Combinatorial omics analysis reveals perturbed lysosomal homeostasis in collagen VII-deficient keratinocytes

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Supplemental Experimental Procedures

Cell culture and stable isotope labelling by amino acids in cell culture

Keratinocytes were isolated from skin samples of the eight patients and, as controls, from the skin of seven healthy, age-matched controls. Cells were subcultured and passaged in keratinocyte growth medium (Keratinocyte-SFM) (Invitrogen, Karlsruhe, Germany), supplemented with keratinocytes supplements (Bovine Pituitary Extract (BPE); EGF, human recombinant).

Normal human keratinocytes where seeded on 6-well-plate culture dishes. Medium was exchanged the following day and 10 ng/mL TGF-β 1 (Peprotech, Hamburg, Germany) was added. RDEB keratinocytes were incubated with 4.4 µg/mL TGF-β receptor type I and type II dual inhibitor LY2109761 (Adooq BioScience LLC, Irvine, CA, USA). Cells were harvested after 48 h by incubation with lysis buffer (25 mM Tris-HCL pH 7.5, 0.1 M NaCl, 1% NP-40, EDTA, Pefablock, Phosphatase inhibitor 3 cocktail, PHJ2) on a shaker for 20 min on ice. Cells were then scraped off, transferred into 1.5 mL tubes, vortexed and centrifuged at 13`000 rpm for 10 min. Supernatants were incubated for 5 min at 95°C in SDS-buffer and directly used for WB analysis or stored at -80°C until use.

For MS analysis, cells were cultured in keratinocyte growth medium (KGM2) (Promocell, Heidelberg, Germany) without arginine and lysine, but with “SupplementMix” (0.004 mL/mL bovine pituitary gland extract, 0.125 ng/mL recombinant human epidermal growth factor, 5 µg/mL recombinant human insulin, 0.33 µg/mL hydrocortisone, 0.39 µg/mL epinephrine, 10 µg/mL human holo transferrin) and 0.06 mM $CaCl_2$, 210 mg/L L-arginine and 63 mg/L L-lysine for the unlabeled condition. Cells were "heavy" labeled for 2 weeks with 210 mg/L L-arginine-$^{13}C_6$-$^{15}N_4$ (Arg_{10}) and 63 mg/L L-lysine-$^{13}C_6$-$^{15}N_2$ (Lys_8) or "medium" labeled with 210 mg/L L-arginine-$^{13}C_6$ (Arg_6) and 63 mg/L L-lysine-$^{2}H_4$ (Lys_4). Biological replicates were obtained by swapping labels.

RNA isolation from primary human keratinocytes and RNAseq

Total RNA from 80-90% confluent keratinocytes was isolated using the RNeasy Mini Kit according to the manufacturer's instructions. Libraries were constructed with the stranded TruSeq GOLD protocol (RS-122-2301) followed by rRNA depletion (Illumina Ribo-Zero rRNA removal kit human, mouse, rat). Sequencing was performed on a HiSeq2500 (50 bp, Illumina, San Diego, USA). RNAseq raw data is available as a NCBI BioProject, ID PRJNA373827 (http://www.ncbi.nlm.nih.gov/bioproject/373827).

Functional annotation was done with a gene ontology analysis based on Cytoscape and ClueGO (2.2.4) (Bindea et al., 2009). Overrepresented GO terms from the categories "biological process", "cellular component" and "molecular function" were corrected by Benjamini–Hochberg procedure for multiple testing-controlled p-values. Significantly enriched terms were functionally grouped and visualized and the most significant term of each group was displayed.

Data analysis

Transcriptomics. RNAseq data were analyzed using the Freiburg instance of Galaxy (Afgan et al., 2016; Blankenberg et al., 2011). Therefore, a workflow was created including steps from quality-control of raw reads to calculation of differentially expressed genes. Quality control was performed using FastQC. After manual quality inspection, reads were trimmed with Trim Galore! accordingly. RNAseq data were mapped to the human (hg19) reference genome, using TopHat2 and the human gene annotation model (GRCh37.75) (Kim et al., 2013). After read mapping, htseqcount was applied to count aligned reads per gene in a BAM file which overlap features in the gtf file (Anders et al., 2015). These count data then were used as input files for DESeq2 to calculate differentially expressed transcripts of RDEB patients compared to controls (Love et al., 2014). The results were filtered first by the adjusted p value 0.1 (FDR controlled with Benjamini-Hochberg procedure) and second by the log2 fold change. The workflow is publicly available on github https://github.com/galaxyproject/training-material/tree/master/RNA-Seq.

To show altered gene expression in RDEB keratinocytes compared to controls, cluster analysis was performed of 301 differentially regulated genes in RDEB keratinocytes (Benjamini–Hochberg corrected q-value 0.1) as determined by high-throughput sequencing of the transcripts. TPM values were log2-transformed and z-score normalized. Columns containing data from the different samples were hierarchically clustered and rows containing gene entries were clustered by k-means.

Functional annotation was done with a Gene Ontology (GO) analysis based on Cytoscape and ClueGO (2.2.4) (Bindea et al., 2009; Shannon et al., 2003). Over represented GO terms from the categories ‘biological process’, ‘cellular component’ and ‘molecular function’ were corrected by Benjamini–Hochberg procedure for multiple testing-controlled p-values. Significantly enriched terms were functionally grouped and visualized and the most significant term of each group was displayed.

Proteomics. To generate a list of extracellular proteins, the data were filtered using the freely available Perseus software to extract proteins that belong to the “matrisome” and/or are annotated as “extracellular” (extracellular region, extracellular region part, extracellular space, extracellular matrix, extracellular matrix part, proteinaceous extracellular matrix, extracellular organelle, extracellular membrane-bounded organelle, extracellular vesicular exosome) and “cell adhesion” (Tyanova et al., 2016). Data were readjusted to a median of 1 and log2 transformed and z-score normalized. SOTA clustering was performed of proteins quantified in intra- (11 clusters) and extracellular (7 clusters) compartments of RDEB cells compared to controls. Proteins in each cluster were tested by DAVID for enriched GO terms (biological process (BP), cellular compartment (CC) and molecular function (MF)) applying the default settings with a minimum significance of $p<0.01$ (Huang da et al., 2009). Network analysis of significantly regulated ECM proteins (Welch's t-test, permutation-based FDR 0.05) was created by STRING DB (confidence score 0.4) and Cytoscape (Szklarczyk et al., 2015).

Immunofluorescence staining of frozen skin biopsy specimens

Immunofluorescence staining of RDEB and site-matched control skin was performed on 5 µm cryosections, which were air dried and incubated with primary antibodies at 4°C overnight. Primary antibodies to the following proteins were used: anti-collagen VII (LH7.2, Abcam), anti-S100A9 (AF2065, R&D Systems, Minneapolis, MN, USA) and anti-cathepsin B (clone 6D5 and 3E4) (Weber et al., 2015). After four washing steps of 5 minutes each, secondary antibodies were applied for 1 h. Secondary antibodies were: Alexa-488 anti-mouse IgG or Alexa-488 anti-rabbit IgG (Invitrogen, Darmstadt, Germany). Nuclei were stained with 4′,6-diamidino-2-phenylindole (DAPI; Millipore, Temecula, CA, USA). Stained sections were observed with an Axiophot fluorescence microscope (Carl Zeiss, Jena, Germany). Images were captured using Zeiss internal software.

Active site labeling for cysteine cathepsins

Keratinocytes (10 cm^2 petri dishes, 80-90% confluent) were washed 3 times with ice-cold DPBS. Cells were lysed by adding 200 µL ice-cold sodium acetate buffer directly onto the petri dish. Cells were scraped off, incubated on ice for 30 min and centrifuged (10,000xg, 10 min, 4°C). Cell lysates (without protease inhibitors) were then used directly for activity assays to avoid degradation of proteins. Cysteine cathepsins were labelled by incubating cell lysates with DCG-04 (final concentration 10 µM) for 1 h on ice (Greenbaum et al., 2000). In order to distinguish western blot signals, prior to DCG-04 treatment cell lysates were incubated for 15 min on ice with the cysteine protease inhibitor E-64 (final concentration 10 µM) or the specific cathepsin B inhibitor Ca074 (final concentration 5 µM). In order to reveal unspecific binding of the substrate, proteases were inactivated in a control sample through incubation for 10 min at 95°C prior to DCG-04 treatment. Afterwards, samples were directly boiled at 95°C for 10 min and then used for WB analysis or stored at -20°C.

Western blot

Cell lysate or ECM samples corresponding to 1/10 of confluent 10 cm^2 cell culture dishes were separated by SDS–PAGE using self-casted SDS gels and transferred onto nitrocellulose membrane. Membranes were blocked with 5% milk powder in 1x TBS-T for a minimum of 1 h at room temperature and incubated with primary antibodies diluted with the same buffer for 1 h or overnight at 4°C. HRP-conjugated secondary antibodies and a chemiluminescent detection assay (Immobilon Western, Millipore, Schwalbach, Germany) were used for visualization according to manufacturer's instructions.

For the active site labeling for cysteine cathepsins, fluorescently labeled streptavidin (LI-COR, Lincoln, NE, USA) was used to detect the biotin tag of the DCG-04 substrate. Detection was carried out on a Li-Cor Odyssey Infrared scanning system. *ß*-actin was used as loading control, using respective fluorescently labeled secondary antibodies.

To quantify changes of cathepsin B amount due to the treatment with TGF-β1 bands corresponding to the single-chain enzyme of four different controls were quantified using image J. To investigate changes of cathepsin B after treatment with LY2109761 bands corresponding to the single-chain enzyme of four different RDEB keratinocytes were quantified. Intensities (AU) were normalized to the β-tubulin signals from the same blots. Antibodies used for WB analysis: Anti-cathepsin B (3E4, Weber et al 2015) 1:1000; Anti-Phospho-Smad3 (phospho S423 + S425;

EP823Y; ab52903, Abcam, Cambridge, UK) 1:1000; Anti-Phospho-Smad2 (Ser465/467 (138D4) Cell Signalling).

Autophagy assay

10 cm cell culture dishes (approximately 50 % confluent) were washed with PBS once and then incubated with fresh medium including 20 nM concanamycin A for 2 h in order to block degradation of autopahgosomes. Cells were then harvested, lysed and used for western blot analysis (anti-LC3 (clone5F10, Nanotools, Teningen, Germany)).

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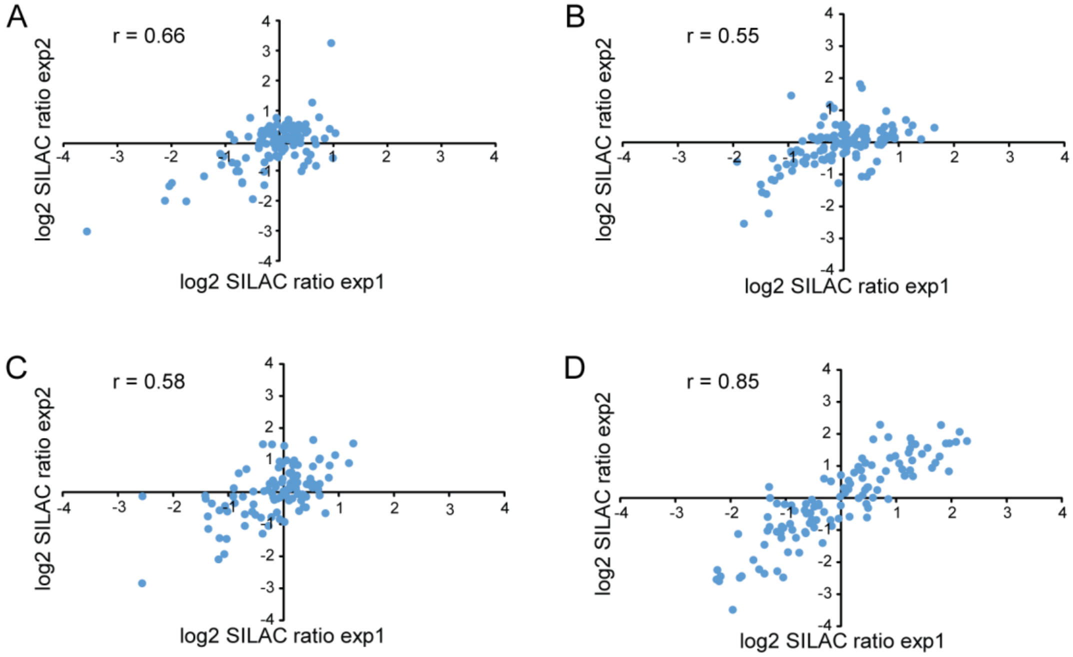
Supplemental Figures

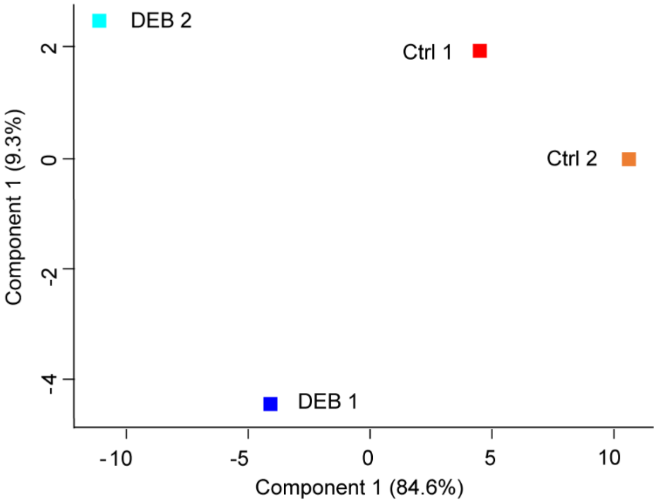
- Supplemental Figure S1: Correlation of replicates of ECM isolated from primary human keratinocytes.
- Supplemental Figure S2: PCA replicates ECM
- Supplemental Figure S3: Relative mRNA and protein abundances of laminin beta 1 and gamma 1
- Supplemental Figure S4: Gene expression analysis of keratin-encoding genes.
- Supplemental Figure S5: Network analysis of significantly regulated intracellular proteins.
- Supplemental Figure S6: Spontaneous restoration of *COL7A1* expression in skin of a DEB patient

Supplemental Figure S1: Correlation of replicates of ECM isolated from primary human keratinocytes.



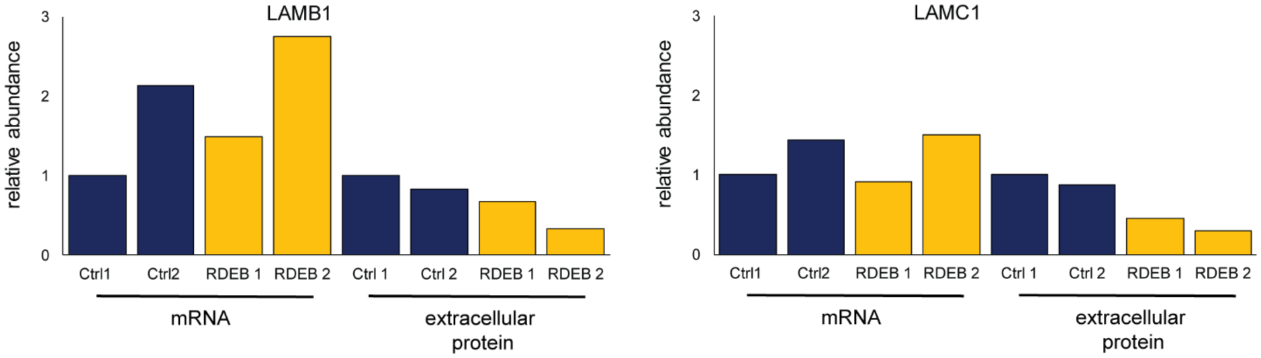
Correlation of biological replicates of the ECM proteome isolated of primary human DEB keratinocytes (A, B) or healthy controls (C, D), r = Pearson correlation coefficient.

Supplemental Figure S2: PCA replicates ECM



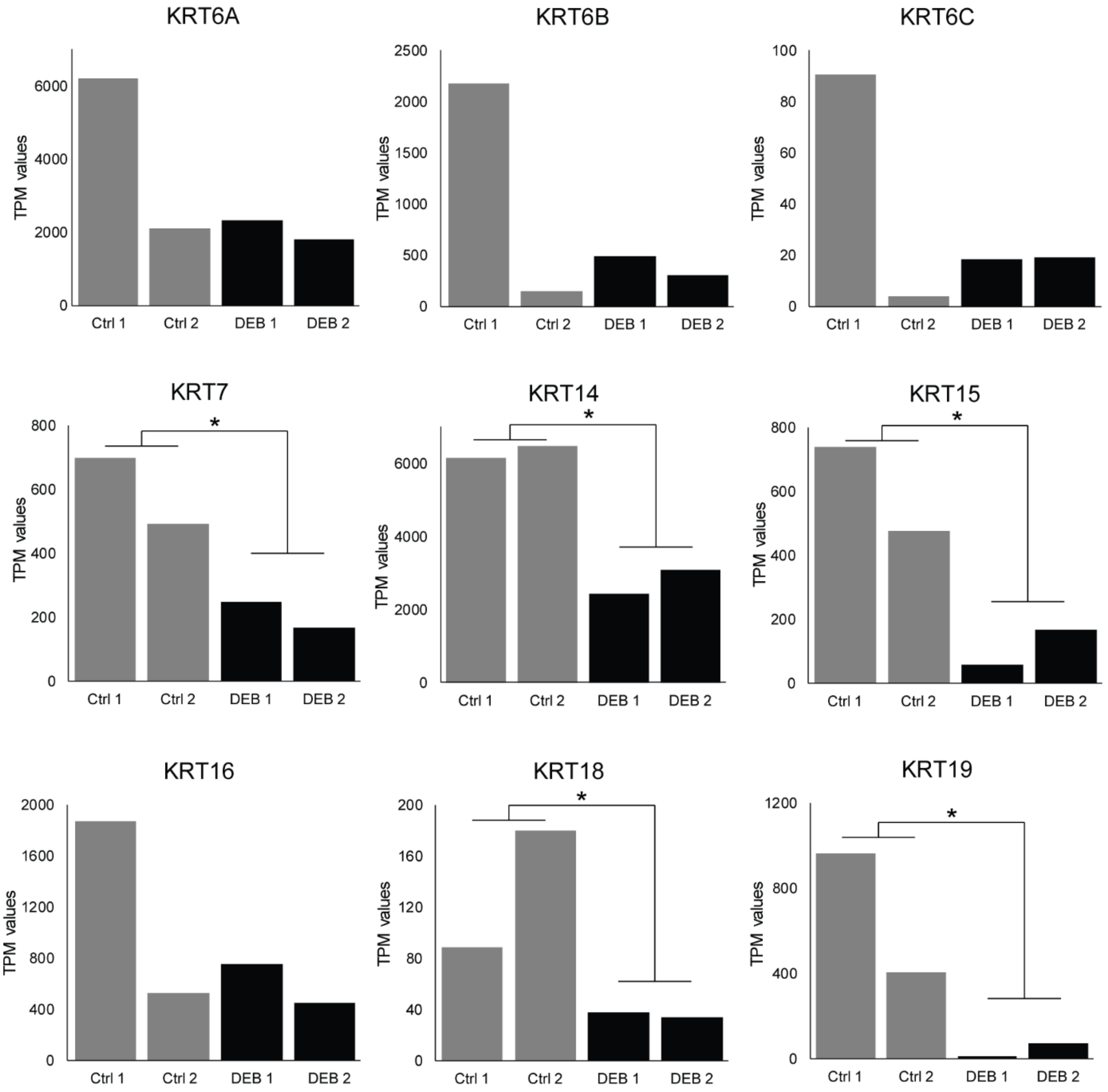
Principle component analysis (PCA) of combined SILAC ratios for each patient and the respective controls.

Supplemental Figure S3: Relative mRNA and protein abundances of laminin beta 1 and gamma 1



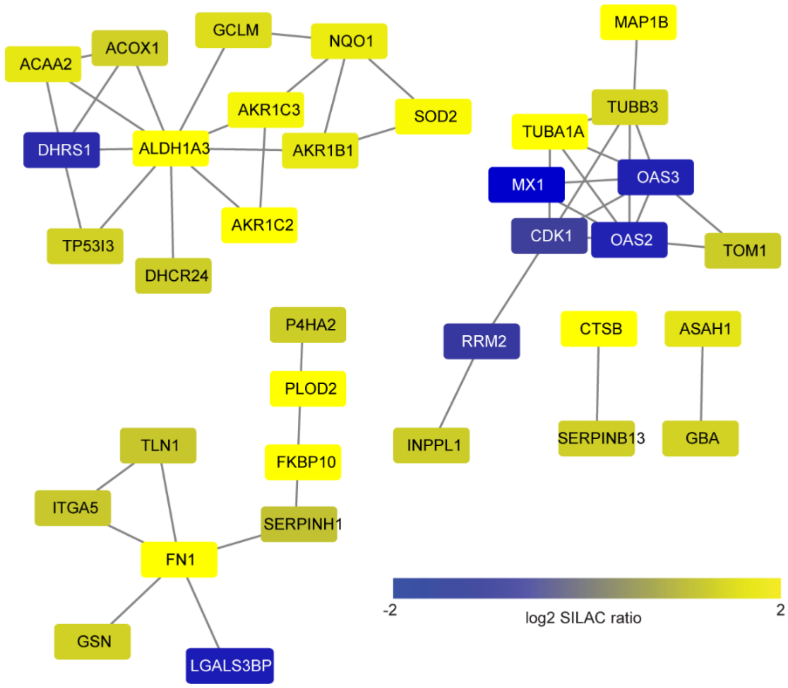
Relative values compared to the respective control 1 (Ctrl 1) are shown. Protein levels were significantly reduced (Welch's t-test, Permutation-based FDR 0.05) in ECM isolated of DEB cells compared to controls while mRNA levels did not change significantly.

Supplemental Figure S4: Gene expression analysis of keratin-encoding genes.



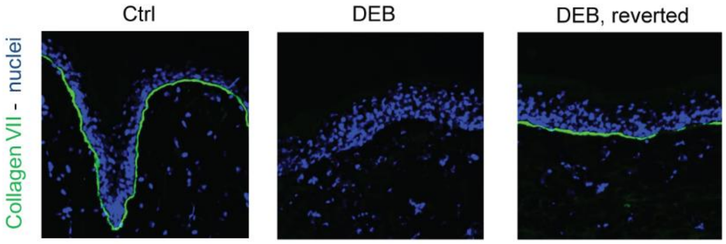
Gene expression analysis of keratin encoding genes. Bar graphs show transcript abundances (TPM values). *: BH-corrected q-value < 0.1.

Supplemental Figure S5: Network analysis of significantly regulated intracellular proteins.



STRING DB was used to identify protein-protein interactions of significantly regulated proteins (confidence score 0.4; Welch's t-test, Permutation-based FDR 0.05, minimal fold change > +/- 2). Color scale indicates log2 transformed SILAC ratios of respective proteins.

Supplemental Figure S6: Spontaneous restoration of *COL7A1* expression in skin of a DEB patient



Immunofluorescence staining of DEB skin reveals spontaneously restored C7 levels (green signal). Blue = DAPI staining.

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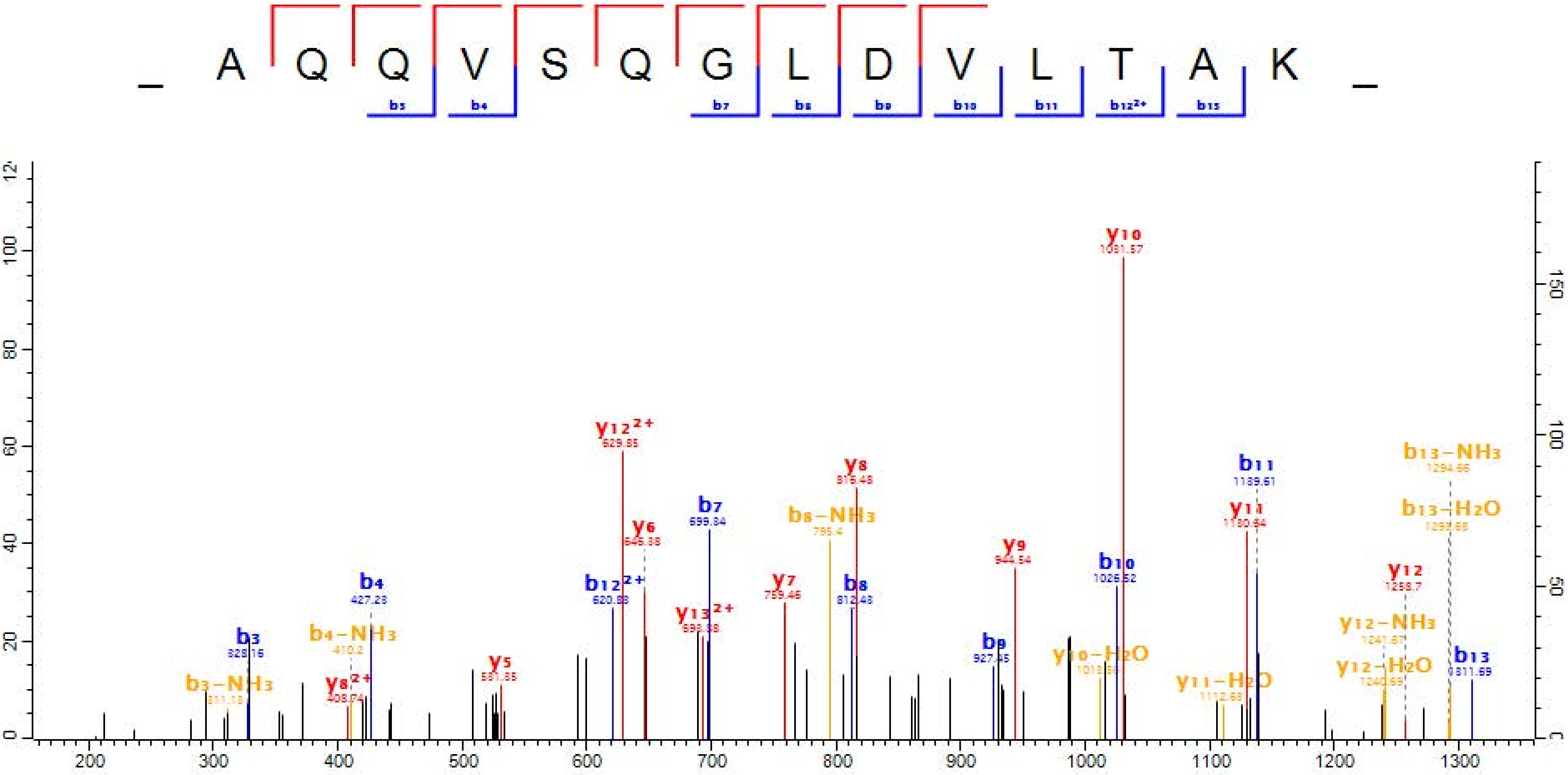

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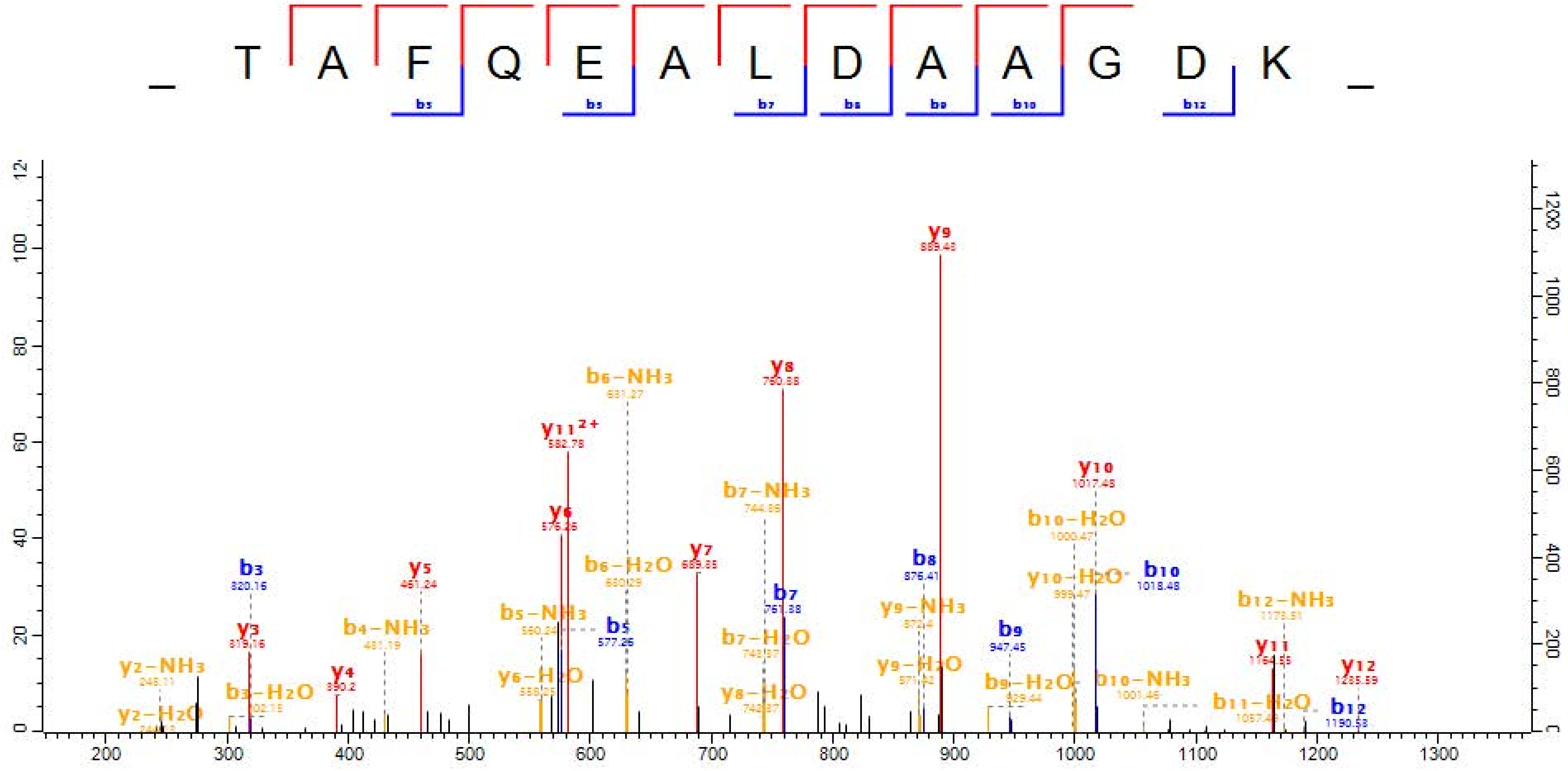

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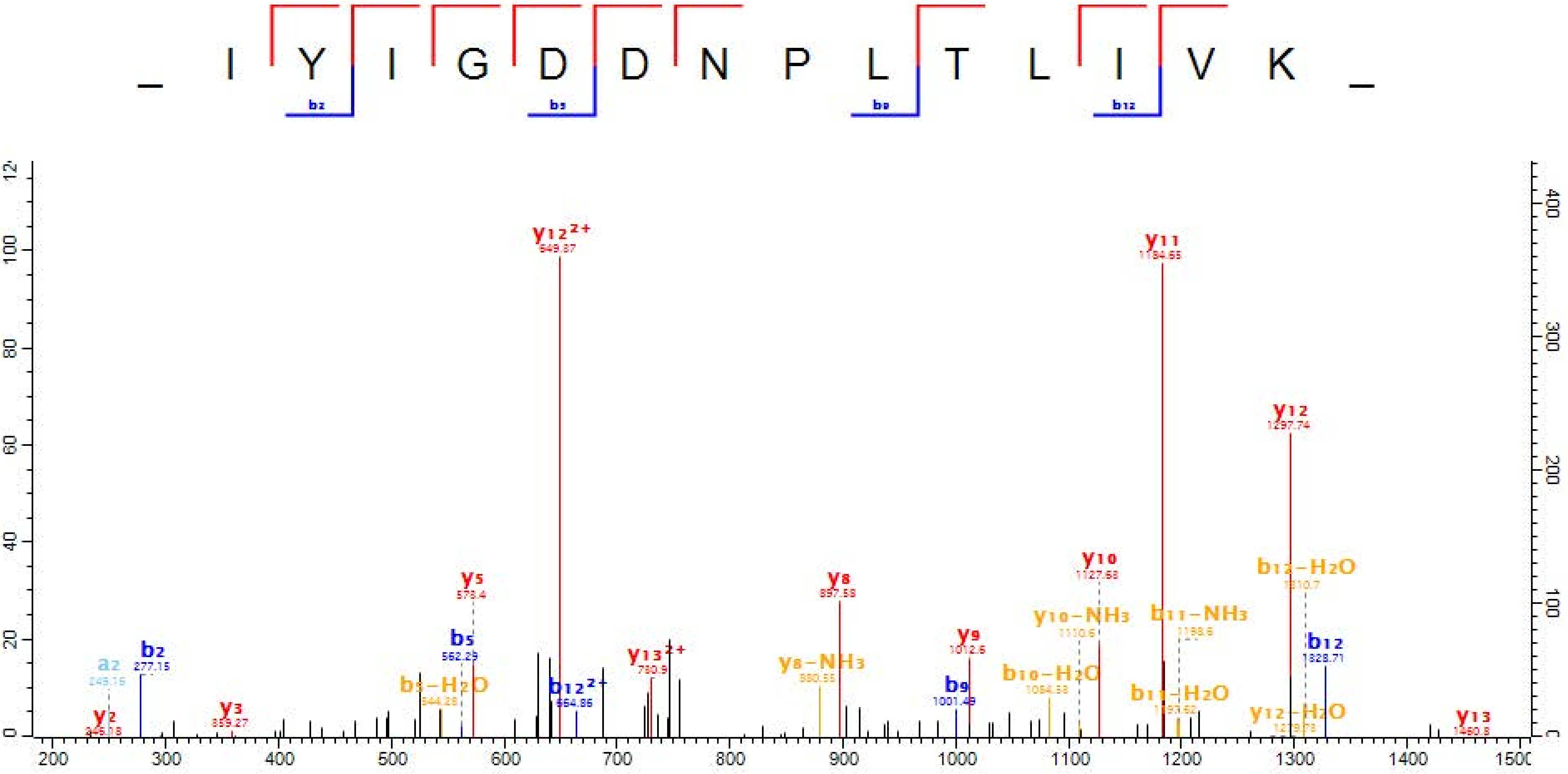

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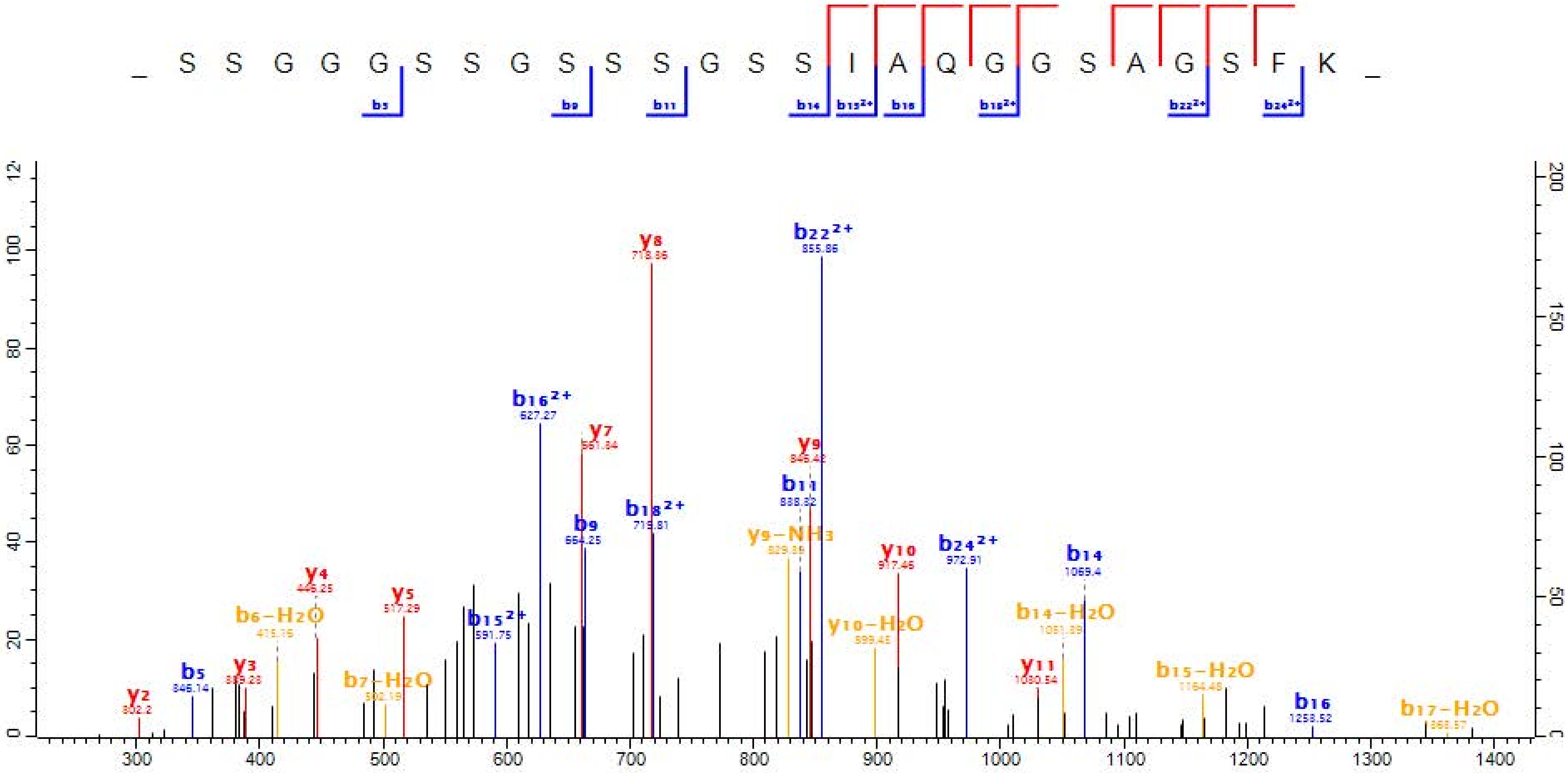

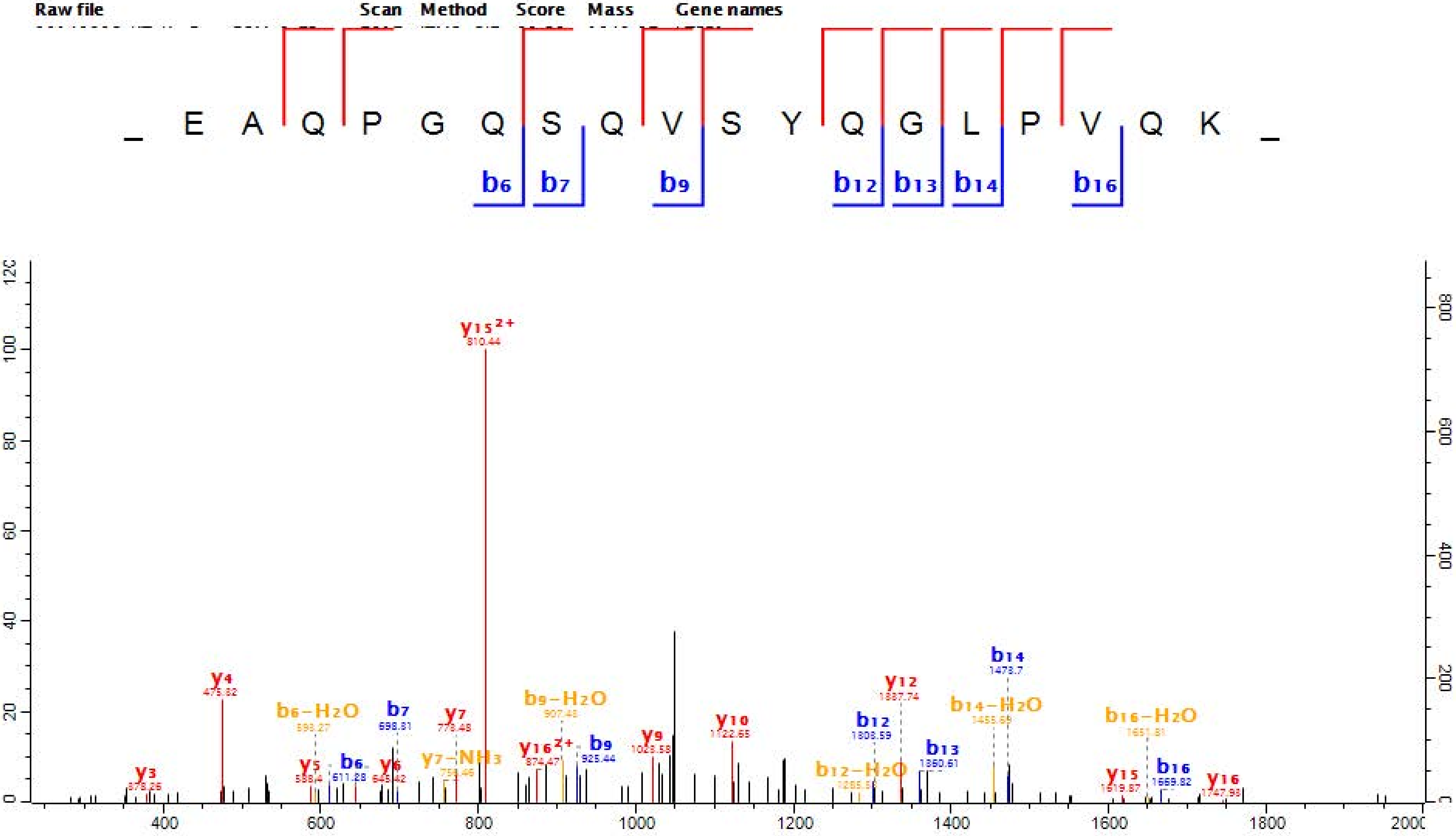
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593.27
y5
588.4
b6
611.28
y6
645.42
b7
698.31
y7
773.48
y7−NH3
755.46
b9−H2O
907.48
y16 2+
874.47
b9
925.44
y9
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y10
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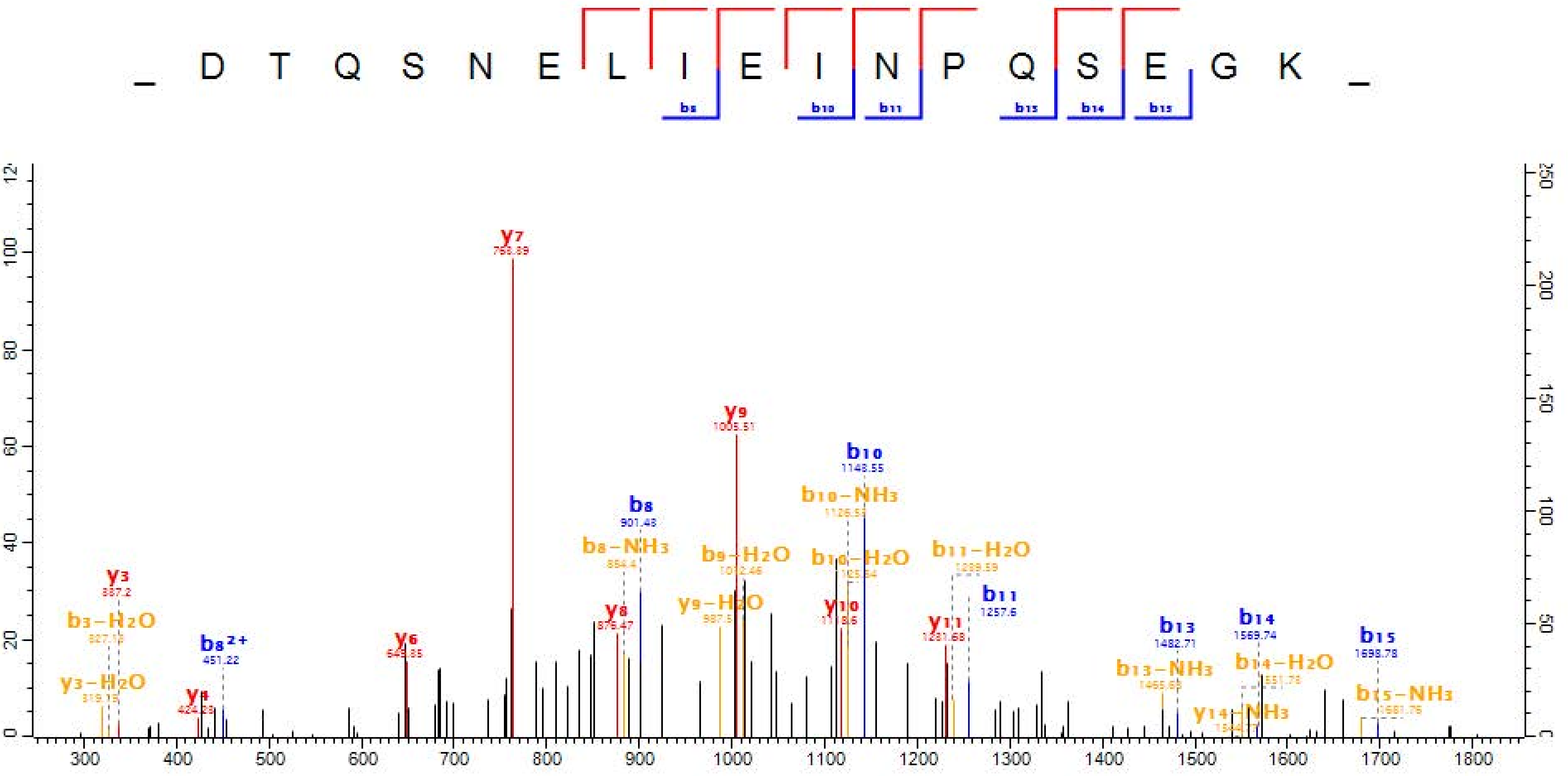

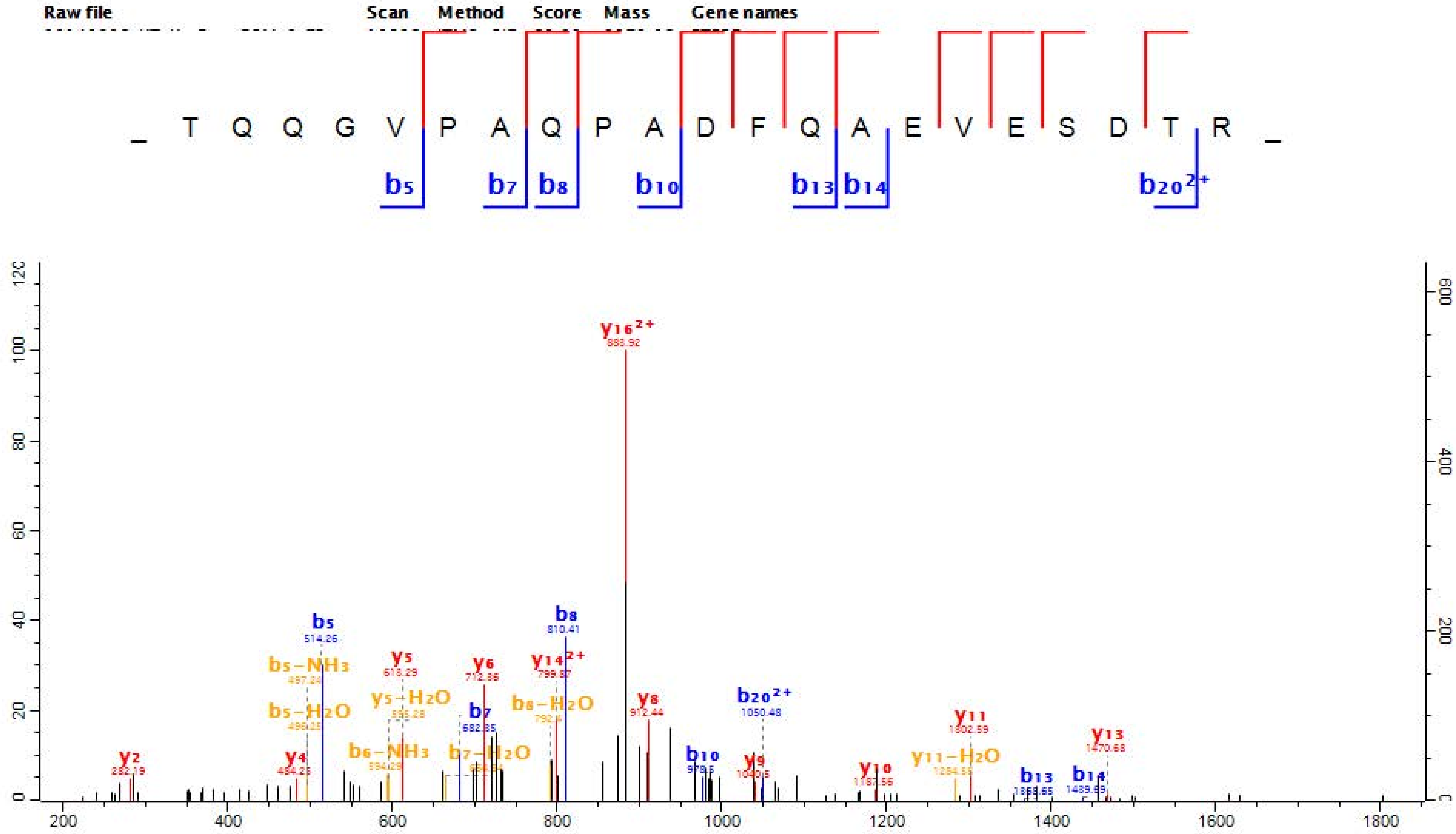
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496.25
y2
282.19
y4
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y5
613.29
y5-H2O
595.28
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594.29
b7
682.35
b7-H2O
664.34
y6
712.36
y14 2+
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b8
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b10
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y9
1040.5
b20 2+
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y10
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b13
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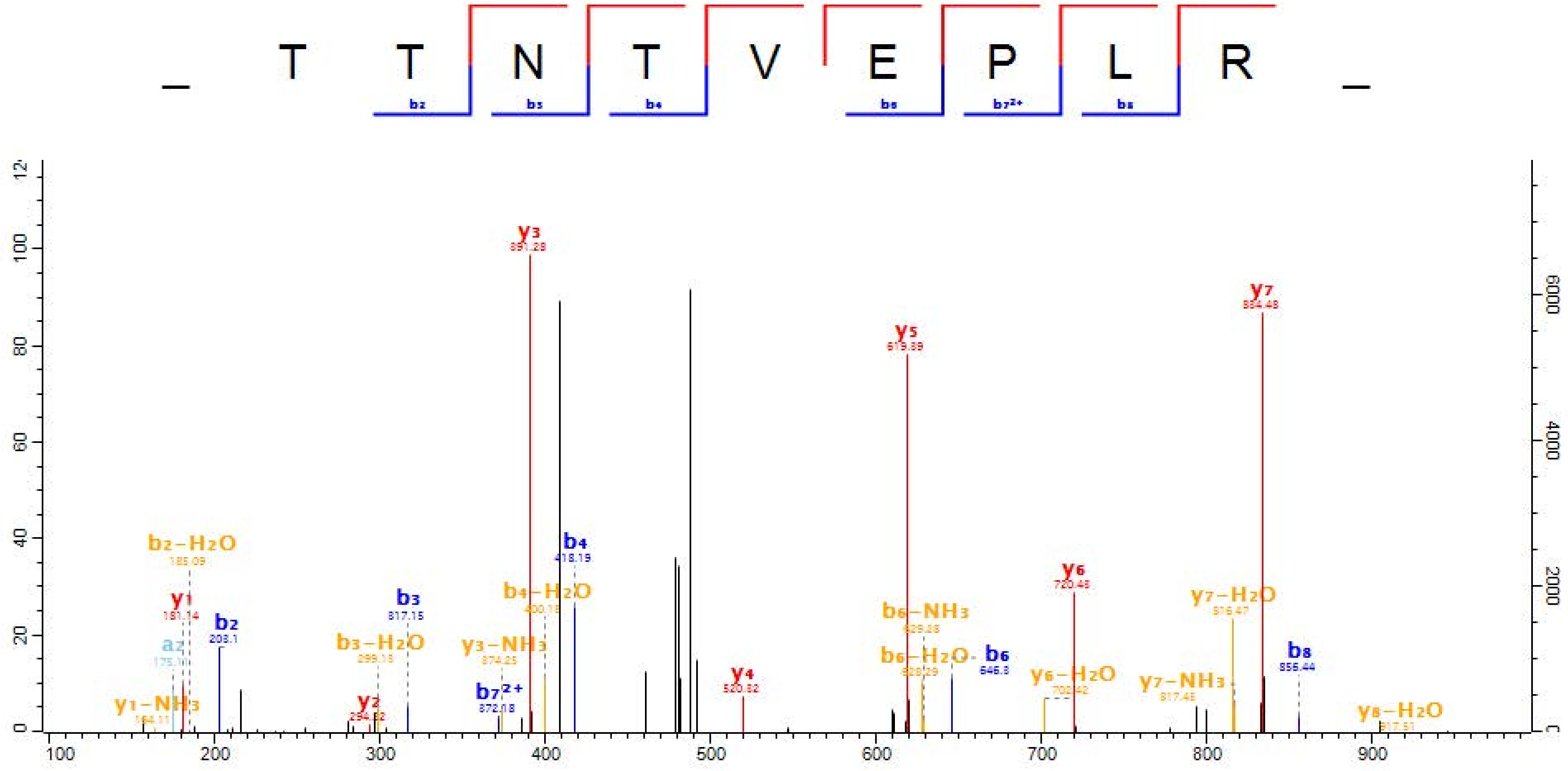

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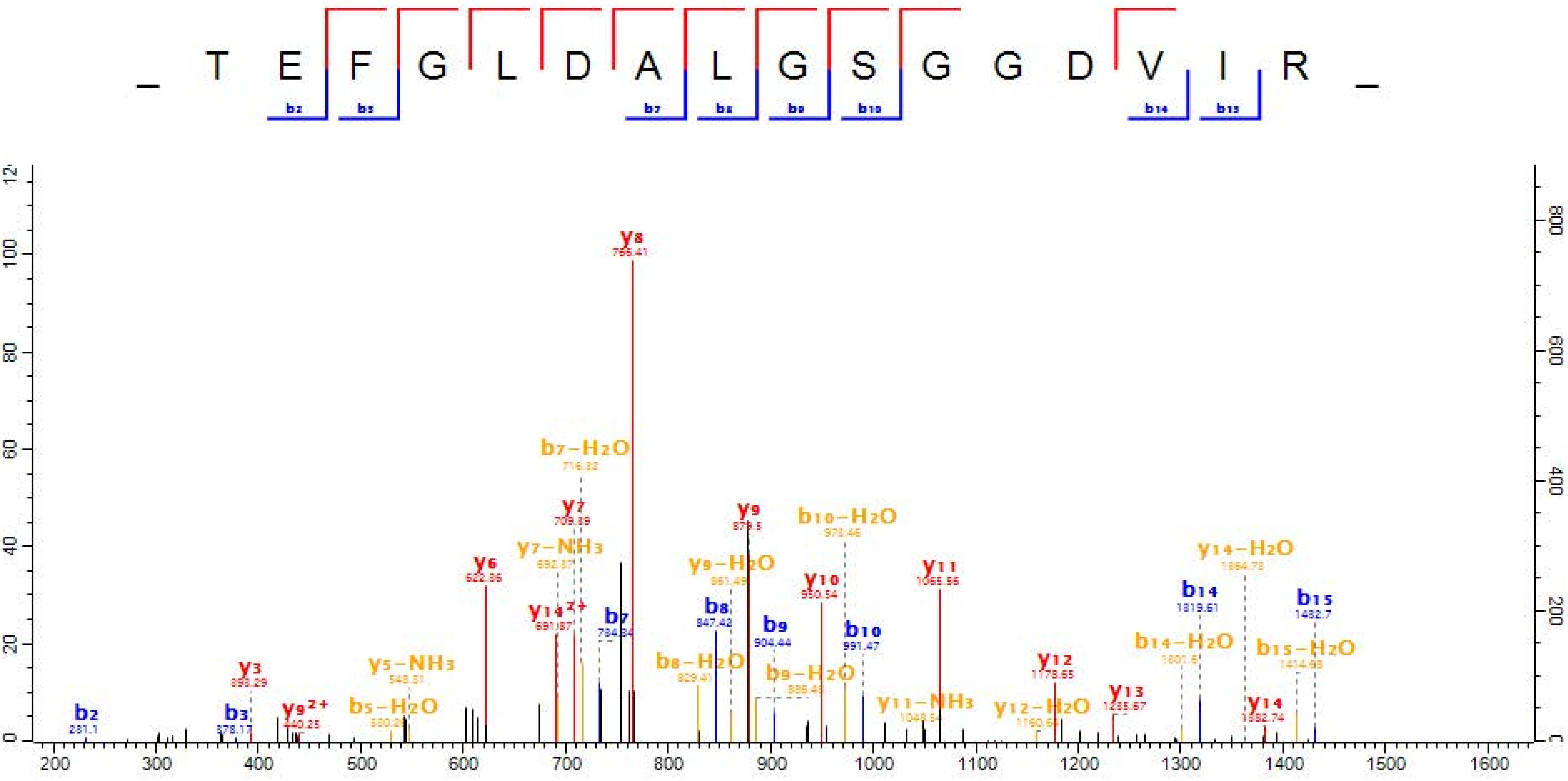

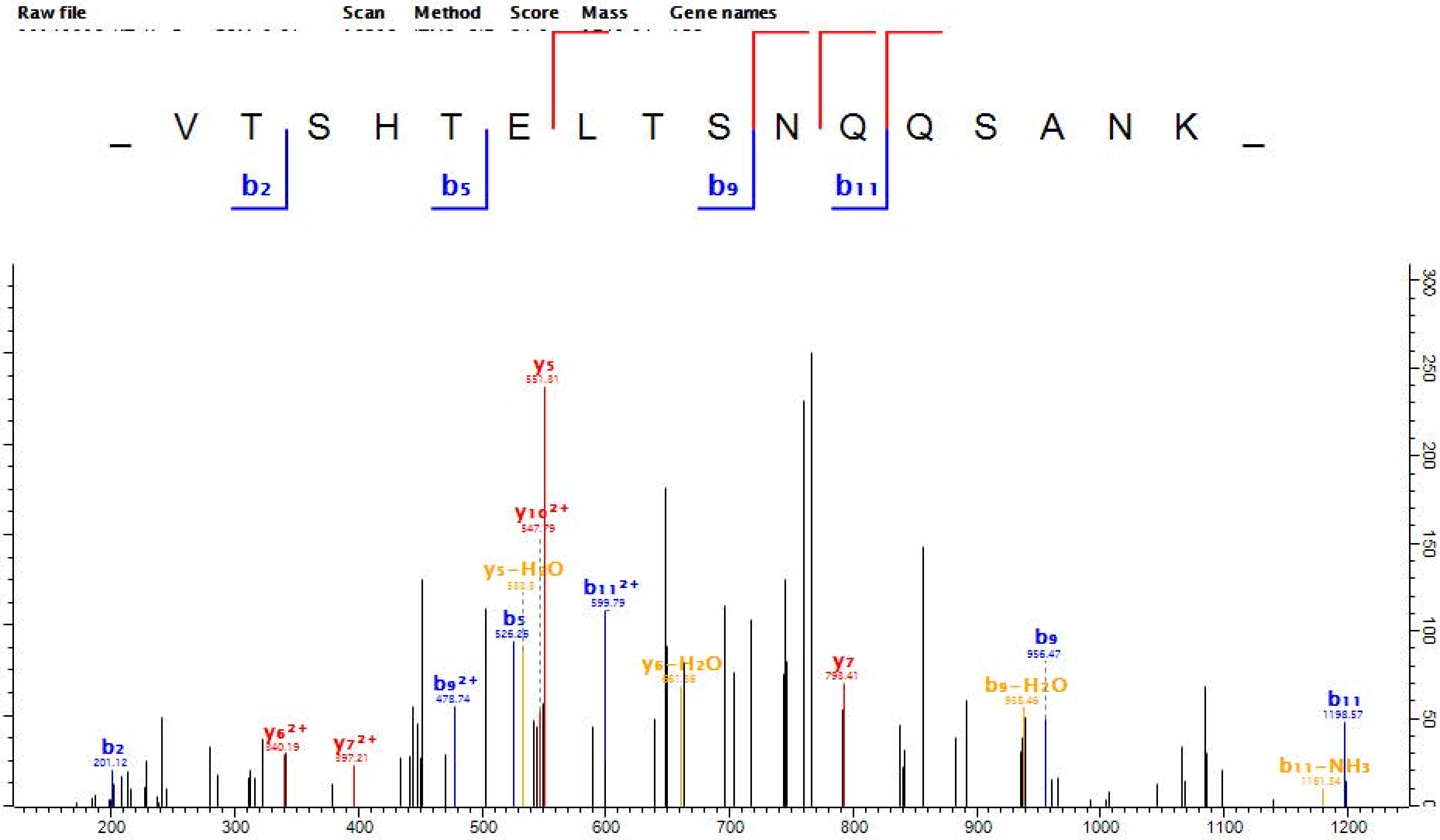
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y10 2+
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b11 2+
599.79
b5
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b9 2+
478.74
y6-H2O
661.36
y7
793.41
b9
956.47
b9-H2O
938.46
b11
1198.57
b11-NH3
1181.54
b2
201.12
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340.19
y7 2+
397.21
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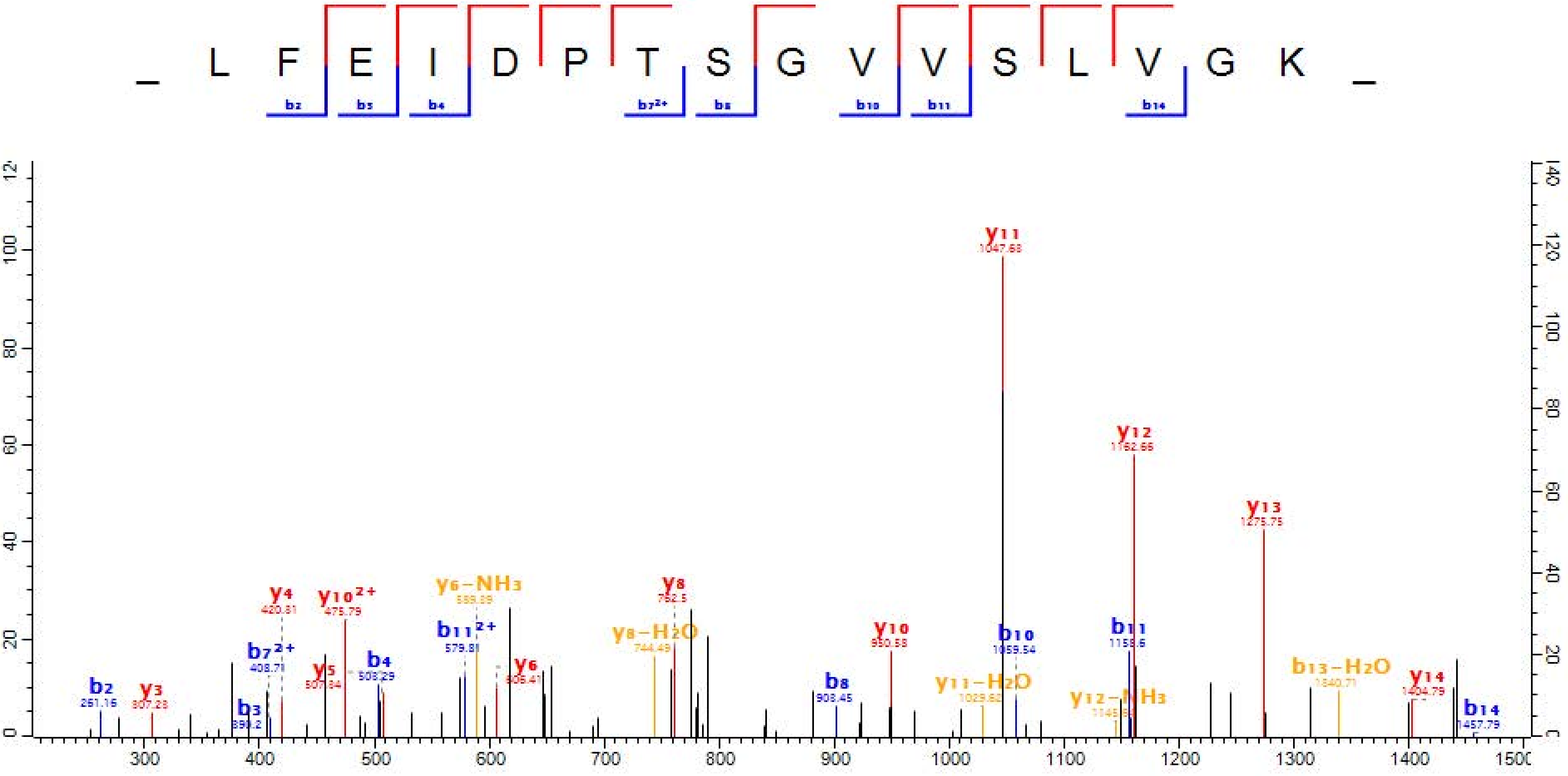

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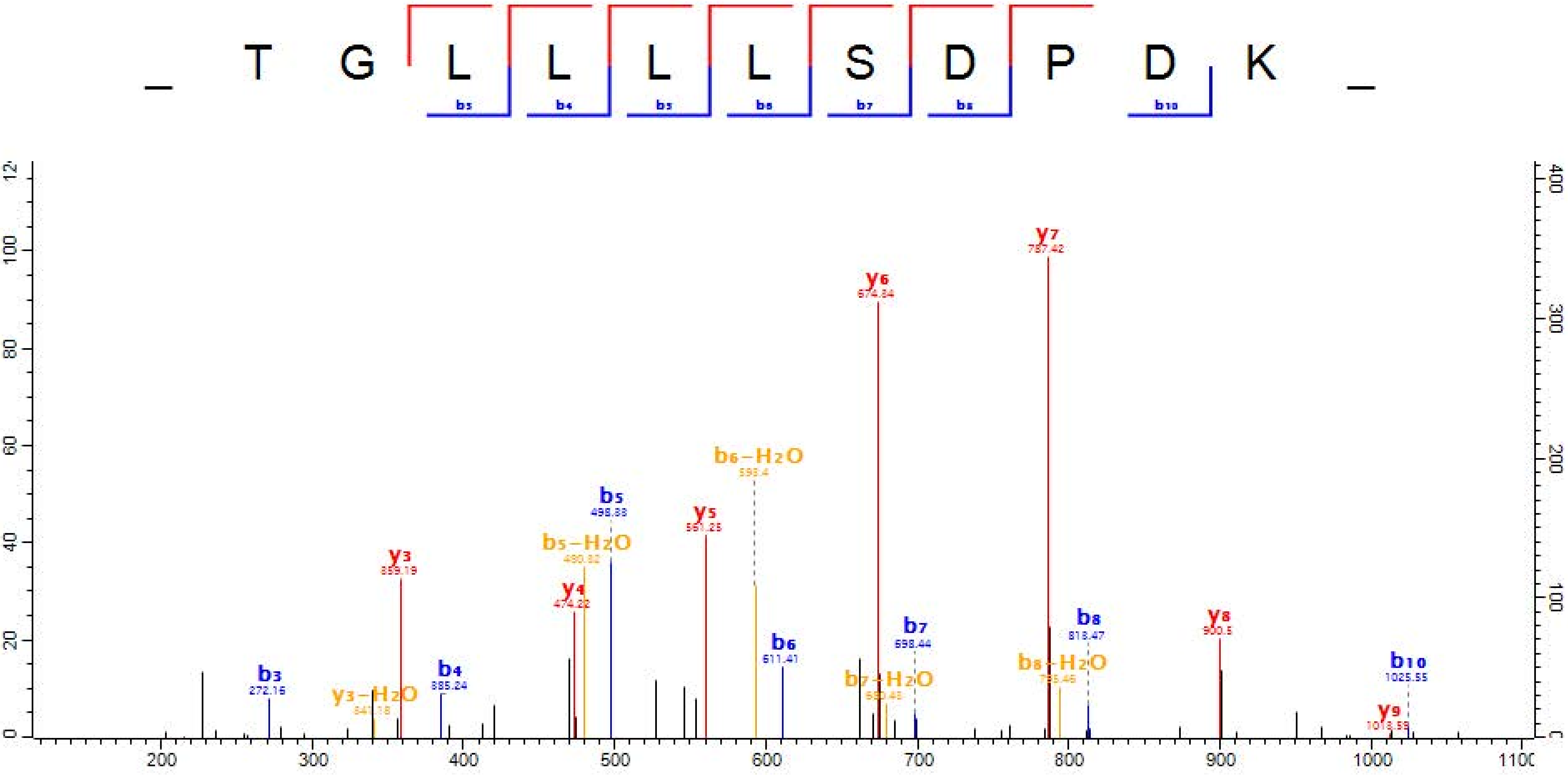

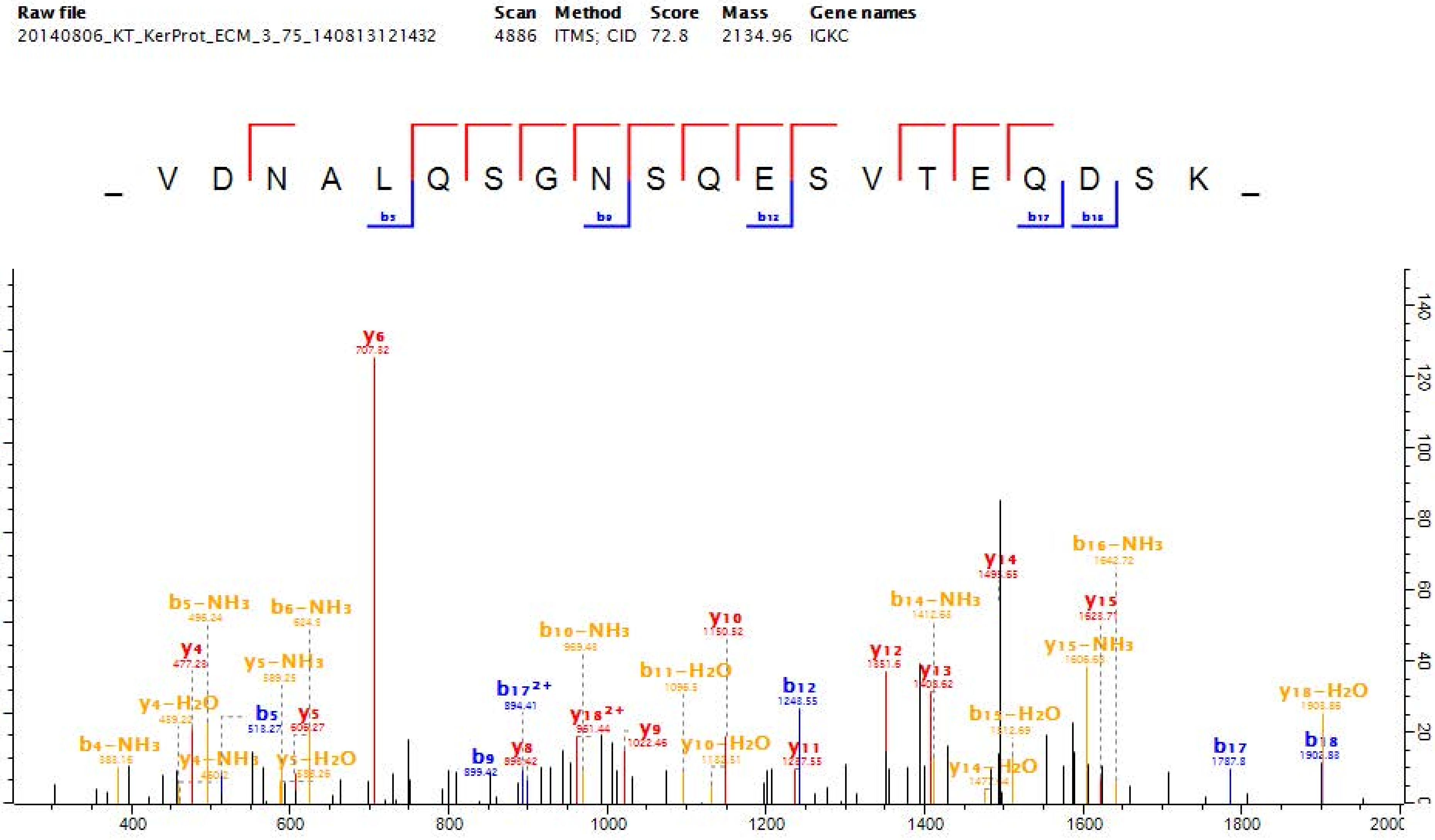

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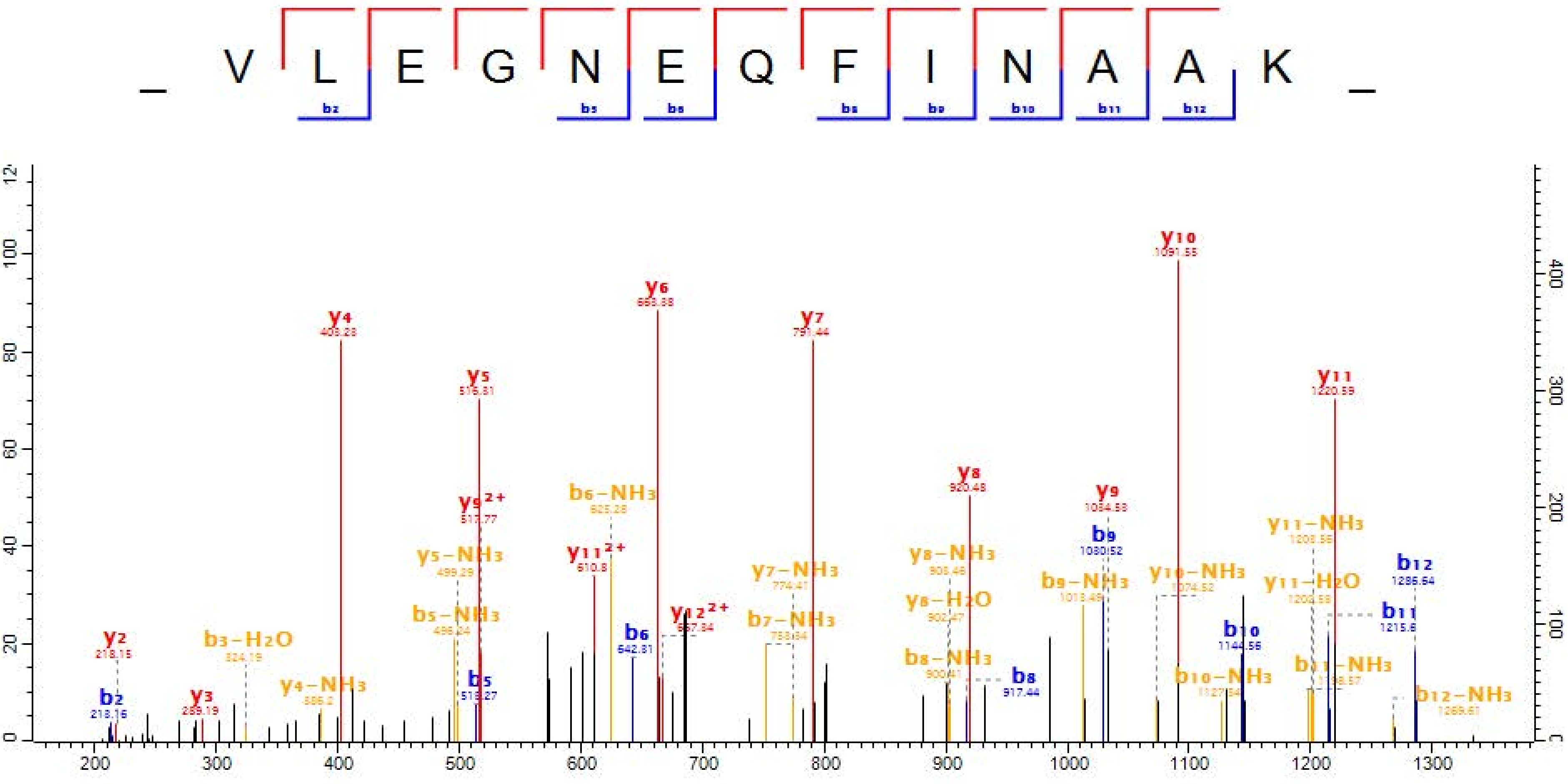

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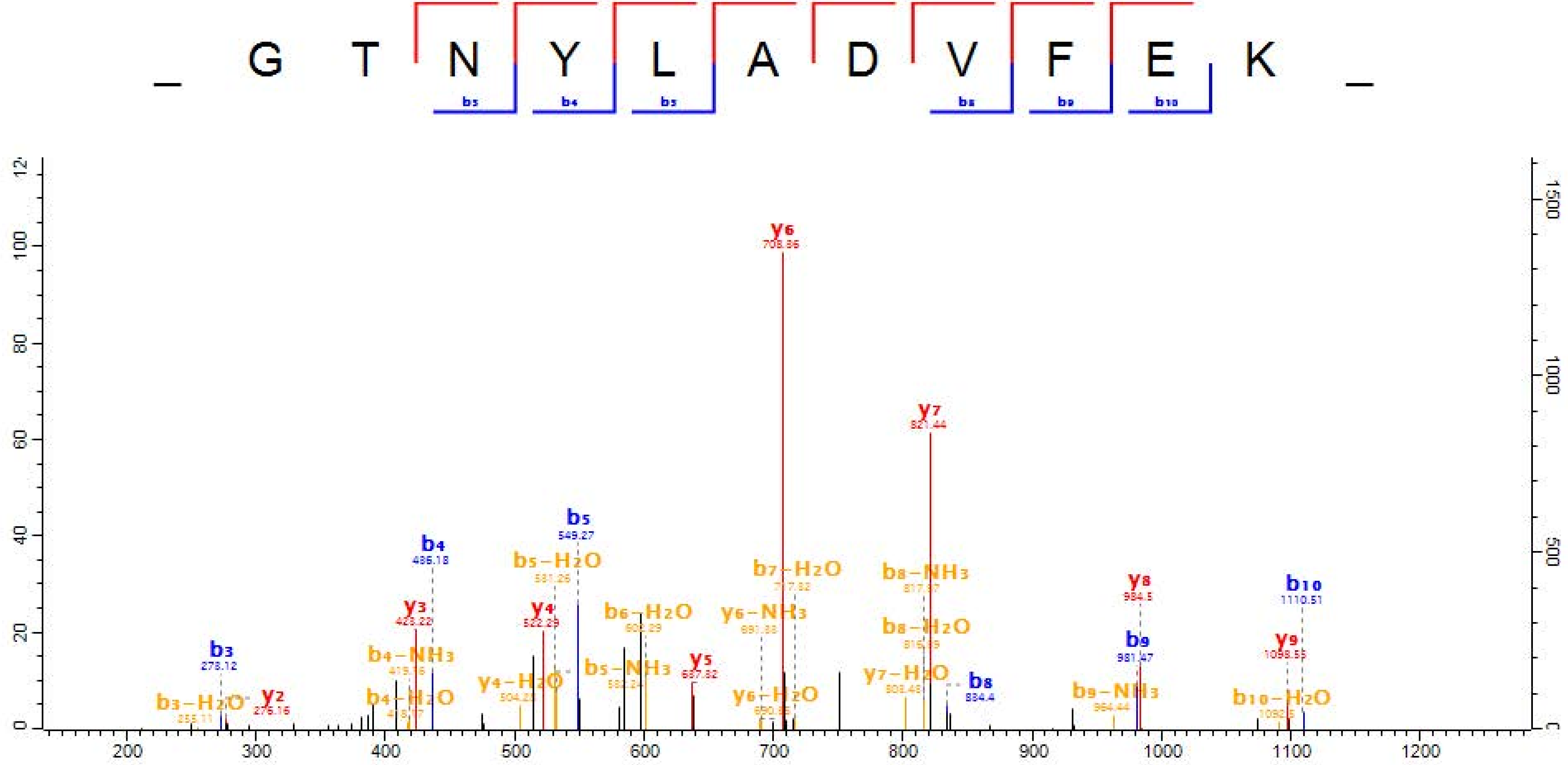

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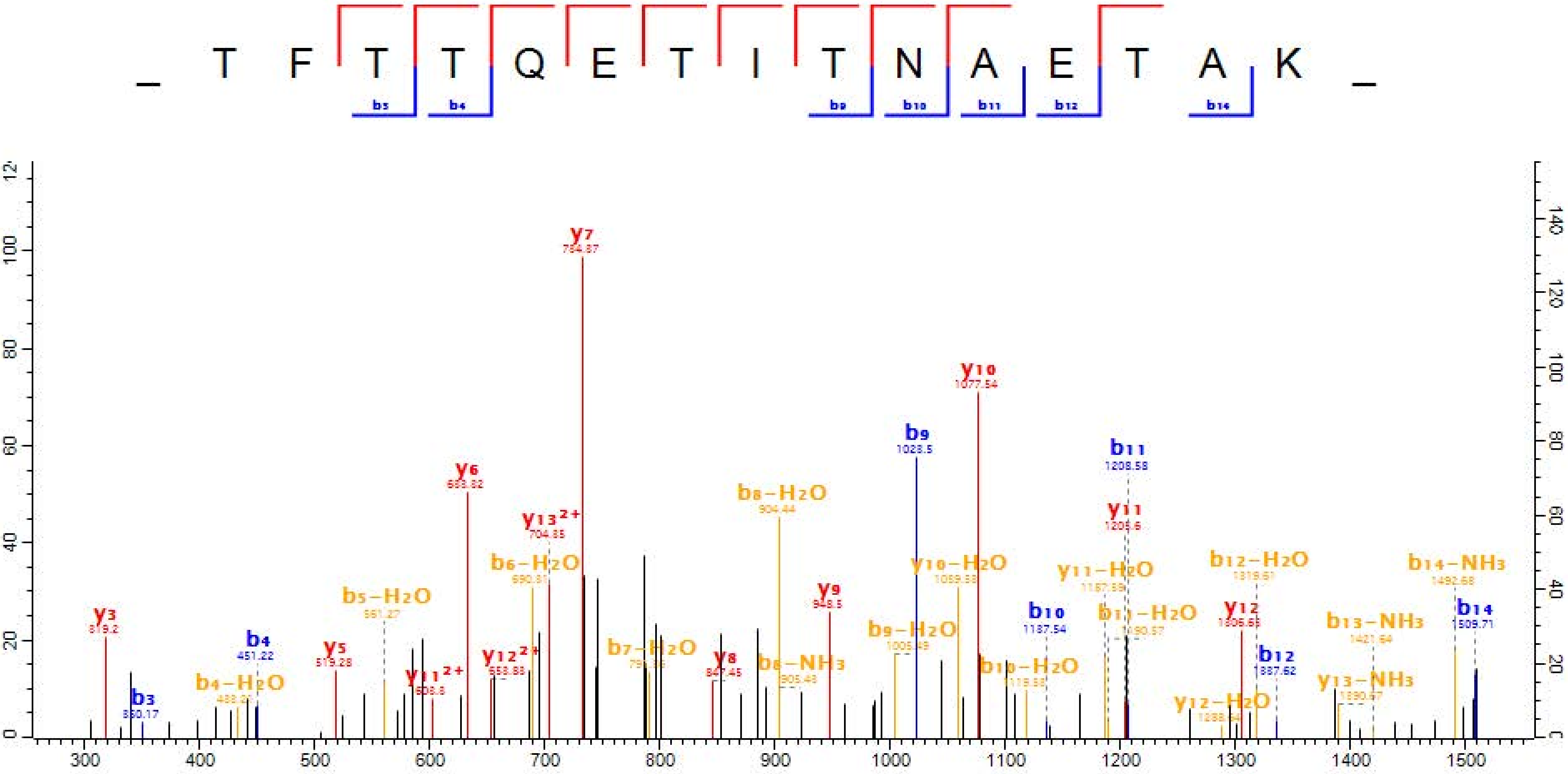

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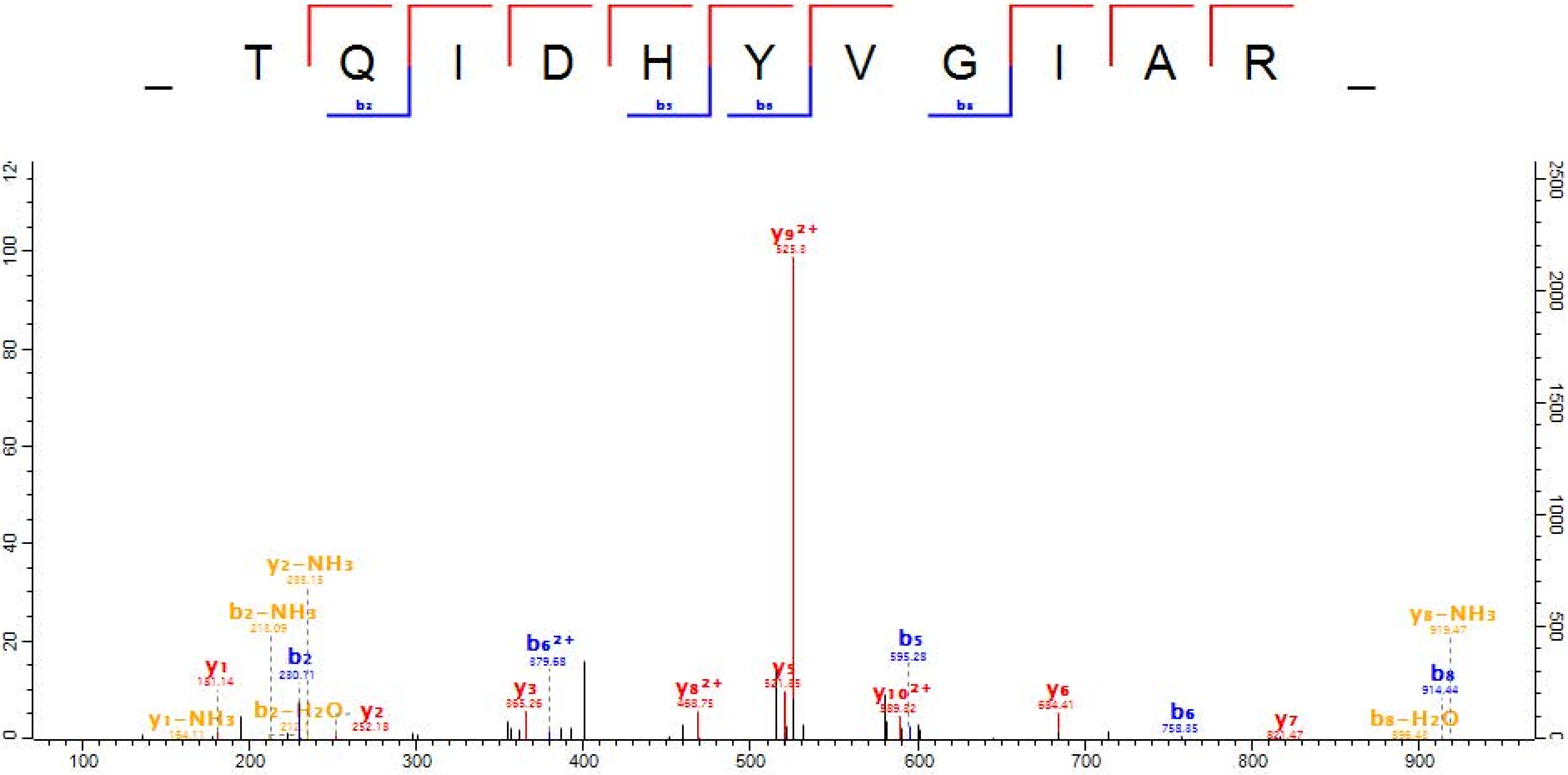

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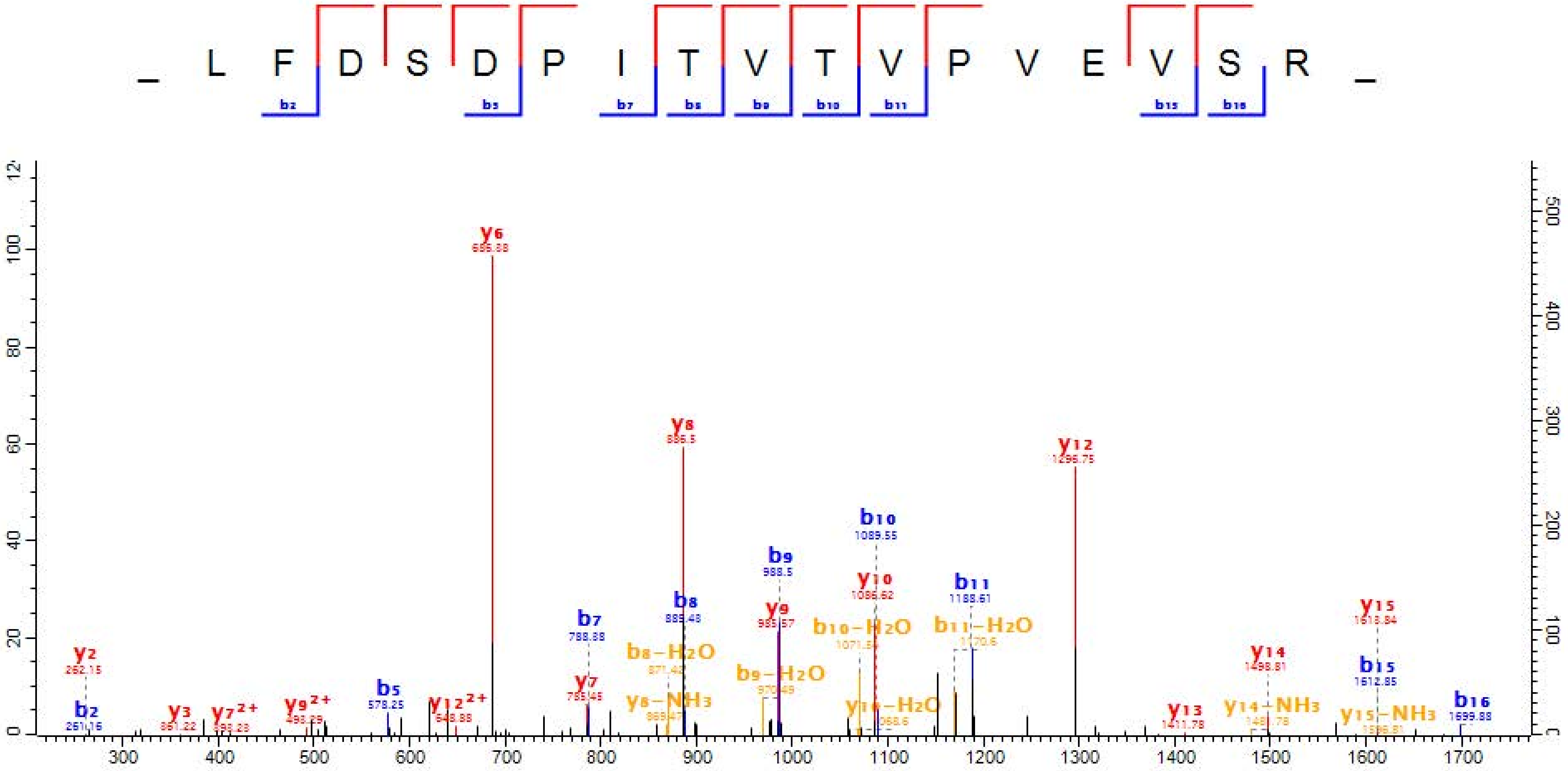

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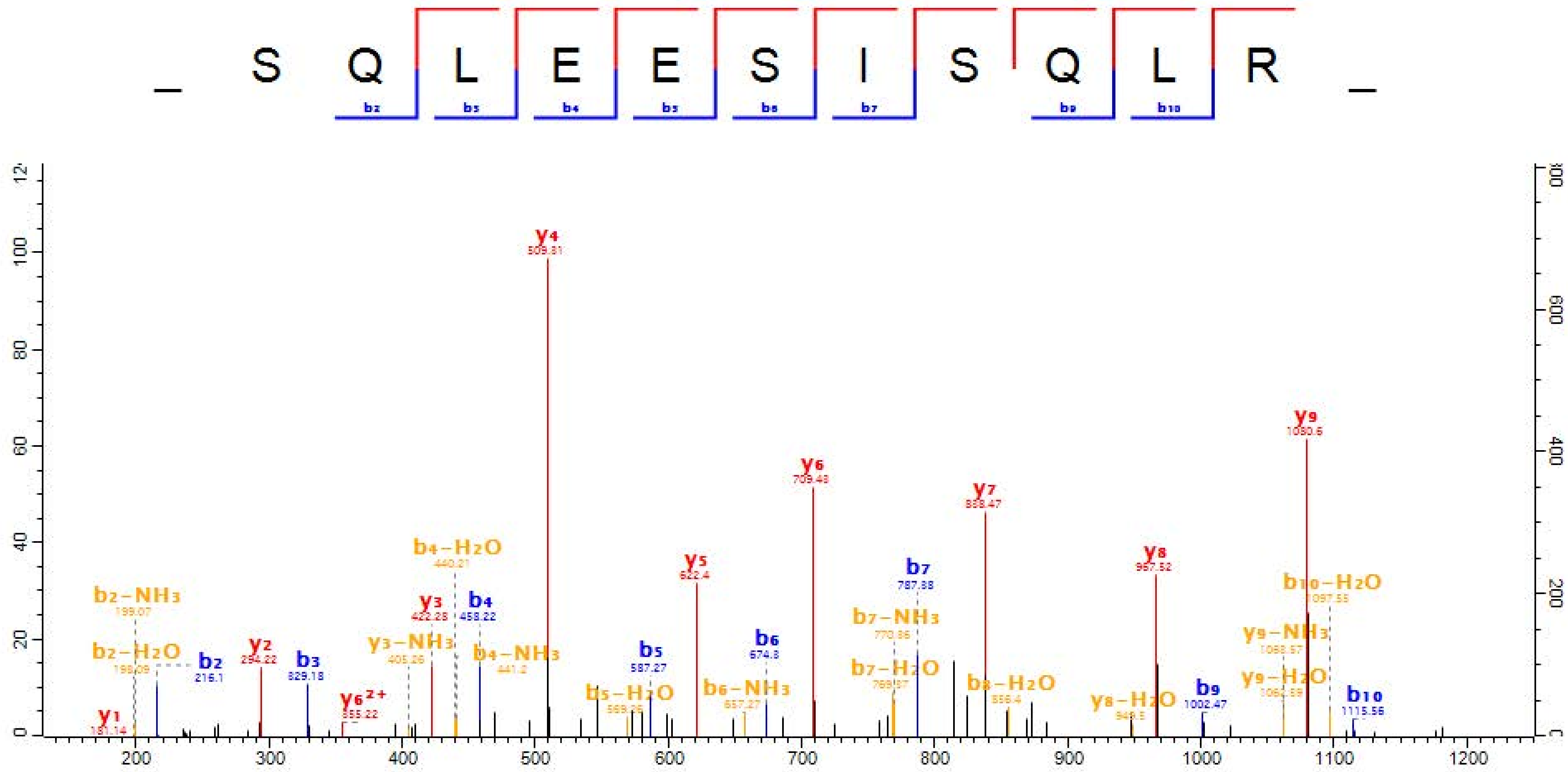

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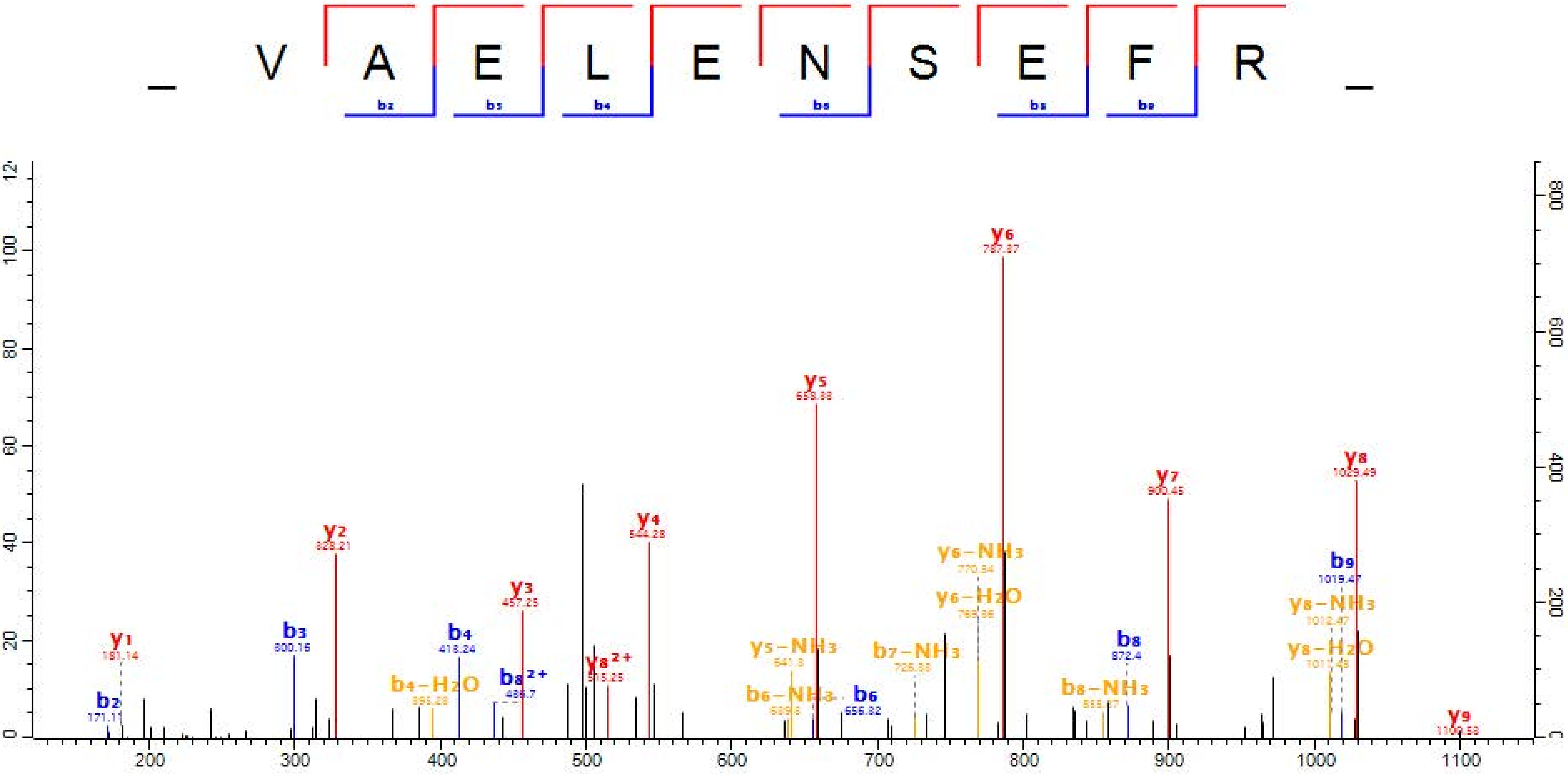

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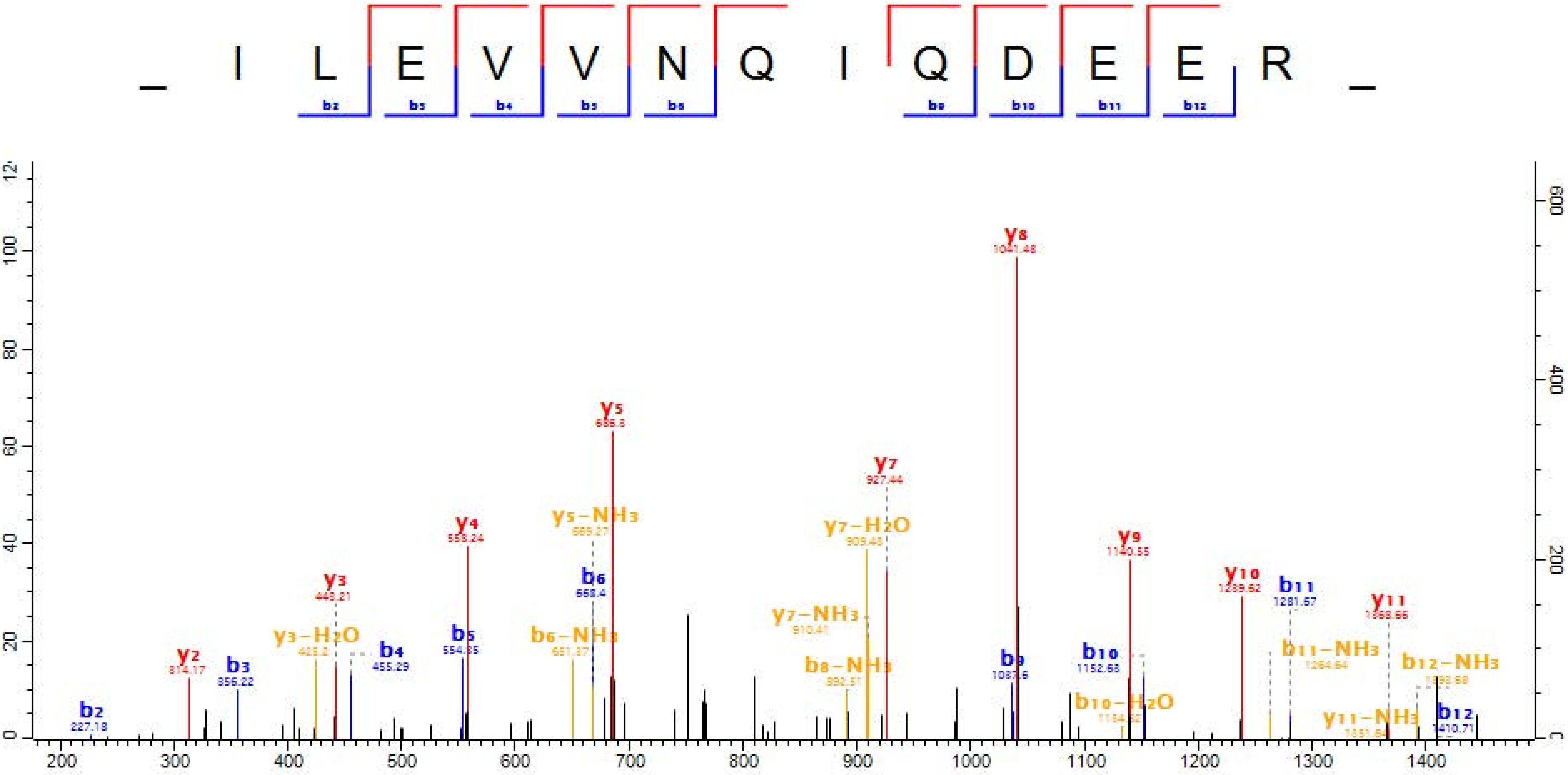

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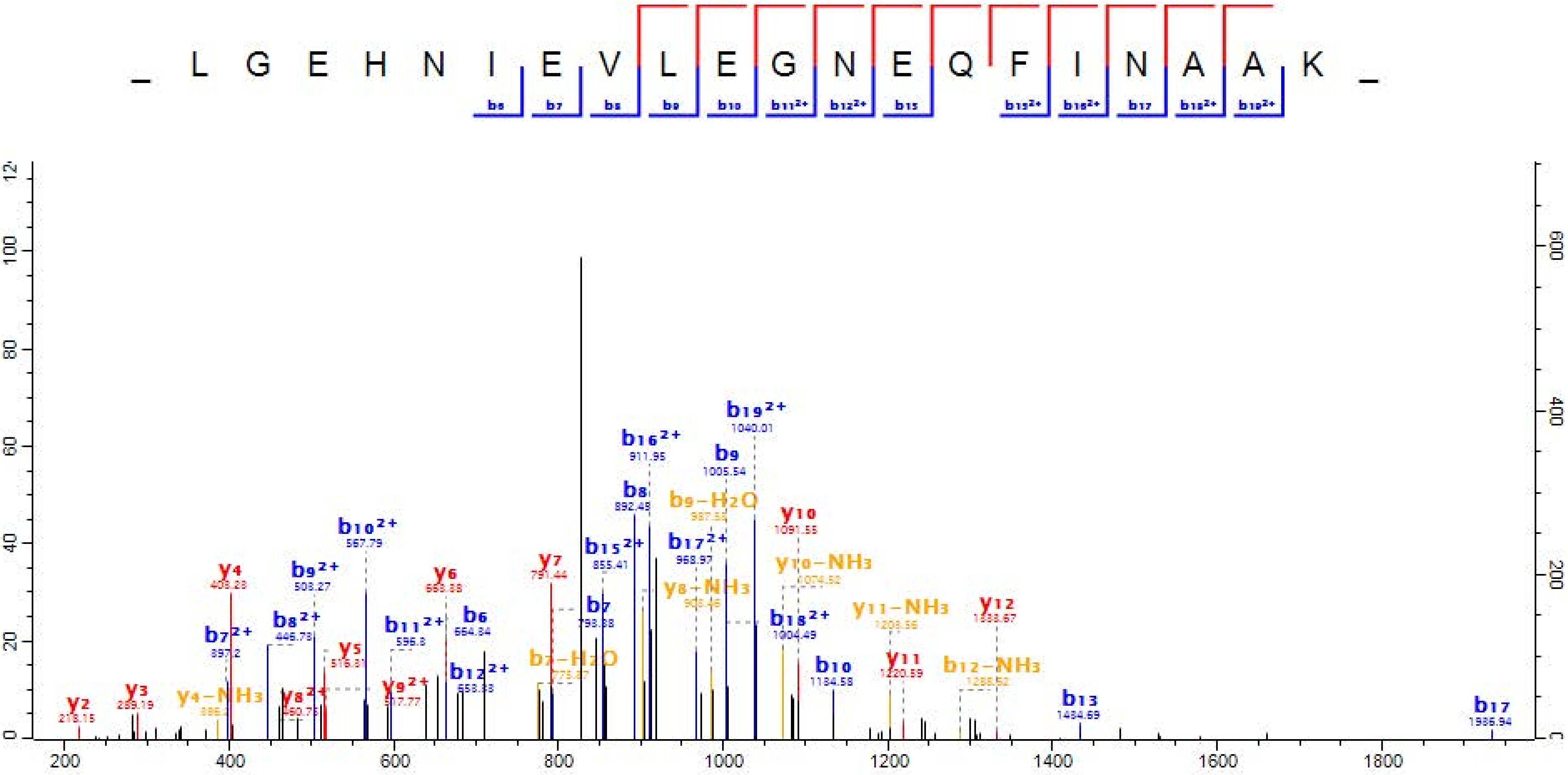
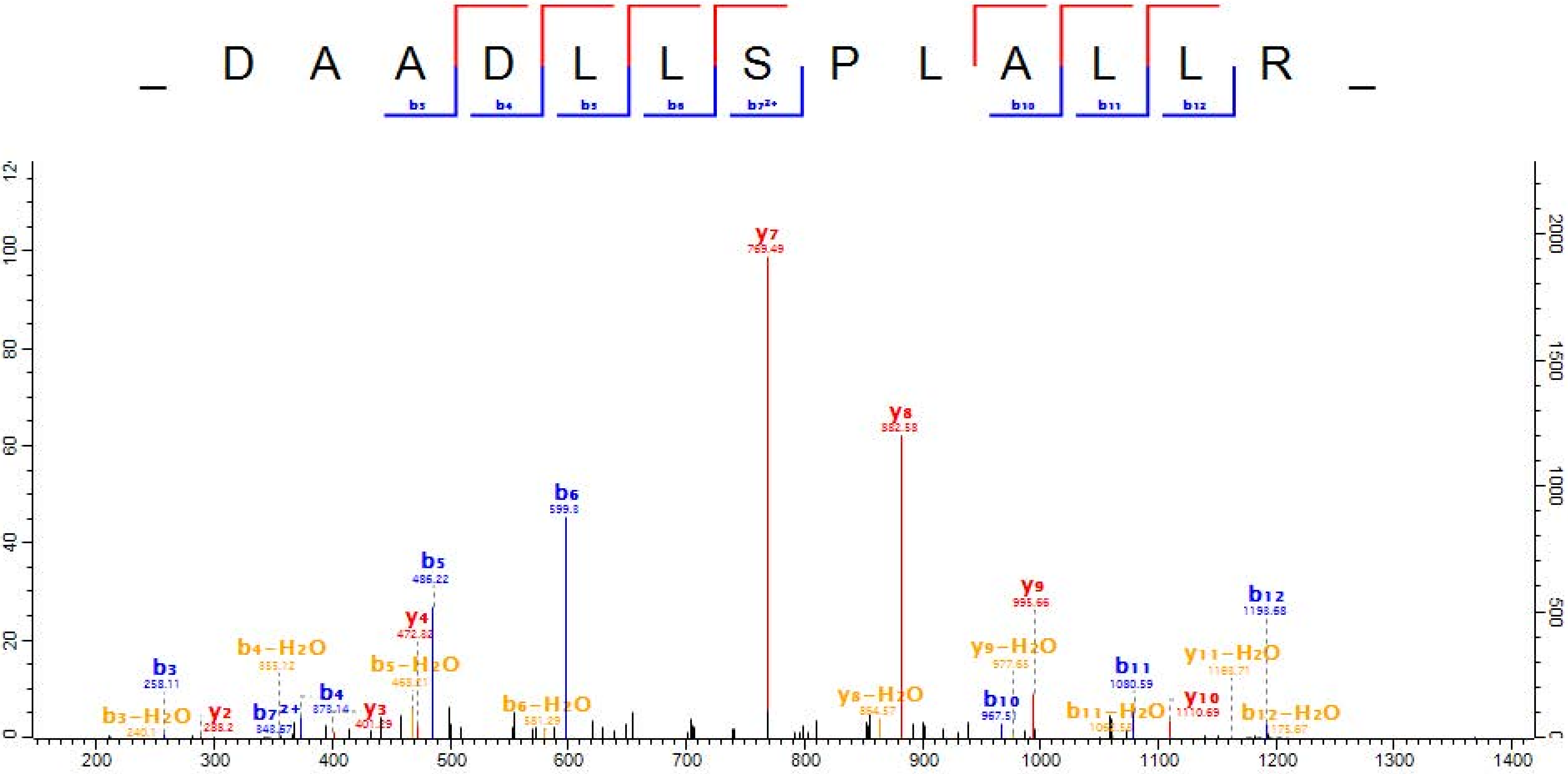
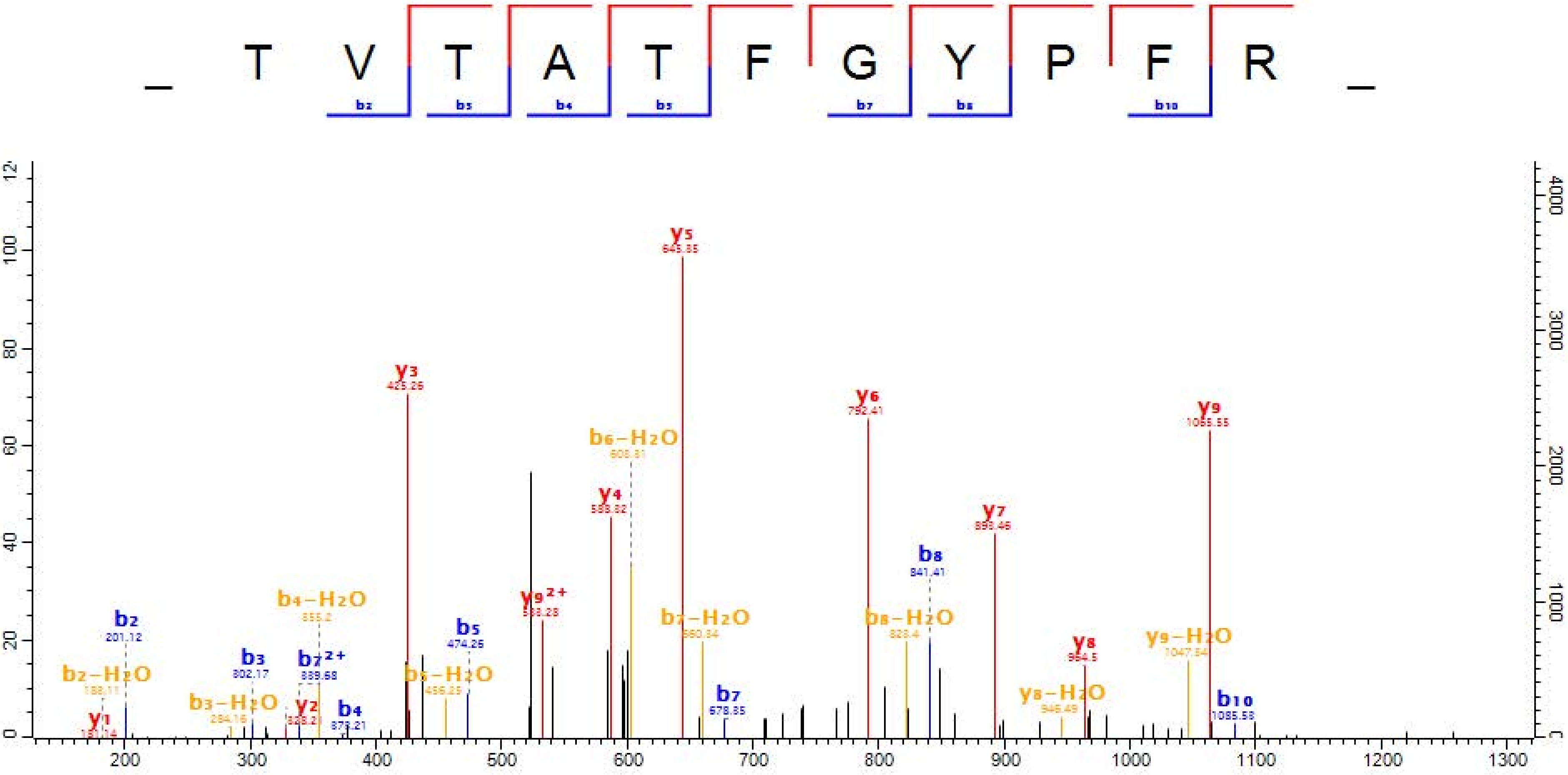
20140917_KT_KeratinocyteProteome_ECM_2_09	9429	ITMS; CID	132.14	2224.11	TRY6;PRSS2;PRSS1



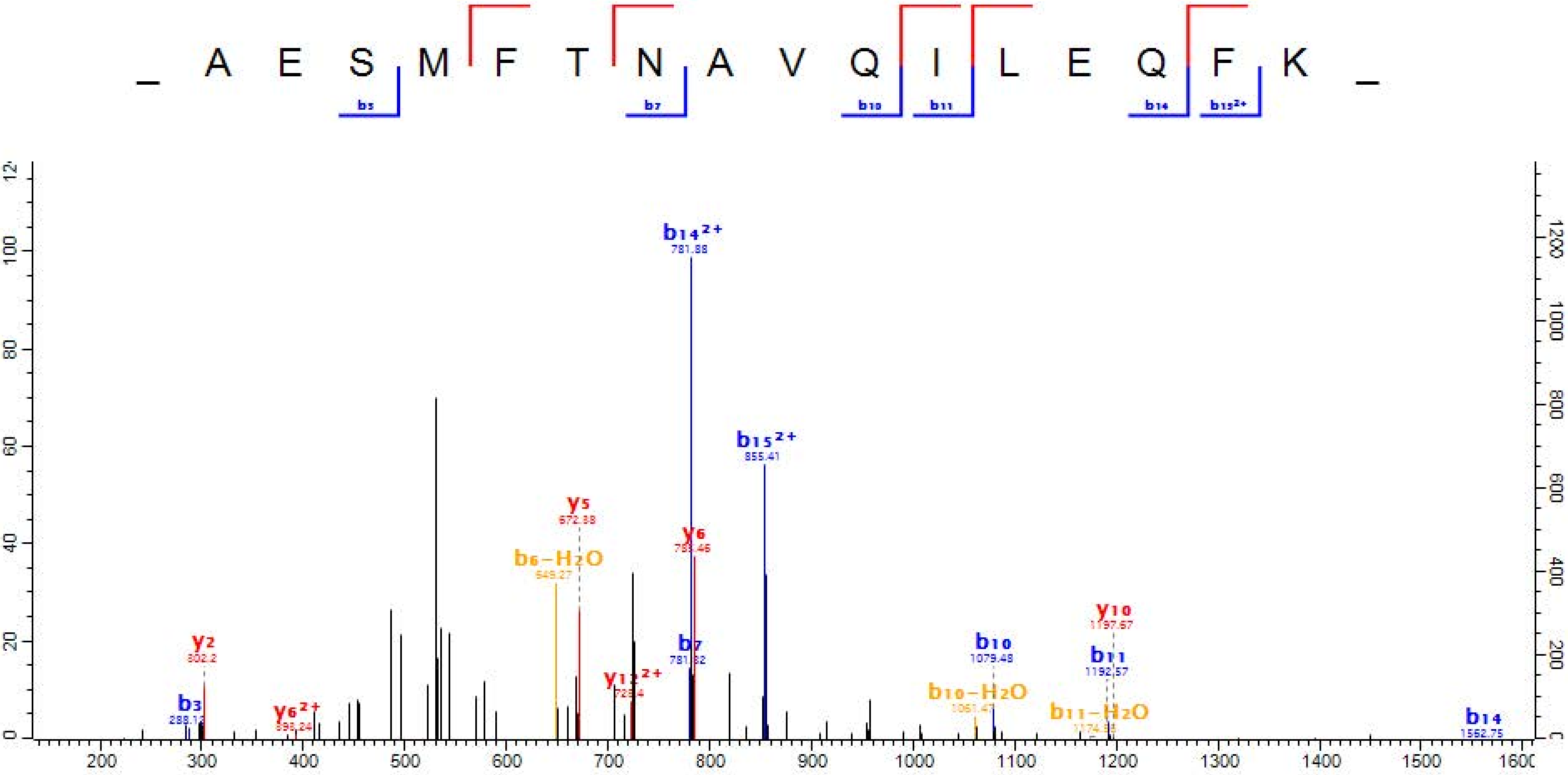
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_7_08	17692	ITMS; CID	99.73	1366.78	MFSD10

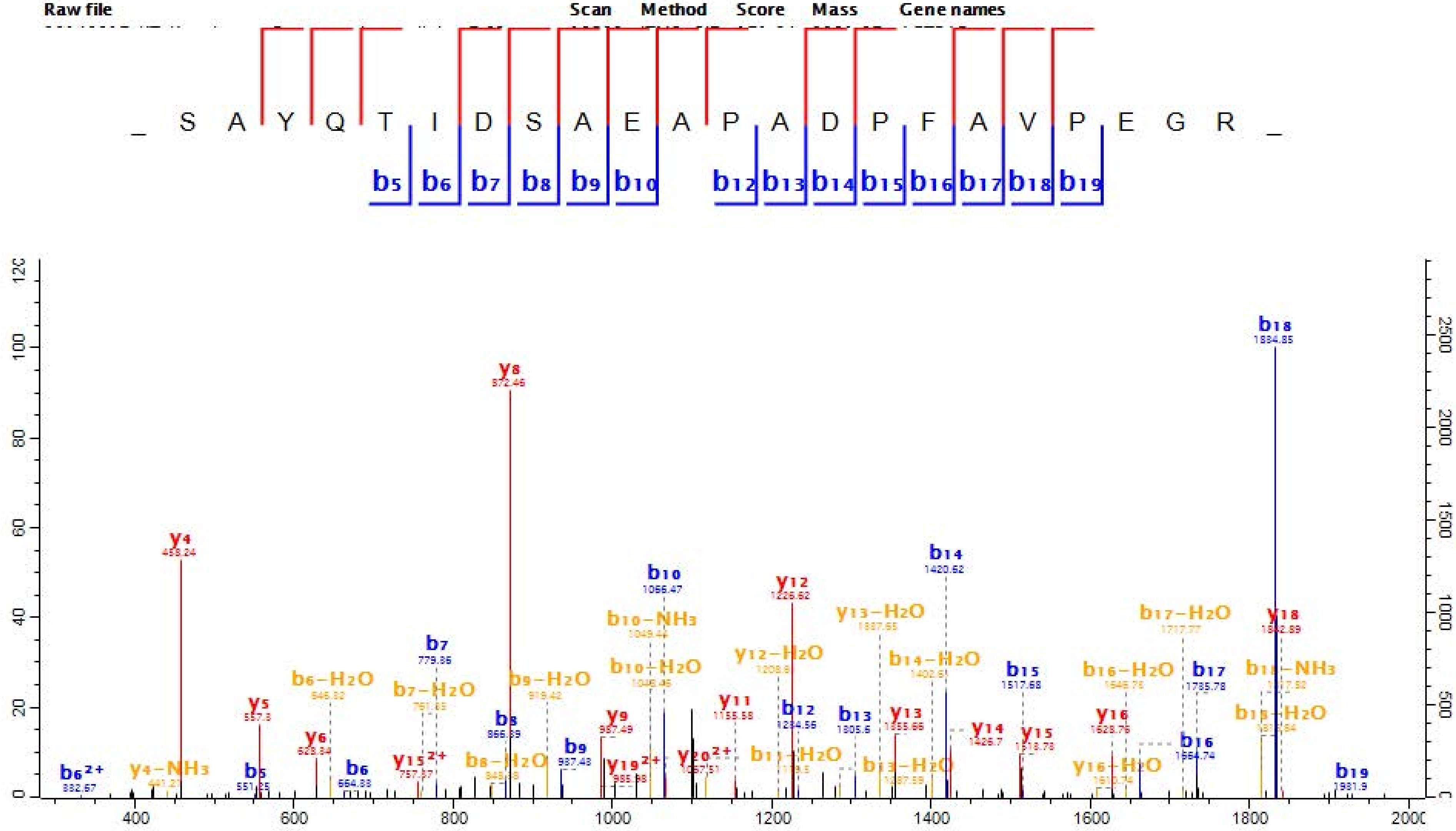


Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_8_04	9818	ITMS; CID	125.23	1258.63	SYPL1



Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_6_04	16334	ITMS; CID	49.59	1854.92	PIGN





Raw file
Scan
Method
Score
Mass
Gene names
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b18 1834.85
y8 872.46
y4 458.24
b14 1420.62
b10 1066.47
y12 1226.62
y18 1842.89
b10-NH3 1049.44
y13-H2O 1337.55
b17-H2O 1717.77
b7 779.36
b10-H2O 1048.46
y12-H2O 1208.6
b14-H2O 1402.61
b15 1517.68
b16-H2O 1646.73
b17 1735.78
b18-NH3 1817.82
b6-H2O 646.32
b7-H2O 761.35
b9-H2O 919.42
b18-H2O 1816.84
y5 557.3
y11 1155.58
b12 1234.56
b13 1305.6
y13 1355.66
y16 1628.76
b8 866.39
y9 987.49
y14 1426.7
y15 1513.78
y6 628.34
b9 937.43
b16 1664.74
y15 2+ 757.37
y19 2+ 985.98
y20 2+ 1057.51
b11-H2O 1119.5
b13-H2O 1287.59
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b6 2+ 332.67
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b5 551.25
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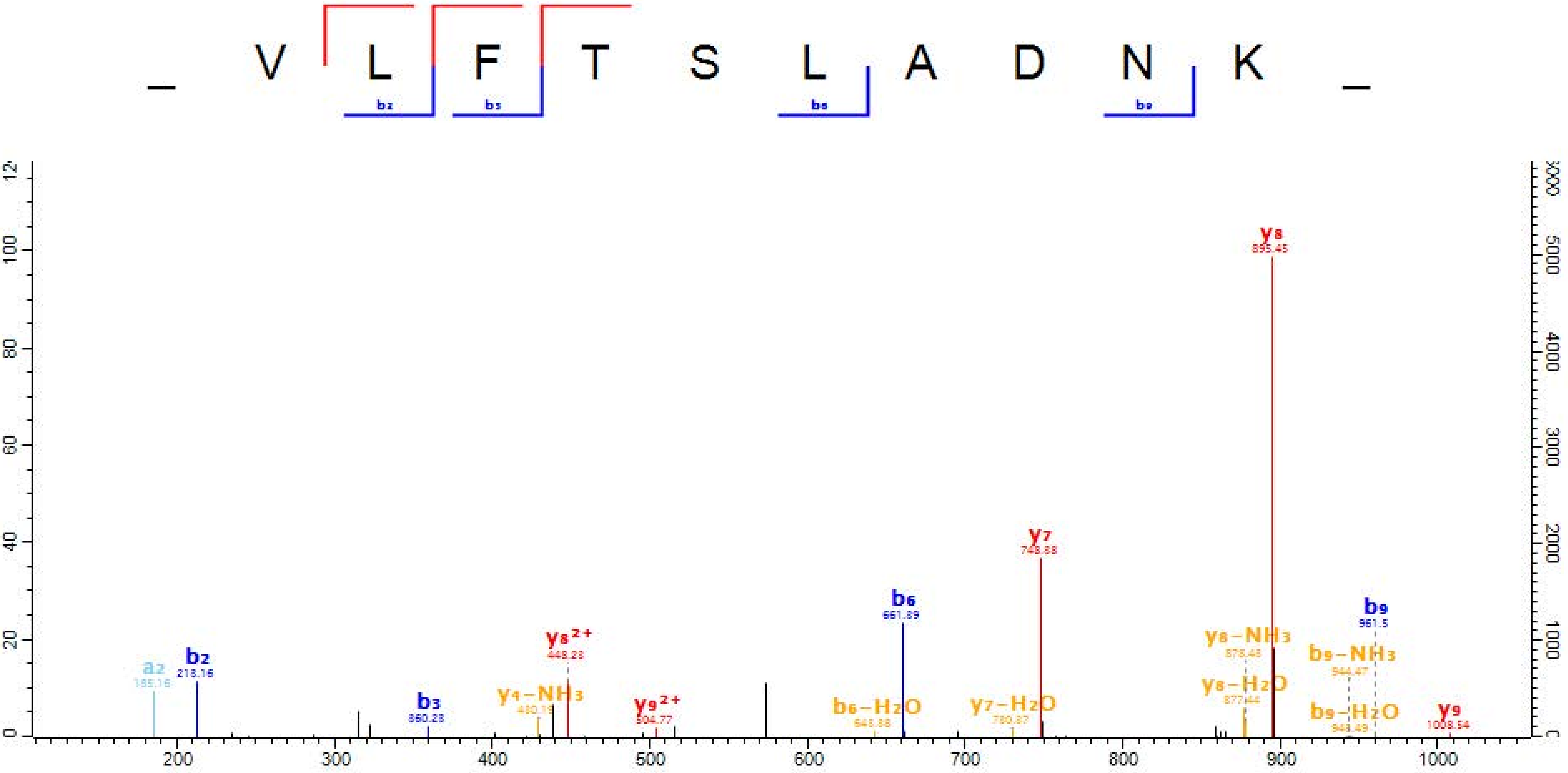
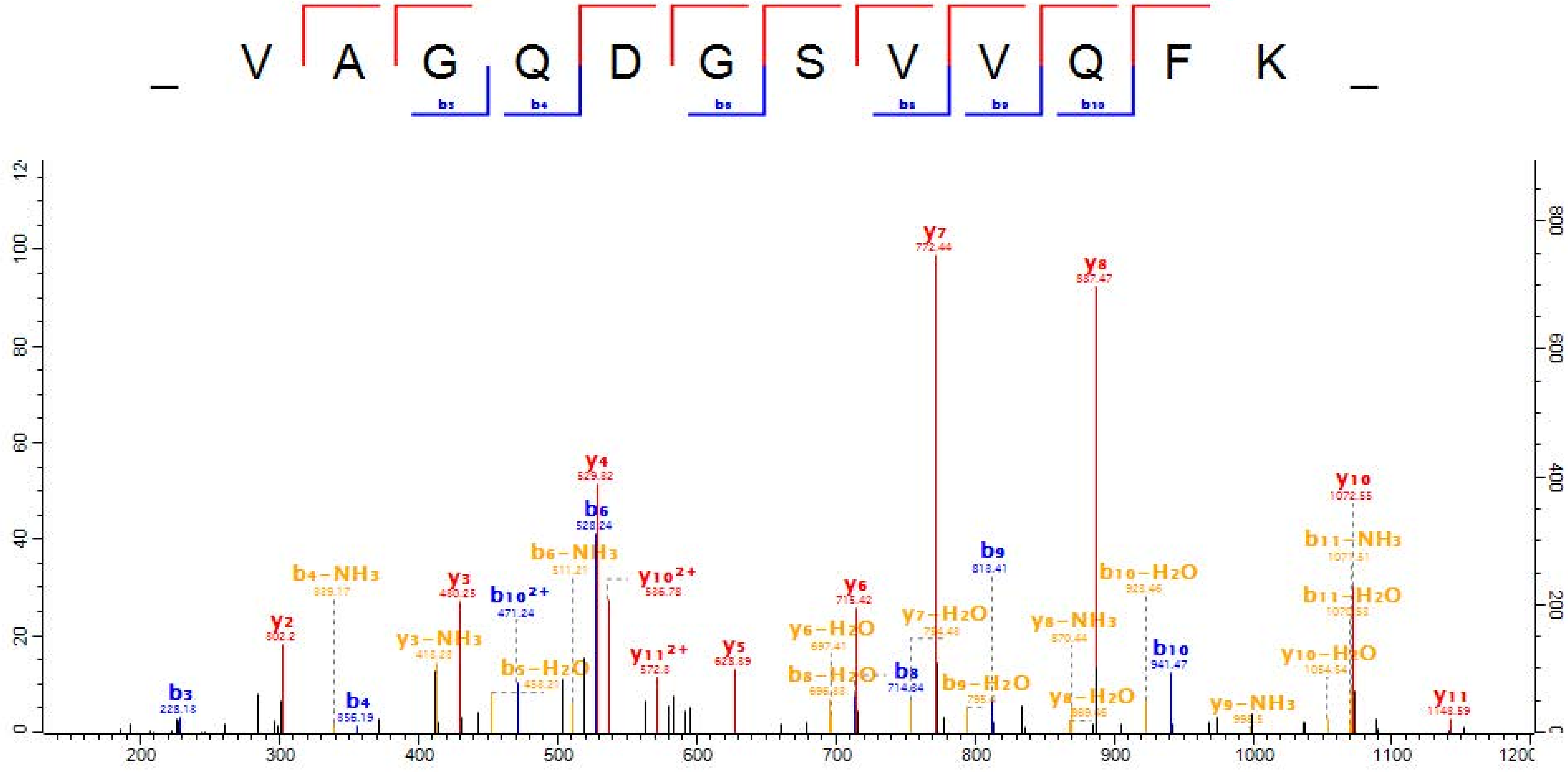
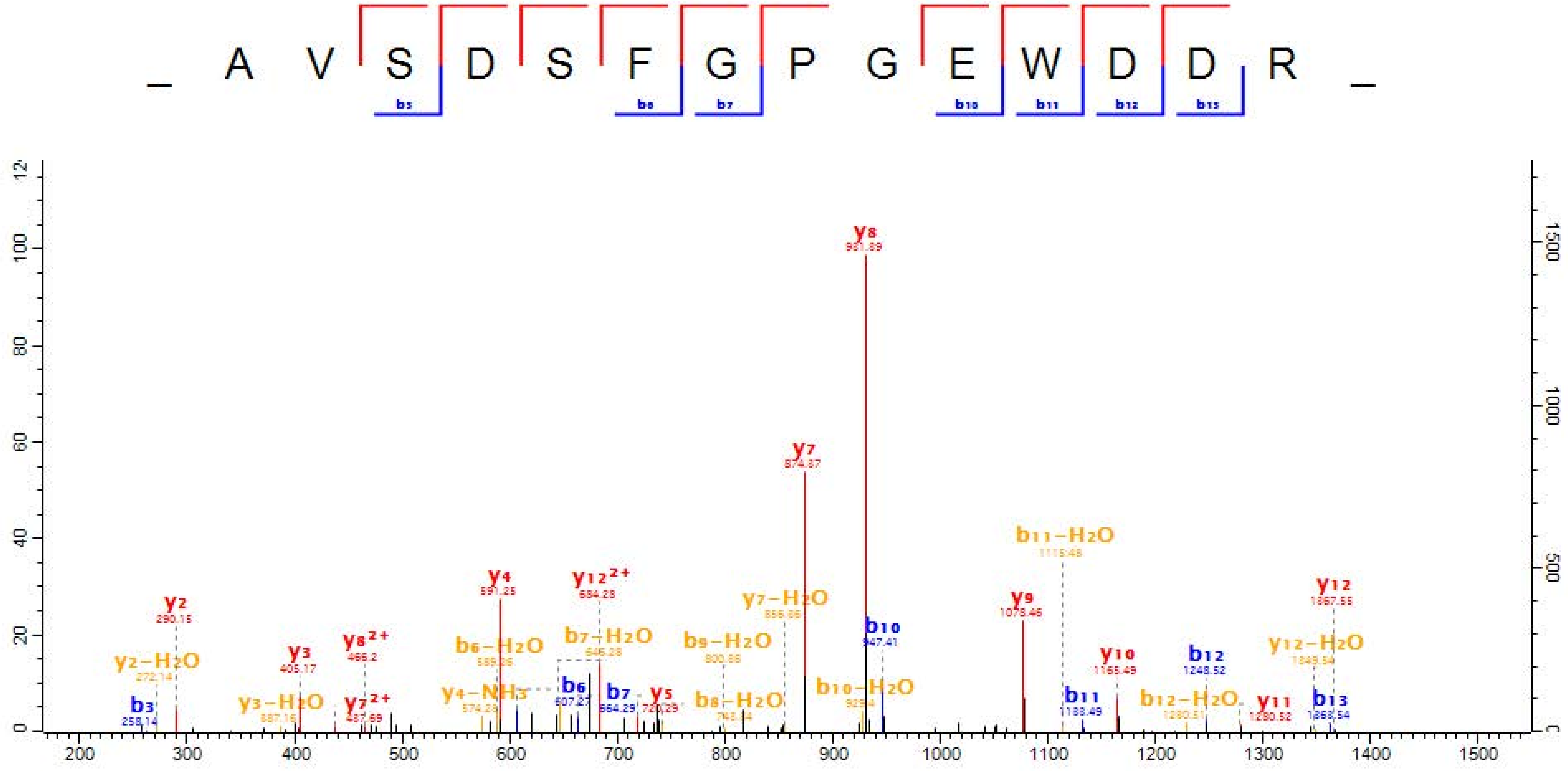
Raw file	**Scan**	**Method**	**Score**	**Mass**	**Gene names**
20140915_KT_KeratinocyteProteome_intracellular_5_05	7171	ITMS; CID	104.2	1106.6	SYNE1



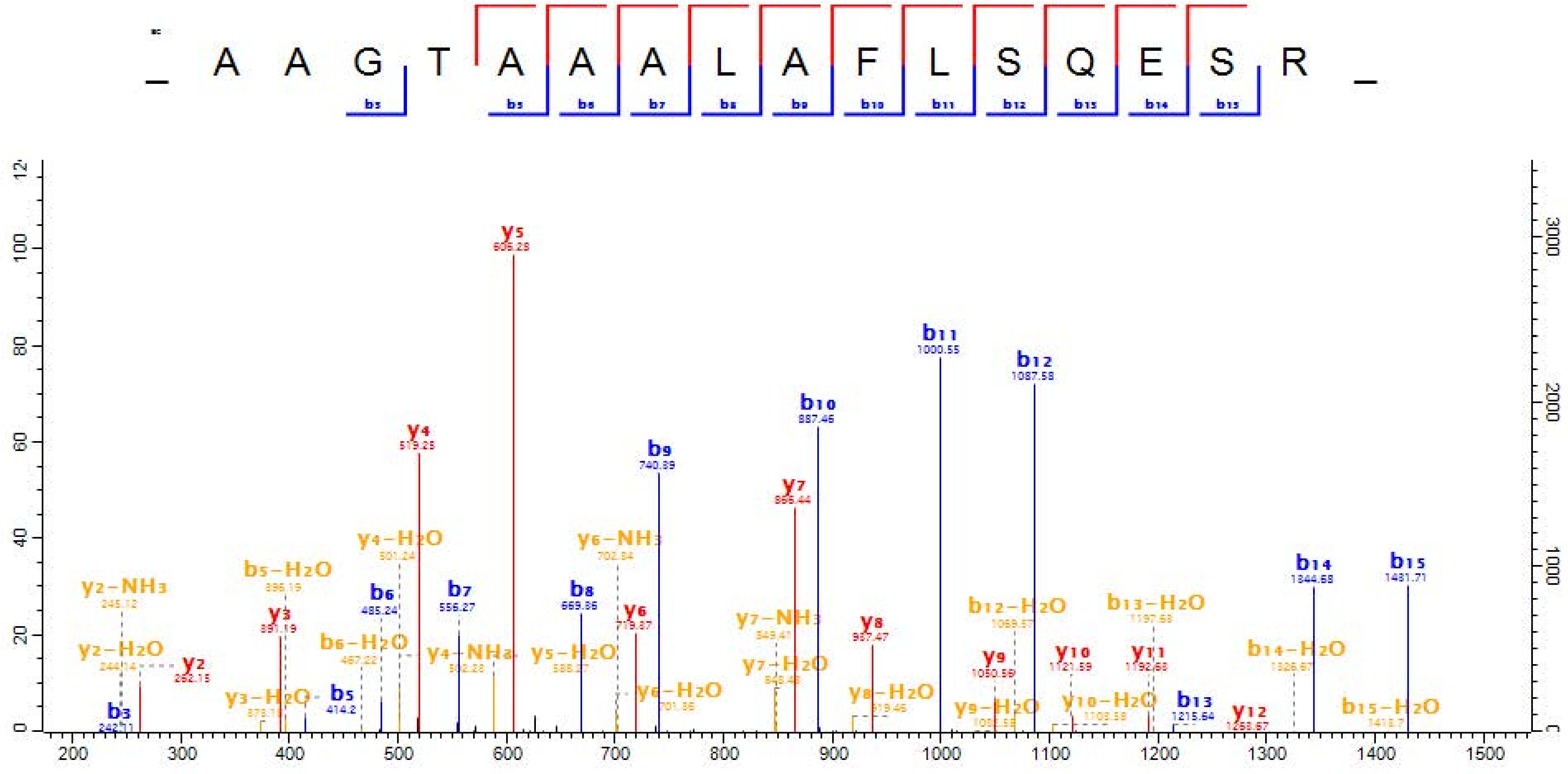
Raw file	**Scan**	**Method**	**Score**	**Mass**	**Gene names**
20140915_KT_KeratinocyteProteome_intracellular_7_02	5297	ITMS; CID	187.58	1233.64	SUMO4;SUMO2;SUMO3



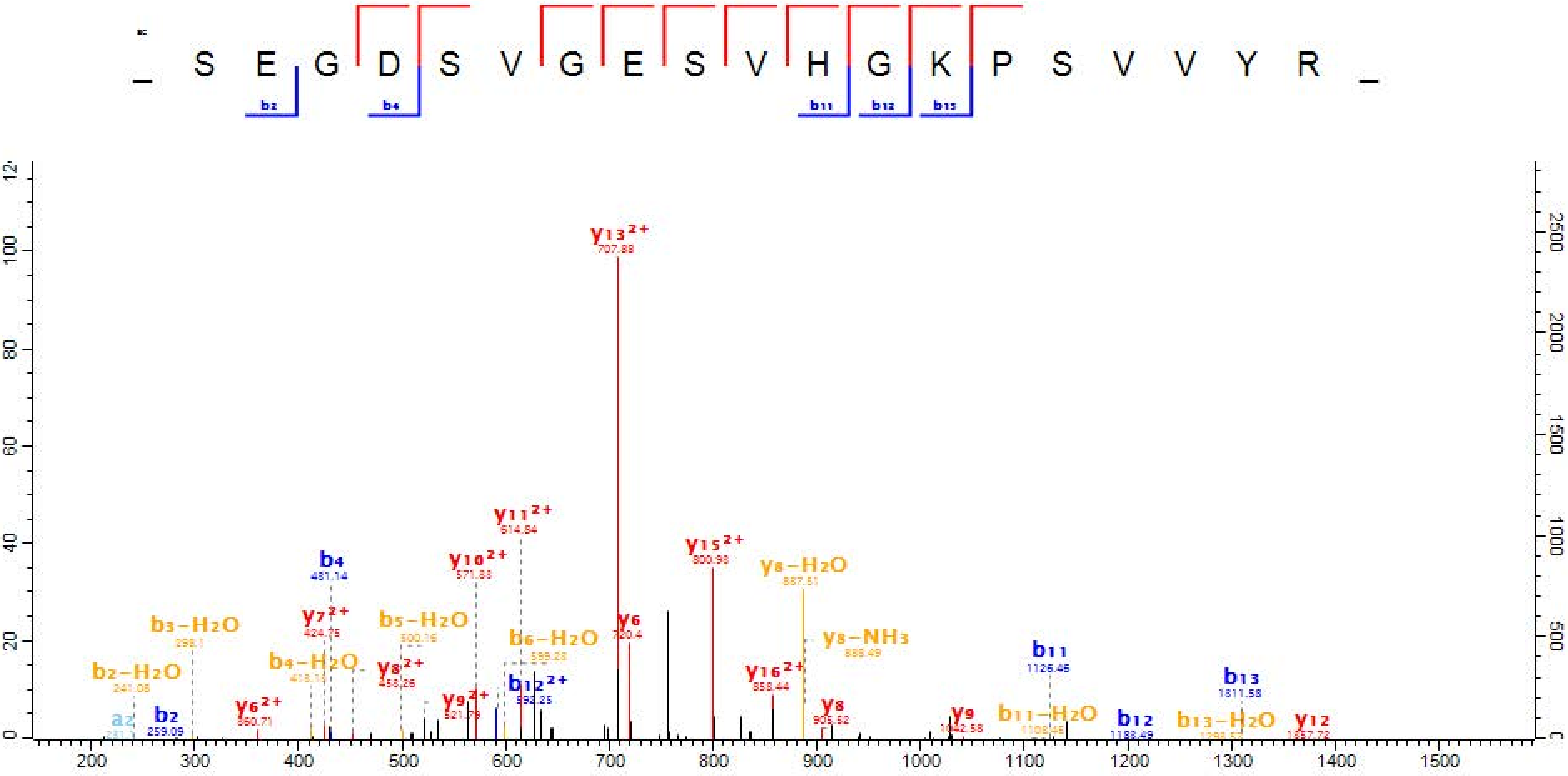
Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_5_10_140916231537	9288	ITMS; CID	150.26	1536.65	TMBIM1



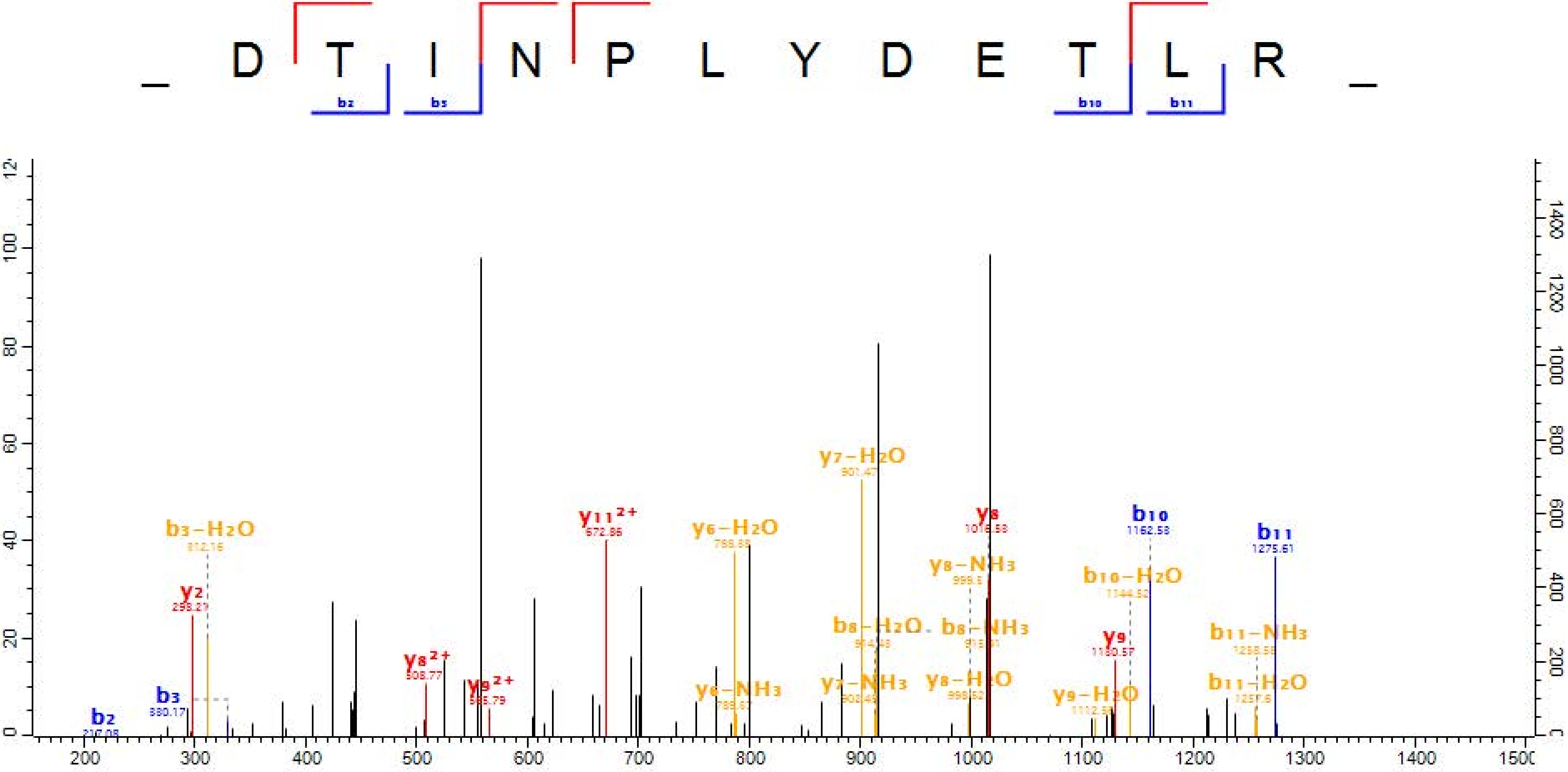
Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_7_02	16308	ITMS; CID	242.19	1562.81	NPM3



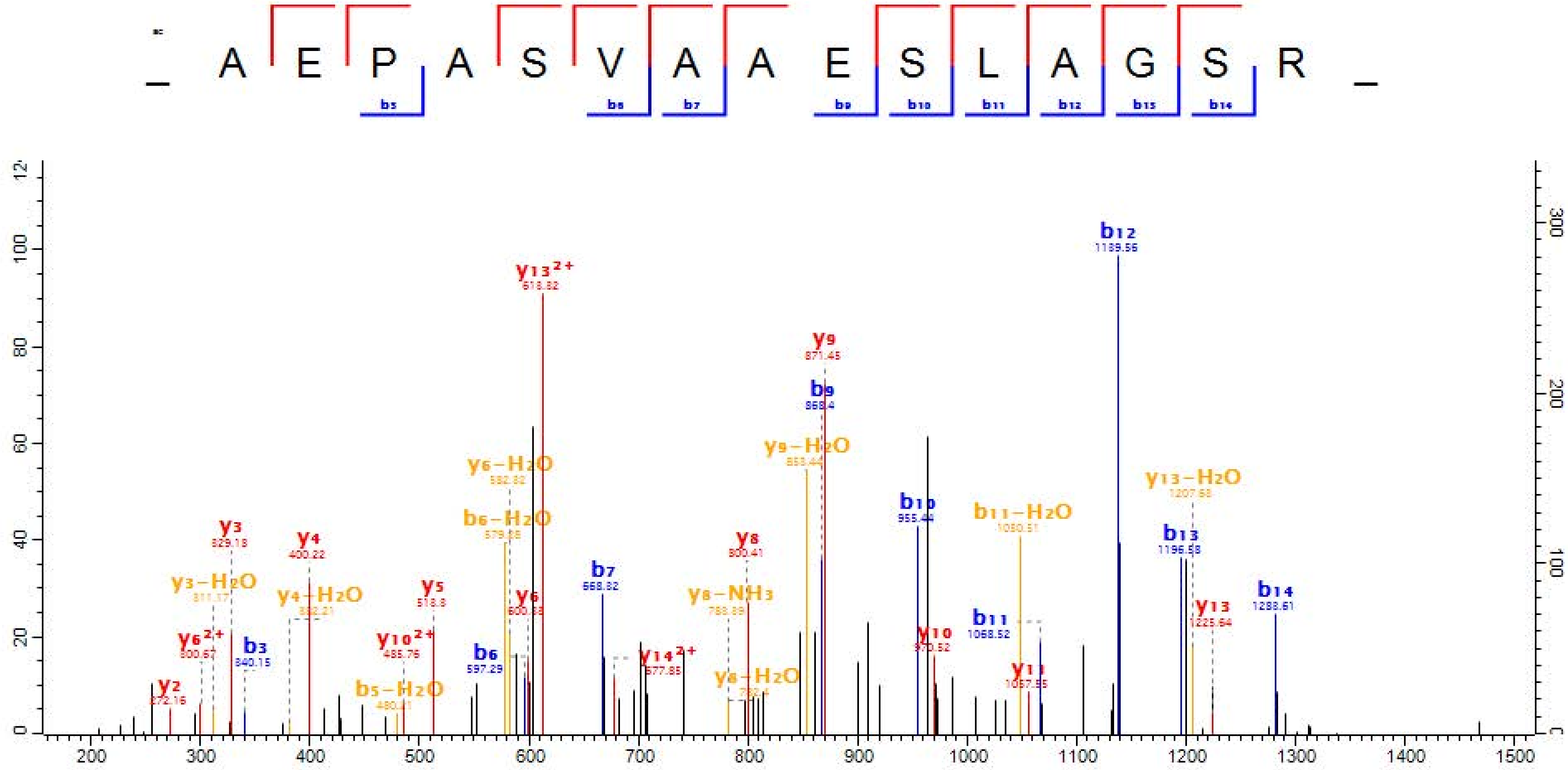
Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_5_09	4912	ITMS; CID	102.29	1987.96	RER1



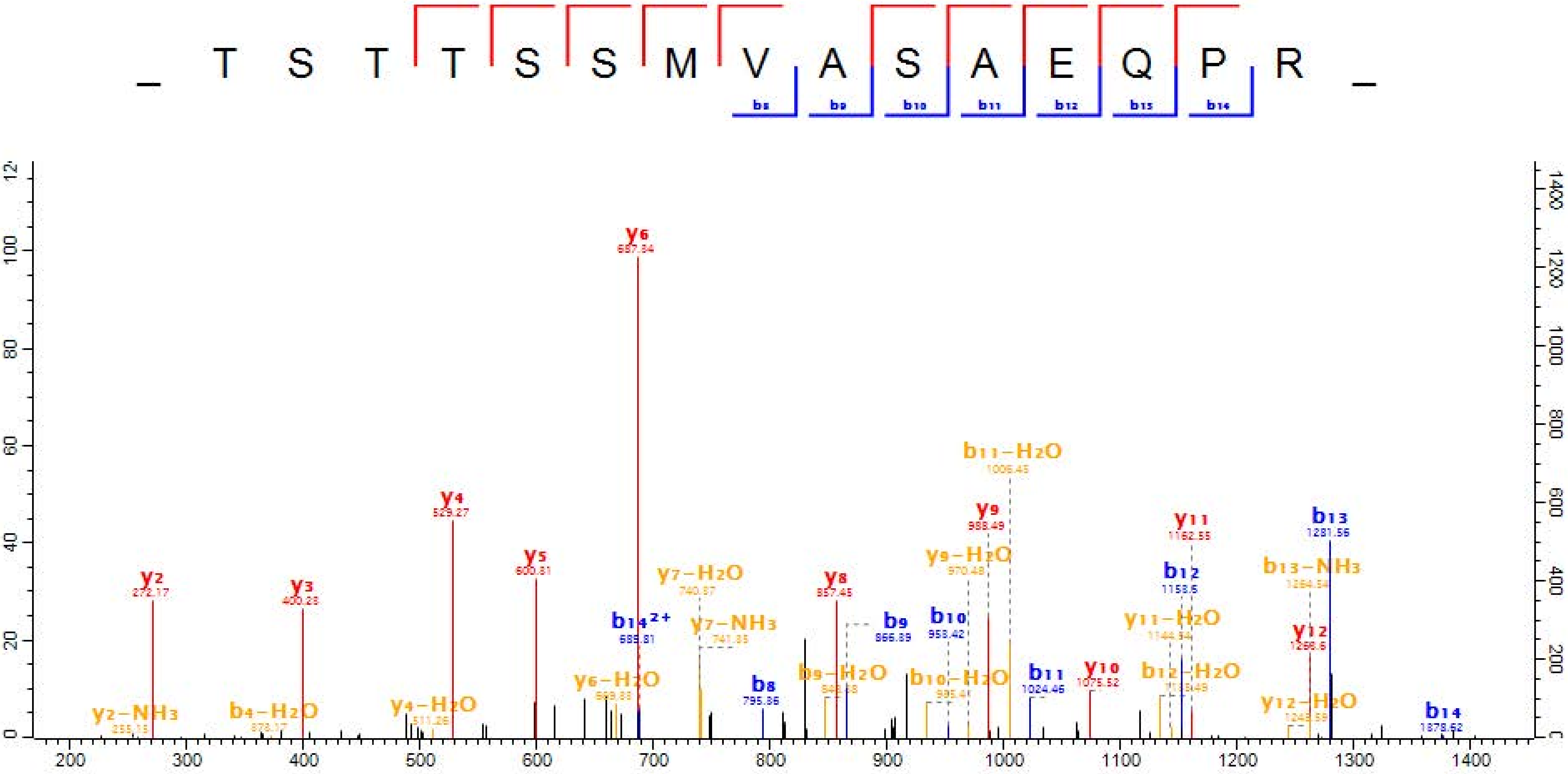
Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_7_05	15556	ITMS; CID	76.33	1448.71	SYTL4



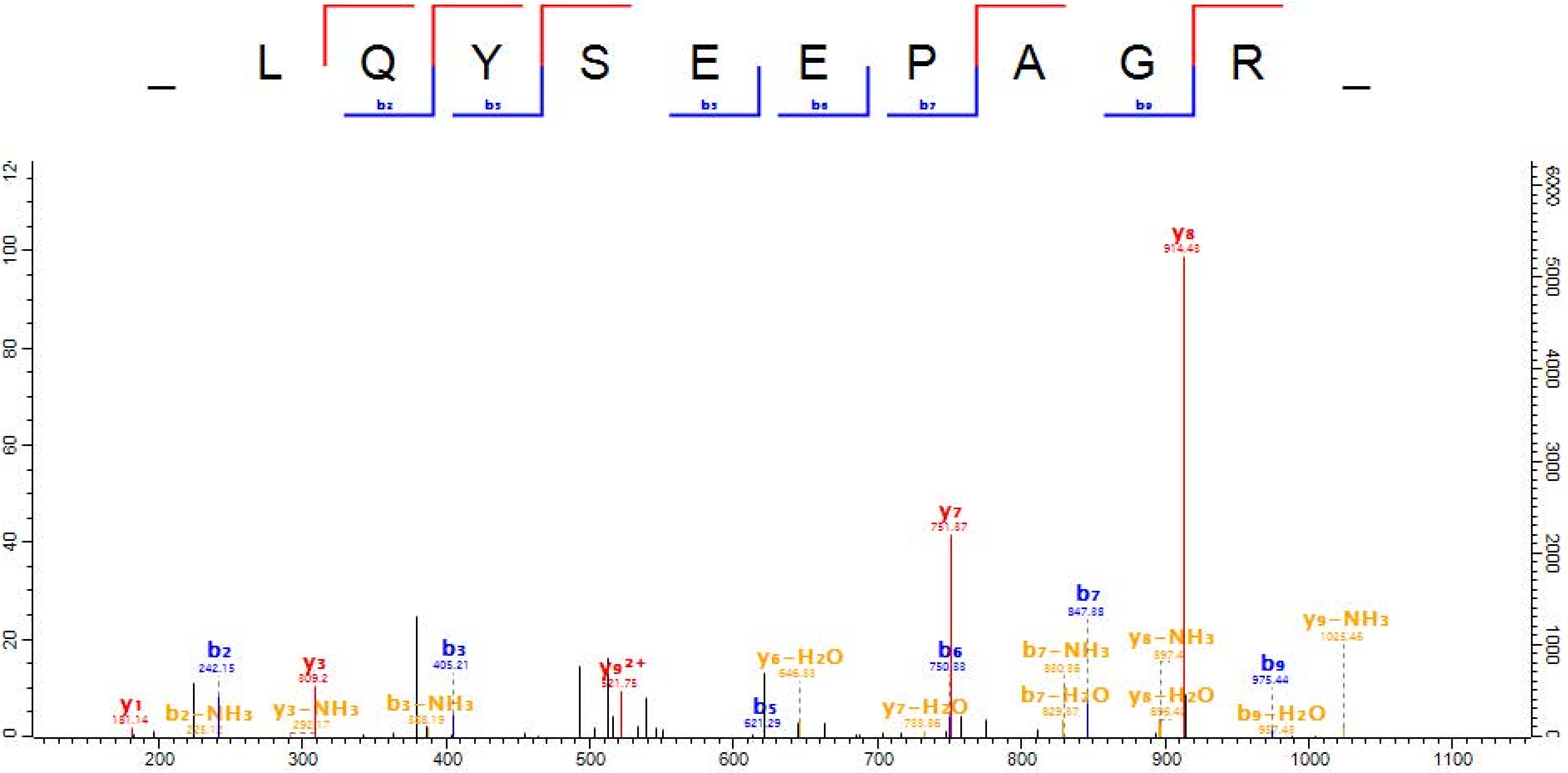
Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_7_03	10229	ITMS; CID	139.66	1414.71	EXOSC3



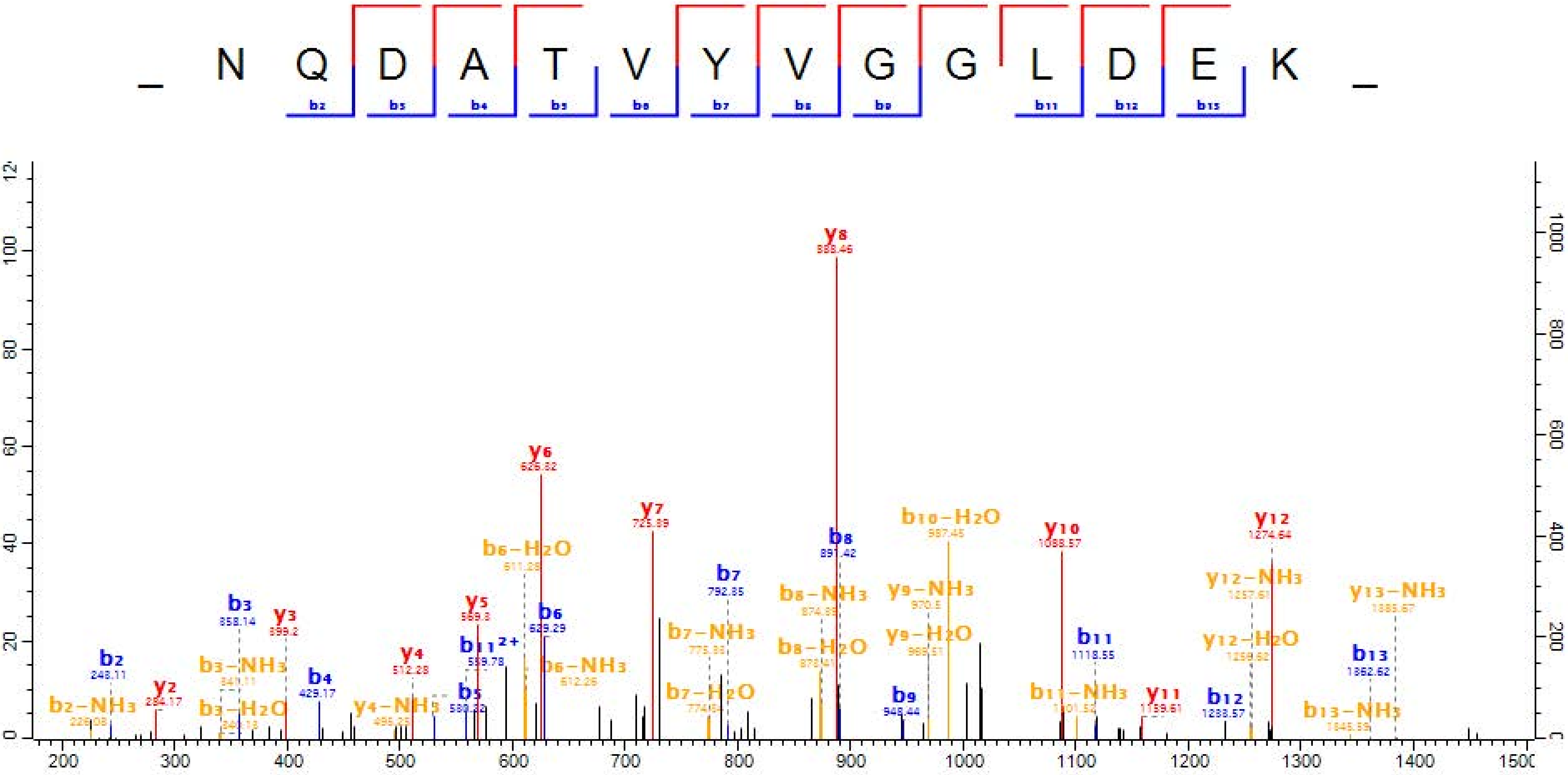
Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_7_03	3868	ITMS; CID	136.14	1551.72	PPP1R2P3;PPP1R2



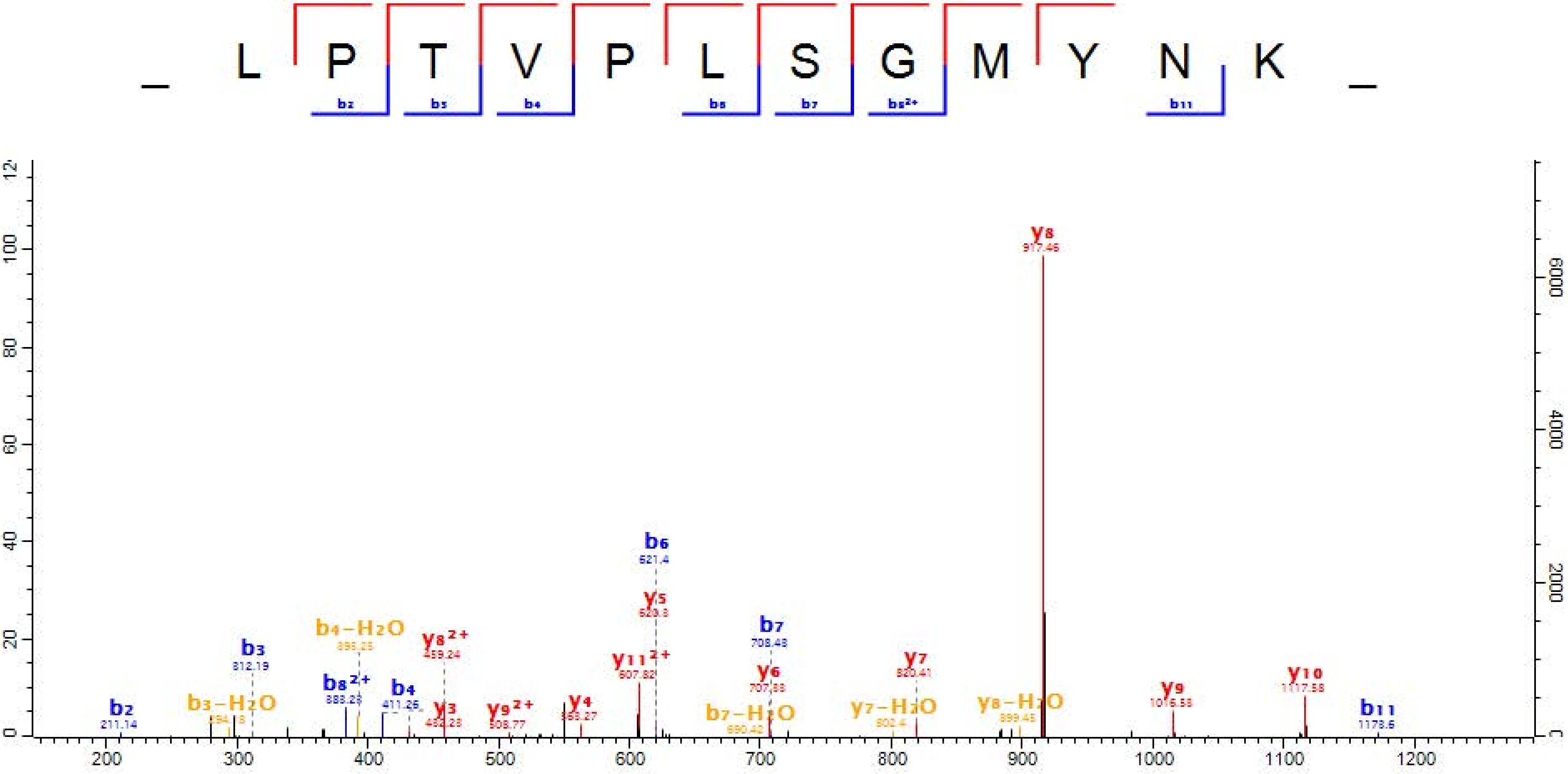
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_6_05	3095	ITMS; CID	99.97	1148.55	RAPGEFL1



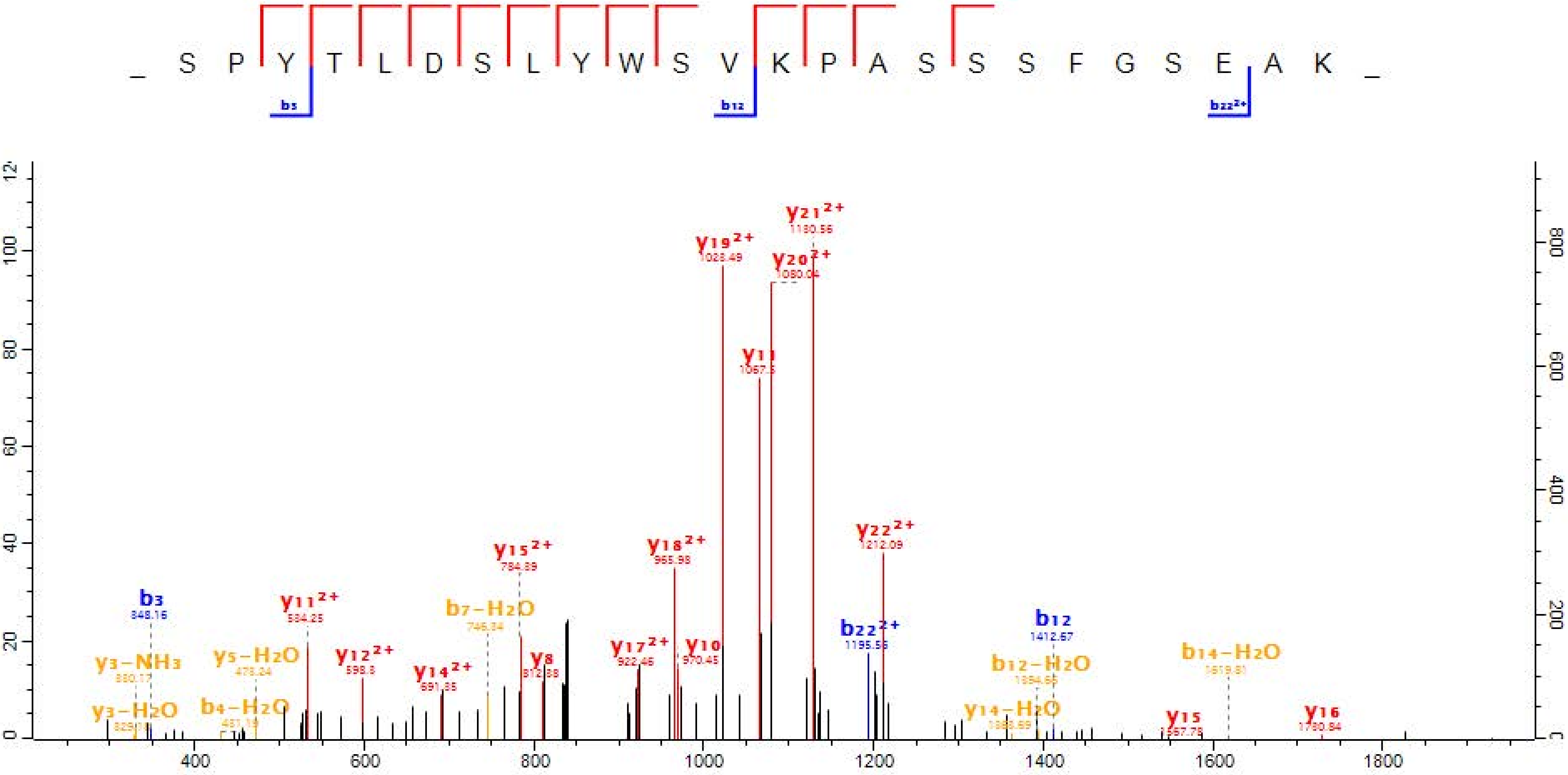
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_6_04	5193	ITMS; CID	171.15	1507.72	SF3B4



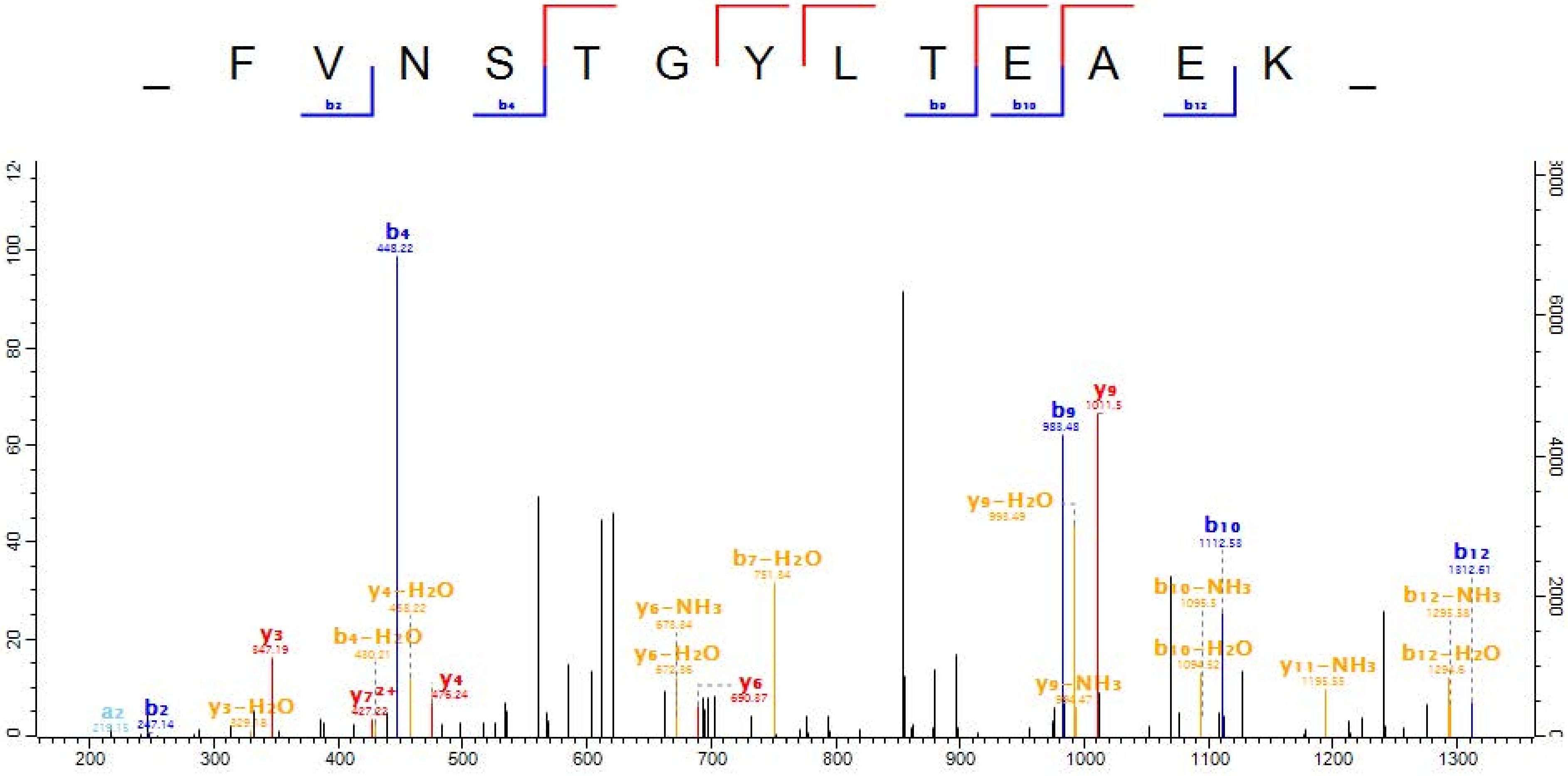
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_7_04	9374	ITMS; CID	122.33	1318.7	UBFD1



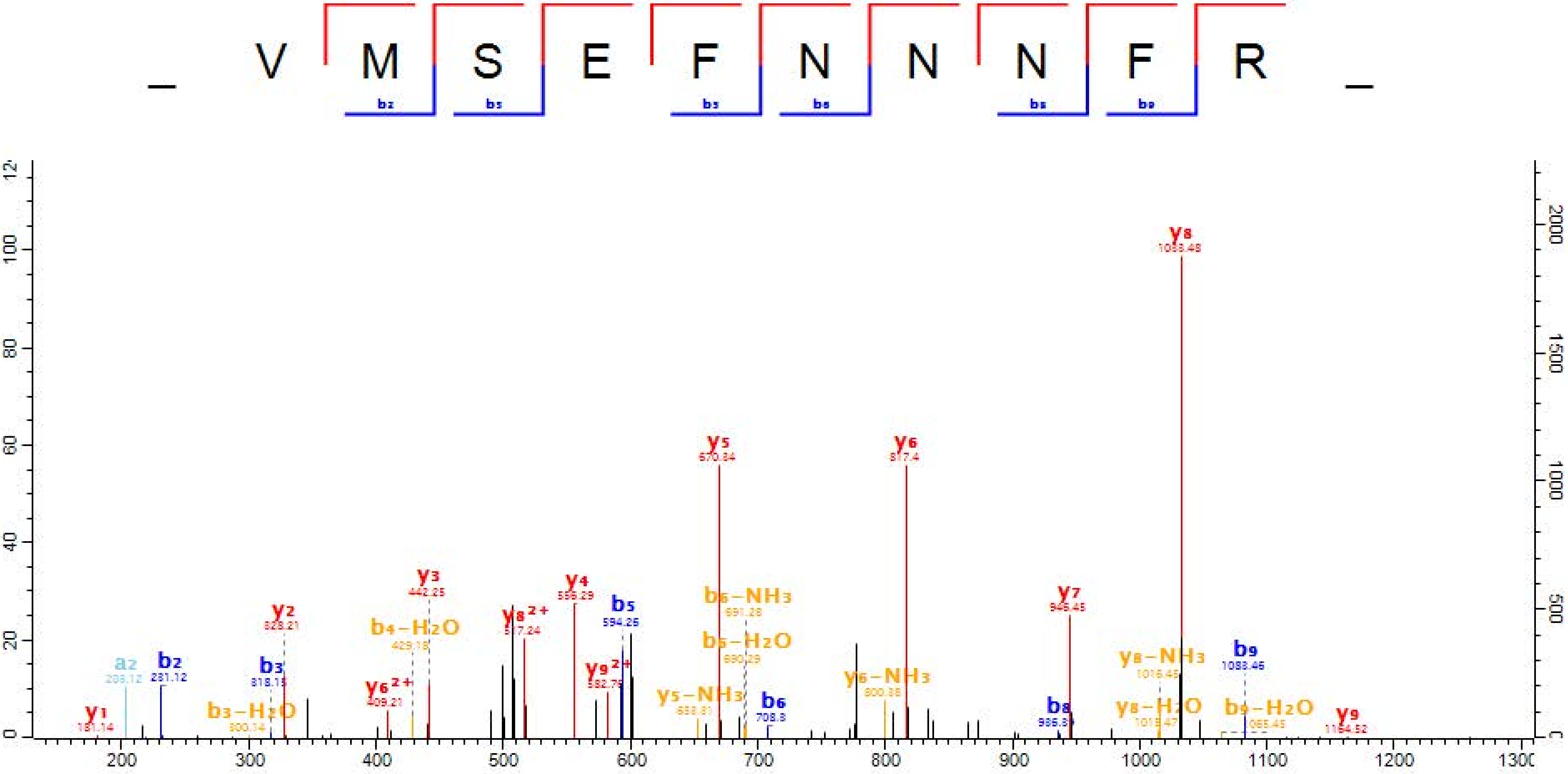
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_5_06	12762	ITMS; CID	73.29	2606.25	LAS1L



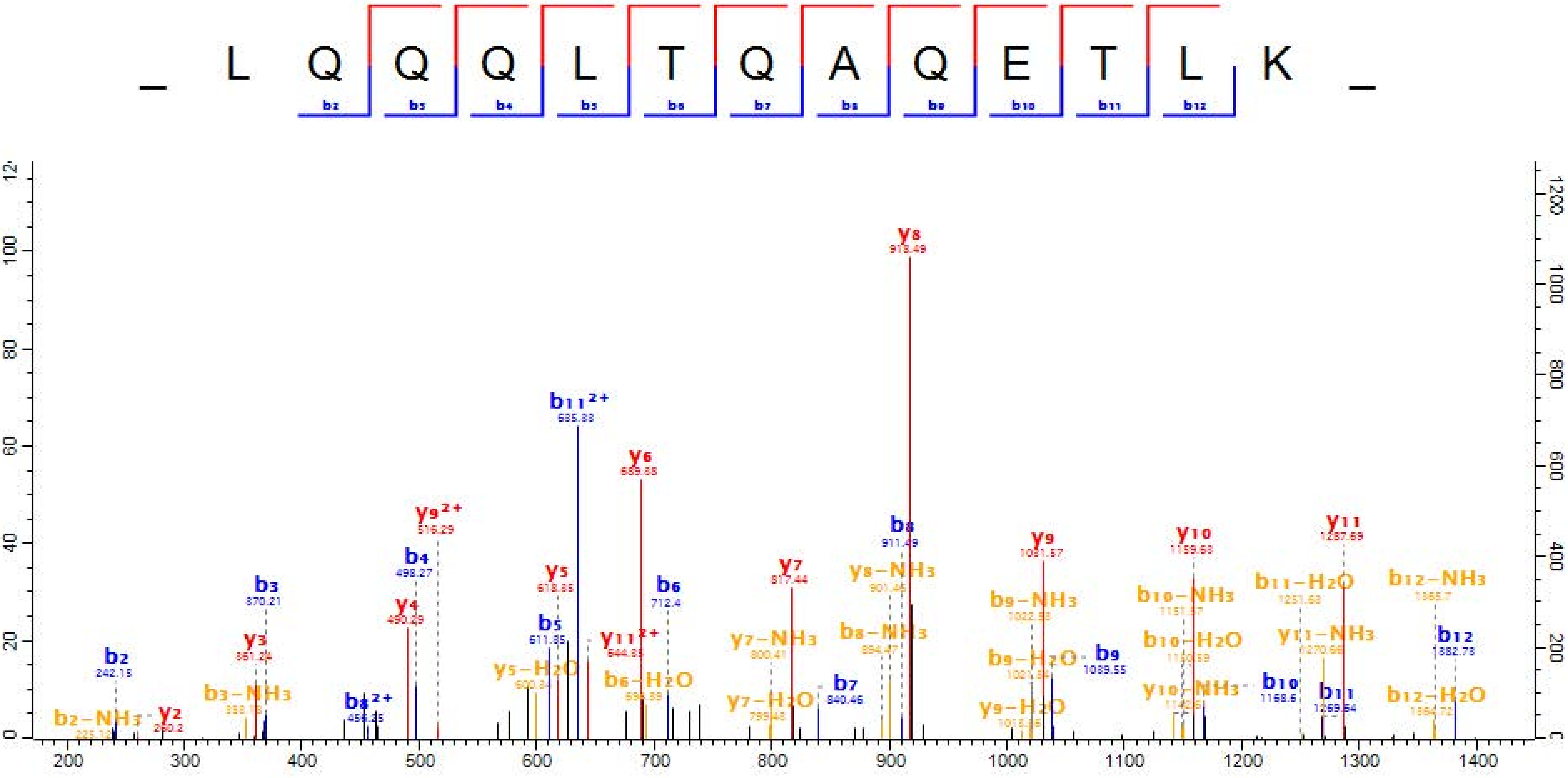
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_7_02_140921214543	10479	ITMS; CID	92.19	1457.7	SUMF1



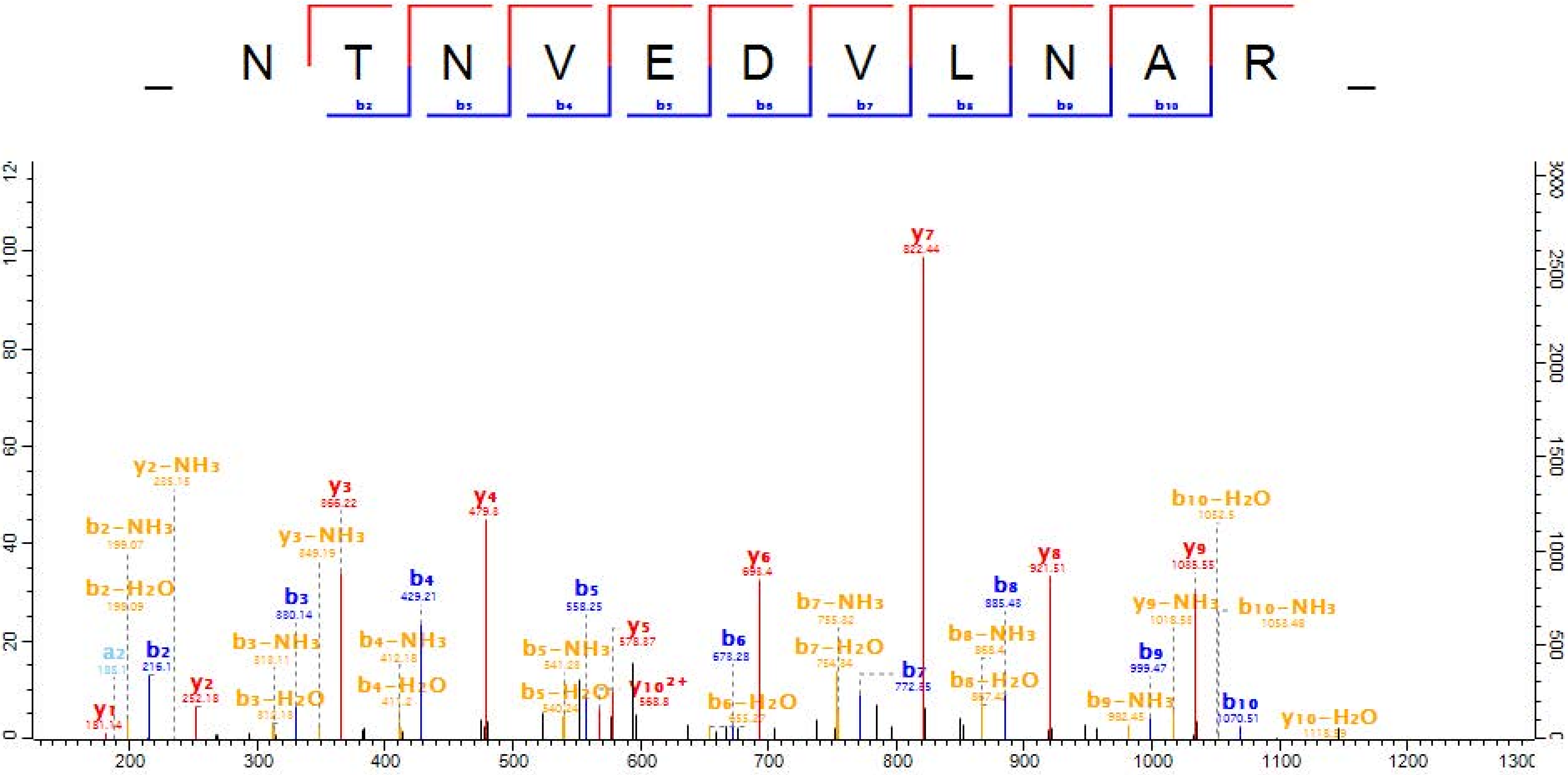
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_5_05	4743	ITMS; CID	178.84	1256.56	CD63



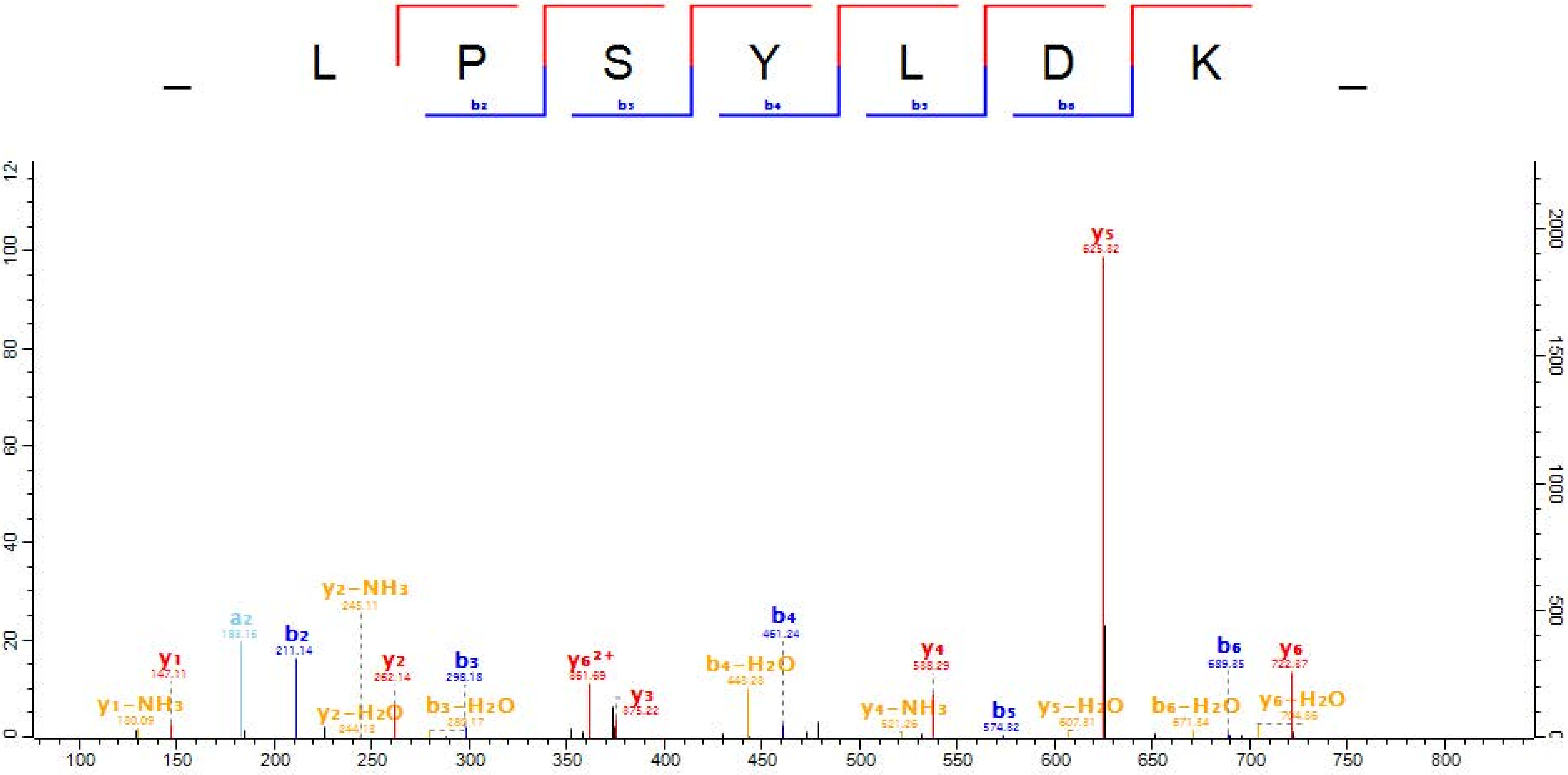
Raw file	**Scan**	**Method**	**Score**	**Mass**	**Gene names**
20140917_KT_KeratinocyteProteome_intracellular_5_04	4297	ITMS; CID	259.27	1527.83	TBL2



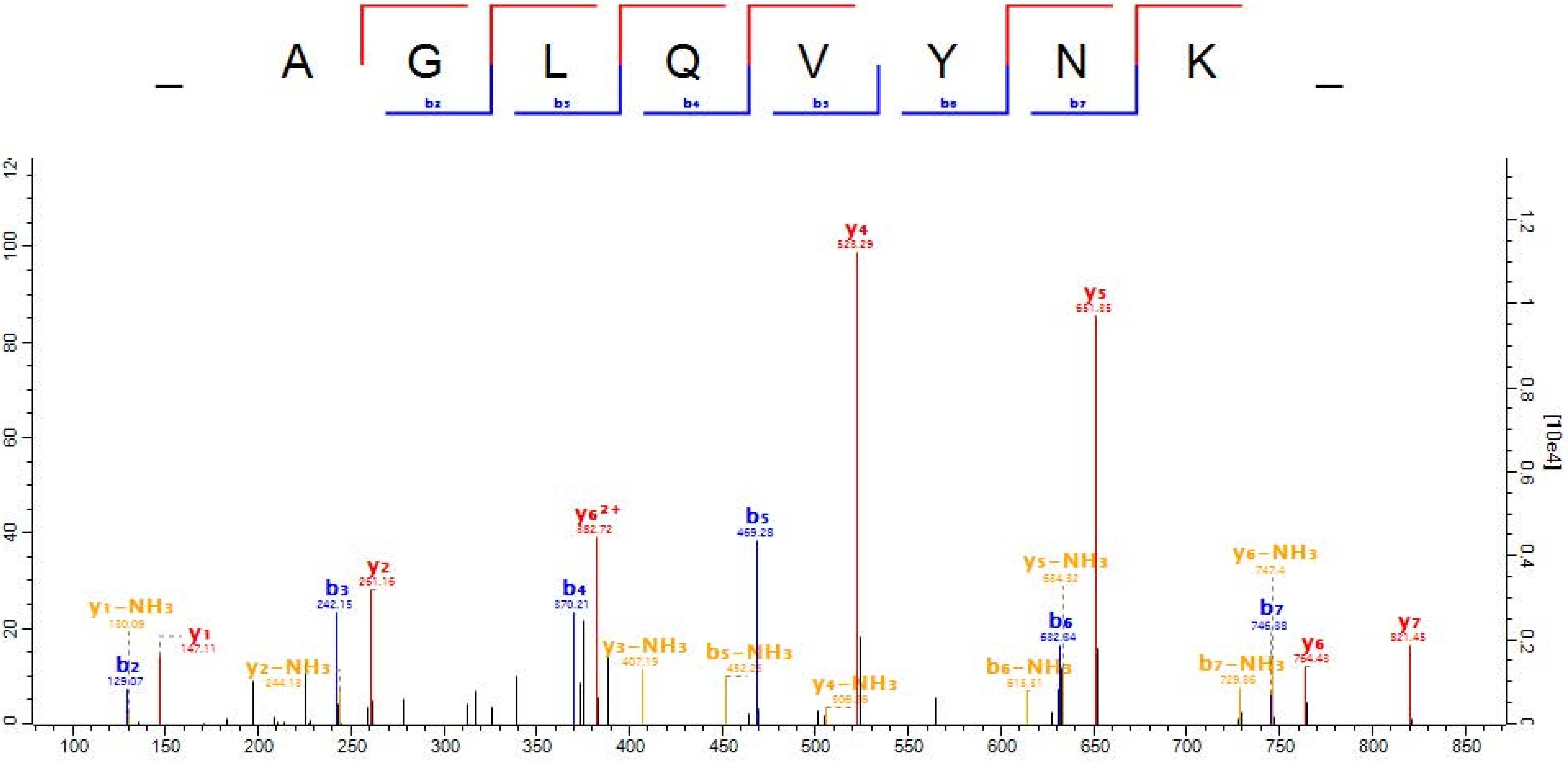
Raw file	Scan	Method	Score	Mass	Gene names
20140917_KT_KeratinocyteProteome_intracellular_5_03	5589	ITMS; CID	225.15	1243.62	CCDC43



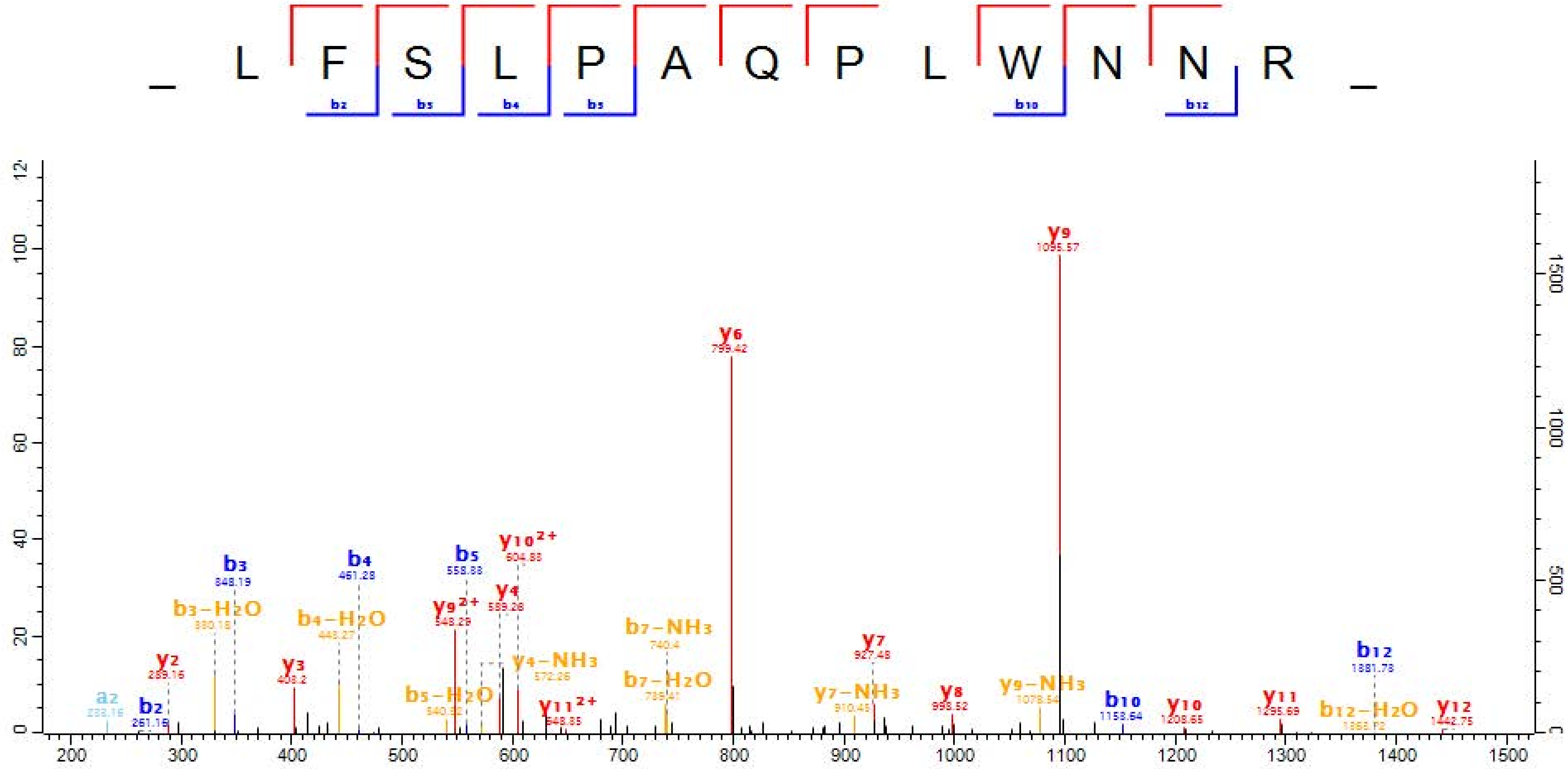
Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_8_04	7274	ITMS; CID	194.25	834.45	TADA2B

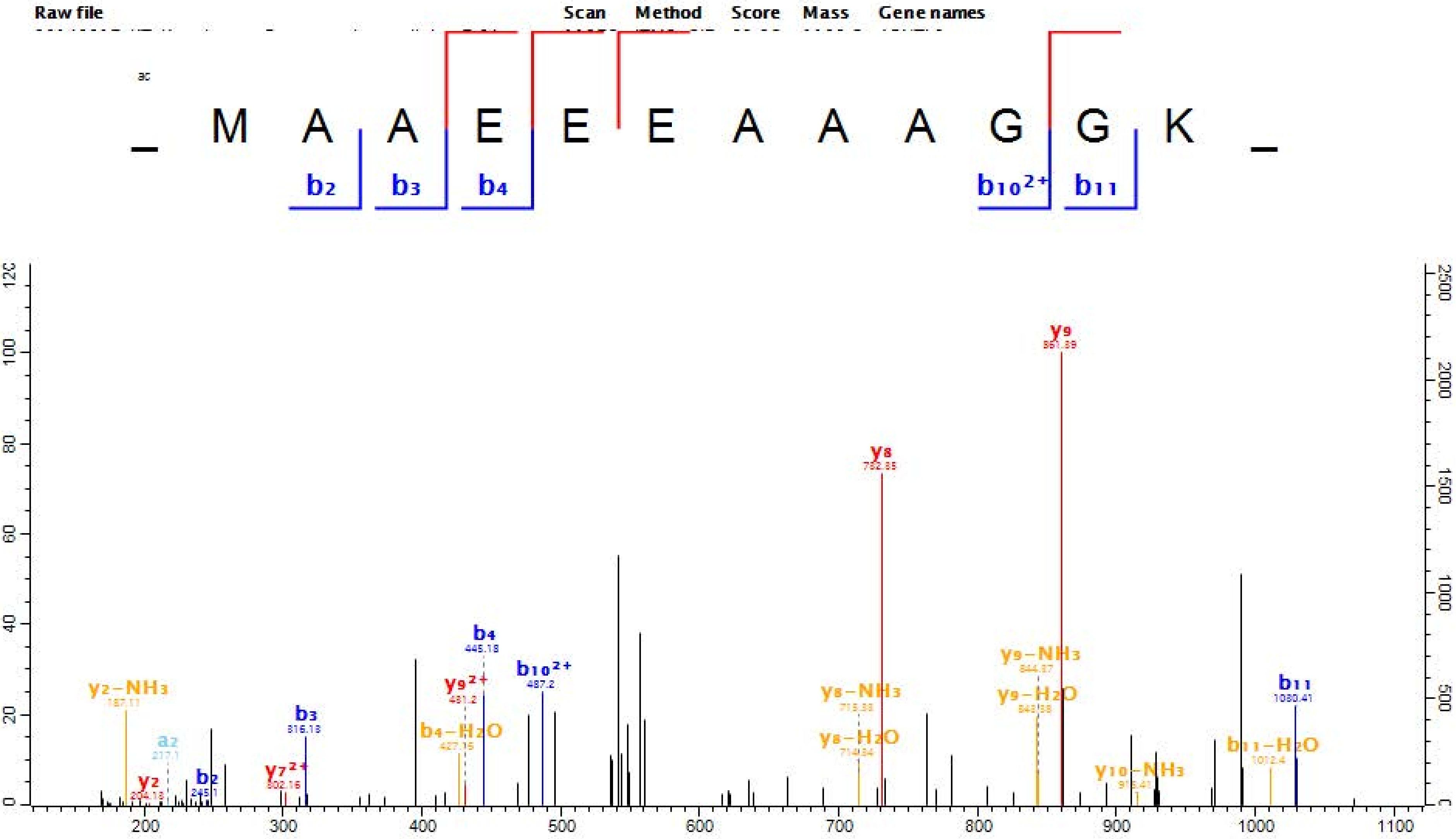


Raw file	**Scan**	**Method**	**Score**	**Mass**	**Gene names**
20140917_KT_KeratinocyteProteome_intracellular_5_02	2616	ITMS; CID	197.65	891.48	CD59



Raw file	Scan	Method	Score	Mass	Gene names
20140915_KT_KeratinocyteProteome_intracellular_7_07	14878	ITMS; CID	128.36	1554.83	RAD21




Raw file
Scan
Method
Score
Mass
Gene names
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b3
b4
b10 2+
b11
y9
861.39
y8
732.35
y9−NH3
844.37
y9−H2O
843.38
y8−NH3
715.38
y8−H2O
714.34
y10−NH3
915.41
b11
1030.41
b11−H2O
1012.4
b4
445.18
b10 2+
487.2
y9 2+
431.2
b4−H2O
427.15
b3
316.13
y7 2+
302.16
y2−NH3
187.11
a2
217.1
y2
204.13
b2
245.1
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800
900
1000
1100

Annotation Cluster 1 Enrichment Score: 4.785469752865533
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007155~cell adhesion 13 1.419213974 1.88E-07 "CD9, COL17A1, LGALS3BP, LY6D, ITGA6, PKP2, ITGB4, DSC3, CTNND1, LAMC1, CD151, CTNNB1, PNN" 38 700 13528 6.611428571 1.17E-04 1.17E-04 2.79E-04
GOTERM_BP_FAT GO:0022610~biological adhesion 13 1.419213974 1.91E-07 "CD9, COL17A1, LGALS3BP, LY6D, ITGA6, PKP2, ITGB4, DSC3, CTNND1, LAMC1, CD151, CTNNB1, PNN" 38 701 13528 6.601997147 1.19E-04 5.97E-05 2.84E-04
GOTERM_CC_FAT GO:0005911~cell-cell junction 6 0.655021834 2.32E-04 "COL17A1, ITGA6, PKP2, DSC3, CTNNB1, PNN" 39 190 12782 10.34979757 0.041357115 0.020896898 0.285969015
GOTERM_CC_FAT GO:0044459~plasma membrane part 14 1.528384279 0.008662785 "MYO1C, ITGB4, SDC4, CD151, EPHA2, PNN, CTNNB1, CD9, CDC42, COL17A1, ITGA6, PKP2, RAB35, DSC3" 39 2203 12782 2.082800843 0.794743634 0.088940249 10.18033999

Annotation Cluster 2 Enrichment Score: 3.3626896856482533
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0031589~cell-substrate adhesion 5 0.545851528 1.42E-04 "COL17A1, ITGA6, ITGB4, LAMC1, CTNNB1" 38 98 13528 18.16326531 0.085139901 0.029225793 0.211227656
GOTERM_CC_FAT GO:0016323~basolateral plasma membrane 6 0.655021834 3.15E-04 "COL17A1, MYO1C, ITGA6, ITGB4, SDC4, CTNNB1" 39 203 12782 9.687002653 0.055762015 0.014241872 0.388279809
GOTERM_BP_FAT GO:0007160~cell-matrix adhesion 4 0.436681223 0.001819412 "COL17A1, ITGA6, ITGB4, CTNNB1" 38 89 13528 16 0.679594593 0.090488238 2.668357659

Annotation Cluster 3 Enrichment Score: 2.8412468653895107
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0016323~basolateral plasma membrane 6 0.655021834 3.15E-04 "COL17A1, MYO1C, ITGA6, ITGB4, SDC4, CTNNB1" 39 203 12782 9.687002653 0.055762015 0.014241872 0.388279809
GOTERM_CC_FAT GO:0009925~basal plasma membrane 3 0.327510917 0.002673947 "COL17A1, MYO1C, ITGB4" 39 26 12782 37.81656805 0.385723565 0.059095638 3.250136712
GOTERM_CC_FAT GO:0045178~basal part of cell 3 0.327510917 0.003552289 "COL17A1, MYO1C, ITGB4" 39 30 12782 32.77435897 0.476735161 0.057179033 4.296377095

Annotation Cluster 4 Enrichment Score: 2.6279046808107944
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0070161~anchoring junction 6 0.655021834 1.46E-04 "ITGA6, PKP2, DSC3, SDC4, CTNNB1, PNN" 39 172 12782 11.43291592 0.026194503 0.026194503 0.179813258
GOTERM_CC_FAT GO:0005911~cell-cell junction 6 0.655021834 2.32E-04 "COL17A1, ITGA6, PKP2, DSC3, CTNNB1, PNN" 39 190 12782 10.34979757 0.041357115 0.020896898 0.285969015
GOTERM_CC_FAT GO:0030057~desmosome 3 0.327510917 0.001580896 "PKP2, DSC3, PNN" 39 20 12782 49.16153846 0.250201457 0.046858384 1.933466446
GOTERM_CC_FAT GO:0043296~apical junction complex 4 0.436681223 0.003123645 "PKP2, DSC3, CTNNB1, PNN" 39 99 12782 13.24216524 0.434131284 0.061306166 3.787102337
GOTERM_CC_FAT GO:0016327~apicolateral plasma membrane 4 0.436681223 0.003398536 "PKP2, DSC3, CTNNB1, PNN" 39 102 12782 12.85268979 0.461833302 0.060078288 4.113987507
GOTERM_CC_FAT GO:0030054~cell junction 7 0.76419214 0.003936286 "COL17A1, ITGA6, PKP2, DSC3, SDC4, CTNNB1, PNN" 39 518 12782 4.428967429 0.512184381 0.058064189 4.75050283
GOTERM_CC_FAT GO:0005912~adherens junction 4 0.436681223 0.01081591 "ITGA6, PKP2, SDC4,

CTNNB1" 39 155 12782 8.45789909 0.861822831 0.104126974 12.55827846
GOTERM_BP_FAT GO:0016337~cell-cell adhesion 4 0.436681223 0.039203969 "PKP2, DSC3, CTNND1,
CTNNB1" 38 276 13528 5.15942029 1 0.590453163 44.78677783

Annotation Cluster 5 Enrichment Score: 2.531760671112018
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment
Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0046847~filopodium assembly 3 0.327510917 7.47E-04 "CDC42, ITGA6,
ITGB4" 38 15 13528 71.2 0.373285399 0.056734986 1.104207818
GOTERM_BP_FAT GO:0030035~microspike assembly 3 0.327510917 8.53E-04 "CDC42, ITGA6,
ITGB4" 38 16 13528 66.75 0.413231449 0.05751577 1.258862253
GOTERM_BP_FAT GO:0030031~cell projection assembly 4 0.436681223 0.001488693 "CDC42, ITGA6,
RAC3, ITGB4" 38 83 13528 17.15662651 0.605890419 0.08890912 2.188316562
GOTERM_BP_FAT GO:0030030~cell projection organization 4 0.436681223 0.078680759 "CDC42,
ITGA6, RAC3, ITGB4" 38 368 13528 3.869565217 1 0.768544874 70.39066531

Annotation Cluster 6 Enrichment Score: 2.309063135684755
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment
Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0030036~actin cytoskeleton organization 6 0.655021834 3.51E-04 "ACTG1,
ALDOA, CDC42, RAC3, CAPZA2, CAPZA1" 38 226 13528 9.451327434 0.196962535 0.042922379
0.519889846
GOTERM_BP_FAT GO:0030029~actin filament-based process 6 0.655021834 4.71E-04 "ACTG1,
ALDOA, CDC42, RAC3, CAPZA2, CAPZA1" 38 241 13528 8.863070539 0.25508262 0.047895354
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GOTERM_CC_FAT GO:0015629~actin cytoskeleton 6 0.655021834 0.001130915 "ACTG1, ALDOA,
MYO1C, RAC3, CAPZA2, CAPZA1" 39 269 12782 7.310265942 0.18612048 0.040351864
1.386658198
GOTERM_BP_FAT GO:0033043~regulation of organelle organization 5 0.545851528 0.002809085
"CDC42, CAPZA2, NPM1, CAPZA1, CTNNB1" 38 217 13528 8.202764977 0.827636308 0.118016595
4.091781158
GOTERM_BP_FAT GO:0031333~negative regulation of protein complex assembly 3 0.327510917
0.003864537 "CDC42, CAPZA2, CAPZA1" 38 34 13528 31.41176471 0.911079701 0.148992487
5.588404976
GOTERM_BP_FAT GO:0051129~negative regulation of cellular component organization 4 0.436681223
0.006777739 "CDC42, CAPZA2, NPM1, CAPZA1" 38 142 13528 10.02816901 0.985743006
0.210329346 9.607049147
GOTERM_MF_FAT GO:0008092~cytoskeletal protein binding 6 0.655021834 0.008344925 "ALDOA,
MYO1C, FYN, CAPZA2, CAPZA1, SDC4" 34 504 12983 4.545868347 0.657893149 0.657893149
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"CDC42, CAPZA2, CAPZA1" 38 90 13528 11.86666667 0.999999872 0.483764849 31.41407383
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CAPZA2, CAPZA1" 34 326 12983 4.685312162 0.998422081 0.960276975 44.30905395
GOTERM_BP_FAT GO:0044087~regulation of cellular component biogenesis 3 0.327510917 0.057383128
"CDC42, CAPZA2, CAPZA1" 38 142 13528 7.521126761 1 0.673469005 58.42491151

Annotation Cluster 7 Enrichment Score: 2.278260490741627
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment
Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007010~cytoskeleton organization 8 0.873362445 1.53E-04 "ACTG1,
ALDOA, CDC42, RAC3, CAPZA2, NPM1, CAPZA1, CTNNB1" 38 436 13528 6.532110092
0.091355036 0.02366568 0.22739055
GOTERM_CC_FAT GO:0015629~actin cytoskeleton 6 0.655021834 0.001130915 "ACTG1, ALDOA,

					MYO1C, RAC3, CAPZA2, CAPZA1"	39	269	12782	7.310265942	0.18612048	0.040351864	1.386658198
GOTERM_CC_FAT	GO:0005856~cytoskeleton	11	1.200873362	0.005839232	"ACTG1, ALDOA, MYO1C, PKP2, RAC3, CAPZA2, NPM1, CAPZA1, KRT13, CTNNB1, PNN"	39	1381	12782	2.610557196	0.655566827	0.064445567	6.971896884
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	8	0.873362445	0.020506066	"MYO1C, RAC3, CAPZA2, NPM1, CAPZA1, KRT13, CTNNB1, PNN"	39	952	12782	2.754147813	0.97696869	0.164367787	22.56100381
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	14	1.528384279	0.032111202	"ALDOA, MYO1C, CAPZA2, CAPZA1, KRT13, PNN, CTNNB1, ACTG1, RPS18, HIST1H4A, PKP2, RAC3, NPM1, H3F3B"	39	2596	12782	1.767492395	0.997368312	0.236625014	33.15279671
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	14	1.528384279	0.032111202	"ALDOA, MYO1C, CAPZA2, CAPZA1, KRT13, PNN, CTNNB1, ACTG1, RPS18, HIST1H4A, PKP2, RAC3, NPM1, H3F3B"	39	2596	12782	1.767492395	0.997368312	0.236625014	33.15279671

Annotation Cluster 8	Enrichment Score: 2.1090130207611875

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030016~myofibril	4	0.436681223	0.004310635	"ALDOA, SDC4, CTNNB1, ENO1"	39	111	12782	11.81057981	0.544441629	0.058686784	5.191311091
GOTERM_CC_FAT	GO:0044449~contractile fiber part	4	0.436681223	0.004531563	"ALDOA, SDC4, CTNNB1, ENO1"	39	113	12782	11.601543	0.562473867	0.0573349	5.450580271
GOTERM_CC_FAT	GO:0043292~contractile fiber	4	0.436681223	0.005483566	"ALDOA, SDC4, CTNNB1, ENO1"	39	121	12782	10.83449883	0.632398369	0.064540129	6.560365074
GOTERM_CC_FAT	GO:0030017~sarcomere	3	0.327510917	0.034205465	"ALDOA, CTNNB1, ENO1"	39	98	12782	10.03296703	0.998225715	0.240736855	34.9159512

Annotation Cluster 9	Enrichment Score: 2.0730433909711294

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	8	0.873362445	1.53E-04	"ACTG1, ALDOA, CDC42, RAC3, CAPZA2, NPM1, CAPZA1, CTNNB1"	38	436	13528	6.532110092	0.091355036	0.02366568	0.22739055
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	8	0.873362445	0.002759053	"HIST1H4A, CAPZA2, NPM1, CAPZA1, LIPG, H3F3B, LAMC1, CTNNB1"	38	710	13528	4.011267606	0.822145825	0.124386154	4.020289927
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	5	0.545851528	0.002809085	"CDC42, CAPZA2, NPM1, CAPZA1, CTNNB1"	38	217	13528	8.202764977	0.827636308	0.118016595	4.091781158
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	4	0.436681223	0.006015836	"CAPZA2, NPM1, CAPZA1, CTNNB1"	38	136	13528	10.47058824	0.976976799	0.198955199	8.571731276
GOTERM_BP_FAT	GO:0051129~negative regulation of cellular component organization	4	0.436681223	0.006777739	"CDC42, CAPZA2, NPM1, CAPZA1"	38	142	13528	10.02816901	0.985743006	0.210329346	9.607049147
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	7	0.76419214	0.008713534	"HIST1H4A, CAPZA2, NPM1, CAPZA1, H3F3B, LAMC1, CTNNB1"	38	665	13528	3.747368421	0.995788029	0.250152558	12.18854827
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	8	0.873362445	0.020506066	"MYO1C, RAC3, CAPZA2, NPM1, CAPZA1, KRT13, CTNNB1, PNN"	39	952	12782	2.754147813	0.97696869	0.164367787	22.56100381
GOTERM_BP_FAT	GO:0010639~negative regulation of organelle organization	3	0.327510917	0.021073646	"CAPZA2, NPM1, CAPZA1"	38	82	13528	13.02439024	0.999998345	0.48602957	27.11776178

GOTERM_BP_FAT GO:0032535~regulation of cellular component size 4 0.436681223 0.03744848 "CAPZA2, NPM1, CAPZA1, ENO1" 38 271 13528 5.254612546 1 0.586670955 43.26940861
GOTERM_BP_FAT GO:0006461~protein complex assembly 5 0.545851528 0.04797944 "CAPZA2, NPM1, CAPZA1, LAMC1, CTNNB1" 38 505 13528 3.524752475 1 0.6289073 51.82066535
GOTERM_BP_FAT GO:0070271~protein complex biogenesis 5 0.545851528 0.04797944 "CAPZA2, NPM1, CAPZA1, LAMC1, CTNNB1" 38 505 13528 3.524752475 1 0.6289073 51.82066535

Annotation Cluster 10 Enrichment Score: 1.677464035961782
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0044421~extracellular region part 10 1.091703057 0.001636367 "ALDOA, COL17A1, LGALS3BP, LGALS3, HTRA1, RAB35, LIPG, CD109, LAMC1, FGFBP1" 39 960 12782 3.413995726 0.257745191 0.04168657 2.000680301
GOTERM_CC_FAT GO:0005578~proteinaceous extracellular matrix 4 0.436681223 0.06895066 "COL17A1, LGALS3BP, LGALS3, LAMC1" 39 320 12782 4.096794872 0.999997746 0.382192764 58.58891996
GOTERM_CC_FAT GO:0031012~extracellular matrix 4 0.436681223 0.082260021 "COL17A1, LGALS3BP, LGALS3, LAMC1" 39 345 12782 3.799925678 0.999999836 0.405936936 65.3300938

Annotation Cluster 11 Enrichment Score: 1.6058444793684967
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0044421~extracellular region part 10 1.091703057 0.001636367 "ALDOA, COL17A1, LGALS3BP, LGALS3, HTRA1, RAB35, LIPG, CD109, LAMC1, FGFBP1" 39 960 12782 3.413995726 0.257745191 0.04168657 2.000680301
GOTERM_CC_FAT GO:0005576~extracellular region 11 1.200873362 0.064488427 "ALDOA, DCD, COL17A1, LGALS3BP, LGALS3, HTRA1, RAB35, LIPG, CD109, LAMC1, FGFBP1" 39 2010 12782 1.793621635 0.999994618 0.372889386 56.07208302
GOTERM_CC_FAT GO:0005615~extracellular space 5 0.545851528 0.144246117 "LGALS3BP, HTRA1, LIPG, CD109, FGFBP1" 39 685 12782 2.392288976 1 0.54502661 85.37247153

Annotation Cluster 12 Enrichment Score: 1.401737255962358
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0030027~lamellipodium 3 0.327510917 0.018304679 "RAC3, CTNND1, CTNNB1" 39 70 12782 14.04615385 0.965345211 0.154744193 20.38570478
GOTERM_CC_FAT GO:0042995~cell projection 6 0.655021834 0.053887008 "CDC42, MYO1C, RAC3, RAB35, CTNND1, CTNNB1" 39 697 12782 2.82132215 0.999958157 0.342996327 49.51857042
GOTERM_CC_FAT GO:0031252~cell leading edge 3 0.327510917 0.063203635 "RAC3, CTNND1, CTNNB1" 39 138 12782 7.124860647 0.999993091 0.378305487 55.32178889

Annotation Cluster 13 Enrichment Score: 1.228395339218993
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006928~cell motion 7 0.76419214 0.00167234 "ACTG1, CD9, ITGA6, FYN, CAPZA2, CAPZA1, LAMC1" 38 475 13528 5.246315789 0.648690392 0.090716954 2.455153445
GOTERM_BP_FAT GO:0016477~cell migration 3 0.327510917 0.174040255 "ITGA6, FYN, LAMC1" 38 276 13528 3.869565217 1 0.941887566 94.15620658
GOTERM_BP_FAT GO:0051674~localization of cell 3 0.327510917 0.204749191 "ITGA6, FYN, LAMC1" 38 307 13528 3.478827362 1 0.958493819 96.67100607
GOTERM_BP_FAT GO:0048870~cell motility 3 0.327510917 0.204749191 "ITGA6, FYN, LAMC1" 38 307 13528 3.478827362 1 0.958493819 96.67100607

Annotation Cluster 14 Enrichment Score: 1.223785095474896

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Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	7	0.76419214	0.008713534
"HIST1H4A, CAPZA2, NPM1, CAPZA1, H3F3B, LAMC1, CTNNB1"	38	665	13528	3.747368421
0.995788029	0.250152558	12.18854827
GOTERM_BP_FAT	GO:0006334~nucleosome assembly	3	0.327510917	0.022045428	"HIST1H4A, NPM1,
H3F3B"	38	84	13528	12.71428571	0.99999911	0.48493087	28.18493298
GOTERM_BP_FAT	GO:0031497~chromatin assembly	3	0.327510917	0.023537499	"HIST1H4A, NPM1,
H3F3B"	38	87	13528	12.27586207	0.999999657	0.476518483	29.79513536
GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	3	0.327510917	0.025589998
"HIST1H4A, NPM1, H3F3B"	38	91	13528	11.73626374	0.999999908	0.476949857	31.95516894
GOTERM_BP_FAT	GO:0034728~nucleosome organization	3	0.327510917	0.026642795	"HIST1H4A,
NPM1, H3F3B"	38	93	13528	11.48387097	0.999999953	0.4775041	33.03891656
GOTERM_BP_FAT	GO:0006323~DNA packaging	3	0.327510917	0.040575609	"HIST1H4A, NPM1,
H3F3B"	38	117	13528	9.128205128	1	0.590455819	45.94592934
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	3	0.327510917	0.047037883
"HIST1H4A, NPM1, H3F3B"	38	127	13528	8.409448819	1	0.633498496	51.10811478
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	3	0.327510917	0.215804386
"HIST1H4A, NPM1, H3F3B"	38	318	13528	3.358490566	1	0.963225309	97.2959251
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	3	0.327510917
0.255402121	"HIST1H4A, NPM1, H3F3B"	38	357	13528	2.991596639	1	0.976753936	98.74739041
GOTERM_BP_FAT	GO:0006325~chromatin organization	3	0.327510917	0.276850243	"HIST1H4A,
NPM1, H3F3B"	38	378	13528	2.825396825	1	0.976520044	99.18848898
GOTERM_BP_FAT	GO:0051276~chromosome organization	3	0.327510917	0.384767364	"HIST1H4A,
NPM1, H3F3B"	38	485	13528	2.202061856	1	0.993654098	99.92640177

Annotation Cluster 15	Enrichment Score: 1.219337804436222
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	6	0.655021834	3.15E-04	"COL17A1,
MYO1C, ITGA6, ITGB4, SDC4, CTNNB1"39	203	12782	9.687002653	0.055762015	0.014241872
0.388279809
GOTERM_CC_FAT	GO:0044459~plasma membrane part	14	1.528384279	0.008662785	"MYO1C, ITGB4,
SDC4, CD151, EPHA2, PNN, CTNNB1, CD9, CDC42, COL17A1, ITGA6, PKP2, RAB35, DSC3"	39	2203
12782	2.082800843	0.794743634	0.088940249	10.18033999
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	7	0.76419214	0.136450796	"CD9,
COL17A1, ITGA6, ITGB4, SDC4, CD151, EPHA2"	39	1188	12782	1.931149098	1	0.544017127
83.64052788
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	7	0.76419214	0.147360477	"CD9,
COL17A1, ITGA6, ITGB4, SDC4, CD151, EPHA2"	39	1215	12782	1.888234673	1	0.543499866
86.01600591
GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	14	1.528384279	0.895358303	"GLG1, CD9,
COL17A1, LY6D, MYO1C, ITGA6, PKP2, ITGB4, DSC3, CD109, CD151, SDC4, NT5E, EPHA2"	39	5485
12782	0.836537877	1	0.999682538	100
GOTERM_CC_FAT	GO:0016021~integral to membrane	11	1.200873362	0.982569733	"GLG1, CD9,
COL17A1, MYO1C, ITGA6, PKP2, ITGB4, DSC3, SDC4, CD151, EPHA2"	39	5297	12782	0.680607794
1	0.999999301	100

Annotation Cluster 16	Enrichment Score: 1.1351396044413542
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_CC_FAT	GO:0031253~cell projection membrane	3	0.327510917	0.015912627	"MYO1C, RAB35,
CTNNB1"	39	65	12782	15.12662722	0.946033286	0.142429589	17.95844345
GOTERM_CC_FAT	GO:0042995~cell projection	6	0.655021834	0.053887008	"CDC42, MYO1C, RAC3,
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RAB35, CTNND1, CTNNB1"	39	697	12782	2.82132215	0.999958157	0.342996327	49.51857042
GOTERM_CC_FAT	GO:0044463~cell projection part	3	0.327510917	0.153137715	"MYO1C, RAB35, CTNNB1"	39	234	12782	4.201840894	1	0.548912006	87.14137014
GOTERM_BP_FAT	GO:0008104~protein localization	5	0.545851528	0.21934789	"CDC42, MYO1C, RAB35, NPM1, CTNNB1"	38	882	13528	2.01814059	1	0.962853828	97.47182425

Annotation Cluster 17	Enrichment Score: 1.114797321541286
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	4	0.436681223	0.039203969	"PKP2, DSC3, CTNND1, CTNNB1"	38	276	13528	5.15942029	1	0.590453163	44.78677783
GOTERM_CC_FAT	GO:0005624~membrane fraction	6	0.655021834	0.089556808	"LY6D, DSC3, CTNND1, CD151, NT5E, CTNNB1"	39	809	12782	2.430731197	0.999999962	0.423532521	68.58249857
GOTERM_CC_FAT	GO:0000267~cell fraction	7	0.76419214	0.098121578	"ACTG1, LY6D, DSC3, CTNND1, CD151, NT5E, CTNNB1"	39	1083	12782	2.11837962	0.999999993	0.444218319	72.04130779
GOTERM_CC_FAT	GO:0005626~insoluble fraction	6	0.655021834	0.100836449	"LY6D, DSC3, CTNND1, CD151, NT5E, CTNNB1"	39	839	12782	2.343815898	0.999999996	0.443566328	73.06234486

Annotation Cluster 18	Enrichment Score: 1.0554719674567417
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	5	0.545851528	0.002809085	"CDC42, CAPZA2, NPM1, CAPZA1, CTNNB1"38	217	13528	8.202764977	0.827636308	0.118016595	4.091781158
GOTERM_BP_FAT	GO:0008104~protein localization	5	0.545851528	0.21934789	"CDC42, MYO1C, RAB35, NPM1, CTNNB1"	38	882	13528	2.01814059	1	0.962853828	97.47182425
GOTERM_BP_FAT	GO:0034613~cellular protein localization	3	0.327510917	0.310515793	"CDC42, NPM1, CTNNB1"	38	411	13528	2.598540146	1	0.985376574	99.60023465
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	3	0.327510917	0.31356684	"CDC42, NPM1, CTNNB1"	38	414	13528	2.579710145	1	0.984992104	99.62571736

Annotation Cluster 19	Enrichment Score: 0.660020459928678
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0042995~cell projection	6	0.655021834	0.053887008	"CDC42, MYO1C, RAC3, RAB35, CTNND1, CTNNB1"	39	697	12782	2.82132215	0.999958157	0.342996327	49.51857042
GOTERM_MF_FAT	GO:0003924~GTPase activity	3	0.327510917	0.100009777	"CDC42, RAC3, RAB35"	34	211	12983	5.429188737	0.999998612	0.894381608	70.58639153
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	3	0.327510917	0.20274672	"CDC42, RAC3, RAB35"	38	305	13528	3.501639344	1	0.959985225	96.54431619
GOTERM_MF_FAT	GO:0005525~GTP binding	3	0.327510917	0.243858227	"CDC42, RAC3, RAB35"	34	372	12983	3.079459203	1	0.981229831	96.10794384
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	3	0.327510917	0.253343392	"CDC42, RAC3, RAB35"	34	382	12983	2.998845088	1	0.97623446	96.63867025
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	3	0.327510917	0.253343392	"CDC42, RAC3, RAB35"	34	382	12983	2.998845088	1	0.97623446	96.63867025
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	6	0.655021834	0.256773945	"CDC42, HIST1H4A, RAC3, FYN, RAB35, CTNNB1"	38	1256	13528	1.700636943	1	0.975508715	98.78123089
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	7	0.76419214	0.320729425	"ACTG1, CDC42, MYO1C, RAC3, FYN, RAB35, EPHA2"	34	1836	12983	1.455866333	1	0.9888932	98.87938249
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	7	0.76419214	0.320729425	"ACTG1, CDC42, MYO1C, RAC3, FYN, RAB35, EPHA2"	34	1836	12983	1.455866333	1	0.9888932
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98.87938249
GOTERM_BP_FAT GO:0030182~neuron differentiation 3 0.327510917 0.337878169 "CDC42, RAC3, EPHA2" 38 438 13528 2.438356164 1 0.988238801 99.78091317
GOTERM_MF_FAT GO:0017076~purine nucleotide binding 7 0.76419214 0.359873034 "ACTG1, CDC42, MYO1C, RAC3, FYN, RAB35, EPHA2" 34 1918 12983 1.393623873 1 0.991419644 99.43752363

Annotation Cluster 20 Enrichment Score: 0.5399886533019197
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0033674~positive regulation of kinase activity 3 0.327510917 0.131219235 "CDC42, NPM1, SDC4" 38 231 13528 4.623376623 1 0.901091526 87.62030068
GOTERM_BP_FAT GO:0051347~positive regulation of transferase activity 3 0.327510917 0.139570517 "CDC42, NPM1, SDC4" 38 240 13528 4.45 1 0.910097749 89.27472766
GOTERM_BP_FAT GO:0043549~regulation of kinase activity 3 0.327510917 0.255402121 "CDC42, NPM1, SDC4" 38 357 13528 2.991596639 1 0.976753936 98.74739041
GOTERM_BP_FAT GO:0051338~regulation of transferase activity 3 0.327510917 0.270719874 "CDC42, NPM1, SDC4" 38 372 13528 2.870967742 1 0.97583491 99.0800952
GOTERM_BP_FAT GO:0042325~regulation of phosphorylation 3 0.327510917 0.365949853 "CDC42, NPM1, SDC4" 38 466 13528 2.291845494 1 0.991985955 99.88486929
GOTERM_BP_FAT GO:0051174~regulation of phosphorus metabolic process 3 0.327510917 0.384767364 "CDC42, NPM1, SDC4" 38 485 13528 2.202061856 1 0.993654098 99.92640177
GOTERM_BP_FAT GO:0019220~regulation of phosphate metabolic process 3 0.327510917 0.384767364 "CDC42, NPM1, SDC4" 38 485 13528 2.202061856 1 0.993654098 99.92640177
GOTERM_BP_FAT GO:0043085~positive regulation of catalytic activity 3 0.327510917 0.418832906 "CDC42, NPM1, SDC4" 38 520 13528 2.053846154 1 0.995411017 99.96841653
GOTERM_BP_FAT GO:0044093~positive regulation of molecular function 3 0.327510917 0.480515569 "CDC42, NPM1, SDC4" 38 586 13528 1.822525597 1 0.998331262 99.99403299

Annotation Cluster 21 Enrichment Score: 0.35462018340034873
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0008104~protein localization 5 0.545851528 0.21934789 "CDC42, MYO1C, RAB35, NPM1, CTNNB1" 38 882 13528 2.01814059 1 0.962853828 97.47182425
GOTERM_BP_FAT GO:0015031~protein transport 3 0.327510917 0.624804891 "MYO1C, RAB35, NPM1" 38 762 13528 1.401574803 1 0.999893213 99.99995247
GOTERM_BP_FAT GO:0045184~establishment of protein localization 3 0.327510917 0.629885439 "MYO1C, RAB35, NPM1" 38 769 13528 1.388816645 1 0.999892229 99.99996118

Annotation Cluster 22 Enrichment Score: 0.3403549878499382
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005829~cytosol 7 0.76419214 0.198179322 "ACTG1, CDC42, RPS18, FYN, NPM1, CTNNB1, ENO1" 39 1330 12782 1.724966262 1 0.633940656 93.44921801
GOTERM_MF_FAT GO:0003712~transcription cofactor activity 3 0.327510917 0.235340081 "NPM1, CTNNB1, ENO1" 34 363 12983 3.155809431 1 0.986338662 95.56719058
GOTERM_BP_FAT GO:0051253~negative regulation of RNA metabolic process 3 0.327510917 0.260505702 "NPM1, CTNNB1, ENO1" 38 362 13528 2.950276243 1 0.973411278 98.86902216
GOTERM_MF_FAT GO:0008134~transcription factor binding 3 0.327510917 0.376843293 "NPM1, CTNNB1, ENO1" 34 513 12983 2.233058136 1 0.99050329 99.58829127
GOTERM_BP_FAT "GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process" 3 0.327510917 0.411121091 "NPM1, CTNNB1, ENO1" 38 512 13528 2.0859375 1 0.995597402 99.96158633
GOTERM_BP_FAT GO:0051172~negative regulation of nitrogen compound metabolic process 3

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0.327510917	0.417871483	"NPM1, CTNNB1, ENO1"	38	519	13528	2.057803468	1	0.995722021
99.96763159
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	3	0.327510917
0.603970694	"NPM1, CTNNB1, ENO1"	38	734	13528	1.455040872	1	0.999844904	99.99989394
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	3	0.327510917	0.910369989	"NPM1,
CTNNB1, ENO1"	34	1512	12983	0.757644725	1	0.999999196	100
GOTERM_BP_FAT	GO:0045449~regulation of transcription	5	0.545851528	0.943782365	"NPM1,
CTNND1, CTNNB1, ENO1, PNN"	38	2601	13528	0.684352172	1	1	100
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	3	0.327510917	0.967385811
"NPM1, CTNNB1, ENO1"	38	1813	13528	0.589078875	1	1	100

Annotation Cluster 23	Enrichment Score: 0.29940216454953406
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_MF_FAT	GO:0000166~nucleotide binding	9	0.982532751	0.199383113	"ACTG1, CDC42,
MYO1C, RAC3, FYN, RAB35, NT5E, RBMX, EPHA2"	34	2245	12983	1.530813573	1	0.982858355
92.44143109
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	7	0.76419214	0.320729425	"ACTG1, CDC42,
MYO1C, RAC3, FYN, RAB35, EPHA2"	34	1836	12983	1.455866333	1	0.9888932	98.87938249
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	7	0.76419214	0.320729425	"ACTG1,
CDC42, MYO1C, RAC3, FYN, RAB35, EPHA2"	34	1836	12983	1.455866333	1	0.9888932
98.87938249
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	7	0.76419214	0.359873034	"ACTG1,
CDC42, MYO1C, RAC3, FYN, RAB35, EPHA2"	34	1918	12983	1.393623873	1	0.991419644
99.43752363
GOTERM_MF_FAT	GO:0005524~ATP binding	4	0.436681223	0.74136561	"ACTG1, MYO1C, FYN,
EPHA2"	34	1477	12983	1.034131188	1	0.999979979	99.99998489
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	4	0.436681223	0.74997068	"ACTG1,
MYO1C, FYN, EPHA2"	34	1497	12983	1.02031514	1	0.999970676	99.9999898
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	4	0.436681223	0.782238425	"ACTG1,
MYO1C, FYN, EPHA2"	34	1577	12983	0.968555336	1	0.999980398	99.99999795
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	4	0.436681223	0.791261115	"ACTG1,
MYO1C, FYN, EPHA2"	34	1601	12983	0.95403608	1	0.999973922	99.99999875
GOTERM_MF_FAT	GO:0001882~nucleoside binding	4	0.436681223	0.795297358	"ACTG1, MYO1C,
FYN, EPHA2"	34	1612	12983	0.947525909	1	0.999960989	99.999999

Annotation Cluster 24	Enrichment Score: 0.1669789531436635
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_CC_FAT	GO:0005654~nucleoplasm	5	0.545851528	0.265561815	"MYO1C, HIST1H4A,
NPM1, CTNNB1, PNN"	39	882	12782	1.857956858	1	0.737493894	97.78252049
GOTERM_CC_FAT	GO:0044451~nucleoplasm part	3	0.327510917	0.495925197	"NPM1, CTNNB1,
PNN"	39	555	12782	1.771586972	1	0.94494551	99.97868302
GOTERM_CC_FAT	GO:0005730~nucleolus	3	0.327510917	0.622208805	"MYO1C, NPM1, PNN"	39	698
12782	1.408640071	1	0.978748593	99.99939299
GOTERM_CC_FAT	GO:0031981~nuclear lumen	5	0.545851528	0.639317293	"MYO1C, HIST1H4A,
NPM1, CTNNB1, PNN"	39	1450	12782	1.130150309	1	0.980723043	99.99965736
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	5	0.545851528	0.794699441	"MYO1C,
HIST1H4A, NPM1, CTNNB1, PNN"	39	1779	12782	0.921145559	1	0.997529342	99.99999967
GOTERM_CC_FAT	GO:0043233~organelle lumen	5	0.545851528	0.809887361	"MYO1C, HIST1H4A,
NPM1, CTNNB1, PNN"	39	1820	12782	0.900394477	1	0.997900863	99.99999987
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	5	0.545851528	0.822496456	"MYO1C,
HIST1H4A, NPM1, CTNNB1, PNN"	39	1856	12782	0.882929929	1	0.998150248	99.99999995
GOTERM_MF_FAT	GO:0003677~DNA binding	5	0.545851528	0.868080745	"HIST1H4A, H3F3B,
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CTNNB1, ENO1, PNN" 34 2331 12983 0.819075378 1 0.999995654 99.99999999
GOTERM_BP_FAT GO:0006350~transcription 4 0.436681223 0.941418036 "CTNND1, CTNNB1, ENO1,
PNN" 38 2101 13528 0.677772489 1 1 100
GOTERM_BP_FAT GO:0045449~regulation of transcription 5 0.545851528 0.943782365 "NPM1,
CTNND1, CTNNB1, ENO1, PNN" 38 2601 13528 0.684352172 1 1 100

Annotation Cluster 25 Enrichment Score: 0.11398627665190735
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0005509~calcium ion binding 4 0.436681223 0.416758421 "S100A16, ITGA6,
DSC3, S100A14" 34 919 12983 1.662036741 1 0.992769205 99.80913743
GOTERM_MF_FAT GO:0046872~metal ion binding 8 0.873362445 0.938583224 "DCD, S100A16,
ITGA6, FYN, DSC3, NT5E, S100A14, ENO1" 34 4140 12983 0.73788008 1 0.999999819 100
GOTERM_MF_FAT GO:0043169~cation binding 8 0.873362445 0.942805235 "DCD, S100A16, ITGA6,
FYN, DSC3, NT5E, S100A14, ENO1" 34 4179 12983 0.730993905 1 0.999999764 100
GOTERM_MF_FAT GO:0043167~ion binding 8 0.873362445 0.949020813 "DCD, S100A16, ITGA6,
FYN, DSC3, NT5E, S100A14, ENO1" 34 4241 12983 0.720307364 1 0.999999759 100

Annotation Cluster 1	Enrichment Score: 52.93834053256461
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	199	40.44715447	3.06E-64	"XRCC5, XRCC6, SRP68, SYNCRIP, INTS3, SART3, XRCC1, U2AF1, PQBP1, RPP30, MRPL39, DHX30, SUPT5H, LUC7L3, EMG1, PTBP1, LIG3, NOP2, RFC2, MYBBP1A, MRPL43, MRE11A, HNRNPA3, VRK1, NAT10, NUP54, PRPF40A, DHX9, MKI67, TP53BP1, DLAT, DDX5, RPS6, RPF2, HNRNPA1, FXR1, CCT5, POP1, SUPT16H, PCNA, PARP1, COPS2, UTP18, TCOF1, UTP15, RRP1B, QKI, MRPL1, SYMPK, PRPF31, RBBP4, EXOSC9, EXOSC6, EXOSC7, SF1, EXOSC2, ADNP, NDUFA10, RBBP7, EIF4A3, NOL11, RBM39, PMPCB, POLR2A, PRPF19, SRRT, SF3B1, SUMO1, MRPL13, NUMA1, TOE1, MORC3, GATAD2A, GATAD2B, ACTL6A, TCEA1, RBM27, RBM28, BUB3, RBM25, TRIM28, KIAA1967, POLR3A, ILF3, SF3A1, SF3A3, ILF2, UBTF, MRPL28, SFPQ, NOP58, NOP56, RBM14, PES1, TEX10, NCBP1, RNMT, SNRPD3, SRP19, CTNNBL1, SMNDC1, PNN, CBX5, EBNA1BP2, CSNK2A1, SRRM2, TARDBP, DDX24, SRRM1, ACIN1, GNL2, GNL3, PABPN1, MTA2, HNRNPA2B1, RRP8, HNRNPR, RSL1D1, MRPS18A, SMARCA5, SNRPB, LRPPRC, XRN2, HMGB1, HMGB2, MRPS15, DAZAP1, HNRNPL, HNRNPM, DDX46, HNRNPK, HIST1H4A, ZNF326, NPM1, RPL3, DNAJA3, DDX42, XPOT, CSTF2, TSR1, MRPS22, SSB, HEATR1, RNPS1, PSMC5, HDAC2, HDAC1, SMARCC1, SMARCC2, GTF2F2, PSMC1, HSPD1, HNRNPH1, DAP3, FOXK1, SKIV2L2, TIMM50, MKI67IP, ZNF207, FUBP1, MCM7, DKC1, GRWD1, TPR, PSMD8, FTSJ3, TBL1XR1, MCM2, CDC5L, MCM3, PRPF4, NCL, MCM4, MCM5, CDK2, MCM6, C1QBP, CPSF6, MATR3, NUP98, HCFC1, PRKDC, WBP11, EXOSC10, RPA1, TFAM, PRPF8, SAFB, NUDT21, GTF3C5, APEX1, CHD4, HSPA9, NUP153, NDUFA9, FBL, SMC3, DIS3, SON"	415	1779	12782	3.445306352	1.19E-61	5.93E-62	4.25E-61
GOTERM_CC_FAT	GO:0031981~nuclear lumen	179	36.38211382	6.37E-63	"XRCC5, NCBP1, RNMT, SNRPD3, XRCC6, SRP68, SYNCRIP, INTS3, SRP19, SART3, XRCC1, CBX5, SMNDC1, PNN, CTNNBL1, EBNA1BP2, CSNK2A1, SRRM2, TARDBP, DDX24, U2AF1, PQBP1, RPP30, SRRM1, ACIN1, GNL2, SUPT5H, LUC7L3, GNL3, PABPN1, EMG1, MTA2, HNRNPA2B1, PTBP1, LIG3, RRP8, HNRNPR, RSL1D1, NOP2, RFC2, SNRPB, SMARCA5, MYBBP1A, LRPPRC, XRN2, HMGB1, HMGB2, MRE11A, DAZAP1, HNRNPA3, HNRNPL, HNRNPM, VRK1, HNRNPK, DDX46, HIST1H4A, ZNF326, NPM1, RPL3, NAT10, NUP54, DDX42, PRPF40A, XPOT, DHX9, CSTF2, TSR1, MKI67, TP53BP1, SSB, HEATR1, RNPS1, DDX5, RPS6, RPF2, HNRNPA1, FXR1, CCT5, PSMC5, HDAC2, HDAC1, SMARCC1, SMARCC2, GTF2F2, PSMC1, PCNA, SUPT16H, POP1, PARP1, HNRNPH1, COPS2, FOXK1, UTP18, TCOF1, UTP15, SKIV2L2, MKI67IP, TIMM50, ZNF207, FUBP1, MCM7, DKC1, RRP1B, GRWD1, QKI, TPR, FTSJ3, PSMD8, PRPF31, SYMPK, TBL1XR1, RBBP4, EXOSC9, EXOSC6, EXOSC7, SF1, EXOSC2, ADNP, CDC5L, MCM2, RBBP7, MCM3, MCM4, NCL, PRPF4, CDK2, MCM5, MCM6, EIF4A3, NOL11, CPSF6, RBM39, MATR3, NUP98, PRKDC, HCFC1, WBP11, POLR2A, PRPF19, EXOSC10, RPA1, SF3B1, SRRT, NUMA1, SUMO1, TOE1, MORC3, SAFB, PRPF8, NUDT21, GATAD2A, GATAD2B, GTF3C5, ACTL6A, TCEA1, RBM27, APEX1, RBM28, CHD4, BUB3, RBM25, NUP153, TRIM28, POLR3A, ILF3, SF3A1, SMC3, FBL, SF3A3, DIS3, SON, UBTF, ILF2, SFPQ, NOP58, NOP56, PES1, RBM14, TEX10"	415	1450	12782	3.802206897	2.47E-60	8.24E-61	8.85E-60
GOTERM_CC_FAT	GO:0043233~organelle lumen	199	40.44715447	1.61E-62	"XRCC5, XRCC6, SRP68, SYNCRIP, INTS3, SART3, XRCC1, U2AF1, PQBP1, RPP30, MRPL39, DHX30, SUPT5H, LUC7L3, EMG1, PTBP1, LIG3, NOP2, RFC2, MYBBP1A, MRPL43, MRE11A, HNRNPA3, VRK1, NAT10, NUP54, PRPF40A, DHX9, MKI67, TP53BP1, DLAT, DDX5, RPS6, RPF2, HNRNPA1, FXR1, CCT5, POP1, SUPT16H, PCNA, PARP1, COPS2, UTP18, TCOF1, UTP15, RRP1B, QKI, MRPL1, SYMPK, PRPF31, RBBP4, EXOSC9, EXOSC6, EXOSC7, SF1, EXOSC2, ADNP, NDUFA10, RBBP7, EIF4A3, NOL11, RBM39, PMPCB, POLR2A, PRPF19, SRRT, SF3B1, SUMO1, MRPL13, NUMA1, TOE1, MORC3, GATAD2A, GATAD2B, ACTL6A, TCEA1, RBM27, RBM28, BUB3, RBM25, TRIM28, KIAA1967, POLR3A, ILF3, SF3A1, SF3A3, ILF2, UBTF, MRPL28, SFPQ, NOP58, NOP56, RBM14, PES1, TEX10, NCBP1, RNMT, SNRPD3, SRP19, CTNNBL1, SMNDC1, PNN, CBX5, EBNA1BP2, CSNK2A1, SRRM2, TARDBP, DDX24, SRRM1, ACIN1, GNL2, GNL3, PABPN1, MTA2, HNRNPA2B1, RRP8, HNRNPR, RSL1D1, MRPS18A, SMARCA5, SNRPB, LRPPRC, XRN2, HMGB1, HMGB2, MRPS15, DAZAP1, HNRNPL, HNRNPM, DDX46, HNRNPK, HIST1H4A, ZNF326, NPM1, RPL3, DNAJA3, DDX42, XPOT, CSTF2, TSR1, MRPS22, SSB, HEATR1, RNPS1, PSMC5, HDAC2, HDAC1, SMARCC1, SMARCC2, GTF2F2, PSMC1, HSPD1, HNRNPH1, DAP3, FOXK1, SKIV2L2, TIMM50, MKI67IP, ZNF207, FUBP1, MCM7, DKC1, GRWD1, TPR, PSMD8, FTSJ3, TBL1XR1, MCM2, CDC5L, MCM3, PRPF4, NCL, MCM4, MCM5, CDK2, MCM6, C1QBP, CPSF6, MATR3, NUP98, HCFC1, PRKDC, WBP11, EXOSC10, RPA1, TFAM, PRPF8, SAFB, NUDT21, GTF3C5,

APEX1, CHD4, HSPA9, NUP153, NDUFA9, FBL, SMC3, DIS3, SON" 415 1820 12782 3.367692308 6.25E-60 1.56E-60 2.24E-59
GOTERM_CC_FAT GO:0031974~membrane-enclosed lumen 200 40.6504065 7.99E-62 "XRCC5, XRCC6, SRP68, SYNCRIP, INTS3, SART3, XRCC1, U2AF1, PQBP1, RPP30, MRPL39, DHX30, SUPT5H, LUC7L3, EMG1, PTBP1, LIG3, NOP2, RFC2, MYBBP1A, MRPL43, MRE11A, HNRNPA3, VRK1, CACYBP, NAT10, NUP54, PRPF40A, DHX9, MKI67, TP53BP1, DLAT, DDX5, RPS6, RPF2, HNRNPA1, FXR1, CCT5, POP1, SUPT16H, PCNA, PARP1, COPS2, UTP18, TCOF1, UTP15, RRP1B, QKI, MRPL1, SYMPK, PRPF31, RBBP4, EXOSC9, EXOSC6, EXOSC7, SF1, EXOSC2, ADNP, NDUFA10, RBBP7, EIF4A3, NOL11, RBM39, PMPCB, POLR2A, PRPF19, SRRT, SF3B1, SUMO1, MRPL13, NUMA1, TOE1, MORC3, GATAD2A, GATAD2B, ACTL6A, TCEA1, RBM27, RBM28, BUB3, RBM25, TRIM28, KIAA1967, POLR3A, ILF3, SF3A1, SF3A3, ILF2, UBTF, MRPL28, SFPQ, NOP58, NOP56, RBM14, PES1, TEX10, NCBP1, RNMT, SNRPD3, SRP19, SMNDC1, CTNNBL1, PNN, CBX5, EBNA1BP2, CSNK2A1, SRRM2, TARDBP, DDX24, SRRM1, ACIN1, GNL2, GNL3, PABPN1, MTA2, HNRNPA2B1, RRP8, HNRNPR, RSL1D1, MRPS18A, SMARCA5, SNRPB, LRPPRC, XRN2, HMGB1, HMGB2, MRPS15, DAZAP1, HNRNPL, HNRNPM, DDX46, HNRNPK, HIST1H4A, ZNF326, NPM1, RPL3, DNAJA3, DDX42, XPOT, CSTF2, TSR1, MRPS22, SSB, HEATR1, RNPS1, PSMC5, HDAC2, HDAC1, SMARCC1, SMARCC2, GTF2F2, PSMC1, HSPD1, HNRNPH1, DAP3, FOXK1, SKIV2L2, TIMM50, MKI67IP, ZNF207, FUBP1, MCM7, DKC1, GRWD1, TPR, PSMD8, FTSJ3, TBL1XR1, MCM2, CDC5L, MCM3, PRPF4, NCL, MCM4, MCM5, CDK2, MCM6, C1QBP, CPSF6, MATR3, NUP98, HCFC1, PRKDC, WBP11, EXOSC10, RPA1, TFAM, PRPF8, SAFB, NUDT21, GTF3C5, APEX1, CHD4, HSPA9, NUP153, NDUFA9, SMC3, FBL, DIS3, SON" 415 1856 12782 3.318965517 3.10E-59 6.20E-60 1.11E-58
GOTERM_CC_FAT GO:0005730~nucleolus 99 20.12195122 4.28E-37 "SNRPD3, SRP68, SRP19, PNN, CTNNBL1, CBX5, EBNA1BP2, TARDBP, DDX24, PQBP1, RPP30, ACIN1, GNL2, GNL3, PABPN1, EMG1, MTA2, HNRNPA2B1, PTBP1, RRP8, RSL1D1, NOP2, SMARCA5, MYBBP1A, XRN2, HMGB1, HMGB2, MRE11A, DAZAP1, HNRNPA3, HNRNPM, VRK1, HNRNPK, NPM1, RPL3, NAT10, DHX9, CSTF2, TSR1, MKI67, HEATR1, SSB, RPS6, DDX5, HNRNPA1, RPF2, FXR1, CCT5, PSMC5, PSMC1, SMARCC2, POP1, HNRNPH1, PARP1, COPS2, FOXK1, UTP18, TCOF1, UTP15, SKIV2L2, MKI67IP, ZNF207, FUBP1, DKC1, RRP1B, GRWD1, QKI, PSMD8, FTSJ3, EXOSC9, EXOSC6, EXOSC7, ADNP, EXOSC2, SF1, CDC5L, MCM3, NCL, MCM4, NOL11, POLR2A, EXOSC10, TOE1, SAFB, GATAD2A, GATAD2B, RBM28, BUB3, ILF3, SF3A1, FBL, DIS3, ILF2, UBTF, NOP58, NOP56, RBM14, PES1, TEX10" 415 698 12782 4.368481375 1.66E-34 2.37E-35 5.94E-34
GOTERM_CC_FAT GO:0005654~nucleoplasm 106 21.54471545 2.18E-33 "XRCC5, NCBP1, RNMT, SNRPD3, XRCC6, SYNCRIP, INTS3, XRCC1, SART3, CBX5, PNN, SMNDC1, CSNK2A1, SRRM2, U2AF1, SRRM1, SUPT5H, LUC7L3, GNL3, PABPN1, MTA2, HNRNPA2B1, PTBP1, LIG3, HNRNPR, RFC2, SMARCA5, SNRPB, LRPPRC, HMGB1, HMGB2, MRE11A, HNRNPL, DDX46, HNRNPK, HIST1H4A, NPM1, NUP54, PRPF40A, DDX42, XPOT, TP53BP1, RNPS1, HNRNPA1, HDAC2, HDAC1, SMARCC1, GTF2F2, SMARCC2, SUPT16H, PCNA, PARP1, HNRNPH1, TIMM50, MKI67IP, MCM7, DKC1, TPR, TBL1XR1, SYMPK, PRPF31, RBBP4, MCM2, CDC5L, MCM3, RBBP7, MCM4, NCL, PRPF4, MCM5, CDK2, MCM6, EIF4A3, CPSF6, RBM39, NUP98, HCFC1, PRKDC, WBP11, POLR2A, RPA1, PRPF19, SRRT, SF3B1, NUMA1, SUMO1, TOE1, MORC3, PRPF8, NUDT21, GATAD2A, GTF3C5, TCEA1, ACTL6A, RBM27, APEX1, RBM25, CHD4, NUP153, TRIM28, POLR3A, SF3A3, SON, UBTF, RBM14, PES1" 415 882 12782 3.701587302 8.47E-31 9.41E-32 3.03E-30

Annotation Cluster 2 Enrichment Score: 49.958628133766084
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006396~RNA processing 123 25 2.71E-71 "RALY, NCBP1, RNMT, CHERP, PRPF4B, RPL14, U2AF2, SNRPD3, RBM3, SYNCRIP, INTS3, SART3, PNN, SMNDC1, NONO, DDX17, DDX23, DHX38, SRRM2, TARDBP, DNAJC8, U2AF1, SRRM1, RPP30, LUC7L3, CCAR1, PABPN1, SNRPA1, EMG1, EFTUD2, HNRNPA2B1, PTBP1, RRP8, HNRNPR, HNRNPU, RSL1D1, NOP2, SNRPB, SNRPA, XRN2, MRPL44, FIP1L1, PABPC4, PUS7, HNRNPA3, HNRNPL, HNRNPM, DDX46, HNRNPK, HNRNPD, HNRNPC, PABPC1, PRPF40A, DHX9, CSTF3, CSTF2, SSB, RNPS1, HEATR1, RPS6, DDX5, HNRNPA1, RBMX, HNRNPA0, HNRNPH3, GTF2F2, POP1, SMC1A, HNRNPH1, PUF60, UTP18, UTP15, SKIV2L2, YBX1, DKC1, RRP1B, TRMT6, QKI, FTSJ3, KHDRBS1, MRPL1, PRPF31, EXOSC9, EXOSC6, EXOSC7, EXOSC2, SF1, CDC5L, PRPF4, PRPF6, HNRPDL, EIF4A3, SNRNP200, CPSF7, CPSF6, RBM39, TRA2B, TRA2A, WBP11, SF3B4, SF3B2,

POLR2A, EXOSC10, PRPF19, SF3B1, SRRT, PRPF8, USP39, NUDT21, DHX15, SNRNP70, RBM28, RBM25, SF3A2, SF3A1, FBL, SF3A3, DIS3, SFPQ, NOP58, NOP56, PES1, RBM14" 430 547 13528 7.074291059 4.27E-68 4.27E-68 4.53E-68

GOTERM_BP_FAT GO:0006397~mRNA processing 86 17.4796748 2.77E-55 "RALY, NCBP1, PRPF4B, RNMT, SNRPD3, U2AF2, SYNCRIP, SKIV2L2, YBX1, SMNDC1, PNN, NONO, DHX38, DDX23, SRRM2, TARDBP, DNAJC8, U2AF1, SRRM1, QKI, LUC7L3, CCAR1, PABPN1, KHDRBS1, PRPF31, SNRPA1, EFTUD2, PTBP1, HNRNPA2B1, SF1, CDC5L, PRPF4, HNRNPR, HNRNPU, PRPF6, EIF4A3, SNRNP200, SNRPB, CPSF7, SNRPA, CPSF6, RBM39, XRN2, FIP1L1, TRA2B, TRA2A, WBP11, SF3B4, POLR2A, SF3B2, HNRNPA3, PRPF19, HNRNPL, SF3B1, HNRNPM, HNRNPK, DDX46, PRPF8, USP39, NUDT21, HNRNPD, DHX15, HNRNPC, PABPC1, SNRNP70, RBM28, RBM25, PRPF40A, DHX9, CSTF3, CSTF2, RNPS1, SF3A2, DDX5, HNRNPA1, RBMX, SF3A1, HNRNPA0, SF3A3, HNRNPH3, SFPQ, GTF2F2, HNRNPH1, RBM14, SMC1A, PUF60" 430 321 13528 8.428660436 4.37E-52 2.19E-52 4.64E-52

GOTERM_BP_FAT GO:0008380~RNA splicing 81 16.46341463 3.06E-54 "RALY, NCBP1, PRPF4B, SNRPD3, U2AF2, SYNCRIP, SKIV2L2, YBX1, SMNDC1, PNN, NONO, DHX38, DDX23, SRRM2, TARDBP, DNAJC8, U2AF1, QKI, SRRM1, LUC7L3, CCAR1, PABPN1, PRPF31, SNRPA1, EFTUD2, PTBP1, HNRNPA2B1, SF1, CDC5L, PRPF4, HNRNPR, HNRNPU, PRPF6, EIF4A3, SNRNP200, CPSF7, SNRPB, SNRPA, RBM39, TRA2B, TRA2A, WBP11, SF3B4, POLR2A, SF3B2, HNRNPA3, PRPF19, HNRNPL, SF3B1, HNRNPM, HNRNPK, DDX46, PRPF8, USP39, NUDT21, HNRNPD, DHX15, HNRNPC, PABPC1, SNRNP70, RBM28, RBM25, PRPF40A, DHX9, CSTF3, CSTF2, RNPS1, SF3A2, DDX5, HNRNPA1, RBMX, SF3A1, HNRNPA0, SF3A3, HNRNPH3, SFPQ, GTF2F2, HNRNPH1, RBM14, SMC1A, PUF60" 430 284 13528 8.972879135 4.83E-51 1.61E-51 5.12E-51

GOTERM_BP_FAT GO:0016071~mRNA metabolic process 89 18.08943089 5.22E-53 "RALY, NCBP1, PRPF4B, RNMT, SNRPD3, U2AF2, SYNCRIP, SKIV2L2, YBX1, SMNDC1, PNN, NONO, DHX38, DDX23, SRRM2, TARDBP, DNAJC8, U2AF1, SRRM1, QKI, LUC7L3, CCAR1, PABPN1, KHDRBS1, PRPF31, SNRPA1, EFTUD2, PTBP1, HNRNPA2B1, SF1, CDC5L, HNRNPR, PRPF4, HNRNPU, PRPF6, EIF4A3, SNRNP200, SNRPB, CPSF7, SNRPA, CPSF6, RBM39, XRN2, FIP1L1, TRA2B, TRA2A, WBP11, SF3B4, POLR2A, SF3B2, HNRNPA3, HNRNPL, EXOSC10, PRPF19, SF3B1, HNRNPM, HNRNPK, DDX46, PRPF8, USP39, NUDT21, HNRNPD, DHX15, HNRNPC, PABPC1, SNRNP70, RBM28, RBM25, PRPF40A, DHX9, CSTF3, CSTF2, ELAVL1, SSB, RNPS1, SF3A2, DDX5, HNRNPA1, RBMX, SF3A1, HNRNPA0, SF3A3, HNRNPH3, SFPQ, GTF2F2, HNRNPH1, RBM14, SMC1A, PUF60" 430 370 13528 7.567517285 8.23E-50 2.06E-50 8.72E-50

GOTERM_BP_FAT "GO:0000375~RNA splicing, via transesterification reactions" 57 11.58536585 5.85E-45 "NCBP1, SNRPD3, U2AF2, YBX1, SMNDC1, DDX23, DHX38, DNAJC8, U2AF1, SRRM1, CCAR1, PABPN1, PRPF31, SNRPA1, EFTUD2, PTBP1, HNRNPA2B1, SF1, PRPF4, HNRNPR, HNRNPU, PRPF6, SNRNP200, CPSF7, SNRPB, SNRPA, TRA2B, TRA2A, SF3B4, SF3B2, POLR2A, HNRNPL, HNRNPA3, HNRNPM, SF3B1, HNRNPK, PRPF8, USP39, NUDT21, HNRNPD, SNRNP70, HNRNPC, RBM25, DHX9, CSTF3, CSTF2, RNPS1, SF3A2, SF3A1, RBMX, HNRNPA1, HNRNPA0, SF3A3, HNRNPH3, GTF2F2, HNRNPH1, SMC1A" 430 153 13528 11.72056544 9.23E-42 1.85E-42 9.78E-42

GOTERM_BP_FAT "GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" 57 11.58536585 5.85E-45 "NCBP1, SNRPD3, U2AF2, YBX1, SMNDC1, DDX23, DHX38, DNAJC8, U2AF1, SRRM1, CCAR1, PABPN1, PRPF31, SNRPA1, EFTUD2, PTBP1, HNRNPA2B1, SF1, PRPF4, HNRNPR, HNRNPU, PRPF6, SNRNP200, CPSF7, SNRPB, SNRPA, TRA2B, TRA2A, SF3B4, SF3B2, POLR2A, HNRNPL, HNRNPA3, HNRNPM, SF3B1, HNRNPK, PRPF8, USP39, NUDT21, HNRNPD, SNRNP70, HNRNPC, RBM25, DHX9, CSTF3, CSTF2, RNPS1, SF3A2, SF3A1, RBMX, HNRNPA1, HNRNPA0, SF3A3, HNRNPH3, GTF2F2, HNRNPH1, SMC1A" 430 153 13528 11.72056544 9.23E-42 1.85E-42 9.78E-42

GOTERM_BP_FAT "GO:0000398~nuclear mRNA splicing, via spliceosome" 57 11.58536585 5.85E-45 "NCBP1, SNRPD3, U2AF2, YBX1, SMNDC1, DDX23, DHX38, DNAJC8, U2AF1, SRRM1, CCAR1, PABPN1, PRPF31, SNRPA1, EFTUD2, PTBP1, HNRNPA2B1, SF1, PRPF4, HNRNPR, HNRNPU, PRPF6, SNRNP200, CPSF7, SNRPB, SNRPA, TRA2B, TRA2A, SF3B4, SF3B2, POLR2A, HNRNPL, HNRNPA3, HNRNPM, SF3B1, HNRNPK, PRPF8, USP39, NUDT21, HNRNPD, SNRNP70, HNRNPC, RBM25, DHX9, CSTF3, CSTF2, RNPS1, SF3A2, SF3A1, RBMX, HNRNPA1, HNRNPA0, SF3A3, HNRNPH3, GTF2F2, HNRNPH1, SMC1A" 430 153 13528 11.72056544 9.23E-42 1.85E-42 9.78E-42

GOTERM_CC_FAT GO:0005681~spliceosome 48 9.756097561 8.90E-37 "RALY, PRPF4B, U2AF2, SNRPD3, SYNCRIP, SKIV2L2, SF3B4, SF3B2, PNN, SMNDC1, PRPF19, HNRNPA3, HNRNPM, SF3B1,

HNRNPK, DHX38, DDX23, PRPF8, SRRM2, DHX15, U2AF1, SRRM1, SNRNP70, HNRNPC, PABPC1, RBM28, API5, PRPF31, SNRPA1, EFTUD2, HNRNPA2B1, SF1, CDC5L, DDX5, SF3A2, SF3A1, HNRNPA1, RBMX, HNRNPR, PRPF4, HNRNPU, PRPF6, SF3A3, EIF4A3, SNRNP200, SNRPB, SNRPA, HNRNPH1" 415 132 12782 11.2 3.46E-34 4.32E-35 1.24E-33

Annotation Cluster 3 Enrichment Score: 42.321312970672125
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0043232~intracellular non-membrane-bounded organelle 213 43.29268293 5.04E-46 "XRCC5, HIST2H2AA3, RPL19, RPL14, RPL13, XRCC6, SRP68, H1FX, HIST1H2BM, RPLP0, RPLP1, PQBP1, RPP30, MRPL39, DHX30, STAG2, H1F0, EMG1, PTBP1, KRT13, NCAPD2, JUP, NOP2, KRT16, RFC2, RPS10, MYBBP1A, MRPL46, NUP43, MRPL43, MRPL44, MRE11A, IGF2BP2, RCC1, HNRNPA3, VRK1, NAT10, DHX9, MKI67, TP53BP1, DDX5, FXR2, RPS6, HNRNPA1, RPF2, RPS8, FXR1, SYNE1, CCT5, POP1, SUPT16H, PCNA, PARP1, COPS2, UTP18, TCOF1, UTP15, RRP1B, QKI, MRPL1, SYMPK, MRPL4, HIST1H1D, EXOSC9, RBBP4, EXOSC6, HIST1H1C, HIST1H1B, EXOSC7, SF1, EXOSC2, ADNP, RAD50, NOL11, RBM39, NUP107, KLC2, POLR2A, NCAPH, MRPL13, NUMA1, TOE1, MRPL15, RPL34, GATAD2A, MRPL19, GATAD2B, TRIP10, RBM28, BUB3, PDS5A, TRIM28, ILF3, SF3A1, RPL29, MRPL22, ILF2, UBTF, MRPL28, RPL7L1, NOP58, NOP56, RBM14, PES1, TEX10, PRPF4B, SNRPD3, CBX3, SRP19, MRPS31, CBX5, CTNNBL1, PNN, EBNA1BP2, RAD21, CSNK2A1, TARDBP, DDX24, TUBG1, ACIN1, GNL2, GNL3, PABPN1, NUP133, MTA2, HNRNPA2B1, RRP8, RSL1D1, MRPS18A, PSMA3, SMARCA5, MAP7D1, LRPPRC, XRN2, SMARCA4, HMGB1, HMGB2, MRPS15, ANLN, C14ORF166, DAZAP1, HNRNPM, HNRNPK, HIST1H4A, RPL6, NPM1, HNRNPD, RPL3, DNAJA3, HIST2H3A, CSTF2, TSR1, MRPS22, CKAP5, HEATR1, SSB, RPL23A, SMEK1, SUGT1, MPRIP, PSMC5, HDAC2, HDAC1, SMARCC1, SMARCC2, GTF2F2, PSMC1, SPTBN2, TMPO, HNRNPH1, SMC1A, DAP3, MYH10, FOXK1, HP1BP3, SKIV2L2, MKI67IP, ZNF207, FUBP1, MCM7, DKC1, GRWD1, GOPC, TPR, PSMD8, FTSJ3, ZW10, TBL1XR1, HMBS, NUP85, MCM2, CDC5L, MCM3, MCM4, NCL, CDK2, KRT6A, NUP98, NUP160, EXOSC10, RPA1, TFAM, SAFB, NUDT21, TGM1, APEX1, CHD4, HSPA9, TCP1, SMC3, FBL, DIS3, KRT79" 415 2596 12782 2.527118644 1.95E-43 3.26E-44 7.00E-43
GOTERM_CC_FAT GO:0043228~non-membrane-bounded organelle 213 43.29268293 5.04E-46 "XRCC5, HIST2H2AA3, RPL19, RPL14, RPL13, XRCC6, SRP68, H1FX, HIST1H2BM, RPLP0, RPLP1, PQBP1, RPP30, MRPL39, DHX30, STAG2, H1F0, EMG1, PTBP1, KRT13, NCAPD2, JUP, NOP2, KRT16, RFC2, RPS10, MYBBP1A, MRPL46, NUP43, MRPL43, MRPL44, MRE11A, IGF2BP2, RCC1, HNRNPA3, VRK1, NAT10, DHX9, MKI67, TP53BP1, DDX5, FXR2, RPS6, HNRNPA1, RPF2, RPS8, FXR1, SYNE1, CCT5, POP1, SUPT16H, PCNA, PARP1, COPS2, UTP18, TCOF1, UTP15, RRP1B, QKI, MRPL1, SYMPK, MRPL4, HIST1H1D, EXOSC9, RBBP4, EXOSC6, HIST1H1C, HIST1H1B, EXOSC7, SF1, EXOSC2, ADNP, RAD50, NOL11, RBM39, NUP107, KLC2, POLR2A, NCAPH, MRPL13, NUMA1, TOE1, MRPL15, RPL34, GATAD2A, MRPL19, GATAD2B, TRIP10, RBM28, BUB3, PDS5A, TRIM28, ILF3, SF3A1, RPL29, MRPL22, ILF2, UBTF, MRPL28, RPL7L1, NOP58, NOP56, RBM14, PES1, TEX10, PRPF4B, SNRPD3, CBX3, SRP19, MRPS31, CBX5, CTNNBL1, PNN, EBNA1BP2, RAD21, CSNK2A1, TARDBP, DDX24, TUBG1, ACIN1, GNL2, GNL3, PABPN1, NUP133, MTA2, HNRNPA2B1, RRP8, RSL1D1, MRPS18A, PSMA3, SMARCA5, MAP7D1, LRPPRC, XRN2, SMARCA4, HMGB1, HMGB2, MRPS15, ANLN, C14ORF166, DAZAP1, HNRNPM, HNRNPK, HIST1H4A, RPL6, NPM1, HNRNPD, RPL3, DNAJA3, HIST2H3A, CSTF2, TSR1, MRPS22, CKAP5, HEATR1, SSB, RPL23A, SMEK1, SUGT1, MPRIP, PSMC5, HDAC2, HDAC1, SMARCC1, SMARCC2, GTF2F2, PSMC1, SPTBN2, TMPO, HNRNPH1, SMC1A, DAP3, MYH10, FOXK1, HP1BP3, SKIV2L2, MKI67IP, ZNF207, FUBP1, MCM7, DKC1, GRWD1, GOPC, TPR, PSMD8, FTSJ3, ZW10, TBL1XR1, HMBS, NUP85, MCM2, CDC5L, MCM3, MCM4, NCL, CDK2, KRT6A, NUP98, NUP160, EXOSC10, RPA1, TFAM, SAFB, NUDT21, TGM1, APEX1, CHD4, HSPA9, TCP1, SMC3, FBL, DIS3, KRT79" 415 2596 12782 2.527118644 1.95E-43 3.26E-44 7.00E-43
GOTERM_CC_FAT GO:0005730~nucleolus 99 20.12195122 4.28E-37 "SNRPD3, SRP68, SRP19, PNN, CTNNBL1, CBX5, EBNA1BP2, TARDBP, DDX24, PQBP1, RPP30, ACIN1, GNL2, GNL3, PABPN1, EMG1, MTA2, HNRNPA2B1, PTBP1, RRP8, RSL1D1, NOP2, SMARCA5, MYBBP1A, XRN2, HMGB1, HMGB2, MRE11A, DAZAP1, HNRNPA3, HNRNPM, VRK1, HNRNPK, NPM1, RPL3, NAT10, DHX9, CSTF2, TSR1, MKI67, HEATR1, SSB, RPS6, DDX5, HNRNPA1, RPF2, FXR1, CCT5, PSMC5, PSMC1, SMARCC2, POP1, HNRNPH1, PARP1, COPS2, FOXK1, UTP18, TCOF1, UTP15, SKIV2L2, MKI67IP, ZNF207, FUBP1, DKC1, RRP1B, GRWD1, QKI, PSMD8, FTSJ3, EXOSC9, EXOSC6, EXOSC7, ADNP, EXOSC2, SF1, CDC5L, MCM3, NCL, MCM4, NOL11, POLR2A, EXOSC10, TOE1, SAFB, GATAD2A, GATAD2B, RBM28, BUB3, ILF3, SF3A1,

FBL, DIS3, ILF2, UBTF, NOP58, NOP56, RBM14, PES1, TEX10" 415 698 12782 4.368481375 1.66E-34 2.37E-35 5.94E-34

Annotation Cluster 4 Enrichment Score: 15.84760213568718

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0005694~chromosome 64 13.00813008 4.80E-23 "XRCC5, HIST2H2AA3, PRPF4B, HP1BP3, XRCC6, CBX3, H1FX, MKI67IP, CBX5, HIST1H2BM, CSNK2A1, MCM7, RAD21, TUBG1, TPR, STAG2, ZW10, H1F0, NUP133, RBBP4, HIST1H1D, HIST1H1C, HIST1H1B, HMBS, NUP85, MCM2, MCM3, RAD50, CDK2, NCAPD2, RFC2, SMARCA5, NUP107, NUP43, LRPPRC, SMARCA4, HMGB1, NUP98, HMGB2, NUP160, RCC1, RPA1, NCAPH, HIST1H4A, HNRNPD, CHD4, BUB3, HIST2H3A, TCP1, PDS5A, MKI67, TP53BP1, TRIM28, SUGT1, SMC3, HDAC2, HDAC1, SMARCC1, SMARCC2, PCNA, SUPT16H, TMPO, SMC1A, PES1" 415 460 12782 4.285217391 1.86E-20 1.86E-21 6.67E-20

GOTERM_CC_FAT GO:0044427~chromosomal part 52 10.56910569 4.33E-18 "XRCC5, HIST2H2AA3, HP1BP3, XRCC6, CBX3, H1FX, CBX5, HIST1H2BM, CSNK2A1, MCM7, TPR, STAG2, ZW10, H1F0, NUP133, RBBP4, HIST1H1D, HIST1H1C, HIST1H1B, NUP85, MCM2, MCM3, RAD50, CDK2, NCAPD2, RFC2, NUP107, NUP43, SMARCA4, NUP98, NUP160, RCC1, RPA1, NCAPH, HIST1H4A, CHD4, BUB3, HIST2H3A, TCP1, PDS5A, MKI67, TP53BP1, TRIM28, SUGT1, SMC3, HDAC2, HDAC1, SMARCC1, SMARCC2, PCNA, TMPO, SMC1A" 415 386 12782 4.149222798 1.68E-15 1.53E-16 6.01E-15

GOTERM_BP_FAT GO:0051276~chromosome organization 52 10.56910569 3.40E-14 "XRCC5, HIST2H2AA3, HP1BP3, XRCC6, NAP1L1, CBX3, H1FX, CBX5, HIST1H2BM, DKC1, ACIN1, SUPT5H, ZW10, H1F0, TBL1XR1, HIST1H1D, RBBP4, HIST1H1C, HIST1H1B, MTA2, MCM2, RBBP7, RAD50, NCAPD2, SMARCA5, SMARCA1, SMARCA4, HMGB1, HMGB2, MRE11A, PRKDC, RPA1, NCAPH, HIST1H4A, SAFB, NPM1, ACTL6A, CHD4, BUB3, HIST2H3A, MSH2, NASP, SMC3, HDAC2, HDAC1, SMARCC1, SMARCC2, SUPT16H, DNMT1, SMC1A, PARP1, RBM14" 430 485 13528 3.373080796 5.36E-11 4.12E-12 5.68E-11

GOTERM_CC_FAT GO:0000785~chromatin 29 5.894308943 5.75E-11 "HIST2H2AA3, HP1BP3, CBX3, H1FX, RCC1, CBX5, HIST1H2BM, CSNK2A1, MCM7, HIST1H4A, CHD4, STAG2, H1F0, HIST2H3A, TCP1, RBBP4, HIST1H1D, PDS5A, HIST1H1C, HIST1H1B, TRIM28, MCM2, SMC3, HDAC2, HDAC1, SMARCC1, SMARCC2, TMPO, SMARCA4" 415 200 12782 4.466 2.23E-08 1.17E-09 7.99E-08

Annotation Cluster 5 Enrichment Score: 15.139757573982429

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0016604~nuclear body 34 6.910569106 3.45E-17 "TIMM50, WBP11, SART3, SMNDC1, PNN, CBX5, RPA1, SF3B1, SUMO1, DDX46, DKC1, TOE1, MORC3, PRPF8, SRRM2, NUDT21, NPM1, U2AF1, GATAD2A, SRRM1, RBM27, RBM25, LUC7L3, PRPF40A, DDX42, PRPF31, RNPS1, CDC5L, PRPF4, SF3A3, EIF4A3, SON, CPSF6, RBM39" 415 168 12782 6.233333333 1.34E-14 1.12E-15 4.79E-14

GOTERM_CC_FAT GO:0016607~nuclear speck 27 5.487804878 1.33E-16 "WBP11, TIMM50, SART3, SMNDC1, PNN, SF3B1, SUMO1, DDX46, TOE1, PRPF8, SRRM2, NPM1, GATAD2A, SRRM1, RBM27, RBM25, LUC7L3, DDX42, PRPF40A, PRPF31, RNPS1, CDC5L, PRPF4, SF3A3, EIF4A3, SON, RBM39" 415 103 12782 8.073786408 4.31E-14 3.11E-15 1.55E-13

GOTERM_CC_FAT GO:0044451~nucleoplasm part 56 11.38211382 8.27E-14 "XRCC6, TIMM50, INTS3, SART3, SMNDC1, PNN, CBX5, CSNK2A1, MCM7, DKC1, SRRM2, U2AF1, SRRM1, LUC7L3, PRPF31, TBL1XR1, RBBP4, MTA2, CDC5L, RBBP7, PRPF4, CDK2, EIF4A3, CPSF6, RBM39, HCFC1, PRKDC, WBP11, POLR2A, RPA1, SF3B1, SUMO1, DDX46, TOE1, MORC3, PRPF8, NUDT21, NPM1, GATAD2A, GTF3C5, ACTL6A, RBM27, CHD4, RBM25, DDX42, PRPF40A, POLR3A, RNPS1, SF3A3, SON, HDAC2, HDAC1, GTF2F2, SMARCC2, RBM14, PARP1" 415 555 12782 3.107747748 3.21E-11 2.01E-12 1.15E-10

Annotation Cluster 6 Enrichment Score: 14.937172148411673

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0022613~ribonucleoprotein complex biogenesis 42 8.536585366 5.54E-24 "NCBP1, RPL14, UTP18, SNRPD3, UTP15, WBP11, SMNDC1, EXOSC10, EBNA1BP2, EIF3A, RRP1B, DKC1, DDX23, RPLP0, USP39, NPM1, GNL2, FTSJ3, PRPF31, EXOSC9, TSR1, EXOSC6, EMG1, EXOSC7, SF1, EXOSC2,

HEATR1, RRP8, RPS6, SF3A2, SF3A1, FBL, PRPF6, SF3A3, DIS3, EIF4A3, NOP2, SNRNP200, SNRPB, NOP58, NOP56, PES1" 430 180 13528 7.340775194 8.73E-21 1.46E-21 9.25E-21
GOTERM_BP_FAT GO:0042254~ribosome biogenesis 28 5.691056911 8.58E-16 "RPL14, UTP18, UTP15, WBP11, EXOSC10, EBNA1BP2, RRP1B, DKC1, RPLP0, NPM1, GNL2, FTSJ3, EXOSC9, TSR1, EXOSC6, EXOSC7, EMG1, EXOSC2, HEATR1, RRP8, RPS6, FBL, DIS3, EIF4A3, NOP2, NOP58, NOP56, PES1" 430 122 13528 7.220434617 1.40E-12 1.40E-13 1.49E-12
GOTERM_BP_FAT GO:0016072~rRNA metabolic process 24 4.87804878 1.91E-14 "EXOSC9, EXOSC6, RPL14, EXOSC7, UTP18, EMG1, EXOSC2, UTP15, WBP11, HEATR1, RRP8, MKI67IP, RPS6, FBL, EXOSC10, DIS3, EIF4A3, NOP2, RRP1B, DKC1, NOP58, NOP56, PES1, FTSJ3" 430 96 13528 7.865116279 3.01E-11 2.51E-12 3.19E-11
GOTERM_BP_FAT GO:0006364~rRNA processing 23 4.674796748 7.45E-14 "EXOSC9, EXOSC6, RPL14, EXOSC7, UTP18, EMG1, EXOSC2, UTP15, WBP11, HEATR1, RRP8, RPS6, FBL, EXOSC10, DIS3, EIF4A3, NOP2, RRP1B, DKC1, NOP58, NOP56, PES1, FTSJ3" 430 92 13528 7.865116279 1.17E-10 8.39E-12 1.25E-10
GOTERM_BP_FAT GO:0034660~ncRNA metabolic process 34 6.910569106 3.00E-13 "RPL14, UTP18, UTP15, MKI67IP, WBP11, INTS3, VARS, PUS7, EXOSC10, RRP1B, DKC1, TRMT6, RPP30, TPR, FTSJ3, EXOSC9, EXOSC6, DARS, EXOSC7, EMG1, EXOSC2, HEATR1, RRP8, SSB, AARSD1, RPS6, FBL, DIS3, EIF4A3, NOP2, POP1, NOP58, NOP56, PES1" 430 230 13528 4.650677452 4.72E-10 2.78E-11 5.01E-10
GOTERM_BP_FAT GO:0034470~ncRNA processing 30 6.097560976 1.18E-12 "RPL14, UTP18, UTP15, WBP11, INTS3, PUS7, EXOSC10, SRRT, RRP1B, DKC1, TRMT6, RPP30, FTSJ3, EXOSC9, EXOSC6, EXOSC7, EMG1, EXOSC2, HEATR1, RRP8, SSB, RPS6, FBL, DIS3, EIF4A3, NOP2, POP1, NOP58, NOP56, PES1"430 187 13528 5.047133441 1.85E-09 9.76E-11 1.97E-09

Annotation Cluster 7 Enrichment Score: 10.000941158189674
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0004386~helicase activity 27 5.487804878 1.79E-13 "XRCC5, XRCC6, SKIV2L2, DDX27, DDX17, MCM7, DDX46, DHX38, DDX23, DDX24, DHX15, DHX36, DHX30, CHD4, DDX42, DHX57, DHX9, DDX5, MCM4, MCM6, DDX6, EIF4A3, SNRNP200, GTF2F2, SMARCA5, SMARCA1, SMARCA4" 408 140 12983 6.136922269 8.55E-11 2.85E-11 2.56E-10
GOTERM_MF_FAT GO:0070035~purine NTP-dependent helicase activity 21 4.268292683 1.91E-11 "XRCC5, DHX9, XRCC6, SKIV2L2, DDX5, DDX6, DDX27, EIF4A3, DDX17, DDX46, DDX23, DHX38, DDX24, SNRNP200, GTF2F2, DHX15, DHX36, DHX30, CHD4, DHX57, DDX42" 408 98 12983 6.818802521 9.16E-09 2.29E-09 2.74E-08
GOTERM_MF_FAT GO:0008026~ATP-dependent helicase activity 21 4.268292683 1.91E-11 "XRCC5, DHX9, XRCC6, SKIV2L2, DDX5, DDX6, DDX27, EIF4A3, DDX17, DDX46, DDX23, DHX38, DDX24, SNRNP200, GTF2F2, DHX15, DHX36, DHX30, CHD4, DHX57, DDX42" 408 98 12983 6.818802521 9.16E-09 2.29E-09 2.74E-08
GOTERM_MF_FAT GO:0016887~ATPase activity 36 7.317073171 3.50E-10 "XRCC5, XRCC6, SKIV2L2, DDX27, DDX17, DDX46, DDX23, DHX38, DDX24, DHX15, DHX36, ACIN1, PSMD6, DHX30, CHD4, DHX57, DDX42, DHX9, RBBP4, MSH2, DDX5, ATP6V1D, DDX6, EIF4A3, PSMC6, PSMC5, RFC2, PSMC2, PSMC1, SNRNP200, GTF2F2, SMARCA5, HSPD1, SMARCA1, SMARCA4, MYH10" 408 334 12983 3.429816837 1.68E-07 3.35E-08 5.01E-07
GOTERM_MF_FAT "GO:0042623~ATPase activity, coupled" 27 5.487804878 4.33E-07 "XRCC5, DHX9, RBBP4, XRCC6, SKIV2L2, DDX5, ATP6V1D, DDX6, DDX27, EIF4A3, DDX17, DDX46, DHX38, DDX23, RFC2, GTF2F2, SNRNP200, DDX24, DHX15, DHX36, SMARCA1, DHX30, CHD4, DHX57, DDX42, SMARCA4, MYH10" 408 272 12983 3.158709991 2.07E-04 1.89E-05 6.20E-04

Annotation Cluster 8 Enrichment Score: 8.649476959900614
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006412~translation 46 9.349593496 7.47E-17 "RPL19, MRPS15, RPL14, RPL13, RBM3, PABPC4, VARS, EIF3C, EIF3D, MRPL13, EIF3A, MRPL15, RPL6, EIF3H, TRMT6, ICT1, RPL34, RPLP0, RPLP1, RPL3, MRPL19, EIF3I, TPR, EIF2B3, EIF2B5, MRPL1, MRPL4, DARS, EIF2S3, RPL23A, AARSD1, RPS6,

RPS8, RPL29, RSL1D1, MRPL22, MRPL28, MRPS18A, EIF4H, EIF2S1, RPL7L1, EIF2S2, EEF1G, RPS10, EEF1D, MRPL43" 430 331 13528 4.372149231 1.75E-13 2.50E-14 1.89E-13

GOTERM_CC_FAT GO:0005840~ribosome 36 7.317073171 1.97E-15 "MRPS15, RPL19, RPL14, RPL13, SRP68, MRPS31, MRPL13, MRPL15, RPL6, RPL34, RPLP0, NPM1, RPLP1, RPL3, MRPL19, MRPL39, APEX1, MRPL1, MRPL4, MRPS22, SF1, RPL23A, RPS6, FXR2, RPS8, RPL29, RSL1D1, MRPL22, MRPL28, MRPS18A, RPL7L1, RPS10, MRPL46, MRPL43, MRPL44, DAP3" 415 215 12782 5.157209302 7.75E-13 5.17E-14 2.78E-12

GOTERM_CC_FAT GO:0033279~ribosomal subunit 24 4.87804878 1.81E-11 "MRPL1, MRPS15, RPL19, RPL14, MRPS22, RPL23A, RPS6, FXR2, RPS8, RPL29, MRPL13, MRPL22, MRPL15, MRPS18A, RPL6, RPL34, RPLP0, RPL7L1, NPM1, RPLP1, RPL3, RPS10, MRPL43, DAP3" 415 128 12782 5.775 7.01E-09 3.89E-10 2.51E-08

GOTERM_CC_FAT GO:0015934~large ribosomal subunit 17 3.455284553 2.72E-10 "MRPL1, RPL19, RPL14, RPL23A, FXR2, RPL29, MRPL22, MRPL13, MRPL15, RPL6, RPL34, RPLP0, RPL7L1, NPM1, RPLP1, RPL3, MRPL43" 415 67 12782 7.814925373 1.06E-07 4.80E-09 3.78E-07

GOTERM_MF_FAT GO:0003735~structural constituent of ribosome 25 5.081300813 4.79E-10 "RPL19, MRPS15, RPL14, RPL13, MRPL13, MRPL15, RPL6, RPLP0, RPL34, RPLP1, RPL3, MRPL19, MRPL1, MRPL4, MRPS22, RPL23A, RPS6, RPS8, RPL29, RSL1D1, MRPL22, MRPL28, MRPS18A, RPL7L1, MRPL43" 408 168 12983 4.735279528 2.30E-07 3.83E-08 6.86E-07

GOTERM_BP_FAT GO:0006414~translational elongation 16 3.25203252 6.34E-07 "RPL19, RPL14, RPL13, RPL23A, RPS6, VARS, RPS8, RPL29, RPL6, RPL34, RPLP0, RPLP1, RPL3, EEF1G, RPS10, EEF1D" 430 101 13528 4.983836058 9.99E-04 2.08E-05 0.001059606

GOTERM_CC_FAT GO:0022626~cytosolic ribosome 14 2.845528455 1.81E-06 "RPL19, RPL14, RPL13, RPL23A, FXR2, RPS6, RPS8, RPL29, RPL6, RPL34, RPLP0, RPLP1, RPL3, RPS10" 415 81 12782 5.32345679 7.03E-04 2.27E-05 0.002518253

GOTERM_CC_FAT GO:0022625~cytosolic large ribosomal subunit 10 2.032520325 2.54E-06 "RPL19, RPL14, RPL6, RPL34, RPLP0, RPLP1, RPL3, RPL23A, FXR2, RPL29" 415 38 12782 8.105263158 9.87E-04 2.90E-05 0.003533526

GOTERM_CC_FAT GO:0044445~cytosolic part 17 3.455284553 3.34E-05 "TCP1, RPL19, RPL14, RPL23A, RPS6, FXR2, RPS8, RPL29, CCT7, CCT5, AKT1S1, RPL6, RPL34, RPLP0, RPLP1, RPL3, RPS10" 415 152 12782 3.444736842 0.012872544 3.08E-04 0.046358185

GOTERM_MF_FAT GO:0005198~structural molecule activity 39 7.926829268 9.44E-05 "NUP98, KRT6A, MRPS15, RPL19, RPL14, VAPB, RPL13, PNN, NUMA1, MRPL13, EIF3A, MRPL15, RPL6, RPL34, RPLP0, RPLP1, RPL3, MRPL19, TUBG1, MRPL1, MRPL4, MRPS22, KRT13, RPL23A, RPS6, NUP155, RPS8, RPL29, RSL1D1, JUP, MRPL22, MRPL28, KRT16, MRPS18A, KRT79, RPL7L1, SPTBN2, MATR3, MRPL43" 408 634 12983 1.957448042 0.044223943 0.001614112 0.135070284

Annotation Cluster 9 Enrichment Score: 7.576089115952402

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0034621~cellular macromolecular complex subunit organization 43 8.739837398 1.69E-13 "HIST2H2AA3, NCBP1, HMGB2, NUP98, HP1BP3, SNRPD3, NAP1L1, ANLN, H1FX, SMNDC1, TFAM, HIST1H2BM, EIF3A, DDX23, HIST1H4A, ICT1, USP39, NPM1, TUBG1, HIST2H3A, H1F0, NUP133, PRPF31, TCP1, HIST1H1D, TSR1, HIST1H1C, HIST1H1B, NASP, SF1, MCM2, SF3A2, SF3A1, PRPF6, SF3A3, ADRM1, NUP205, SNRNP200, SMARCA5, SNRPB, SUPT16H, HSPD1, XRN2" 430 357 13528 3.789355742 2.67E-10 1.78E-11 2.83E-10

GOTERM_BP_FAT GO:0034622~cellular macromolecular complex assembly 38 7.723577236 7.08E-12 "NCBP1, HIST2H2AA3, HMGB2, NUP98, HP1BP3, SNRPD3, NAP1L1, H1FX, ANLN, SMNDC1, TFAM, HIST1H2BM, EIF3A, DDX23, HIST1H4A, USP39, NPM1, TUBG1, HIST2H3A, H1F0, PRPF31, TCP1, HIST1H1D, TSR1, HIST1H1C, HIST1H1B, SF1, MCM2, SF3A2, SF3A1, PRPF6, SF3A3, ADRM1, NUP205, SNRNP200, SMARCA5, SNRPB, HSPD1" 430 318 13528 3.759426649 1.12E-08 5.58E-10 1.18E-08

GOTERM_BP_FAT GO:0006333~chromatin assembly or disassembly 22 4.471544715 4.79E-10 "HIST2H3A, H1F0, HIST2H2AA3, HMGB2, HIST1H1D, HIST1H1C, HIST1H1B, HP1BP3, MTA2, NAP1L1, CBX3, H1FX, MCM2, CBX5, HIST1H2BM, HIST1H4A, SMARCC1, SMARCC2, NPM1, SMARCA5, SUPT16H, CHD4" 430 127 13528 5.449844351 7.56E-07 3.29E-08 8.01E-07

GOTERM_BP_FAT	GO:0006325~chromatin organization	36	7.317073171	1.29E-08	"HMGB1, HIST2H2AA3, HMGB2, HP1BP3, NAP1L1, CBX3, H1FX, CBX5, HIST1H2BM, HIST1H4A, SAFB, NPM1, ACTL6A, SUPT5H, CHD4, HIST2H3A, H1F0, TBL1XR1, RBBP4, HIST1H1D, HIST1H1C, HIST1H1B, NASP, MTA2, MCM2, RBBP7, HDAC2, HDAC1, SMARCC1, SMARCC2, SMARCA5, SUPT16H, DNMT1, RBM14, SMARCA1, SMARCA4"	430	378	13528	2.996234773	2.03E-05	6.36E-07	2.16E-05

GOTERM_BP_FAT	GO:0034728~nucleosome organization	17	3.455284553	3.21E-08	"H1F0, HIST2H3A, HIST2H2AA3, HMGB2, HIST1H1D, HIST1H1C, HIST1H1B, HP1BP3, NASP, NAP1L1, H1FX, MCM2, HIST1H2BM, HIST1H4A, NPM1, SMARCA5, SUPT16H"	430	93	13528	5.750837709	5.06E-05	1.41E-06	5.37E-05

GOTERM_BP_FAT	GO:0006323~DNA packaging	18	3.658536585	1.57E-07	"H1F0, HIST2H3A, HIST2H2AA3, HMGB2, HIST1H1D, HIST1H1C, HIST1H1B, HP1BP3, NAP1L1, H1FX, MCM2, NCAPD2, NCAPH, HIST1H2BM, HIST1H4A, NPM1, SMARCA5, ACIN1"	430	117	13528	4.840071556	2.48E-04	5.63E-06	2.63E-04

GOTERM_BP_FAT	GO:0006334~nucleosome assembly	15	3.048780488	3.52E-07	"H1F0, HIST2H3A, HIST2H2AA3, HMGB2, HIST1H1D, HIST1H1C, HIST1H1B, HP1BP3, NAP1L1, H1FX, MCM2, HIST1H2BM, HIST1H4A, NPM1, SMARCA5"	430	84	13528	5.617940199	5.55E-04	1.21E-05	5.89E-04

GOTERM_BP_FAT	GO:0031497~chromatin assembly	15	3.048780488	5.50E-07	"H1F0, HIST2H3A, HIST2H2AA3, HMGB2, HIST1H1D, HIST1H1C, HIST1H1B, HP1BP3, NAP1L1, H1FX, MCM2, HIST1H2BM, HIST1H4A, NPM1, SMARCA5"	430	87	13528	5.424218123	8.67E-04	1.85E-05	9.20E-04

GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	15	3.048780488	9.68E-07	"H1F0, HIST2H3A, HIST2H2AA3, HMGB2, HIST1H1D, HIST1H1C, HIST1H1B, HP1BP3, NAP1L1, H1FX, MCM2, HIST1H2BM, HIST1H4A, NPM1, SMARCA5"	430	91	13528	5.185790953	0.001525646	3.12E-05	0.001618384

GOTERM_CC_FAT	GO:0032993~protein-DNA complex	14	2.845528455	3.63E-06	"H1F0, XRCC5, HIST2H3A, HIST2H2AA3, HIST1H1D, HIST1H1C, HIST1H1B, HP1BP3, XRCC6, H1FX, MCM3, RPA1, HIST1H2BM, HIST1H4A"	415	86	12782	5.013953488	0.001407616	4.02E-05	0.005041172

GOTERM_CC_FAT	GO:0000786~nucleosome	10	2.032520325	1.81E-04	"H1F0, HIST2H3A, HIST2H2AA3, HIST1H2BM, HIST1H1D, HIST1H1C, HIST1H4A, HP1BP3, HIST1H1B, H1FX"	415	63	12782	4.888888889	0.067660003	0.00148948	0.250417145

Annotation Cluster 10	Enrichment Score: 7.558215714880222

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_CC_FAT	GO:0000785~chromatin	29	5.894308943	5.75E-11	"HIST2H2AA3, HP1BP3, CBX3, H1FX, RCC1, CBX5, HIST1H2BM, CSNK2A1, MCM7, HIST1H4A, CHD4, STAG2, H1F0, HIST2H3A, TCP1, RBBP4, HIST1H1D, PDS5A, HIST1H1C, HIST1H1B, TRIM28, MCM2, SMC3, HDAC2, HDAC1, SMARCC1, SMARCC2, TMPO, SMARCA4"	415	200	12782	4.466	2.23E-08	1.17E-09	7.99E-08

GOTERM_CC_FAT	GO:0000228~nuclear chromosome	25	5.081300813	4.30E-10	"XRCC5, HMGB2, XRCC6, CBX3, MKI67IP, RCC1, CBX5, RPA1, RAD21, MCM7, CSNK2A1, TUBG1, TCP1, RBBP4, TRIM28, MCM2, MCM3, SMC3, RAD50, NCAPD2, HDAC2, HDAC1, SMARCC1, SMC1A, LRPPRC"	415	162	12782	4.75308642	1.67E-07	7.25E-09	5.97E-07

GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	18	3.658536585	3.88E-07	"XRCC5, TCP1, RBBP4, XRCC6, TRIM28, CBX3, MCM2, MCM3, RCC1, RAD50, SMC3, CBX5, RPA1, CSNK2A1, HDAC2, MCM7, HDAC1, SMARCC1"	415	122	12782	4.544262295	1.51E-04	5.19E-06	5.39E-04

GOTERM_CC_FAT	GO:0000790~nuclear chromatin	10	2.032520325	6.10E-05	"TCP1, CSNK2A1, RBBP4, HDAC2, HDAC1, SMARCC1, TRIM28, CBX3, RCC1, CBX5"	415	55	12782	5.6	0.023375357	5.25E-04	0.08461607

Annotation Cluster 11	Enrichment Score: 7.30462231999961

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_MF_FAT	GO:0000166~nucleotide binding	157	31.91056911	6.25E-25	"RALY, XRCC5, PRPF4B, RBM3, U2AF2, XRCC6, DTYMK, SYNCRIP, SART3, HIBADH, DDX27, NONO, DDX17, CSNK2A1, DDX23, DHX38, RAVER1, TARDBP, DDX24, U2AF1, DHX36, TUBG1, MRPL39, ACIN1, DHX30, GNL2, RAB21,

RBM12, GNL3, PABPN1, GTPBP1, DARS, EFTUD2, HNRNPA2B1, PTBP1, LIG3, EIF2S3, HNRNPR, HNRNPU, SLTM, GLUL, RFC2, SMARCA5, SNRPA, YME1L1, SMARCA1, NEK7, SMARCA4, PABPC4, IGF2BP2, DAZAP1, HNRNPA3, HNRNPL, HNRNPM, VRK1, DDX46, HNRNPD, NAT10, HNRNPC, PABPC1, EWSR1, DHX57, DDX42, DHX9, CSTF2, MKI67, RBM12B, SSB, DOCK7, RNPS1, RPL23A, AARSD1, DDX5, RBMX, HNRNPA1, HNRNPA0, DDX6, CCT7, PSMC6, CCT5, HNRNPH3, PSMC5, PSMC3, PSMC2, EIF4H, NDUFV1, UBA2, GTF2F2, PSMC1, HSPD1, PARP1, SMC1A, HNRNPH1, PUF60, MYH10, SKIV2L2, MKI67IP, GSR, ATAD3A, MCM7, HNRNPCL1, TPR, SUCLA2, NT5E, CDK13, RAP2B, MCM2, NDUFA10, MCM3, MCM4, NCL, GMPS, RAD50, CDK2, MCM5, MCM6, HNRPDL, TRAP1, EIF4A3, GNAQ, RRM1, SNRNP200, CPSF7, CPSF6, CDK11B, GNAS, RBM39, MATR3, TRA2B, TRA2A, HK2, PRKDC, VARS, SF3B4, PFAS, MORC3, SAFB, DHX15, ACTL6A, SNRNP70, RBM27, RBM28, CHD4, RBM25, HSPA9, TCP1, MSH2, ELAVL1, SPATA5L1, SMC3, SDHA, NRAS, ILF2, SFPQ, POLDIP3, RBM14, RBM15" 408 2245 12983 2.22534936 2.99E-22 1.50E-22 8.94E-22

GOTERM_MF_FAT GO:0016887~ATPase activity 36 7.317073171 3.50E-10 "XRCC5, XRCC6, SKIV2L2, DDX27, DDX17, DDX46, DDX23, DHX38, DDX24, DHX15, DHX36, ACIN1, PSMD6, DHX30, CHD4, DHX57, DDX42, DHX9, RBBP4, MSH2, DDX5, ATP6V1D, DDX6, EIF4A3, PSMC6, PSMC5, RFC2, PSMC2, PSMC1, SNRNP200, GTF2F2, SMARCA5, HSPD1, SMARCA1, SMARCA4, MYH10" 408 334 12983 3.429816837 1.68E-07 3.35E-08 5.01E-07

GOTERM_MF_FAT GO:0005524~ATP binding 78 15.85365854 4.11E-06 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TPR, DHX30, SUCLA2, CDK13, DARS, LIG3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50, CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, RFC2, SNRNP200, RRM1, SMARCA5, YME1L1, CDK11B, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, DDX42, DHX57, HSPA9, DHX9, TCP1, MKI67, MSH2, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, CCT7, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10"408 1477 12983 1.680463181 0.001966094 1.31E-04 0.005880709

GOTERM_MF_FAT GO:0032559~adenyl ribonucleotide binding 78 15.85365854 6.73E-06 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TPR, DHX30, SUCLA2, CDK13, DARS, LIG3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50, CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, RFC2, SNRNP200, RRM1, SMARCA5, YME1L1, CDK11B, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, DDX42, DHX57, HSPA9, DHX9, TCP1, MKI67, MSH2, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, CCT7, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10" 408 1497 12983 1.658012103 0.00321798 1.90E-04 0.009631037

GOTERM_MF_FAT GO:0032555~purine ribonucleotide binding 90 18.29268293 1.21E-05 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TUBG1, TPR, DHX30, SUCLA2, GNL2, RAB21, GNL3, CDK13, RAP2B, GTPBP1, DARS, EFTUD2, LIG3, EIF2S3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50, CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, GNAQ, RFC2, SNRNP200, RRM1, SMARCA5, GNAS, CDK11B, YME1L1, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, HSPA9, DDX42, DHX57, DHX9, TCP1, MKI67, MSH2, DOCK7, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, CCT7, NRAS, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10"408 1836 12983 1.559856786 0.00575803 3.21E-04 0.017254434

GOTERM_MF_FAT GO:0032553~ribonucleotide binding 90 18.29268293 1.21E-05 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TUBG1, TPR, DHX30, SUCLA2, GNL2, RAB21, GNL3, CDK13, RAP2B, GTPBP1, DARS, EFTUD2, LIG3, EIF2S3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50, CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, GNAQ, RFC2, SNRNP200, RRM1, SMARCA5, GNAS, CDK11B, YME1L1, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, HSPA9, DDX42, DHX57, DHX9, TCP1, MKI67, MSH2, DOCK7, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, CCT7, NRAS, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10"408 1836 12983 1.559856786 0.00575803 3.21E-04 0.017254434

GOTERM_MF_FAT GO:0030554~adenyl nucleotide binding 80 16.2601626 1.31E-05 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, GSR, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TPR, DHX30, SUCLA2, CDK13, DARS, LIG3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50,

CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, RFC2, SNRNP200, RRM1, SMARCA5, YME1L1, CDK11B, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, DDX42, DHX57, HSPA9, DHX9, TCP1, MKI67, MSH2, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, SDHA, CCT7, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10" 408 1577 12983 1.614258893 0.006258515 3.30E-04 0.018758757
GOTERM_MF_FAT GO:0001882~nucleoside binding 81 16.46341463 1.59E-05 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, GSR, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TPR, DHX30, SUCLA2, CDK13, DARS, LIG3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50, CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, RFC2, SNRNP200, RRM1, SMARCA5, YME1L1, CDK11B, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, DDX42, DHX57, HSPA9, DHX9, TCP1, MKI67, MSH2, POLR3A, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, SDHA, CCT7, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10" 408 1612 12983 1.598949971 0.007607911 3.64E-04 0.022818343
GOTERM_MF_FAT GO:0017076~purine nucleotide binding 92 18.69918699 2.18E-05 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, GSR, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TUBG1, TPR, DHX30, SUCLA2, GNL2, RAB21, GNL3, CDK13, RAP2B, GTPBP1, DARS, EFTUD2, LIG3, EIF2S3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50, CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, GNAQ, RFC2, SNRNP200, RRM1, SMARCA5, GNAS, CDK11B, YME1L1, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, HSPA9, DDX42, DHX57, DHX9, TCP1, MKI67, MSH2, DOCK7, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, SDHA, CCT7, NRAS, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10" 408 1918 12983 1.526349956 0.010373251 4.53E-04 0.031154478
GOTERM_MF_FAT GO:0001883~purine nucleoside binding 80 16.2601626 2.25E-05 "XRCC5, PRPF4B, DTYMK, XRCC6, SKIV2L2, DDX27, GSR, DDX17, ATAD3A, MCM7, CSNK2A1, DHX38, DDX23, DDX24, DHX36, TPR, DHX30, SUCLA2, CDK13, DARS, LIG3, MCM2, MCM3, NDUFA10, MCM4, GMPS, RAD50, CDK2, HNRNPU, MCM5, MCM6, TRAP1, EIF4A3, GLUL, RFC2, SNRNP200, RRM1, SMARCA5, YME1L1, CDK11B, SMARCA1, SMARCA4, NEK7, HK2, PRKDC, VARS, PFAS, VRK1, DDX46, MORC3, DHX15, NAT10, ACTL6A, CHD4, DDX42, DHX57, HSPA9, DHX9, TCP1, MKI67, MSH2, SPATA5L1, AARSD1, DDX5, SMC3, DDX6, SDHA, CCT7, PSMC6, CCT5, PSMC5, ILF2, PSMC3, PSMC2, UBA2, PSMC1, GTF2F2, HSPD1, SMC1A, MYH10" 408 1601 12983 1.590060134 0.01072587 4.49E-04 0.032219073

Annotation Cluster 12 Enrichment Score: 7.2341109061813595
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006259~DNA metabolic process 51 10.36585366 6.78E-13 "XRCC5, HMGB1, HMGB2, NUP98, MRE11A, XRCC6, NAP1L1, PRKDC, INTS3, XRCC1, PRPF19, RPA1, NONO, TFAM, SUMO1, MCM7, RAD21, DKC1, GATAD2A, PSIP1, APEX1, NT5E, DNAJA3, FEN1, RBBP4, NUDT1, MSH2, NASP, TP53BP1, LIG3, MCM2, MCM3, RBBP7, MCM4, RAD50, MCM5, SMC3, CDK2, MCM6, UHRF1, RFC2, SFPQ, RRM1, SUPT16H, PCNA, DNMT1, HSPD1, RBM14, PARP1, SMC1A, XRN2" 430 506 13528 3.170916445 1.07E-09 5.94E-11 1.13E-09
GOTERM_BP_FAT GO:0006281~DNA repair 29 5.894308943 1.04E-07 "XRCC5, HMGB1, HMGB2, MRE11A, XRCC6, PRKDC, INTS3, XRCC1, NONO, RPA1, PRPF19, SUMO1, RAD21, APEX1, FEN1, NUDT1, MSH2, TP53BP1, LIG3, RAD50, SMC3, UHRF1, RFC2, SFPQ, SUPT16H, PCNA, SMC1A, PARP1, RBM14" 430 284 13528 3.212512283 1.65E-04 3.92E-06 1.74E-04
GOTERM_BP_FAT GO:0006974~response to DNA damage stimulus 31 6.300813008 2.89E-06 "XRCC5, HMGB1, HMGB2, MRE11A, XRCC6, PRKDC, INTS3, XRCC1, NONO, RPA1, PRPF19, SUMO1, RAD21, MCM7, APEX1, FEN1, NUDT1, MSH2, TP53BP1, LIG3, RAD50, SMC3, UHRF1, RFC2, UBR5, SFPQ, SUPT16H, PCNA, SMC1A, PARP1, RBM14" 430 373 13528 2.614676725 0.004548063 8.29E-05 0.004831757
GOTERM_BP_FAT GO:0033554~cellular response to stress 37 7.520325203 5.66E-05 "XRCC5, HMGB1, HMGB2, VAPB, MRE11A, XRCC6, PRKDC, INTS3, XRCC1, PRPF19, RPA1, NONO, SUMO1, RAD21, MCM7, EIF2B3, APEX1, FEN1, EIF2B5, DHX9, NUDT1, MSH2, TP53BP1, LIG3, RAD50, SMC3, UHRF1, HDAC2, RFC2, UBR5, SFPQ, EIF2S1, SUPT16H, PCNA, RBM14, SMC1A, PARP1" 430 566 13528 2.056602843 0.085438544 0.001352276 0.094623089

Annotation Cluster 13 Enrichment Score: 5.9162340601512415
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0034621~cellular macromolecular complex subunit organization 43 8.739837398 1.69E-13 "HIST2H2AA3, NCBP1, HMGB2, NUP98, HP1BP3, SNRPD3, NAP1L1, ANLN, H1FX, SMNDC1, TFAM, HIST1H2BM, EIF3A, DDX23, HIST1H4A, ICT1, USP39, NPM1, TUBG1, HIST2H3A, H1F0, NUP133, PRPF31, TCP1, HIST1H1D, TSR1, HIST1H1C, HIST1H1B, NASP, SF1, MCM2, SF3A2, SF3A1, PRPF6, SF3A3, ADRM1, NUP205, SNRNP200, SMARCA5, SNRPB, SUPT16H, HSPD1, XRN2" 430 357 13528 3.789355742 2.67E-10 1.78E-11 2.83E-10
GOTERM_BP_FAT GO:0034622~cellular macromolecular complex assembly 38 7.723577236 7.08E-12 "NCBP1, HIST2H2AA3, HMGB2, NUP98, HP1BP3, SNRPD3, NAP1L1, H1FX, ANLN, SMNDC1, TFAM, HIST1H2BM, EIF3A, DDX23, HIST1H4A, USP39, NPM1, TUBG1, HIST2H3A, H1F0, PRPF31, TCP1, HIST1H1D, TSR1, HIST1H1C, HIST1H1B, SF1, MCM2, SF3A2, SF3A1, PRPF6, SF3A3, ADRM1, NUP205, SNRNP200, SMARCA5, SNRPB, HSPD1" 430 318 13528 3.759426649 1.12E-08 5.58E-10 1.18E-08
GOTERM_BP_FAT GO:0043933~macromolecular complex subunit organization 54 10.97560976 4.87E-09 "HIST2H2AA3, NCBP1, HP1BP3, SNRPD3, NAP1L1, H1FX, MKI67IP, SMNDC1, HIST1H2BM, DDX23, GOPC, TUBG1, ZW10, H1F0, PRPF31, NUP133, HIST1H1D, HIST1H1C, DARS, HIST1H1B, SF1, MPP6, MCM2, PRPF6, JUP, ADRM1, GTF2I, NUP205, RRM1, SNRNP200, SNRPB, SMARCA5, XRN2, PPP5C, HMGB2, NUP98, ANLN, POLR2A, TFAM, EIF3A, HIST1H4A, ICT1, NPM1, USP39, HIST2H3A, TCP1, TSR1, NASP, SF3A2, SF3A1, SF3A3, GTF2F2, SUPT16H, HSPD1" 430 710 13528 2.392767769 7.68E-06 2.65E-07 8.14E-06
GOTERM_BP_FAT GO:0065003~macromolecular complex assembly 49 9.959349593 7.85E-08 "NCBP1, HIST2H2AA3, HP1BP3, SNRPD3, NAP1L1, MKI67IP, H1FX, SMNDC1, HIST1H2BM, DDX23, GOPC, TUBG1, ZW10, H1F0, PRPF31, HIST1H1D, DARS, HIST1H1C, HIST1H1B, SF1, MPP6, MCM2, PRPF6, JUP, ADRM1, GTF2I, NUP205, RRM1, SNRNP200, SNRPB, SMARCA5, PPP5C, NUP98, HMGB2, ANLN, POLR2A, TFAM, EIF3A, HIST1H4A, NPM1, USP39, HIST2H3A, TCP1, TSR1, SF3A2, SF3A1, SF3A3, GTF2F2, HSPD1" 430 665 13528 2.318139535 1.24E-04 3.09E-06 1.31E-04
GOTERM_BP_FAT GO:0006461~protein complex assembly 21 4.268292683 0.181579753 "NUP98, TCP1, DARS, MPP6, ANLN, MKI67IP, POLR2A, JUP, TFAM, ADRM1, GTF2I, NUP205, GOPC, RRM1, NPM1, GTF2F2, SMARCA5, HSPD1, TUBG1, ZW10, PPP5C" 430 505 13528 1.308256965 1 0.797284241 96.48992452
GOTERM_BP_FAT GO:0070271~protein complex biogenesis 21 4.268292683 0.181579753 "NUP98, TCP1, DARS, MPP6, ANLN, MKI67IP, POLR2A, JUP, TFAM, ADRM1, GTF2I, NUP205, GOPC, RRM1, NPM1, GTF2F2, SMARCA5, HSPD1, TUBG1, ZW10, PPP5C" 430 505 13528 1.308256965 1 0.797284241 96.48992452
GOTERM_BP_FAT GO:0043623~cellular protein complex assembly 8 1.62601626 0.255226631 "ADRM1, TFAM, NUP98, TCP1, NUP205, ANLN, TUBG1, HSPD1" 430 162 13528 1.553603216 1 0.888306315 99.274294

Annotation Cluster 14 Enrichment Score: 5.439511371946516
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0016585~chromatin remodeling complex 16 3.25203252 6.13E-09 "TBL1XR1, RBBP4, MTA2, RBBP7, CBX5, HDAC2, CSNK2A1, HDAC1, SMARCC1, SMARCC2, GATAD2A, SMARCA5, ACTL6A, SMARCA1, CHD4, SMARCA4" 415 71 12782 6.94084507 2.38E-06 9.14E-08 8.51E-06
GOTERM_CC_FAT GO:0016581~NuRD complex 8 1.62601626 5.16E-08 "CSNK2A1, RBBP4, HDAC2, HDAC1, MTA2, GATAD2A, RBBP7, CHD4" 415 13 12782 18.95384615 2.00E-05 7.14E-07 7.16E-05
GOTERM_CC_FAT GO:0017053~transcriptional repressor complex 11 2.235772358 5.20E-07 "TBL1XR1, CSNK2A1, RBBP4, HDAC2, HDAC1, MTA2, SMARCC2, GATAD2A, RBBP7, CHD4, CBX5" 415 41 12782 8.263414634 2.02E-04 6.72E-06 7.22E-04
GOTERM_CC_FAT GO:0000118~histone deacetylase complex 10 2.032520325 5.02E-06 "TBL1XR1, CSNK2A1, RBBP4, HDAC2, HDAC1, MTA2, GATAD2A, RBBP7, CHD4, CBX5" 415 41 12782 7.512195122 0.001944822 5.41E-05 0.006966902
GOTERM_CC_FAT GO:0070822~Sin3-type complex 4 0.81300813 0.001672981 "CSNK2A1, RBBP4,

HDAC2, HDAC1" 415 8 12782 15.4 0.477776709 0.012182916 2.298261447

GOTERM_CC_FAT GO:0016580~Sin3 complex 4 0.81300813 0.001672981 "CSNK2A1, RBBP4, HDAC2, HDAC1" 415 8 12782 15.4 0.477776709 0.012182916 2.298261447

Annotation Cluster 15 Enrichment Score: 5.102989438724152

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0000502~proteasome complex 18 3.658536585 4.98E-12 "UBE3A, PSMA7, PAAF1, PSMA1, ADRM1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8" 415 61 12782 9.08852459 1.93E-09 1.14E-10 6.92E-09

GOTERM_BP_FAT GO:0051436~negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle 16 3.25203252 1.26E-09 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 65 13528 7.74411449 1.98E-06 8.25E-08 2.10E-06

GOTERM_BP_FAT GO:0031145~anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process 16 3.25203252 1.26E-09 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 65 13528 7.74411449 1.98E-06 8.25E-08 2.10E-06

GOTERM_BP_FAT GO:0051444~negative regulation of ubiquitin-protein ligase activity 16 3.25203252 1.98E-09 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 67 13528 7.512946893 3.12E-06 1.20E-07 3.30E-06

GOTERM_BP_FAT GO:0051352~negative regulation of ligase activity 16 3.25203252 1.98E-09 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 67 13528 7.512946893 3.12E-06 1.20E-07 3.30E-06

GOTERM_BP_FAT GO:0051439~regulation of ubiquitin-protein ligase activity during mitotic cell cycle 16 3.25203252 4.65E-09 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 71 13528 7.08968228 7.34E-06 2.62E-07 7.78E-06

GOTERM_BP_FAT GO:0000278~mitotic cell cycle 36 7.317073171 7.46E-09 "ANLN, PSMA7, RCC1, NUMA1, PSMB7, NCAPH, RAD21, TARDBP, PSMB2, PSMD4, PSMD6, STAG2, BUB3, PSMD8, ZW10, KHDRBS1, PDS5A, CKAP5, SUGT1, SMC3, CDK2, NCAPD2, PSMA1, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMC1, PSMA3, CDK11B, PES1, SMC1A, NUP43, PPP5C" 430 370 13528 3.061018228 1.18E-05 3.92E-07 1.25E-05

GOTERM_BP_FAT GO:0031397~negative regulation of protein ubiquitination 16 3.25203252 8.51E-09 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 74 13528 6.802262728 1.34E-05 4.33E-07 1.42E-05

GOTERM_BP_FAT GO:0051438~regulation of ubiquitin-protein ligase activity 16 3.25203252 1.81E-08 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 78 13528 6.453428742 2.86E-05 8.67E-07 3.03E-05

GOTERM_BP_FAT GO:0051437~positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle 15 3.048780488 2.17E-08 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8" 430 68 13528 6.939808482 3.43E-05 1.01E-06 3.63E-05

GOTERM_BP_FAT GO:0051340~regulation of ligase activity 16 3.25203252 3.10E-08 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 81 13528 6.214412862 4.89E-05 1.40E-06 5.18E-05

GOTERM_BP_FAT GO:0051443~positive regulation of ubiquitin-protein ligase activity 15 3.048780488 3.22E-08 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8" 430 70 13528 6.741528239 5.07E-05 1.37E-06 5.37E-05

GOTERM_BP_FAT GO:0031398~positive regulation of protein ubiquitination 16 3.25203252 5.17E-08 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, DNAJA3, PSMD8" 430 84 13528 5.992469546 8.15E-05 2.14E-06 8.64E-05

GOTERM_BP_FAT GO:0051351~positive regulation of ligase activity 15 3.048780488 5.64E-08 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8" 430 73 13528 6.464479133 8.89E-05 2.28E-06 9.43E-05

GOTERM_BP_FAT GO:0031396~regulation of protein ubiquitination 17 3.455284553 9.26E-08 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, DNAJA3, PSMD8, BUB3" 430 100 13528 5.34827907 1.46E-04 3.56E-06 1.55E-04

GOTERM_BP_FAT GO:0043161~proteasomal ubiquitin-dependent protein catabolic process 17 3.455284553 1.23E-07 "TBL1XR1, PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 102 13528 5.243410853 1.94E-04 4.52E-06 2.06E-04

GOTERM_BP_FAT GO:0010498~proteasomal protein catabolic process 17 3.455284553 1.23E-07 "TBL1XR1, PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 102 13528 5.243410853 1.94E-04 4.52E-06 2.06E-04

GOTERM_BP_FAT GO:0031400~negative regulation of protein modification process 17 3.455284553 1.07E-06 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, DNMT1, PSMD4, PSMD6, PSMD8, BUB3" 430 119 13528 4.494352159 0.001679302 3.36E-05 0.001781515

GOTERM_BP_FAT GO:0032269~negative regulation of cellular protein metabolic process 21 4.268292683 1.11E-06 "IGF2BP2, PSMA7, EIF4A3, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, DNMT1, PSMD4, PSMD6, EIF2B3, PSMD8, BUB3, EIF2B5" 430 180 13528 3.670387597 0.001754727 3.44E-05 0.001861601

GOTERM_BP_FAT GO:0051248~negative regulation of protein metabolic process 21 4.268292683 2.03E-06 "IGF2BP2, PSMA7, EIF4A3, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, DNMT1, PSMD4, PSMD6, EIF2B3, PSMD8, BUB3, EIF2B5" 430 187 13528 3.532993409 0.00319913 5.93E-05 0.003396407

GOTERM_BP_FAT GO:0010605~negative regulation of macromolecule metabolic process 48 9.756097561 3.27E-06 "HMGB1, COPS2, HMGB2, FOXK1, RBM3, CBX3, IGF2BP2, PSMA7, CBX5, SRRT, SUMO1, PSMB7, HEXIM1, DRAP1, NPM1, PSMB2, GATAD2A, PSMD4, PSMD6, SUPT5H, EIF2B3, PSMD8, BUB3, EIF2B5, KHDRBS1, TBL1XR1, MSH2, MTA2, TRIM28, ILF3, RBBP7, EIF4A3, PSMA1, PSMC6, PSMD13, HDAC2, PSMC5, HDAC1, TRIM33, PSMC3, PSMC2, PSMA4, PSMA3, SMARCC2, PSMC1, DNMT1, RBM15, SMARCA4" 430 734 13528 2.057360117 0.005136471 9.20E-05 0.005458463

GOTERM_BP_FAT GO:0006511~ubiquitin-dependent protein catabolic process 21 4.268292683 9.07E-05 "USP7, TBL1XR1, UBE3A, PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, UBR5, PSMC2, PSMA4, PSMB2, USP39, PSMC1, PSMA3, PSMD4, PSMD6, PSMD8, BUB3" 430 242 13528 2.730040361 0.133346627 0.001985751 0.151585962

GOTERM_BP_FAT GO:0031401~positive regulation of protein modification process 18 3.658536585 9.56E-05 "DOCK7, PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, DNMT1, PSMD4, PSMD6, DNAJA3, PSMD8" 430 187 13528 3.028280065 0.139941704 0.002063008 0.159670502

GOTERM_BP_FAT GO:0032270~positive regulation of cellular protein metabolic process 20 4.06504065 1.61E-04 "DOCK7, PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, HDAC2, PSMC5, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, DNMT1, PSMD4, PSMD6, DNAJA3, PSMD8, EIF2B5" 430 233 13528 2.700469109 0.224528785 0.003213615 0.269174672

GOTERM_BP_FAT GO:0032268~regulation of cellular protein metabolic process 31 6.300813008 2.59E-04 "NCBP1, IGF2BP2, PSMA7, PSMB7, EIF3H, TRMT6, PSMB2, QKI, PSMD4, PSMD6, EIF2B3, BUB3, DNAJA3, PSMD8, EIF2B5, DOCK7, SARNP, EIF4A3, PSMA1, PSMC6, PSMD13, PSMC5, HDAC2, PSMC3, PSMC2, EIF2S1, EIF4H, PSMA4, PSMC1, PSMA3, DNMT1" 430 474 13528 2.057540968 0.335628208 0.004856187 0.432503915

GOTERM_BP_FAT GO:0051247~positive regulation of protein metabolic process 20 4.06504065 2.76E-04 "DOCK7, PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, HDAC2, PSMC5, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, DNMT1, PSMD4, PSMD6, DNAJA3, PSMD8, EIF2B5" 430 243 13528 2.589338693 0.353070278 0.005051357 0.460578093

GOTERM_MF_FAT GO:0004298~threonine-type endopeptidase activity 6 1.219512195 3.10E-04 "PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, PSMA7" 408 20 12983 9.546323529 0.138098656 0.004782542 0.443106395

GOTERM_MF_FAT GO:0070003~threonine-type peptidase activity 6 1.219512195 3.10E-04 "PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, PSMA7" 408 20 12983 9.546323529 0.138098656 0.004782542 0.443106395

GOTERM_CC_FAT GO:0005839~proteasome core complex 6 1.219512195 3.61E-04 "PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, PSMA7" 415 20 12782 9.24 0.130593967 0.002794987 0.49960029

GOTERM_BP_FAT GO:0044265~cellular macromolecule catabolic process 41 8.333333333 4.60E-04 "USP7, NCBP1, UBE3A, PABPC4, SAE1, PSMA7, EXOSC10, RPA1, SUMO1, PSMB7, USP39, PSMB2, CACYBP, HNRNPD, PSMD4, RANBP2, PSMD6, PSMD8, FEN1, BUB3, TBL1XR1, EXOSC7, RNPS1, SUGT1, ATG3, EIF4A3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, PSMC2, PSMA4, UBR5, UBA2, PSMA3, PSMC1, POP1, XRN2" 430 725 13528 1.779143545 0.515881332 0.008209584 0.765990885

GOTERM_BP_FAT GO:0009057~macromolecule catabolic process 42 8.536585366 0.001023923 "USP7, NCBP1, UBE3A, PABPC4, SAE1, PSMA7, EXOSC10, RPA1, SUMO1, PSMB7, USP39, PSMB2, CACYBP, HNRNPD, PSMD4, RANBP2, PSMD6, PSMD8, FEN1, BUB3, TBL1XR1, EXOSC7, RNPS1, SUGT1, ATG3, EIF4A3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, PSMC2, PSMA4, UBR5, UBA2, PSMA3, PSMC1, POP1, YME1L1, XRN2" 430 781 13528 1.691855999 0.80121951 0.017790449 1.697883418

GOTERM_BP_FAT GO:0043086~negative regulation of catalytic activity 19 3.861788618 0.003237997 "PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, AKT1S1, HEXIM1, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, DNAJA3, PSMD8, BUB3" 430 277 13528 2.15793804 0.993991653 0.051361892 5.277065918

GOTERM_BP_FAT GO:0044092~negative regulation of molecular function 21 4.268292683 0.004967902 "PSMA7, PSMA1, SUMO1, PSMB7, PSMC6, PSMD13, HDAC2, PSMC5, AKT1S1, HEXIM1, PSMC3, PSMC2, PSMA4, PSMB2, PSMC1, PSMA3, PSMD4, PSMD6, DNAJA3, PSMD8, BUB3" 430 334 13528 1.978053196 0.999611767 0.075534049 7.98790994

GOTERM_BP_FAT GO:0031399~regulation of protein modification process 19 3.861788618 0.00620694 "DOCK7, PSMA7, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMB2, PSMC1, PSMA3, DNMT1, PSMD4, PSMD6, DNAJA3, PSMD8, BUB3" 430 295 13528 2.026267245 0.999945584 0.092640297 9.884526154

GOTERM_BP_FAT GO:0019941~modification-dependent protein catabolic process 30 6.097560976 0.009144492 "USP7, UBE3A, SAE1, PSMA7, SUMO1, PSMB7, PSMB2, CACYBP, USP39, PSMD4, RANBP2, PSMD6, BUB3, PSMD8, TBL1XR1, SUGT1, ATG3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, UBA2, UBR5, PSMA4, PSMC2, PSMC1, PSMA3" 430 574 13528 1.64427518 0.999999489 0.12774349 14.23525414

GOTERM_BP_FAT GO:0043632~modification-dependent macromolecule catabolic process 30 6.097560976 0.009144492 "USP7, UBE3A, SAE1, PSMA7, SUMO1, PSMB7, PSMB2, CACYBP, USP39, PSMD4, RANBP2, PSMD6, BUB3, PSMD8, TBL1XR1, SUGT1, ATG3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, UBA2, UBR5, PSMA4, PSMC2, PSMC1, PSMA3" 430 574 13528 1.64427518 0.999999489 0.12774349 14.23525414

GOTERM_BP_FAT GO:0030163~protein catabolic process 31 6.300813008 0.014747335 "USP7, UBE3A, SAE1, PSMA7, SUMO1, PSMB7, PSMB2, CACYBP, USP39, PSMD4, RANBP2, PSMD6, BUB3, PSMD8, TBL1XR1, SUGT1, ATG3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, UBA2, UBR5, PSMA4, PSMC2, PSMC1, PSMA3, YME1L1" 430 622 13528 1.567965303 1 0.174731948 21.99144207

GOTERM_BP_FAT GO:0051603~proteolysis involved in cellular protein catabolic process 30 6.097560976 0.01612555 "USP7, UBE3A, SAE1, PSMA7, SUMO1, PSMB7, PSMB2, CACYBP, USP39, PSMD4, RANBP2, PSMD6, BUB3, PSMD8, TBL1XR1, SUGT1, ATG3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, UBA2, UBR5, PSMA4, PSMC2, PSMC1, PSMA3" 430 600 13528 1.573023256 1 0.186778779 23.7956052

GOTERM_BP_FAT GO:0044257~cellular protein catabolic process 30 6.097560976 0.017559102 "USP7, UBE3A, SAE1, PSMA7, SUMO1, PSMB7, PSMB2, CACYBP, USP39, PSMD4, RANBP2, PSMD6, BUB3, PSMD8, TBL1XR1, SUGT1, ATG3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, UBA2, UBR5, PSMA4, PSMC2, PSMC1, PSMA3" 430 603 13528 1.565197269 1 0.200279993 25.63053624

GOTERM_BP_FAT GO:0043085~positive regulation of catalytic activity 23 4.674796748 0.103733855 "MSH2, DOCK7, PSMA7, SCRIB, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, GNAQ, PSMC3, PSMC2, PSMA4, PSMB2, NPM1, PSMC1, PSMA3, GNAS, PSMD4, HSPD1, PSMD6, DNAJA3, PSMD8" 430 520 13528 1.391520572 1 0.635780351 83.96980909

GOTERM_BP_FAT GO:0044093~positive regulation of molecular function 24 4.87804878 0.171381592 "MSH2, DOCK7, PSMA7, SCRIB, PSMA1, PSMB7, PSMC6, PSMD13, PSMC5, GNAQ, PSMC3, PSMC2, PSMA4, PSMB2, NPM1, PSMC1, PSMA3, GNAS, PSMD4, HSPD1, PSMD6, DNAJA3, PSMD8, SMARCA4" 430 586

13528 1.288483213 1 0.784783027 95.68263832
GOTERM_BP_FAT GO:0006508~proteolysis 36 7.317073171 0.407130428 "UQCRC2, USP7, METAP2, UBE3A, SAE1, PSMA7, SUMO1, PSMB7, USP39, PSMB2, CACYBP, PSMD4, RANBP2, PSMD6, BUB3, PSMD8, TBL1XR1, OSGEP, SUGT1, ATG3, PSMA1, UHRF1, PSMC6, PSMD13, PSMC5, TRIM33, PSMC3, PSMC2, UBR5, UBA2, PSMA4, PSMC1, PSMA3, YME1L1, CPD, PMPCB" 430 1054 13528 1.074550991 1 0.968694838 99.98397513

Annotation Cluster 16 Enrichment Score: 5.095043468863092
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007049~cell cycle 60 12.19512195 2.87E-10 "DTYMK, MCM7, RAD21, TARDBP, PSMD4, TUBG1, PSMD6, SUPT5H, STAG2, PSMD8, ZW10, CCAR1, KHDRBS1, RBBP4, LIG3, SF1, CDC5L, MCM2, MCM3, RAD50, CDK2, NCAPD2, MCM6, PSMA1, PPM1G, UHRF1, PSMA4, PSMA3, CDK11B, NUP43, PPP5C, MRE11A, HCFC1, ANLN, RCC1, PSMA7, RPA1, NUMA1, PSMB7, NCAPH, PSMB2, NPM1, BUB3, PDS5A, MKI67, CKAP5, MSH2, NASP, ILF3, SUGT1, SMC3, PSMC6, PSMD13, PSMC5, PSMC3, PSMC2, PSMC1, SMC1A, PES1, MYH10"430 776 13528 2.432510189 4.53E-07 2.16E-08 4.81E-07
GOTERM_BP_FAT GO:0022402~cell cycle process 48 9.756097561 1.29E-09 "MRE11A, ANLN, PSMA7, RCC1, RPA1, NUMA1, PSMB7, NCAPH, RAD21, TARDBP, PSMB2, NPM1, PSMD4, TUBG1, PSMD6, STAG2, PSMD8, BUB3, ZW10, KHDRBS1, MKI67, PDS5A, CKAP5, MSH2, SF1, LIG3, ILF3, SUGT1, RAD50, SMC3, CDK2, NCAPD2, PPM1G, PSMA1, PSMC6, PSMD13, PSMC5, PSMC3, PSMC2, PSMA4, PSMA3, PSMC1, CDK11B, PES1, SMC1A, NUP43, PPP5C, MYH10" 430 565 13528 2.672747479 2.03E-06 8.12E-08 2.15E-06
GOTERM_BP_FAT GO:0000278~mitotic cell cycle 36 7.317073171 7.46E-09 "ANLN, PSMA7, RCC1, NUMA1, PSMB7, NCAPH, RAD21, TARDBP, PSMB2, PSMD4, PSMD6, STAG2, BUB3, PSMD8, ZW10, KHDRBS1, PDS5A, CKAP5, SUGT1, SMC3, CDK2, NCAPD2, PSMA1, PSMC6, PSMD13, PSMC5, PSMC3, PSMA4, PSMC2, PSMC1, PSMA3, CDK11B, PES1, SMC1A, NUP43, PPP5C" 430 370 13528 3.061018228 1.18E-05 3.92E-07 1.25E-05
GOTERM_BP_FAT GO:0000279~M phase 28 5.691056911 6.27E-06 "MRE11A, ANLN, RCC1, RPA1, NCAPH, NUMA1, RAD21, TARDBP, TUBG1, BUB3, STAG2, ZW10, MKI67, PDS5A, CKAP5, LIG3, ILF3, SUGT1, RAD50, CDK2, SMC3, NCAPD2, PSMD13, CDK11B, PES1, SMC1A, NUP43, PPP5C" 430 329 13528 2.677486393 0.009844821 1.65E-04 0.010486517
GOTERM_BP_FAT GO:0007067~mitosis 20 4.06504065 7.56E-05 "PDS5A, CKAP5, ANLN, SUGT1, RCC1, CDK2, SMC3, NCAPD2, NCAPH, NUMA1, RAD21, TARDBP, CDK11B, PES1, SMC1A, NUP43, BUB3, STAG2, ZW10, PPP5C"430 220 13528 2.860042283 0.112334846 0.001700847 0.126228773
GOTERM_BP_FAT GO:0000280~nuclear division 20 4.06504065 7.56E-05 "PDS5A, CKAP5, ANLN, SUGT1, RCC1, CDK2, SMC3, NCAPD2, NCAPH, NUMA1, RAD21, TARDBP, CDK11B, PES1, SMC1A, NUP43, BUB3, STAG2, ZW10, PPP5C" 430 220 13528 2.860042283 0.112334846 0.001700847 0.126228773
GOTERM_BP_FAT GO:0000087~M phase of mitotic cell cycle 20 4.06504065 9.60E-05 "PDS5A, CKAP5, ANLN, SUGT1, RCC1, CDK2, SMC3, NCAPD2, NCAPH, NUMA1, RAD21, TARDBP, CDK11B, PES1, SMC1A, NUP43, BUB3, STAG2, ZW10, PPP5C" 430 224 13528 2.8089701 0.14054577 0.002044633 0.160414057
GOTERM_BP_FAT GO:0048285~organelle fission 20 4.06504065 1.29E-04 "PDS5A, CKAP5, ANLN, SUGT1, RCC1, CDK2, SMC3, NCAPD2, NCAPH, NUMA1, RAD21, TARDBP, CDK11B, PES1, SMC1A, NUP43, BUB3, STAG2, ZW10, PPP5C" 430 229 13528 2.747638875 0.183535956 0.002629943 0.214704832
GOTERM_BP_FAT GO:0022403~cell cycle phase 29 5.894308943 1.38E-04 "MRE11A, ANLN, RCC1, RPA1, NCAPH, NUMA1, RAD21, TARDBP, TUBG1, BUB3, STAG2, ZW10, KHDRBS1, MKI67, PDS5A, CKAP5, LIG3, ILF3, SUGT1, RAD50, CDK2, SMC3, NCAPD2, PSMD13, CDK11B, PES1, SMC1A, NUP43, PPP5C" 430 414 13528 2.203752387 0.195774235 0.002789375 0.230677965
GOTERM_BP_FAT GO:0007059~chromosome segregation 9 1.829268293 0.004078612 "NCAPH, RAD21, SMC1A, NUP43, SMC3, BUB3, STAG2, NCAPD2, ZW10" 430 81 13528 3.495607235 0.998411752 0.063028355 6.603594497
GOTERM_BP_FAT GO:0051301~cell division 18 3.658536585 0.013103156 "PDS5A, CKAP5, LIG3, ANLN, RCC1, SMC3, CDK2, MCM5, NCAPD2, NCAPH, RAD21, CDK11B, SMC1A, NUP43, STAG2, MYH10, ZW10, CDK13" 430 295 13528 1.9196216 0.999999999 0.162873367 19.78659097

Annotation Cluster 17 Enrichment Score: 5.073809361051923

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0050658~RNA transport 26 5.284552846 1.92E-16 "NCBP1, NUP98, NUP160, NUP93, NUP214, NPM1, QKI, NUP54, RANBP2, TPR, NUP35, XPOT, PABPN1, NUP133, NUP153, NUP88, CKAP5, HNRNPA2B1, NUP85, NUP155, HNRNPA1, EIF4A3, NUP205, NUP107, NUP43, LRPPRC" 430 97 13528 8.43270199 3.50E-13 4.37E-14 3.66E-13

GOTERM_BP_FAT GO:0050657~nucleic acid transport 26 5.284552846 1.92E-16 "NCBP1, NUP98, NUP160, NUP93, NUP214, NPM1, QKI, NUP54, RANBP2, TPR, NUP35, XPOT, PABPN1, NUP133, NUP153, NUP88, CKAP5, HNRNPA2B1, NUP85, NUP155, HNRNPA1, EIF4A3, NUP205, NUP107, NUP43, LRPPRC" 430 97 13528 8.43270199 3.50E-13 4.37E-14 3.66E-13

GOTERM_BP_FAT GO:0051236~establishment of RNA localization 26 5.284552846 1.92E-16 "NCBP1, NUP98, NUP160, NUP93, NUP214, NPM1, QKI, NUP54, RANBP2, TPR, NUP35, XPOT, PABPN1, NUP133, NUP153, NUP88, CKAP5, HNRNPA2B1, NUP85, NUP155, HNRNPA1, EIF4A3, NUP205, NUP107, NUP43, LRPPRC" 430 97 13528 8.43270199 3.50E-13 4.37E-14 3.66E-13

GOTERM_BP_FAT GO:0006403~RNA localization 26 5.284552846 4.20E-16 "NCBP1, NUP98, NUP160, NUP93, NUP214, NPM1, QKI, NUP54, RANBP2, TPR, NUP35, XPOT, PABPN1, NUP133, NUP153, NUP88, CKAP5, HNRNPA2B1, NUP85, NUP155, HNRNPA1, EIF4A3, NUP205, NUP107, NUP43, LRPPRC" 430 100 13528 8.17972093 7.00E-13 7.78E-14 7.44E-13

GOTERM_BP_FAT "GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport" 26 5.284552846 1.00E-14 "NCBP1, NUP98, NUP160, NUP93, NUP214, NPM1, QKI, NUP54, RANBP2, TPR, NUP35, XPOT, PABPN1, NUP133, NUP153, NUP88, CKAP5, HNRNPA2B1, NUP85, NUP155, HNRNPA1, EIF4A3, NUP205, NUP107, NUP43, LRPPRC" 430 113 13528 7.238691089 1.58E-11 1.43E-12 1.67E-11

GOTERM_BP_FAT GO:0051028~mRNA transport 22 4.471544715 2.28E-13 "PABPN1, NUP133, NCBP1, NUP153, NUP98, NUP160, NUP88, NUP93, NUP85, NUP155, HNRNPA1, EIF4A3, NUP214, NUP205, QKI, NUP54, NUP107, RANBP2, NUP35, TPR, NUP43, LRPPRC" 430 87 13528 7.955519914 3.59E-10 2.24E-11 3.80E-10

GOTERM_CC_FAT GO:0005635~nuclear envelope 29 5.894308943 1.04E-10 "NUP98, NUP160, CBX3, NUP93, CBX5, SUMO1, NUP214, CACYBP, MRPL19, NUP54, RANBP2, TPR, NUP35, XPOT, NUP133, NUP153, NUP88, NUP85, NUP155, SYNE1, BNIP1, NUP205, PCNA, TMPO, NUP107, PARP1, NUP43, MATR3, LRPPRC" 415 205 12782 4.357073171 4.04E-08 2.02E-09 1.45E-07

GOTERM_CC_FAT GO:0005643~nuclear pore 18 3.658536585 4.34E-10 "XPOT, NUP133, NUP98, NUP153, NUP160, NUP88, NUP93, NUP85, NUP155, SUMO1, NUP214, NUP205, NUP54, RANBP2, NUP107, NUP35, TPR, NUP43" 415 79 12782 7.017721519 1.68E-07 7.02E-09 6.03E-07

GOTERM_CC_FAT GO:0046930~pore complex 19 3.861788618 1.20E-09 "XPOT, NUP133, NUP98, NUP153, NUP160, NUP88, TOMM40, NUP93, NUP85, NUP155, SUMO1, NUP214, NUP205, NUP54, RANBP2, NUP107, NUP35, TPR, NUP43" 415 95 12782 6.16 4.65E-07 1.86E-08 1.66E-06

GOTERM_CC_FAT GO:0031967~organelle envelope 44 8.943089431 1.94E-06 "UQCRC2, NUP98, NUP160, HK2, CHCHD3, NUP93, CBX3, TIMM50, CBX5, SUMO1, NUP214, CACYBP, MRPL19, CSDE1, RANBP2, NUP54, NUP35, TPR, TOMM34, GPD2, XPOT, NUP133, NUP153, NUP88, NDUFA9, TOMM40, NUP85, NUP155, NDUFA10, SDHA, SDHB, SYNE1, BNIP1, NUP205, NDUFV1, PCNA, NUP107, TMPO, HSPD1, PARP1, NUP43, MATR3, LRPPRC, PMPCB" 415 620 12782 2.185806452 7.52E-04 2.35E-05 0.002693591

GOTERM_CC_FAT GO:0031975~envelope 44 8.943089431 2.11E-06 "UQCRC2, NUP98, NUP160, HK2, CHCHD3, NUP93, CBX3, TIMM50, CBX5, SUMO1, NUP214, CACYBP, MRPL19, CSDE1, RANBP2, NUP54, NUP35, TPR, TOMM34, GPD2, XPOT, NUP133, NUP153, NUP88, NDUFA9, TOMM40, NUP85, NUP155, NDUFA10, SDHA, SDHB, SYNE1, BNIP1, NUP205, NDUFV1, PCNA, NUP107, TMPO, HSPD1, PARP1, NUP43, MATR3, LRPPRC, PMPCB" 415 622 12782 2.178778135 8.18E-04 2.48E-05 0.002929989

GOTERM_BP_FAT GO:0006913~nucleocytoplasmic transport 18 3.658536585 9.24E-06 "XPOT, PABPN1, NUP133, NCBP1, NUP98, NUP160, NUP155, HNRNPA1, NUP214, NUP205, NPM1, NOP58, NUP54, NUP107, RANBP2, TPR, MYBBP1A, HSPA9" 430 156 13528 3.630053667 0.014460186 2.39E-04 0.015438284

GOTERM_BP_FAT GO:0051169~nuclear transport 18 3.658536585 1.10E-05 "XPOT, PABPN1, NUP133, NCBP1, NUP98, NUP160, NUP155, HNRNPA1, NUP214, NUP205, NPM1, NOP58, NUP54, NUP107, RANBP2, TPR, MYBBP1A, HSPA9" 430 158 13528 3.584103621 0.017123004 2.74E-04 0.018305637

GOTERM_BP_FAT GO:0051168~nuclear export 10 2.032520325 1.05E-04 "XPOT, PABPN1, NUP133,

NCBP1, NUP214, NUP160, NPM1, NUP107, HNRNPA1, HSPA9"	430	60	13528	5.243410853	0.152565901	0.002175816	0.175318345
GOTERM_BP_FAT	GO:0006405~RNA export from nucleus	8	1.62601626	2.71E-04	"XPOT, PABPN1, NUP133, NCBP1, NUP160, NPM1, NUP107, HNRNPA1"	430	41	13528	6.13862734	0.348232499	0.005023427	0.452717016
GOTERM_BP_FAT	GO:0015031~protein transport	37	7.520325203	0.010861901	"NUP98, NUP160, VPS52, NUP93, TIMM50, SRP19, AIP, NUP214, GOPC, NPM1, RANBP3, NUP54, RANBP2, TPR, NUP35, RAB21, ZW10, HSPA9, TNPO3, TOMM34, NUP133, NUP153, SNX27, NUP88, NASP, TOMM40, NUP85, NUP155, ATG3, COG6, NUP205, PCNA, NOP58, GNAS, NUP107, NUP43, COG1"	430	762	13528	1.527607886	0.999999967	0.14493009	16.68656609
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	37	7.520325203	0.012471869	"NUP98, NUP160, VPS52, NUP93, TIMM50, SRP19, AIP, NUP214, GOPC, NPM1, RANBP3, NUP54, RANBP2, TPR, NUP35, RAB21, ZW10, HSPA9, TNPO3, TOMM34, NUP133, NUP153, SNX27, NUP88, NASP, TOMM40, NUP85, NUP155, ATG3, COG6, NUP205, PCNA, NOP58, GNAS, NUP107, NUP43, COG1"	430	769	13528	1.513702483	0.999999997	0.158107336	18.92457022
GOTERM_CC_FAT	GO:0012505~endomembrane system	38	7.723577236	0.013029435	"NUP98, NUP160, VAPB, RER1, NUP93, CBX3, CBX5, SUMO1, NUP214, CACYBP, MRPL19, PCYT1A, RANBP2, NUP54, NUP35, TPR, RAB21, XPOT, NUP133, NUP153, SPTLC1, SPTLC2, NUP88, NUP85, NUP155, SYNE1, BNIP1, NUP205, PCNA, GNAS, NUP107, TMPO, HSPD1, PARP1, NUP43, MATR3, LRPPRC, GOLGB1"	415	782	12782	1.496675192	0.993833627	0.075300849	16.64975747
GOTERM_BP_FAT	GO:0046907~intracellular transport	32	6.504065041	0.017736035	"NCBP1, NUP98, NUP160, RER1, KLC2, SRP19, AIP, NUP214, GOPC, NPM1, RANBP3, NUP54, RANBP2, TPR, ZW10, TOMM34, HSPA9, XPOT, PABPN1, NUP133, TOMM40, NUP155, HNRNPA1, NUP205, PCNA, NOP58, GNAS, NUP107, MYBBP1A, LRPPRC, COG1, MYH10"	430	657	13528	1.53232098	1	0.200664158	25.8541059
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	10	2.032520325	0.042924971	"NUP98, MORC3, NUP205, TOMM40, NOP58, RANBP2, SRP19, TPR, AIP, TOMM34"	430	146	13528	2.154826378	1	0.379458028	51.97207087
GOTERM_BP_FAT	GO:0008104~protein localization	38	7.723577236	0.04907305	"NUP98, NUP160, VPS52, NUP93, TIMM50, SRP19, AIP, NUP214, MORC3, GOPC, NPM1, RANBP3, NUP54, RANBP2, TPR, NUP35, RAB21, ZW10, HSPA9, TNPO3, TOMM34, NUP133, NUP153, SNX27, NUP88, NASP, TOMM40, NUP85, NUP155, ATG3, COG6, NUP205, PCNA, NOP58, GNAS, NUP107, NUP43, COG1"	430	882	13528	1.35543954	1	0.41290032	56.87702196
GOTERM_BP_FAT	GO:0006605~protein targeting	12	2.43902439	0.081304938	"NUP214, NUP98, NUP205, TOMM40, NOP58, NUP54, RANBP2, SRP19, TPR, AIP, HSPA9, TOMM34"	430	215	13528	1.755932937	1	0.564224766	75.7688335
GOTERM_BP_FAT	GO:0017038~protein import	8	1.62601626	0.122984018	"NUP98, NUP205, TOMM40, NOP58, RANBP2, TPR, AIP, TOMM34"	430	131	13528	1.921249778	1	0.687340138	88.84894869
GOTERM_BP_FAT	GO:0051170~nuclear import	6	1.219512195	0.147185233	"NUP98, NUP205, NOP58, RANBP2, TPR, HNRNPA1"	430	88	13528	2.145031712	1	0.740730132	93.01493942
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	6	1.219512195	0.178148529	"NUP98, MORC3, NUP205, NOP58, RANBP2, TPR"	430	94	13528	2.008114795	1	0.793730915	96.23565966
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	5	1.016260163	0.290700905	"NUP98, NUP205, NOP58, RANBP2, TPR"	430	86	13528	1.829096809	1	0.915698463	99.67902558
GOTERM_BP_FAT	GO:0034613~cellular protein localization	16	3.25203252	0.325392318	"NUP98, TOMM40, SRP19, AIP, NUP214, MORC3, NUP205, NPM1, PCNA, NOP58, NUP54, RANBP2, TPR, TOMM34, HSPA9, ZW10"	430	411	13528	1.224738301	1	0.93663646	99.86118762
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	16	3.25203252	0.334535306	"NUP98, TOMM40, SRP19, AIP, NUP214, MORC3, NUP205, NPM1, PCNA, NOP58, NUP54, RANBP2, TPR, TOMM34, HSPA9, ZW10"	430	414	13528	1.215863386	1	0.940949259	99.8894993
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	14	2.845528455	0.411917298	"NUP98, TOMM40, SRP19, AIP, NUP214, NUP205, NPM1, PCNA, NOP58, NUP54, RANBP2, TPR, TOMM34, HSPA9"	430	374	13528	1.17766447	1	0.968105069	99.986006
GOTERM_BP_FAT	GO:0055085~transmembrane transport	20	4.06504065	0.44449567	"NUP133, NUP98, NUP153, NUP160, NUP88, TOMM40, NUP93, NUP85, TIMM50, NUP155, ATP6V1D, NUP214, NUP205, MFSD10,

NUP54, NUP107, RANBP2, NUP35, TPR, NUP43"	430	569	13528	1.105815997	1	0.974749484	99.99460234

GOTERM_CC_FAT	GO:0016021~integral to membrane	44	8.943089431	1	"NUP98, TMEM214, NUP160, VAPB, RER1, NUP93, TIMM50, HNRNPM, SUMO1, NUP214, RANBP2, NUP54, NUP35, TPR, HIGD1A, TOMM34, XPOT, NUP133, NUP153, SPTLC1, SPTLC2, NUP88, TOMM40, NUP85, NUP155, TMEM209, TECR, CAPRIN1, ADRM1, SYNE1, BNIP1, DSG3, SLC7A1, FER1L4, NUP205, TMEM165, MFSD10, NUP107, TMPO, HSPD1, CPD, NUP43, TEX10, GOLGB1"	415	5297	12782	0.25584293	1	1	100

GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	49	9.959349593	1	"VAPB, TIMM50, RANBP2, TPR, NUP35, NT5E, HIGD1A, RAB21, TOMM34, NUP133, SPTLC1, SPTLC2, NUP88, NUP85, TMEM209, TECR, ADRM1, BNIP1, FER1L4, NUP205, MFSD10, GNAS, CPD, NUP107, NUP43, NUP98, TMEM214, NUP160, RER1, NUP93, HNRNPM, SUMO1, NUP214, TGM1, NUP54, XPOT, NUP153, TOMM40, NUP155, CAPRIN1, NRAS, SYNE1, DSG3, SLC7A1, TMEM165, HSPD1, TMPO, TEX10, GOLGB1"	415	5485	12782	0.27515041	1	1	100

Annotation Cluster 18	Enrichment Score: 4.810173168547029

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_BP_FAT	GO:0048255~mRNA stabilization	7	1.422764228	3.85E-06	"DHX9, HNRNPD, ELAVL1, SYNCRIP, PABPC1, HNRNPU, YBX1"	430	15	13528	14.68155039	0.006060079	1.07E-04	0.006442926

GOTERM_BP_FAT	GO:0043489~RNA stabilization	7	1.422764228	3.85E-06	"DHX9, HNRNPD, ELAVL1, SYNCRIP, PABPC1, HNRNPU, YBX1"	430	15	13528	14.68155039	0.006060079	1.07E-04	0.006442926

GOTERM_BP_FAT	GO:0043488~regulation of mRNA stability	7	1.422764228	4.76E-05	"DHX9, HNRNPD, ELAVL1, SYNCRIP, PABPC1, HNRNPU, YBX1"	430	22	13528	10.01014799	0.072265972	0.001171348	0.079478061

GOTERM_BP_FAT	GO:0043487~regulation of RNA stability	7	1.422764228	8.13E-05	"DHX9, HNRNPD, ELAVL1, SYNCRIP, PABPC1, HNRNPU, YBX1"	430	24	13528	9.175968992	0.120338256	0.001804255	0.135816625

Annotation Cluster 19	Enrichment Score: 4.780130849609733

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_MF_FAT	GO:0003729~mRNA binding	13	2.642276423	8.15E-07	"PABPC4, ELAVL1, SYNCRIP, RNPS1, IGF2BP2, SSB, HNRPDL, EIF4A3, HNRNPD, HNRNPC, PABPC1, LUC7L3, RBM25"	408	66	12983	6.267788176	3.90E-04	3.25E-05	0.00116697

GOTERM_MF_FAT	GO:0003727~single-stranded RNA binding	8	1.62601626	1.46E-05	"HNRPDL, EIF4A3, PTBP1, PABPC4, SYNCRIP, PABPC1, HNRNPH1, HNRNPA1"	408	27	12983	9.428467683	0.006955713	3.49E-04	0.020855572

GOTERM_MF_FAT	GO:0008143~poly(A) RNA binding	5	1.016260163	6.03E-05	"HNRPDL, EIF4A3, PABPC4, SYNCRIP, PABPC1"	408	8	12983	19.88817402	0.028458984	0.001109837	0.086237731

GOTERM_MF_FAT	GO:0070717~poly-purine tract binding	5	1.016260163	1.06E-04	"HNRPDL, EIF4A3, PABPC4, SYNCRIP, PABPC1"	408	9	12983	17.67837691	0.049421617	0.001688062	0.151341687

Annotation Cluster 20	Enrichment Score: 4.762576218541677

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_CC_FAT	GO:0016585~chromatin remodeling complex	16	3.25203252	6.13E-09	"TBL1XR1, RBBP4, MTA2, RBBP7, CBX5, HDAC2, CSNK2A1, HDAC1, SMARCC1, SMARCC2, GATAD2A, SMARCA5, ACTL6A, SMARCA1, CHD4, SMARCA4"	415	71	12782	6.94084507	2.38E-06	9.14E-08	8.51E-06

GOTERM_BP_FAT	GO:0006338~chromatin remodeling	12	2.43902439	1.18E-06	"RBBP4, HDAC2, HDAC1, SMARCC1, NASP, SMARCC2, SMARCA5, CBX3, ACTL6A, SMARCA1, SUPT5H, SMARCA4"	430	56	13528	6.741528239	0.001859022	3.58E-05	0.001972349

GOTERM_MF_FAT	GO:0003682~chromatin binding	14	2.845528455	8.75E-04	"ADNP, CBX3, RCC1, CBX5, RPA1, SF3B1, SMARCC1, SMARCC2, SMARCA5, ACTL6A, SMARCA1, SMC1A, CHD4, SMARCA4"	408	150	12983	2.96996732	0.34242478	0.011905593	1.244832493

GOTERM_BP_FAT GO:0016568~chromatin modification 17 3.455284553 0.014082234 "TBL1XR1, RBBP4, NASP, CBX3, RBBP7, HDAC2, HDAC1, SMARCC1, SMARCC2, SMARCA5, DNMT1, ACTL6A, SMARCA1, RBM14, SUPT5H, CHD4, SMARCA4" 430 274 13528 1.951926668 1 0.170041389 21.10649193

Annotation Cluster 21 Enrichment Score: 4.553168520209698
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT "GO:0008135~translation factor activity, nucleic acid binding" 16 3.25203252 3.64E-07 "EIF2S3, EIF3C, EIF3D, EIF3A, EIF3H, TRMT6, EIF4H, ICT1, EIF2S1, EIF2S2, EEF1G, TCEA1, EIF3I, EEF1D, EIF2B3, EIF2B5" 408 98 12983 5.195278111 1.74E-04 1.74E-05 5.21E-04
GOTERM_MF_FAT GO:0003743~translation initiation factor activity 12 2.43902439 2.56E-06 "EIF3C, EIF3D, EIF3A, EIF3H, EIF4H, TRMT6, EIF2S1, EIF2S2, EIF2S3, EIF3I, EIF2B3, EIF2B5" 408 61 12983 6.259884282 0.001225441 8.76E-05 0.00366405
GOTERM_BP_FAT GO:0006413~translational initiation 10 2.032520325 9.58E-06 "EIF3C, EIF3D, EIF3A, EIF3H, TRMT6, EIF2S2, EIF2S3, EIF3I, EIF2B3, EIF2B5" 430 45 13528 6.99121447 0.014998699 2.44E-04 0.016017542
GOTERM_CC_FAT GO:0005852~eukaryotic translation initiation factor 3 complex 5 1.016260163 0.001114459 "EIF3C, EIF3D, EIF3A, EIF3H, EIF3I" 415 15 12782 10.26666667 0.351213308 0.0082857 1.536499196
GOTERM_BP_FAT GO:0006446~regulation of translational initiation 7 1.422764228 0.001722587 "NCBP1, EIF3H, EIF4H, TRMT6, EIF2S1, EIF2B3, EIF2B5" 430 41 13528 5.371298922 0.934050293 0.028213947 2.840820942

Annotation Cluster 22 Enrichment Score: 4.300544002282962
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006261~DNA-dependent DNA replication 12 2.43902439 1.70E-06 "RPA1, HMGB1, TFAM, HMGB2, MCM7, MCM2, MCM3, MCM4, DNAJA3, FEN1, MCM5, MCM6" 430 58 13528 6.509061748 0.002683827 5.07E-05 0.002848599
GOTERM_BP_FAT GO:0006268~DNA unwinding during replication 6 1.219512195 4.95E-05 "HMGB1, HMGB2, MCM7, MCM2, MCM4, MCM6" 430 14 13528 13.48305648 0.075086663 0.001200129 0.082703141
GOTERM_BP_FAT GO:0006270~DNA replication initiation 6 1.219512195 1.02E-04 "MCM7, MCM2, MCM3, MCM4, MCM5, MCM6" 430 16 13528 11.79767442 0.149204014 0.00215212 0.17112883
GOTERM_BP_FAT GO:0032508~DNA duplex unwinding 6 1.219512195 1.91E-04 "HMGB1, HMGB2, MCM7, MCM2, MCM4, MCM6" 430 18 13528 10.48682171 0.25973922 0.003752352 0.318285718
GOTERM_BP_FAT GO:0032392~DNA geometric change 6 1.219512195 1.91E-04 "HMGB1, HMGB2, MCM7, MCM2, MCM4, MCM6" 430 18 13528 10.48682171 0.25973922 0.003752352 0.318285718

Annotation Cluster 23 Enrichment Score: 3.8088536113982596
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0004527~exonuclease activity 11 2.235772358 4.79E-06 "DIS3, EXOSC10, EXOSC9, EXOSC6, EXOSC7, MRE11A, EXOSC2, APEX1, XRN2, RAD50, FEN1" 408 53 12983 6.604374769 0.002292525 1.43E-04 0.006858173
GOTERM_MF_FAT GO:0008408~3'-5' exonuclease activity 8 1.62601626 1.89E-05 "EXOSC10, EXOSC9, EXOSC6, EXOSC7, MRE11A, EXOSC2, APEX1, RAD50" 408 28 12983 9.091736695 0.009016761 4.12E-04 0.027062508
GOTERM_CC_FAT GO:0000178~exosome (RNase complex) 6 1.219512195 2.28E-05 "DIS3, EXOSC10, EXOSC9, EXOSC6, EXOSC7, EXOSC2" 415 12 12782 15.4 0.008819483 2.21E-04 0.031699238
GOTERM_MF_FAT GO:0004540~ribonuclease activity 11 2.235772358 3.61E-05 "DIS3, EXOSC9, EXOSC6, EXOSC7, POP1, EXOSC2, RPP30, APEX1, XRN2, FEN1, MRPL44" 408 66 12983 5.303513072 0.017121891 6.91E-04 0.051593542

GOTERM_MF_FAT "GO:0016796~exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters" 6 1.219512195 3.10E-04 "EXOSC9, EXOSC6, EXOSC7, EXOSC2, XRN2, FEN1" 408 20 12983 9.546323529 0.138098656 0.004782542 0.443106395
GOTERM_MF_FAT "GO:0016896~exoribonuclease activity, producing 5'-phosphomonoesters" 5 1.016260163 5.43E-04 "EXOSC9, EXOSC6, EXOSC7, EXOSC2, XRN2" 408 13 12983 12.23887632 0.229192661 0.007627142 0.774863294
GOTERM_MF_FAT GO:0004532~exoribonuclease activity 5 1.016260163 5.43E-04 "EXOSC9, EXOSC6, EXOSC7, EXOSC2, XRN2" 408 13 12983 12.23887632 0.229192661 0.007627142 0.774863294
GOTERM_MF_FAT GO:0004518~nuclease activity 14 2.845528455 0.001411556 "EXOSC10, DIS3, EXOSC9, EXOSC6, EXOSC7, MRE11A, POP1, EXOSC2, RPP30, APEX1, RAD50, FEN1, XRN2, MRPL44" 408 158 12983 2.819589228 0.491664229 0.018619287 2.001558474
GOTERM_MF_FAT GO:0000175~3'-5'-exoribonuclease activity 4 0.81300813 0.005447908 "EXOSC9, EXOSC6, EXOSC7, EXOSC2" 408 12 12983 10.60702614 0.926955187 0.056490167 7.521307605

Annotation Cluster 24 Enrichment Score: 3.8026272920005333
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0003724~RNA helicase activity 9 1.829268293 2.10E-06 "EIF4A3, DHX9, DDX17, DHX38, DDX23, DDX24, DHX15, DDX5, DDX6" 408 29 12983 9.875507099 0.00100324 7.72E-05 0.002999351
GOTERM_MF_FAT GO:0008186~RNA-dependent ATPase activity 6 1.219512195 5.00E-04 "EIF4A3, DHX9, DDX17, DHX38, DDX23, DDX24" 408 22 12983 8.678475936 0.213157812 0.007238149 0.713796279
GOTERM_MF_FAT GO:0004004~ATP-dependent RNA helicase activity 5 1.016260163 0.0037287 "EIF4A3, DHX9, DHX38, DDX23, DDX24" 408 21 12983 7.576447246 0.832937175 0.040759653 5.206615824

Annotation Cluster 25 Enrichment Score: 3.77605016470583
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0000776~kinetochore 13 2.642276423 6.21E-06 "NUP133, NUP98, NUP160, TP53BP1, NUP85, NUP107, TPR, SMC1A, SUGT1, NUP43, BUB3, ZW10, CBX5" 415 77 12782 5.2 0.002407556 6.51E-05 0.008626475
GOTERM_CC_FAT GO:0031080~Nup107-160 complex 6 1.219512195 7.67E-06 "NUP133, NUP98, NUP160, NUP85, NUP107, NUP43" 415 10 12782 18.48 0.002970169 7.63E-05 0.010645258
GOTERM_CC_FAT "GO:0000775~chromosome, centromeric region" 15 3.048780488 4.76E-05 "NUP133, NUP98, MKI67, NUP160, TP53BP1, CBX3, NUP85, SUGT1, CBX5, NUP107, SMC1A, TPR, NUP43, BUB3, ZW10" 415 124 12782 3.725806452 0.018291873 4.29E-04 0.066049527
GOTERM_CC_FAT "GO:0000779~condensed chromosome, centromeric region" 8 1.62601626 0.005341 "NUP133, TP53BP1, CBX3, NUP85, NUP107, SMC1A, NUP43, ZW10" 415 66 12782 3.733333333 0.874802392 0.034605062 7.166728327
GOTERM_CC_FAT GO:0000777~condensed chromosome kinetochore 7 1.422764228 0.010885481 "NUP133, TP53BP1, NUP85, NUP107, SMC1A, NUP43, ZW10" 415 58 12782 3.717241379 0.985688938 0.065186554 14.1000491

Annotation Cluster 26 Enrichment Score: 3.623129907412316
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT "GO:0006351~transcription, DNA-dependent" 24 4.87804878 5.79E-05 "COPS2, TCOF1, HCFC1, POLR3A, MKI67IP, YBX1, POLR2A, FUBP1, ADRM1, TFAM, TCERG1, PSMC5, GTF2I, TARDBP, GTF2F2, SMARCA5, CEBPZ, SUPT16H, GTF3C5, TCEA1, SUPT5H, PARP1, APEX1, XRN2" 430 292 13528 2.585791653 0.087262033 0.001361855 0.096736614
GOTERM_BP_FAT GO:0032774~RNA biosynthetic process 24 4.87804878 7.13E-05 "COPS2, TCOF1, HCFC1, POLR3A, MKI67IP, YBX1, POLR2A, FUBP1, ADRM1, TFAM, TCERG1, PSMC5, GTF2I, TARDBP,

GTF2F2, SMARCA5, CEBPZ, SUPT16H, GTF3C5, TCEA1, SUPT5H, PARP1, APEX1, XRN2" 430 296 13528
2.550848523 0.106345097 0.001652098 0.119109021
GOTERM_BP_FAT GO:0006366~transcription from RNA polymerase II promoter 17 3.455284553
0.003272627 "COPS2, HCFC1, YBX1, POLR2A, FUBP1, ADRM1, PSMC5, TCERG1, GTF2I, TARDBP, GTF2F2,
CEBPZ, SUPT16H, TCEA1, SUPT5H, PARP1, APEX1" 430 234 13528 2.285589346 0.994311996
0.051381856 5.33206209

Annotation Cluster 27 Enrichment Score: 3.6196355299064216
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0000245~spliceosome assembly 9 1.829268293 5.16E-06 "DDX23, USP39,
SNRNP200, SF1, SF3A2, SF3A1, PRPF6, SMNDC1, SF3A3" 430 32 13528 8.848255814 0.008103111
1.40E-04 0.00862379
GOTERM_BP_FAT GO:0000389~nuclear mRNA 3'-splice site recognition 4 0.81300813 3.02E-04 "SF1,
SF3A2, SF3A1, SF3A3" 430 5 13528 25.16837209 0.378917859 0.005459662 0.503589894
GOTERM_BP_FAT GO:0006376~mRNA splice site selection 4 0.81300813 0.008882454 "SF1, SF3A2,
SF3A1, SF3A3" 430 14 13528 8.988704319 0.999999225 0.126537865 13.8553304

Annotation Cluster 28 Enrichment Score: 3.4956302275924793
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0005732~small nucleolar ribonucleoprotein complex 7 1.422764228 2.93E-05
"EMG1, UTP18, POP1, SNRPB, NOP58, NOP56, FBL" 415 20 12782 10.78 0.011316374 2.78E-04
0.040723039
GOTERM_CC_FAT GO:0044452~nucleolar part 7 1.422764228 1.85E-04 "NPM1, POP1, RPP30, NOP58,
NOP56, PES1, FBL" 415 27 12782 7.985185185 0.069194726 0.001492743 0.256298322
GOTERM_CC_FAT GO:0031428~box C/D snoRNP complex 3 0.609756098 0.006013017 "NOP58,
NOP56, FBL" 415 4 12782 23.1 0.903681355 0.038250787 8.033898704

Annotation Cluster 29 Enrichment Score: 3.1572558665154915
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0031080~Nup107-160 complex 6 1.219512195 7.67E-06 "NUP133, NUP98,
NUP160, NUP85, NUP107, NUP43" 415 10 12782 18.48 0.002970169 7.63E-05 0.010645258
GOTERM_MF_FAT GO:0005487~nucleocytoplasmic transporter activity 4 0.81300813 0.002231111
"NUP133, NUP160, NUP54, NUP107" 408 9 12983 14.14270153 0.656955817 0.026392857 3.146506433
GOTERM_BP_FAT GO:0006406~mRNA export from nucleus 5 1.016260163 0.019729574 "PABPN1,
NUP133, NCBP1, NUP160, NUP107" 430 33 13528 4.766737139 1 0.217690164 28.32983141

Annotation Cluster 30 Enrichment Score: 3.128161814830609
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0000279~M phase 28 5.691056911 6.27E-06 "MRE11A, ANLN, RCC1, RPA1,
NCAPH, NUMA1, RAD21, TARDBP, TUBG1, BUB3, STAG2, ZW10, MKI67, PDS5A, CKAP5, LIG3, ILF3,
SUGT1, RAD50, CDK2, SMC3, NCAPD2, PSMD13, CDK11B, PES1, SMC1A, NUP43, PPP5C" 430 329 13528
2.677486393 0.009844821 1.65E-04 0.010486517
GOTERM_BP_FAT GO:0051321~meiotic cell cycle 13 2.642276423 7.46E-05 "MKI67, MRE11A, LIG3,
SMC3, RAD50, RPA1, NUMA1, RAD21, PSMD13, TUBG1, SMC1A, STAG2, ZW10" 430 100 13528
4.089860465 0.11099649 0.001703679 0.124633813
GOTERM_BP_FAT GO:0022403~cell cycle phase 29 5.894308943 1.38E-04 "MRE11A, ANLN, RCC1,
RPA1, NCAPH, NUMA1, RAD21, TARDBP, TUBG1, BUB3, STAG2, ZW10, KHDRBS1, MKI67, PDS5A, CKAP5,
LIG3, ILF3, SUGT1, RAD50, CDK2, SMC3, NCAPD2, PSMD13, CDK11B, PES1, SMC1A, NUP43, PPP5C" 430
414 13528 2.203752387 0.195774235 0.002789375 0.230677965
GOTERM_BP_FAT GO:0051327~M phase of meiotic cell cycle 11 2.235772358 0.001075798 "RPA1,

RAD21, PSMD13, MKI67, MRE11A, LIG3, SMC1A, SMC3, RAD50, STAG2, ZW10" 430 98 13528 3.531276697 0.816849498 0.018281343 1.783177788

GOTERM_BP_FAT GO:0007126~meiosis 11 2.235772358 0.001075798 "RPA1, RAD21, PSMD13, MKI67, MRE11A, LIG3, SMC1A, SMC3, RAD50, STAG2, ZW10" 430 98 13528 3.531276697 0.816849498 0.018281343 1.783177788

GOTERM_BP_FAT GO:0007131~reciprocal meiotic recombination 4 0.81300813 0.039125424 "RAD21, MRE11A, LIG3, RAD50" 430 24 13528 5.243410853 1 0.356054845 48.68346744

GOTERM_BP_FAT GO:0007127~meiosis I 5 1.016260163 0.04328325 "RAD21, PSMD13, MRE11A, LIG3, RAD50" 430 42 13528 3.745293466 1 0.379939378 52.27172725

Annotation Cluster 31 Enrichment Score: 2.9334198865872816

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0000790~nuclear chromatin 10 2.032520325 6.10E-05 "TCP1, CSNK2A1, RBBP4, HDAC2, HDAC1, SMARCC1, TRIM28, CBX3, RCC1, CBX5" 415 55 12782 5.6 0.023375357 5.25E-04 0.08461607

GOTERM_CC_FAT GO:0000792~heterochromatin 7 1.422764228 0.001914875 "TCP1, HDAC2, SMARCC1, TRIM28, CBX3, SMARCA4, CBX5" 415 41 12782 5.258536585 0.52464041 0.013677522 2.62647879

GOTERM_CC_FAT GO:0005720~nuclear heterochromatin 5 1.016260163 0.013569398 "TCP1, SMARCC1, TRIM28, CBX3, CBX5" 415 29 12782 5.310344828 0.995013265 0.077176962 17.28074484

Annotation Cluster 32 Enrichment Score: 2.459484835003045

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0031980~mitochondrial lumen 21 4.268292683 4.92E-05 "MRPL1, MRPS15, MRPS22, NDUFA9, KIAA1967, DLAT, NDUFA10, TFAM, MRPL13, C1QBP, MRPL28, MRPS18A, MRPL39, HSPD1, DHX30, DNAJA3, LRPPRC, MRPL43, PMPCB, DAP3, HSPA9" 415 227 12782 2.849339207 0.018921968 4.34E-04 0.068345801

GOTERM_CC_FAT GO:0005759~mitochondrial matrix 21 4.268292683 4.92E-05 "MRPL1, MRPS15, MRPS22, NDUFA9, KIAA1967, DLAT, NDUFA10, TFAM, MRPL13, C1QBP, MRPL28, MRPS18A, MRPL39, HSPD1, DHX30, DNAJA3, LRPPRC, MRPL43, PMPCB, DAP3, HSPA9" 415 227 12782 2.849339207 0.018921968 4.34E-04 0.068345801

GOTERM_CC_FAT GO:0000313~organellar ribosome 9 1.829268293 1.37E-04 "MRPL1, MRPL13, MRPS15, MRPL28, MRPS18A, MRPS22, MRPL39, MRPL43, DAP3" 415 48 12782 5.775 0.051760734 0.001154733 0.190033308

GOTERM_CC_FAT GO:0005761~mitochondrial ribosome 9 1.829268293 1.37E-04 "MRPL1, MRPL13, MRPS15, MRPL28, MRPS18A, MRPS22, MRPL39, MRPL43, DAP3" 415 48 12782 5.775 0.051760734 0.001154733 0.190033308

GOTERM_CC_FAT GO:0015935~small ribosomal subunit 8 1.62601626 0.00412095 "MRPS15, MRPS18A, MRPS22, NPM1, RPS10, RPS6, RPS8, DAP3" 415 63 12782 3.911111111 0.798553644 0.028205861 5.572954596

GOTERM_CC_FAT GO:0005739~mitochondrion 52 10.56910569 0.004503243 "UQCRC2, TIMM50, MRPS31, HIBADH, GSR, MRPL39, DHX30, SUCLA2, TOMM34, PABPN1, MRPL1, MRPL4, HMBS, NDUFA10, TRAP1, GLUL, C1QBP, MRPS18A, YME1L1, MRPL46, LRPPRC, MRPL43, PMPCB, MRPL44, MRPS15, HK2, CHCHD3, VARS, TFAM, MRPL13, MRPL15, C12ORF10, MRPL19, CSDE1, DNAJA3, FEN1, HSPA9, GPD2, NDUFA9, MRPS22, KIAA1967, TOMM40, ILF3, DLAT, SDHA, SDHB, MRPL22, MRPL28, PTCD3, NDUFV1, HSPD1, DAP3" 415 1087 12782 1.473413063 0.826435219 0.030255732 6.075062229

GOTERM_CC_FAT GO:0044429~mitochondrial part 32 6.504065041 0.006205251 "UQCRC2, MRPS15, HK2, CHCHD3, TIMM50, TFAM, MRPL13, CSDE1, MRPL39, DHX30, DNAJA3, HSPA9, TOMM34, GPD2, MRPL1, MRPS22, NDUFA9, TOMM40, KIAA1967, DLAT, NDUFA10, SDHA, SDHB, MRPL28, C1QBP, MRPS18A, NDUFV1, HSPD1, LRPPRC, PMPCB, MRPL43, DAP3" 415 595 12782 1.656470588 0.910645046 0.038818898 8.280570866

GOTERM_CC_FAT GO:0000315~organellar large ribosomal subunit 3 0.609756098 0.113932855 "MRPL1,

MRPL13, MRPL43" 415 18 12782 5.133333333 1 0.447937788 81.35724746
GOTERM_CC_FAT GO:0000314~organellar small ribosomal subunit 3 0.609756098 0.113932855
"MRPS15, MRPS18A, MRPS22" 415 18 12782 5.133333333 1 0.447937788 81.35724746
GOTERM_CC_FAT GO:0005762~mitochondrial large ribosomal subunit 3 0.609756098 0.113932855
"MRPL1, MRPL13, MRPL43" 415 18 12782 5.133333333 1 0.447937788 81.35724746
GOTERM_CC_FAT GO:0005763~mitochondrial small ribosomal subunit 3 0.609756098 0.113932855
"MRPS15, MRPS18A, MRPS22" 415 18 12782 5.133333333 1 0.447937788 81.35724746

Annotation Cluster 33 Enrichment Score: 2.3117661190862546
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0003678~DNA helicase activity 7 1.422764228 0.001422495 "XRCC5, DHX9,
MCM7, XRCC6, MCM4, CHD4, MCM6" 408 40 12983 5.568688725 0.494324643 0.01825989
2.016923507
GOTERM_MF_FAT GO:0008094~DNA-dependent ATPase activity 8 1.62601626 0.001933028 "XRCC5,
DHX9, RBBP4, RFC2, XRCC6, SMARCA1, CHD4, SMARCA4" 408 57 12983 4.466116271 0.604188218
0.023484372 2.731521337
GOTERM_MF_FAT GO:0004003~ATP-dependent DNA helicase activity 4 0.81300813 0.042209734
"XRCC5, DHX9, XRCC6, CHD4" 408 25 12983 5.091372549 0.999999999 0.317878593 46.05964703

Annotation Cluster 34 Enrichment Score: 2.228213992248928
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0004527~exonuclease activity 11 2.235772358 4.79E-06 "DIS3, EXOSC10, EXOSC9,
EXOSC6, EXOSC7, MRE11A, EXOSC2, APEX1, XRN2, RAD50, FEN1" 408 53 12983 6.604374769
0.002292525 1.43E-04 0.006858173
GOTERM_MF_FAT GO:0004520~endodeoxyribonuclease activity 4 0.81300813 0.030267303
"MRE11A, APEX1, RAD50, FEN1" 408 22 12983 5.785650624 0.999999596 0.246566813 35.59142234
GOTERM_MF_FAT GO:0004536~deoxyribonuclease activity 4 0.81300813 0.089607319 "MRE11A,
APEX1, RAD50, FEN1" 408 34 12983 3.743656286 1 0.515817296 73.91324615
GOTERM_MF_FAT GO:0004519~endonuclease activity 7 1.422764228 0.0940483 "MRE11A, POP1,
RPP30, APEX1, RAD50, FEN1, MRPL44" 408 100 12983 2.22747549 1 0.528086758 75.67671464

Annotation Cluster 35 Enrichment Score: 2.2086762462974696
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0004540~ribonuclease activity 11 2.235772358 3.61E-05 "DIS3, EXOSC9,
EXOSC6, EXOSC7, POP1, EXOSC2, RPP30, APEX1, XRN2, FEN1, MRPL44" 408 66 12983 5.303513072
0.017121891 6.91E-04 0.051593542
GOTERM_MF_FAT GO:0004518~nuclease activity 14 2.845528455 0.001411556 "EXOSC10, DIS3,
EXOSC9, EXOSC6, EXOSC7, MRE11A, POP1, EXOSC2, RPP30, APEX1, RAD50, FEN1, XRN2, MRPL44" 408
158 12983 2.819589228 0.491664229 0.018619287 2.001558474
GOTERM_MF_FAT "GO:0016891~endoribonuclease activity, producing 5'-phosphomonoesters" 5
1.016260163 0.009431723 "POP1, RPP30, APEX1, FEN1, MRPL44" 408 27 12983 5.892792302
0.989318432 0.093966534 12.68446847
GOTERM_MF_FAT "GO:0016893~endonuclease activity, active with either ribo- or deoxyribonucleic acids and
producing 5'-phosphomonoesters" 5 1.016260163 0.02100409 "POP1, RPP30, APEX1, FEN1, MRPL44" 408
34 12983 4.679570358 0.999961626 0.187397091 26.20245534
GOTERM_MF_FAT GO:0004521~endoribonuclease activity 5 1.016260163 0.059026268 "POP1, RPP30,
APEX1, FEN1, MRPL44" 408 47 12983 3.38522111 1 0.411313542 58.13982477
GOTERM_MF_FAT GO:0004519~endonuclease activity 7 1.422764228 0.0940483 "MRE11A, POP1,
RPP30, APEX1, RAD50, FEN1, MRPL44" 408 100 12983 2.22747549 1 0.528086758 75.67671464

Annotation Cluster 36 Enrichment Score: 2.2052807202747915

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0016581~NuRD complex 8 1.62601626 5.16E-08 "CSNK2A1, RBBP4,
HDAC2, HDAC1, MTA2, GATAD2A, RBBP7, CHD4" 415 13 12782 18.95384615 2.00E-05 7.14E-07
7.16E-05
GOTERM_MF_FAT GO:0004407~histone deacetylase activity 3 0.609756098 0.078672456 "HDAC2,
HDAC1, MTA2" 408 15 12983 6.364215686 1 0.485849361 69.05147908
GOTERM_MF_FAT GO:0033558~protein deacetylase activity 3 0.609756098 0.078672456 "HDAC2,
HDAC1, MTA2" 408 15 12983 6.364215686 1 0.485849361 69.05147908
GOTERM_MF_FAT GO:0019213~deacetylase activity 3 0.609756098 0.107888296 "HDAC2, HDAC1,
MTA2" 408 18 12983 5.303513072 1 0.574480979 80.48696592
GOTERM_MF_FAT "GO:0016811~hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear
amides" 4 0.81300813 0.273325342 "HDAC2, HDAC1, DARS, MTA2" 408 58 12983 2.194557133
1 0.869855777 98.96417198

Annotation Cluster 37 Enrichment Score: 1.9835540178713669
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0006446~regulation of translational initiation 7 1.422764228 0.001722587 "NCBP1,
EIF3H, EIF4H, TRMT6, EIF2S1, EIF2B3, EIF2B5" 430 41 13528 5.371298922 0.934050293 0.028213947
2.840820942
GOTERM_CC_FAT GO:0005851~eukaryotic translation initiation factor 2B complex 3 0.609756098
0.014397595 "EIF2S1, EIF2B3, EIF2B5" 415 6 12782 15.4 0.99640018 0.079416997 18.23994617
GOTERM_BP_FAT GO:0043558~regulation of translational initiation in response to stress 3 0.609756098
0.018955874 "EIF2S1, EIF2B3, EIF2B5" 430 7 13528 13.48305648 1 0.211514087 27.37836866
GOTERM_BP_FAT GO:0043555~regulation of translation in response to stress 3 0.609756098 0.024749639
"EIF2S1, EIF2B3, EIF2B5" 430 8 13528 11.79767442 1 0.258739921 34.22429688

Annotation Cluster 38 Enrichment Score: 1.85260612358451
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0008134~transcription factor binding 30 6.097560976 0.001569714 "COPS2,
HMGB1, PRKDC, HCFC1, VARS, AIP, TCERG1, DRAP1, NPM1, PQBP1, APEX1, DNAJA3, CHD4, TBL1XR1,
TRIM28, SF1, DDX5, PRPF6, PSMC5, HDAC2, HDAC1, PSMC3, SMARCC1, UBA2, SMARCC2, DNMT1, PARP1,
RBM14, MYBBP1A, SMARCA4" 408 513 12983 1.86088178 0.528805153 0.019607424 2.223485812
GOTERM_MF_FAT GO:0016563~transcription activator activity 24 4.87804878 0.005164938 "TBL1XR1,
FOXK1, MTA2, TP53BP1, XRCC6, TRIM28, HCFC1, ILF3, PRPF6, AIP, FUBP3, TCERG1, HDAC2, HDAC1,
PSMC3, SMARCC1, SMARCC2, NPM1, SMARCA5, HNRNPD, PQBP1, RBM14, APEX1, SMARCA4" 408 410
12983 1.862697274 0.916291631 0.054813577 7.143975259
GOTERM_MF_FAT GO:0003712~transcription cofactor activity 18 3.658536585 0.064639623 "COPS2,
TBL1XR1, TRIM28, SF1, HCFC1, DDX5, PRPF6, AIP, PSMC5, TCERG1, DRAP1, PSMC3, SMARCC1, NPM1,
SMARCC2, PQBP1, RBM14, APEX1" 408 363 12983 1.577904716 1 0.429676181 61.57561589
GOTERM_MF_FAT GO:0003713~transcription coactivator activity 12 2.43902439 0.074163662
"TCERG1, PSMC3, SMARCC1, TRIM28, NPM1, SMARCC2, PQBP1, HCFC1, RBM14, APEX1, PRPF6, AIP" 408
214 12983 1.784359538 1 0.470801216 66.81155117

Annotation Cluster 39 Enrichment Score: 1.8258851006404588
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0000723~telomere maintenance 7 1.422764228 2.04E-04 "XRCC5, DKC1,
MRE11A, XRCC6, PRKDC, PARP1, RAD50" 430 28 13528 7.865116279 0.275525672 0.003922882
0.341059636
GOTERM_BP_FAT GO:0032200~telomere organization 7 1.422764228 2.51E-04 "XRCC5, DKC1,
MRE11A, XRCC6, PRKDC, PARP1, RAD50" 430 29 13528 7.593905373 0.326745786 0.004755312

0.418486084
GOTERM_BP_FAT GO:0006302~double-strand break repair 9 1.829268293 7.22E-04 "RPA1, XRCC5, RAD21, MSH2, MRE11A, XRCC6, PRKDC, RAD50, FEN1" 430 62 13528 4.56684171 0.679949217 0.012719267 1.200352343
GOTERM_BP_FAT GO:0006303~double-strand break repair via nonhomologous end joining 4 0.81300813 0.003217918 "XRCC5, MRE11A, XRCC6, PRKDC"430 10 13528 12.58418605 0.993797727 0.051569006 5.245165824
GOTERM_BP_FAT GO:0000726~non-recombinational repair 4 0.81300813 0.008882454 "XRCC5, MRE11A, XRCC6, PRKDC" 430 14 13528 8.988704319 0.999999225 0.126537865 13.8553304
GOTERM_BP_FAT GO:0007004~telomere maintenance via telomerase 3 0.609756098 0.045665016 "DKC1, MRE11A, RAD50" 430 11 13528 8.58012685 1 0.394334451 54.21954077
GOTERM_BP_FAT GO:0060249~anatomical structure homeostasis 8 1.62601626 0.051482904 "RPA1, XRCC5, DKC1, MRE11A, XRCC6, PRKDC, PARP1, RAD50" 430 106 13528 2.374374726 1 0.424207012 58.66786114
GOTERM_BP_FAT GO:0010833~telomere maintenance via telomere lengthening 3 0.609756098 0.053672556 "DKC1, MRE11A, RAD50" 430 12 13528 7.865116279 1 0.435804148 60.23421101
GOTERM_CC_FAT "GO:0000781~chromosome, telomeric region" 4 0.81300813 0.066222248 "XRCC5, XRCC6, RAD50, CDK2" 415 29 12782 4.248275862 1 0.295168426 61.38153909
GOTERM_BP_FAT GO:0006278~RNA-dependent DNA replication 3 0.609756098 0.099785944 "DKC1, MRE11A, RAD50"430 17 13528 5.551846785 1 0.622870887 82.74773677
GOTERM_CC_FAT "GO:0000784~nuclear chromosome, telomeric region" 3 0.609756098 0.146968189 "XRCC5, XRCC6, RAD50" 415 21 12782 4.4 1 0.528645499 89.00062895
GOTERM_BP_FAT GO:0042592~homeostatic process 18 3.658536585 0.947399556 "XRCC5, MRE11A, XRCC6, PRKDC, RPS6, RAD50, RPA1, GSR, GNAQ, DKC1, NPM1, QKI, TCEA1, ACIN1, PARP1, APEX1, DNAJA3, EIF2B5" 430 751 13528 0.754045768 1 0.999997124 100

Annotation Cluster 40 Enrichment Score: 1.8021712058896642
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006401~RNA catabolic process 10 2.032520325 1.97E-04 "EXOSC10, EIF4A3, NCBP1, EXOSC7, PABPC4, HNRNPD, POP1, RNPS1, XRN2, FEN1" 430 65 13528 4.840071556 0.267488119 0.003835536 0.329403783
GOTERM_BP_FAT GO:0006402~mRNA catabolic process 5 1.016260163 0.046574428 "EXOSC10, EIF4A3, NCBP1, HNRNPD, RNPS1" 430 43 13528 3.658193618 1 0.398421352 54.94334748
GOTERM_BP_FAT "GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay" 4 0.81300813 0.068380615 "EXOSC10, EIF4A3, NCBP1, RNPS1"430 30 13528 4.194728682 1 0.513562873 69.39500623
GOTERM_BP_FAT GO:0000956~nuclear-transcribed mRNA catabolic process 4 0.81300813 0.098392943 "EXOSC10, EIF4A3, NCBP1, RNPS1"430 35 13528 3.595481728 1 0.6195915 82.29601404

Annotation Cluster 41 Enrichment Score: 1.5743524974102867
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007059~chromosome segregation 9 1.829268293 0.004078612 "NCAPH, RAD21, SMC1A, NUP43, SMC3, BUB3, STAG2, NCAPD2, ZW10" 430 81 13528 3.495607235 0.998411752 0.063028355 6.603594497
GOTERM_BP_FAT GO:0000070~mitotic sister chromatid segregation 5 1.016260163 0.026380011 "NCAPH, SMC1A, BUB3, NCAPD2, ZW10" 430 36 13528 4.369509044 1 0.269937912 36.03843974
GOTERM_BP_FAT GO:0000819~sister chromatid segregation 5 1.016260163 0.028860471 "NCAPH, SMC1A, BUB3, NCAPD2, ZW10" 430 37 13528 4.251414205 1 0.289718314 38.70849664
GOTERM_BP_FAT GO:0000075~cell cycle checkpoint 6 1.219512195 0.162367549 "MSH2, INTS3, TPR, SMC1A, BUB3, ZW10" 430 91 13528 2.074316381 1 0.770203187 94.82672772

Annotation Cluster 42 Enrichment Score: 1.5437864888435988

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0004298~threonine-type endopeptidase activity 6 1.219512195 3.10E-04 "PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, PSMA7" 408 20 12983 9.546323529 0.138098656 0.004782542 0.443106395

GOTERM_MF_FAT GO:0070003~threonine-type peptidase activity 6 1.219512195 3.10E-04 "PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, PSMA7" 408 20 12983 9.546323529 0.138098656 0.004782542 0.443106395

GOTERM_CC_FAT GO:0005839~proteasome core complex 6 1.219512195 3.61E-04 "PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, PSMA7" 415 20 12782 9.24 0.130593967 0.002794987 0.49960029

GOTERM_MF_FAT GO:0008237~metallopeptidase activity 6 1.219512195 0.683986056 "UQCRC2, OSGEP, METAP2, YME1L1, CPD, PMPCB" 408 183 12983 1.043314047 1 0.99620347 99.9999931

GOTERM_MF_FAT GO:0004175~endopeptidase activity 11 2.235772358 0.743427025 "UQCRC2, USP7, PSMA1, PSMB7, OSGEP, PSMA4, PSMA3, PSMB2, YME1L1, PSMA7, PMPCB"408 375 12983 0.933418301 1 0.998318844 99.99999965

GOTERM_MF_FAT "GO:0070011~peptidase activity, acting on L-amino acid peptides" 13 2.642276423 0.930030463 "UQCRC2, USP7, METAP2, OSGEP, PSMA7, PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, YME1L1, CPD, PMPCB" 408 549 12983 0.753504589 1 0.99998852 100

GOTERM_MF_FAT GO:0008233~peptidase activity 13 2.642276423 0.951366822 "UQCRC2, USP7, METAP2, OSGEP, PSMA7, PSMA1, PSMB7, PSMA4, PSMA3, PSMB2, YME1L1, CPD, PMPCB" 408 574 12983 0.720686445 1 0.999996216 100

Annotation Cluster 43 Enrichment Score: 1.5329765206288233

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0010605~negative regulation of macromolecule metabolic process 48 9.756097561 3.27E-06 "HMGB1, COPS2, HMGB2, FOXK1, RBM3, CBX3, IGF2BP2, PSMA7, CBX5, SRRT, SUMO1, PSMB7, HEXIM1, DRAP1, NPM1, PSMB2, GATAD2A, PSMD4, PSMD6, SUPT5H, EIF2B3, PSMD8, BUB3, EIF2B5, KHDRBS1, TBL1XR1, MSH2, MTA2, TRIM28, ILF3, RBBP7, EIF4A3, PSMA1, PSMC6, PSMD13, HDAC2, PSMC5, HDAC1, TRIM33, PSMC3, PSMC2, PSMA4, PSMA3, SMARCC2, PSMC1, DNMT1, RBM15, SMARCA4" 430 734 13528 2.057360117 0.005136471 9.20E-05 0.005458463

GOTERM_MF_FAT GO:0003677~DNA binding 104 21.13821138 1.05E-04 "XRCC5, HIST2H2AA3, XRCC6, H1FX, XRCC1, PNN, NONO, HIST1H2BM, TARDBP, PQBP1, PSIP1, SRRM1, LUC7L3, H1F0, MTA2, HNRNPA2B1, LIG3, HNRNPU, UHRF1, TRIM33, RFC2, SMARCA5, SMARCA1, MYBBP1A, LRPPRC, SMARCA4, HMGB1, HMGB2, MRE11A, HNRNPK, HIST1H4A, DRAP1, RPL6, ZNF326, HNRNPD, EWSR1, HIST2H3A, DHX9, TP53BP1, HNRNPA1, HDAC2, HDAC1, SMARCC1, GTF2F2, SMARCC2, PCNA, DNMT1, HSPD1, TMPO, PARP1, PUF60, FOXK1, HP1BP3, DEK, YBX1, ZNF207, FUBP1, FUBP3, MCM7, ZW10, KHDRBS1, TBL1XR1, HIST1H1D, HIST1H1C, HIST1H1B, ADNP, MCM2, CDC5L, MCM3, MCM4, NCL, RAD50, MCM5, MCM6, HNRPDL, SARNP, GTF2I, HCFC1, PRKDC, WBP11, POLR2A, RPA1, PRPF19, TFAM, SAFB, GATAD2A, CEBPZ, CSDE1, GTF3C5, GATAD2B, TCEA1, APEX1, FEN1, CHD4, NUP153, MSH2, TRIM28, ILF3, POLR3A, SON, ILF2, MRPL28, UBTF, SFPQ" 408 2331 12983 1.419730655 0.04884072 0.001725191 0.149518898

GOTERM_BP_FAT GO:0010604~positive regulation of macromolecule metabolic process 45 9.146341463 0.001061998 "NCBP1, HMGB2, FOXK1, XRCC6, PRKDC, PSMA7, SCRIB, PSMB7, PSMB2, PSMD4, TCEA1, PSMD6, SUPT5H, PSMD8, DNAJA3, EIF2B5, TBL1XR1, MTA2, TP53BP1, TRIM28, DOCK7, ILF3, DDX5, CDK2, PRPF6, PSMA1, PSMC6, PSMD13, PSMC5, HDAC2, HDAC1, ILF2, PSMC3, PSMC2, PSMA4, SMARCC1, PSMA3, GTF2F2, SMARCC2, PSMC1, DNMT1, RBM14, SMARCA1, RBM15, SMARCA4" 430 857 13528 1.651949744 0.812815584 0.018245358 1.76049404

GOTERM_BP_FAT GO:0043193~positive regulation of gene-specific transcription 10 2.032520325 0.001716535 "HMGB2, HDAC2, PSMC5, HDAC1, TRIM28, XRCC6, PRKDC, SMARCA1, RBM15, SMARCA4" 430 87 13528 3.616145416 0.93341669 0.028410952 2.830973293

GOTERM_MF_FAT GO:0016563~transcription activator activity 24 4.87804878 0.005164938 "TBL1XR1, FOXK1, MTA2, TP53BP1, XRCC6, TRIM28, HCFC1, ILF3, PRPF6, AIP, FUBP3, TCERG1, HDAC2, HDAC1, PSMC3, SMARCC1, SMARCC2, NPM1, SMARCA5, HNRNPD, PQBP1, RBM14, APEX1, SMARCA4" 408 410

12983 1.862697274 0.916291631 0.054813577 7.143975259

GOTERM_BP_FAT GO:0010558~negative regulation of macromolecule biosynthetic process 29 5.894308943 0.008815791 "HMGB1, COPS2, HMGB2, FOXK1, CBX3, IGF2BP2, CBX5, SUMO1, HEXIM1, DRAP1, GATAD2A, SUPT5H, EIF2B3, EIF2B5, KHDRBS1, TBL1XR1, MTA2, TRIM28, ILF3, RBBP7, EIF4A3, PSMC5, HDAC2, HDAC1, TRIM33, SMARCC2, DNMT1, RBM15, SMARCA4" 430 547 13528 1.667922282 0.999999138 0.12678566 13.75842491

GOTERM_BP_FAT GO:0010552~positive regulation of specific transcription from RNA polymerase II promoter 7 1.422764228 0.009097766 "HMGB2, HDAC2, HDAC1, XRCC6, PRKDC, RBM15, SMARCA4" 430 57 13528 3.863565891 0.99999945 0.128260935 14.1676232

GOTERM_BP_FAT GO:0010629~negative regulation of gene expression 27 5.487804878 0.010184672 "KHDRBS1, HMGB1, TBL1XR1, COPS2, HMGB2, FOXK1, RBM3, MTA2, TRIM28, CBX3, ILF3, RBBP7, CBX5, SRRT, SUMO1, HDAC2, PSMC5, TRIM33, HDAC1, HEXIM1, DRAP1, SMARCC2, GATAD2A, DNMT1, SUPT5H, RBM15, SMARCA4" 430 504 13528 1.68538206 0.999999903 0.138842241 15.7279097

GOTERM_BP_FAT GO:0032583~regulation of gene-specific transcription 11 2.235772358 0.010278342 "TBL1XR1, HMGB2, HDAC2, PSMC5, HDAC1, TRIM28, XRCC6, PRKDC, SMARCA1, RBM15, SMARCA4" 430 134 13528 2.582575495 0.999999916 0.138840392 15.86111923

GOTERM_MF_FAT GO:0016564~transcription repressor activity 19 3.861788618 0.010860134 "KHDRBS1, COPS2, TBL1XR1, HMGB2, FOXK1, MTA2, TRIM28, SF1, CBX3, ILF3, RBBP7, YBX1, CBX5, HDAC2, DRAP1, HEXIM1, PSMC3, GATAD2A, APEX1" 408 316 12983 1.91329269 0.994648924 0.105317465 14.46948602

GOTERM_BP_FAT GO:0016481~negative regulation of transcription 25 5.081300813 0.011466529 "KHDRBS1, HMGB1, TBL1XR1, COPS2, HMGB2, FOXK1, MTA2, TRIM28, CBX3, ILF3, RBBP7, CBX5, SUMO1, HDAC2, PSMC5, TRIM33, HDAC1, HEXIM1, DRAP1, SMARCC2, GATAD2A, DNMT1, SUPT5H, RBM15, SMARCA4" 430 459 13528 1.713532958 0.999999987 0.15112942 17.53377906

GOTERM_BP_FAT GO:0031327~negative regulation of cellular biosynthetic process 29 5.894308943 0.011931938 "HMGB1, COPS2, HMGB2, FOXK1, CBX3, IGF2BP2, CBX5, SUMO1, HEXIM1, DRAP1, GATAD2A, SUPT5H, EIF2B3, EIF2B5, KHDRBS1, TBL1XR1, MTA2, TRIM28, ILF3, RBBP7, EIF4A3, PSMC5, HDAC2, HDAC1, TRIM33, SMARCC2, DNMT1, RBM15, SMARCA4" 430 561 13528 1.626298553 0.999999994 0.154240797 18.18039272

GOTERM_BP_FAT "GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process" 27 5.487804878 0.012394308 "KHDRBS1, HMGB1, TBL1XR1, COPS2, HMGB2, FOXK1, MSH2, MTA2, TRIM28, CBX3, ILF3, RBBP7, CBX5, SUMO1, HDAC2, PSMC5, TRIM33, HDAC1, HEXIM1, DRAP1, NPM1, SMARCC2, GATAD2A, DNMT1, SUPT5H, RBM15, SMARCA4" 430 512 13528 1.659047965 0.999999997 0.158463581 18.81806198

GOTERM_BP_FAT GO:0051172~negative regulation of nitrogen compound metabolic process 27 5.487804878 0.014520359 "KHDRBS1, HMGB1, TBL1XR1, COPS2, HMGB2, FOXK1, MSH2, MTA2, TRIM28, CBX3, ILF3, RBBP7, CBX5, SUMO1, HDAC2, PSMC5, TRIM33, HDAC1, HEXIM1, DRAP1, NPM1, SMARCC2, GATAD2A, DNMT1, SUPT5H, RBM15, SMARCA4" 430 519 13528 1.636671596 1 0.1735634 21.69049337

GOTERM_BP_FAT GO:0009890~negative regulation of biosynthetic process 29 5.894308943 0.015610404 "HMGB1, COPS2, HMGB2, FOXK1, CBX3, IGF2BP2, CBX5, SUMO1, HEXIM1, DRAP1, GATAD2A, SUPT5H, EIF2B3, EIF2B5, KHDRBS1, TBL1XR1, MTA2, TRIM28, ILF3, RBBP7, EIF4A3, PSMC5, HDAC2, HDAC1, TRIM33, SMARCC2, DNMT1, RBM15, SMARCA4"430 573 13528 1.592239945 1 0.182677689 23.12589011

GOTERM_BP_FAT GO:0051253~negative regulation of RNA metabolic process 20 4.06504065 0.022180658 "TBL1XR1, HMGB1, FOXK1, MTA2, TRIM28, CBX3, ILF3, RBBP7, CBX5, HDAC2, HDAC1, DRAP1, HEXIM1, SMARCC2, NPM1, GATAD2A, DNMT1, SUPT5H, RBM15, SMARCA4" 430 362 13528 1.738147244 1 0.23982504 31.26727752

GOTERM_BP_FAT GO:0006350~transcription 83 16.8699187 0.023889348 "COPS2, FOXK1, TCOF1, CNOT3, CBX3, MKI67IP, YBX1, PNN, NONO, FUBP1, FUBP3, MCM7, TARDBP, PSIP1, PQBP1, SUPT5H, CCAR1, KHDRBS1, TBL1XR1, RBBP4, ADNP, SF1, IRF2BP2, CDC5L, MCM2, RBBP7, MCM3, MCM4, MCM5, MCM6, SARNP, HNRPDL, SLTM, ADRM1, UHRF1, TRIM33, GTF2I, SMARCA5, RBM39, SMARCA1, MYBBP1A, LRPPRC, XRN2, PPP5C, SMARCA4, HCFC1, POLR2A, TFAM, TCERG1, DRAP1, HEXIM1, ZNF326, PELP1, SAFB, CEBPZ, GATAD2A, HNRNPD, GTF3C5, GATAD2B, TCEA1, ACTL6A, APEX1, EWSR1, CHD4,

TP53BP1, TRIM28, RNPS1, POLR3A, ILF3, HDAC2, PSMC5, ILF2, HDAC1, UBTF, SMARCC1, SFPQ,
SMARCC2, GTF2F2, SUPT16H, DNMT1, RBM14, PARP1, PUF60"	430	2101	13528	1.2428456	1
0.254211945	33.24764683
GOTERM_BP_FAT	GO:0010551~regulation of specific transcription from RNA polymerase II promoter	8
1.62601626	0.029677951	"TBL1XR1, HMGB2, HDAC2, HDAC1, XRCC6, PRKDC, RBM15, SMARCA4"	430
94	13528	2.677486393	1	0.29484894	39.56525199
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	24	4.87804878
0.033884189	"TBL1XR1, NCBP1, HMGB2, FOXK1, MTA2, TP53BP1, TRIM28, XRCC6, PRKDC, ILF3, PRPF6,
HDAC2, PSMC5, ILF2, HDAC1, SMARCC1, SMARCC2, GTF2F2, TCEA1, SMARCA1, SUPT5H, RBM14,
RBM15, SMARCA4"	430	481	13528	1.569752937	1	0.325595402	43.79841763
GOTERM_BP_FAT	"GO:0045892~negative regulation of transcription, DNA-dependent"	19	3.861788618
0.034787592	"TBL1XR1, HMGB1, FOXK1, MTA2, TRIM28, CBX3, ILF3, RBBP7, CBX5, HDAC2, HDAC1,
DRAP1, HEXIM1, SMARCC2, GATAD2A, DNMT1, SUPT5H, RBM15, SMARCA4"	430	356	13528
1.679069767	1	0.330821806	44.67047264
GOTERM_BP_FAT	GO:0010553~negative regulation of specific transcription from RNA polymerase II promoter
5	1.016260163	0.040127713	"TBL1XR1, HDAC2, HDAC1, RBM15, SMARCA4"	430	41	13528
3.836642087	1	0.361423973	49.57094742
GOTERM_BP_FAT	"GO:0045893~positive regulation of transcription, DNA-dependent"	23	4.674796748
0.050772773	"TBL1XR1, HMGB2, FOXK1, MTA2, TP53BP1, XRCC6, TRIM28, PRKDC, ILF3, PRPF6, HDAC2,
PSMC5, ILF2, HDAC1, SMARCC1, SMARCC2, GTF2F2, TCEA1, SMARCA1, SUPT5H, RBM14, RBM15,
SMARCA4"	430	477	13528	1.51696163	1	0.42179049	58.1475426
GOTERM_BP_FAT	GO:0032582~negative regulation of gene-specific transcription	5	1.016260163
0.065047082	"TBL1XR1, HDAC2, HDAC1, RBM15, SMARCA4"	430	48	13528	3.277131783	1
0.497796926	67.51203498
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	26	5.284552846	0.075296881
"TBL1XR1, HMGB2, FOXK1, MTA2, TP53BP1, TRIM28, XRCC6, PRKDC, ILF3, DDX5, CDK2, PRPF6, HDAC2,
PSMC5, ILF2, HDAC1, SMARCC1, GTF2F2, SMARCC2, DNMT1, TCEA1, RBM14, SUPT5H, SMARCA1,
RBM15, SMARCA4"	430	581	13528	1.407869351	1	0.54220742	72.97932438
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	58	11.78861789	0.080570688	"COPS2,
FOXK1, XRCC6, CNOT3, CBX3, DEK, YBX1, CBX5, ZNF207, AIP, FUBP1, FUBP3, TARDBP, PQBP1, SUPT5H,
KHDRBS1, TBL1XR1, MTA2, ADNP, SF1, RBBP7, PRPF6, UHRF1, GTF2I, SMARCA5, SMARCA1, SMARCA4,
HMGB2, HCFC1, TFAM, TCERG1, HEXIM1, DRAP1, NPM1, HNRNPD, GATAD2A, GTF3C5, GATAD2B,
TCEA1, APEX1, EWSR1, TP53BP1, TRIM28, ILF3, DDX5, PSMC5, HDAC2, ILF2, HDAC1, UBTF, MRPL28,
PSMC3, SMARCC1, GTF2F2, RPL7L1, SMARCC2, SUPT16H, RBM14"	408	1512	12983	1.220649834
1	0.488606986	69.95175304
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	25	5.081300813	0.088992691
"TBL1XR1, HMGB2, FOXK1, MTA2, TP53BP1, XRCC6, TRIM28, PRKDC, ILF3, DDX5, CDK2, PRPF6, HDAC2,
PSMC5, ILF2, HDAC1, SMARCC1, SMARCC2, GTF2F2, TCEA1, SMARCA1, SUPT5H, RBM14, RBM15,
SMARCA4"	430	564	13528	1.394524163	1	0.591898547	78.94432934
GOTERM_BP_FAT	GO:0045786~negative regulation of cell cycle	6	1.219512195	0.114341285	"HDAC2,
HDAC1, HEXIM1, TPR, SCRIB, SMARCA4"	430	81	13528	2.330404823	1	0.66310469	86.86266429
GOTERM_BP_FAT	GO:0045449~regulation of transcription	93	18.90243902	0.13134829	"COPS2,
FOXK1, XRCC6, CNOT3, CBX3, DEK, YBX1, CBX5, PNN, ZNF207, FUBP1, NONO, FUBP3, MCM7, TARDBP,
PSIP1, PQBP1, SUPT5H, CCAR1, KHDRBS1, TBL1XR1, RBBP4, MTA2, ADNP, SF1, IRF2BP2, CDC5L, MCM2,
MCM3, RBBP7, MCM4, CDK2, MCM5, PRPF6, MCM6, SARNP, HNRPDL, SLTM, UHRF1, TRIM33, GTF2I,
SMARCA5, CDK11B, RBM39, SMARCA1, MYBBP1A, LRPPRC, XRN2, SMARCA4, HMGB1, HMGB2, HCFC1,
PRKDC, POLR2A, TFAM, SUMO1, TCERG1, DRAP1, HEXIM1, RPL6, ZNF326, SAFB, NPM1, CEBPZ, CSDE1,
GATAD2A, HNRNPD, GATAD2B, ACTL6A, TCEA1, EWSR1, DNAJA3, CHD4, TP53BP1, TRIM28, ILF3, DDX5,
HDAC2, PSMC5, ILF2, MRPL28, UBTF, HDAC1, SMARCC1, SFPQ, SMARCC2, GTF2F2, SUPT16H, DNMT1,
TMPO, RBM14, RBM15, PUF60"430	2601	13528	1.124883989	1	0.706788967	90.49949136
GOTERM_BP_FAT	"GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid
metabolic process"	26	5.284552846	0.136710086	"NCBP1, TBL1XR1, HMGB2, FOXK1, MTA2, TP53BP1,
TRIM28, XRCC6, PRKDC, ILF3, DDX5, CDK2, PRPF6, HDAC2, PSMC5, ILF2, HDAC1, SMARCC1, GTF2F2,
SMARCC2, TCEA1, RBM14, SUPT5H, SMARCA1, RBM15, SMARCA4"	430	624	13528	1.310852713	1

0.720225555 91.43361791
GOTERM_BP_FAT GO:0000122~negative regulation of transcription from RNA polymerase II promoter 13
2.642276423 0.140041813 "HMGB1, TBL1XR1, MTA2, TRIM28, RBBP7, HDAC2, HDAC1, HEXIM1, DRAP1,
DNMT1, SUPT5H, RBM15, SMARCA4" 430 266 13528 1.537541528 1 0.727504502 91.96981038
GOTERM_BP_FAT GO:0051173~positive regulation of nitrogen compound metabolic process 26 5.284552846
0.17282986 "NCBP1, TBL1XR1, HMGB2, FOXK1, MTA2, TP53BP1, TRIM28, XRCC6, PRKDC, ILF3, DDX5,
CDK2, PRPF6, HDAC2, PSMC5, ILF2, HDAC1, SMARCC1, GTF2F2, SMARCC2, TCEA1, RBM14, SUPT5H,
SMARCA1, RBM15, SMARCA4" 430 644 13528 1.270143002 1 0.786135074 95.80705818
GOTERM_BP_FAT GO:0010557~positive regulation of macromolecule biosynthetic process 26 5.284552846
0.191149813 "HMGB2, FOXK1, XRCC6, PRKDC, TCEA1, SUPT5H, EIF2B5, TBL1XR1, TP53BP1, MTA2,
TRIM28, ILF3, DDX5, CDK2, PRPF6, PSMC5, HDAC2, HDAC1, ILF2, SMARCC1, GTF2F2, SMARCC2,
SMARCA1, RBM14, RBM15, SMARCA4" 430 654 13528 1.250721855 1 0.810698472 97.11645496
GOTERM_BP_FAT GO:0031328~positive regulation of cellular biosynthetic process 27 5.487804878
0.196545467 "TBL1XR1, HMGB2, FOXK1, MTA2, TP53BP1, TRIM28, XRCC6, PRKDC, ILF3, DDX5, CDK2,
PRPF6, HDAC2, PSMC5, ILF2, HDAC1, SMARCC1, GTF2F2, NPM1, SMARCC2, TCEA1, RBM14, SUPT5H,
SMARCA1, RBM15, EIF2B5, SMARCA4" 430 685 13528 1.24004753 1 0.817318539 97.42167863
GOTERM_BP_FAT GO:0009891~positive regulation of biosynthetic process 27 5.487804878 0.21831638
"TBL1XR1, HMGB2, FOXK1, MTA2, TP53BP1, TRIM28, XRCC6, PRKDC, ILF3, DDX5, CDK2, PRPF6, HDAC2,
PSMC5, ILF2, HDAC1, SMARCC1, GTF2F2, NPM1, SMARCC2, TCEA1, RBM14, SUPT5H, SMARCA1, RBM15,
EIF2B5, SMARCA4" 430 695 13528 1.22220512 1 0.846865867 98.37103882
GOTERM_BP_FAT GO:0006357~regulation of transcription from RNA polymerase II promoter 27
5.487804878 0.287323454 "HMGB1, TBL1XR1, HMGB2, FOXK1, MTA2, TRIM28, XRCC6, PRKDC, DEK,
RBBP7, PRPF6, UHRF1, HDAC2, HDAC1, HEXIM1, DRAP1, SMARCC1, GTF2F2, SMARCC2, SMARCA5,
DNMT1, TCEA1, RBM14, SUPT5H, RBM15, CHD4, SMARCA4" 430 727 13528 1.16840792 1
0.913735482 99.65249868
GOTERM_BP_FAT GO:0045944~positive regulation of transcription from RNA polymerase II promoter 14
2.845528455 0.396752286 "TBL1XR1, HMGB2, MTA2, XRCC6, PRKDC, PRPF6, HDAC2, HDAC1, GTF2F2,
TCEA1, RBM14, SUPT5H, RBM15, SMARCA4" 430 371 13528 1.187187363 1 0.966349933
99.9785822
GOTERM_BP_FAT GO:0051252~regulation of RNA metabolic process 59 11.99186992 0.495069709
"NCBP1, FOXK1, XRCC6, CBX3, SYNCRIP, DEK, YBX1, CBX5, ZNF207, PQBP1, SUPT5H, TBL1XR1, MTA2,
ADNP, CDC5L, RBBP7, HNRNPU, PRPF6, SARNP, UHRF1, SMARCA5, CDK11B, SMARCA1, MYBBP1A,
SMARCA4, HMGB1, HMGB2, PRKDC, POLR2A, TFAM, RPL6, HEXIM1, DRAP1, NPM1, HNRNPD, GATAD2A,
CSDE1, GATAD2B, TCEA1, PABPC1, SNRNP70, EWSR1, CHD4, DHX9, TP53BP1, TRIM28, ELAVL1, ILF3,
PSMC5, HDAC2, ILF2, HDAC1, UBTF, SMARCC1, GTF2F2, SMARCC2, DNMT1, RBM14, RBM15" 430 1813
13528 1.023809951 1 0.982332469 99.99890547
GOTERM_BP_FAT GO:0016569~covalent chromatin modification 5 1.016260163 0.569730695 "HDAC2,
HDAC1, ACTL6A, RBM14, SMARCA4" 430 126 13528 1.248431155 1 0.991346866 99.99992456
GOTERM_BP_FAT "GO:0006355~regulation of transcription, DNA-dependent" 51 10.36585366
0.835822843 "FOXK1, XRCC6, CBX3, DEK, YBX1, ZNF207, CBX5, PQBP1, SUPT5H, TBL1XR1, MTA2, ADNP,
CDC5L, RBBP7, PRPF6, SARNP, UHRF1, SMARCA5, CDK11B, SMARCA1, MYBBP1A, SMARCA4, HMGB1,
HMGB2, PRKDC, POLR2A, TFAM, RPL6, HEXIM1, DRAP1, HNRNPD, GATAD2A, CSDE1, GATAD2B, TCEA1,
EWSR1, CHD4, TP53BP1, TRIM28, ILF3, PSMC5, HDAC2, HDAC1, UBTF, ILF2, SMARCC1, GTF2F2,
SMARCC2, DNMT1, RBM14, RBM15" 430 1773 13528 0.904954157 1 0.999831236 100

Annotation Cluster 44 Enrichment Score: 1.3879028079243805
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0022415~viral reproductive process 7 1.422764228 0.013512583 "XRCC5,
VAPB, XRCC6, PSIP1, HCFC1, DEK, SUPT5H" 430 62 13528 3.551987997 1 0.166247649
20.34104757
GOTERM_BP_FAT GO:0030069~lysogeny 3 0.609756098 0.024749639 "XRCC5, XRCC6, PSIP1" 430
8 13528 11.79767442 1 0.258739921 34.22429688
GOTERM_BP_FAT GO:0019047~provirus integration 3 0.609756098 0.024749639 "XRCC5, XRCC6,

PSIP1"	430	8	13528	11.79767442	1	0.258739921	34.22429688
GOTERM_BP_FAT	GO:0016032~viral reproduction	7	1.422764228	0.024874399	"XRCC5, VAPB, XRCC6, PSIP1, HCFC1, DEK, SUPT5H"	430	71	13528	3.101735997	1	0.258195475	34.36481114
GOTERM_BP_FAT	GO:0019058~viral infectious cycle	5	1.016260163	0.046574428	"XRCC5, XRCC6, PSIP1, DEK, SUPT5H"	430	43	13528	3.658193618	1	0.398421352	54.94334748
GOTERM_BP_FAT	GO:0015074~DNA integration	3	0.609756098	0.131156219	"XRCC5, XRCC6, PSIP1"	430	20	13528	4.719069767	1	0.708216033	90.46431509
GOTERM_BP_FAT	GO:0019059~initiation of viral infection	3	0.609756098	0.153149367	"XRCC5, XRCC6, PSIP1"	430	22	13528	4.290063425	1	0.752016906	93.78813963

Annotation Cluster 45	Enrichment Score: 1.249762988361075
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005657~replication fork	6	1.219512195	0.00340359	"RPA1, HDAC2, RFC2, TP53BP1, PCNA, MCM3"	415	32	12782	5.775	0.733623778	0.0237648	4.62403955
GOTERM_BP_FAT	"GO:0006297~nucleotide-excision repair, DNA gap filling"	3	0.609756098	0.099785944	"RPA1, RFC2, PCNA"	430	17	13528	5.551846785	1	0.622870887	82.74773677
GOTERM_BP_FAT	GO:0006289~nucleotide-excision repair	3	0.609756098	0.524450329	"RPA1, RFC2, PCNA"	430	55	13528	1.71602537	1	0.98677054	99.99959819

Annotation Cluster 46	Enrichment Score: 1.0530185506792582
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006378~mRNA polyadenylation	3	0.609756098	0.045665016	"CSTF3, CSTF2, PABPC1"	430	11	13528	8.58012685	1	0.394334451	54.21954077
GOTERM_BP_FAT	GO:0043631~RNA polyadenylation	3	0.609756098	0.071007019	"CSTF3, CSTF2, PABPC1"	430	14	13528	6.741528239	1	0.525060267	70.80576303
GOTERM_BP_FAT	GO:0031124~mRNA 3'-end processing	3	0.609756098	0.089866043	"CSTF3, CSTF2, PABPC1"	430	16	13528	5.898837209	1	0.593420028	79.27921692
GOTERM_BP_FAT	GO:0031123~RNA 3'-end processing	3	0.609756098	0.210593659	"CSTF3, CSTF2, PABPC1"	430	27	13528	3.495607235	1	0.836393228	98.08008862

Annotation Cluster 47	Enrichment Score: 1.0309946034373338
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0000922~spindle pole	5	1.016260163	0.023357894	"NUMA1, NPM1, TUBG1, SMC3, ZW10"	415	34	12782	4.529411765	0.999895924	0.121166971	27.9781781
GOTERM_CC_FAT	GO:0005819~spindle	10	2.032520325	0.049619998	"TBL1XR1, NUMA1, NPM1, CBX3, NUP85, TUBG1, MAP7D1, SMC3, MYH10, ZW10"	415	147	12782	2.095238095	0.999999997	0.234209259	50.67389036
GOTERM_CC_FAT	GO:0005876~spindle microtubule	4	0.81300813	0.066222248	"TBL1XR1, NUMA1, TUBG1, ZW10"	415	29	12782	4.248275862	1	0.295168426	61.38153909
GOTERM_CC_FAT	GO:0005874~microtubule	5	1.016260163	0.979325899	"TBL1XR1, NUMA1, KLC2, TUBG1, ZW10"	415	274	12782	0.562043796	1	0.999992172	100

Annotation Cluster 48	Enrichment Score: 0.9085287413219587
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006399~tRNA metabolic process	10	2.032520325	0.01273086	"DARS, TRMT6, POP1, RPP30, SSB, AARSD1, VARS, TPR, PUS7, FBL"	430	118	13528	2.666141112	0.999999998	0.159858525	19.27926998
GOTERM_BP_FAT	GO:0043039~tRNA aminoacylation	4	0.81300813	0.178425879	"DARS, AARSD1, VARS, TPR"	430	46	13528	2.735692619	1	0.792632477	96.25683857
GOTERM_BP_FAT	GO:0043038~amino acid activation	4	0.81300813	0.178425879	"DARS, AARSD1,

VARS, TPR" 430 46 13528 2.735692619 1 0.792632477 96.25683857
GOTERM_BP_FAT GO:0006418~tRNA aminoacylation for protein translation 4 0.81300813 0.178425879 "DARS, AARSD1, VARS, TPR" 430 46 13528 2.735692619 1 0.792632477 96.25683857
GOTERM_MF_FAT "GO:0016875~ligase activity, forming carbon-oxygen bonds" 4 0.81300813 0.182119245 "DARS, AARSD1, VARS, TPR" 408 47 12983 2.708176888 1 0.747332102 94.37287596
GOTERM_MF_FAT GO:0004812~aminoacyl-tRNA ligase activity 4 0.81300813 0.182119245 "DARS, AARSD1, VARS, TPR" 408 47 12983 2.708176888 1 0.747332102 94.37287596
GOTERM_MF_FAT "GO:0016876~ligase activity, forming aminoacyl-tRNA and related compounds" 4 0.81300813 0.182119245 "DARS, AARSD1, VARS, TPR" 408 47 12983 2.708176888 1 0.747332102 94.37287596

Annotation Cluster 49 Enrichment Score: 0.9058484107319819
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0000794~condensed nuclear chromosome 7 1.422764228 0.004793676 "RPA1, MKI67IP, TUBG1, RCC1, SMC1A, SMC3, LRPPRC" 415 49 12782 4.4 0.845013689 0.031633983 6.454861623
GOTERM_BP_FAT GO:0007052~mitotic spindle organization 3 0.609756098 0.080262653 "RCC1, SMC1A, SMC3" 430 15 13528 6.292093023 1 0.561609086 75.30517661
GOTERM_BP_FAT GO:0007051~spindle organization 4 0.81300813 0.170523607 "TUBG1, RCC1, SMC1A, SMC3" 430 45 13528 2.796485788 1 0.784675463 95.60730067
GOTERM_BP_FAT GO:0000226~microtubule cytoskeleton organization 8 1.62601626 0.18624966 "CKAP5, NPM1, DOCK7, TUBG1, RCC1, SMC1A, SMC3, ZW10" 430 147 13528 1.712134156 1 0.80471164 96.81012067
GOTERM_BP_FAT GO:0007017~microtubule-based process 10 2.032520325 0.409913393 "CKAP5, NPM1, DOCK7, KLC2, TUBG1, RCC1, SMC1A, SMC3, LRPPRC, ZW10" 430 253 13528 1.243496645 1 0.967851115 99.9851872
GOTERM_BP_FAT GO:0007010~cytoskeleton organization 13 2.642276423 0.73308657 "CKAP5, DOCK7, ANLN, RCC1, SMC3, NRAS, KRT16, NPM1, TUBG1, TRIP10, SMC1A, MYH10, ZW10" 430 436 13528 0.938041391 1 0.998818464 99.99999997

Annotation Cluster 50 Enrichment Score: 0.7313582597117626
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0001824~blastocyst development 5 1.016260163 0.046574428 "PRPF19, TJP1, PSMC3, NASP, SMARCA4" 430 43 13528 3.658193618 1 0.398421352 54.94334748
GOTERM_BP_FAT GO:0001701~in utero embryonic development 10 2.032520325 0.10782734 "RPA1, PRPF19, TJP1, PSMC3, MSH2, NASP, COPS3, YBX1, MYH10, SMARCA4" 430 176 13528 1.787526427 1 0.648693932 85.15069919
GOTERM_BP_FAT GO:0043009~chordate embryonic development 12 2.43902439 0.480818212 "RPA1, PRPF19, TJP1, PSMC3, MSH2, NASP, COPS3, PRKDC, GNAS, YBX1, MYH10, SMARCA4" 430 331 13528 1.140560669 1 0.98123697 99.99825702
GOTERM_BP_FAT GO:0009792~embryonic development ending in birth or egg hatching 12 2.43902439 0.491710666 "RPA1, PRPF19, TJP1, PSMC3, MSH2, NASP, COPS3, PRKDC, GNAS, YBX1, MYH10, SMARCA4" 430 334 13528 1.130316112 1 0.982442669 99.99877718

Annotation Cluster 51 Enrichment Score: 0.6923755405334542
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0002200~somatic diversification of immune receptors 6 1.219512195 0.001420124 "MSH2, XRCC6, LIG3, PRKDC, HSPD1, CTNNBL1" 430 27 13528 6.99121447 0.893661514 0.023810109 2.347567134
GOTERM_BP_FAT GO:0002562~somatic diversification of immune receptors via germline recombination within a single locus 5 1.016260163 0.006403888 "MSH2, XRCC6, LIG3, PRKDC, HSPD1" 430 24 13528

6.554263566 0.999960191 0.094553879 10.18258985
GOTERM_BP_FAT GO:0016444~somatic cell DNA recombination 5 1.016260163 0.006403888 "MSH2, XRCC6, LIG3, PRKDC, HSPD1" 430 24 13528 6.554263566 0.999960191 0.094553879 10.18258985
GOTERM_BP_FAT GO:0016445~somatic diversification of immunoglobulins 4 0.81300813 0.03117907 "MSH2, PRKDC, HSPD1, CTNNBL1" 430 22 13528 5.720084567 1 0.305535942 41.10924636
GOTERM_BP_FAT GO:0033151~V(D)J recombination 3 0.609756098 0.038147971 "XRCC6, LIG3, PRKDC" 430 10 13528 9.438139535 1 0.35075804 47.80385243
GOTERM_BP_FAT GO:0002377~immunoglobulin production 4 0.81300813 0.068380615 "MSH2, PRKDC, HSPD1, CTNNBL1" 430 30 13528 4.194728682 1 0.513562873 69.39500623
GOTERM_BP_FAT GO:0002440~production of molecular mediator of immune response 4 0.81300813 0.073999405 "MSH2, PRKDC, HSPD1, CTNNBL1" 430 31 13528 4.059414854 1 0.538019133 72.33852847
GOTERM_BP_FAT GO:0016447~somatic recombination of immunoglobulin gene segments 3 0.609756098 0.109992738 "MSH2, PRKDC, HSPD1" 430 18 13528 5.243410853 1 0.654306276 85.74180195
GOTERM_BP_FAT GO:0031647~regulation of protein stability 4 0.81300813 0.14747298 "MORC3, PRKDC, HSPD1, DNAJA3" 430 42 13528 2.996234773 1 0.739593931 93.05423173
GOTERM_BP_FAT GO:0002520~immune system development 12 2.43902439 0.258239635 "RPA1, XRCC5, MSH2, XRCC6, LIG3, PRKDC, TCEA1, ACIN1, HSPD1, TPD52, DNAJA3, CTNNBL1" 430 276 13528 1.367846309 1 0.889349845 99.32184026
GOTERM_BP_FAT GO:0010212~response to ionizing radiation 4 0.81300813 0.296483698 "MSH2, XRCC6, PRKDC, INTS3" 430 60 13528 2.097364341 1 0.917757517 99.72007534
GOTERM_BP_FAT GO:0042113~B cell activation 4 0.81300813 0.434930877 "MSH2, PRKDC, HSPD1, TPD52" 430 76 13528 1.655813953 1 0.972694084 99.99281974
GOTERM_BP_FAT GO:0030183~B cell differentiation 3 0.609756098 0.452656421 "MSH2, PRKDC, TPD52" 430 48 13528 1.96627907 1 0.976289259 99.99578531
GOTERM_BP_FAT GO:0048872~homeostasis of number of cells 4 0.81300813 0.61894244 "RPA1, TCEA1, ACIN1, DNAJA3" 430 100 13528 1.258418605 1 0.99501531 99.99999009
GOTERM_BP_FAT GO:0030097~hemopoiesis 8 1.62601626 0.624726672 "RPA1, XRCC5, MSH2, PRKDC, TCEA1, ACIN1, TPD52, DNAJA3" 430 236 13528 1.066456445 1 0.995243112 99.99999233
GOTERM_BP_FAT GO:0030098~lymphocyte differentiation 4 0.81300813 0.638896218 "MSH2, PRKDC, TPD52, DNAJA3" 430 103 13528 1.221765636 1 0.9959941 99.99999597
GOTERM_BP_FAT GO:0051345~positive regulation of hydrolase activity 6 1.219512195 0.674959418 "GNAQ, MSH2, DOCK7, HSPD1, DNAJA3, SCRIB" 430 179 13528 1.05454073 1 0.997438445 99.99999931
GOTERM_BP_FAT GO:0048534~hemopoietic or lymphoid organ development 8 1.62601626 0.722273653 "RPA1, XRCC5, MSH2, PRKDC, TCEA1, ACIN1, TPD52, DNAJA3" 430 260 13528 0.968014311 1 0.99864285 99.99999995
GOTERM_BP_FAT GO:0002521~leukocyte differentiation 4 0.81300813 0.789732347 "MSH2, PRKDC, TPD52, DNAJA3" 430 131 13528 0.960624889 1 0.999572483 100
GOTERM_BP_FAT GO:0002252~immune effector process 4 0.81300813 0.802292229 "MSH2, PRKDC, HSPD1, CTNNBL1" 430 134 13528 0.939118362 1 0.99966899 100
GOTERM_BP_FAT GO:0046649~lymphocyte activation 5 1.016260163 0.880303643 "MSH2, PRKDC, HSPD1, TPD52, DNAJA3" 430 199 13528 0.790463948 1 0.999947043 100
GOTERM_BP_FAT GO:0042110~T cell activation 3 0.609756098 0.912617769 "PRKDC, HSPD1, DNAJA3" 430 126 13528 0.749058693 1 0.99998353 100
GOTERM_BP_FAT GO:0045321~leukocyte activation 5 1.016260163 0.951303395 "MSH2, PRKDC, HSPD1, TPD52, DNAJA3" 430 242 13528 0.65000961 1 0.999997708 100
GOTERM_BP_FAT GO:0001775~cell activation 5 1.016260163 0.982444066 "MSH2, PRKDC, HSPD1, TPD52, DNAJA3" 430 287 13528 0.548091727 1 0.999999924 100
GOTERM_BP_FAT GO:0006955~immune response 11 2.235772358 0.998853643 "GTPBP1, EXOSC9, C1QBP, ILF2, MSH2, IL18, PRKDC, POLR3A, HSPD1, DNAJA3, CTNNBL1" 430 690 13528 0.501543647 1 1 100

Annotation Cluster 52 Enrichment Score: 0.6549307090738717

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0006084~acetyl-CoA metabolic process 4 0.81300813 0.073999405 "SDHA, SDHB, DLAT, SUCLA2" 430 31 13528 4.059414854 1 0.538019133 72.33852847

GOTERM_BP_FAT GO:0045333~cellular respiration 7 1.422764228 0.087747635 "SDHA, UQCRC2, SDHB, NDUFA9, NDUFV1, SUCLA2, NDUFA10" 430 97 13528 2.270342843 1 0.588737866 78.45810368

GOTERM_BP_FAT GO:0009060~aerobic respiration 4 0.81300813 0.098392943 "SDHA, UQCRC2, SDHB, SUCLA2" 430 35 13528 3.595481728 1 0.6195915 82.29601404

GOTERM_BP_FAT GO:0006099~tricarboxylic acid cycle 3 0.609756098 0.164398332 "SDHA, SDHB, SUCLA2" 430 23 13528 4.103538928 1 0.773022015 95.03243631

GOTERM_BP_FAT GO:0046356~acetyl-CoA catabolic process 3 0.609756098 0.164398332 "SDHA, SDHB, SUCLA2" 430 23 13528 4.103538928 1 0.773022015 95.03243631

GOTERM_BP_FAT GO:0015980~energy derivation by oxidation of organic compounds 8 1.62601626 0.173478867 "SDHA, UQCRC2, SDHB, NDUFA9, NDUFV1, GNAS, SUCLA2, NDUFA10" 430 144 13528 1.747803618 1 0.785800752 95.86171305

GOTERM_BP_FAT GO:0009109~coenzyme catabolic process 3 0.609756098 0.198902868 "SDHA, SDHB, SUCLA2" 430 26 13528 3.630053667 1 0.81992698 97.54526091

GOTERM_BP_FAT GO:0051187~cofactor catabolic process 3 0.609756098 0.257859462 "SDHA, SDHB, SUCLA2" 430 31 13528 3.04456114 1 0.890071296 99.31600673

GOTERM_BP_FAT GO:0006732~coenzyme metabolic process 7 1.422764228 0.357457461 "SDHA, SDHB, GSR, DLAT, SUCLA2, HIBADH, NAPRT1" 430 153 13528 1.439367685 1 0.951819079 99.93849708

GOTERM_BP_FAT GO:0051186~cofactor metabolic process 8 1.62601626 0.423841758 "SDHA, SDHB, GSR, HMBS, DLAT, SUCLA2, HIBADH, NAPRT1" 430 195 13528 1.290685748 1 0.96998654 99.99006367

GOTERM_BP_FAT GO:0051188~cofactor biosynthetic process 4 0.81300813 0.598255267 "HMBS, DLAT, SUCLA2, NAPRT1" 430 97 13528 1.297338768 1 0.993678678 99.99997603

GOTERM_MF_FAT GO:0009055~electron carrier activity 3 0.609756098 0.993170368 "SDHA, SDHB, GSR" 408 221 12983 0.431960341 1 0.999999988 100

Annotation Cluster 53 Enrichment Score: 0.6420015352497231

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0051726~regulation of cell cycle 18 3.658536585 0.035143845 "MSH2, HCFC1, ANLN, INTS3, RCC1, SCRIB, CDK2, HDAC2, HDAC1, HEXIM1, NPM1, PES1, SMC1A, TPR, BUB3, SMARCA4, ZW10, CDK13" 430 331 13528 1.710841003 1 0.331683829 45.01085307

GOTERM_BP_FAT GO:0007346~regulation of mitotic cell cycle 9 1.829268293 0.110665892 "ANLN, RCC1, TPR, SCRIB, BUB3, CDK2, SMARCA4, ZW10, CDK13" 430 152 13528 1.862790698 1 0.652461897 85.92100164

GOTERM_BP_FAT GO:0010564~regulation of cell cycle process 7 1.422764228 0.154021512 "NPM1, ANLN, RCC1, TPR, SMARCA4, ZW10, CDK13" 430 114 13528 1.931782946 1 0.752319217 93.89421735

GOTERM_BP_FAT GO:0007088~regulation of mitosis 3 0.609756098 0.534178694 "RCC1, TPR, CDK13" 430 56 13528 1.68538206 1 0.988076491 99.99971557

GOTERM_BP_FAT GO:0051783~regulation of nuclear division 3 0.609756098 0.534178694 "RCC1, TPR, CDK13" 430 56 13528 1.68538206 1 0.988076491 99.99971557

GOTERM_BP_FAT GO:0033043~regulation of organelle organization 6 1.219512195 0.822570677 "NPM1, SPTBN2, DNMT1, RCC1, TPR, CDK13" 430 217 13528 0.869874612 1 0.999778796 100

Annotation Cluster 54 Enrichment Score: 0.566593685323689

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0032984~macromolecular complex disassembly 3 0.609756098 0.198902868

"ICT1, SUPT16H, XRN2" 430 26 13528 3.630053667 1 0.81992698 97.54526091
GOTERM_BP_FAT GO:0034623~cellular macromolecular complex disassembly 3 0.609756098
0.198902868 "ICT1, SUPT16H, XRN2" 430 26 13528 3.630053667 1 0.81992698 97.54526091
GOTERM_BP_FAT GO:0022411~cellular component disassembly 3 0.609756098 0.504587927 "ICT1,
SUPT16H, XRN2" 430 53 13528 1.780781044 1 0.983964473 99.99920371

Annotation Cluster 55 Enrichment Score: 0.5481197760944709
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0044429~mitochondrial part 32 6.504065041 0.006205251 "UQCRC2, MRPS15,
HK2, CHCHD3, TIMM50, TFAM, MRPL13, CSDE1, MRPL39, DHX30, DNAJA3, HSPA9, TOMM34, GPD2,
MRPL1, MRPS22, NDUFA9, TOMM40, KIAA1967, DLAT, NDUFA10, SDHA, SDHB, MRPL28, C1QBP,
MRPS18A, NDUFV1, HSPD1, LRPPRC, PMPCB, MRPL43, DAP3" 415 595 12782 1.656470588
0.910645046 0.038818898 8.280570866
GOTERM_BP_FAT GO:0045333~cellular respiration 7 1.422764228 0.087747635 "SDHA, UQCRC2,
SDHB, NDUFA9, NDUFV1, SUCLA2, NDUFA10" 430 97 13528 2.270342843 1 0.588737866
78.45810368
GOTERM_CC_FAT GO:0019866~organelle inner membrane 16 3.25203252 0.115554465 "UQCRC2,
GPD2, NDUFA9, CHCHD3, CBX3, TIMM50, NDUFA10, SDHA, SDHB, NDUFV1, CSDE1, PCNA, HSPD1,
MATR3, LRPPRC, PMPCB" 415 329 12782 1.49787234 1 0.448742128 81.82547803
GOTERM_BP_FAT GO:0022904~respiratory electron transport chain 5 1.016260163 0.144912949 "SDHA,
SDHB, NDUFA9, NDUFV1, NDUFA10" 430 64 13528 2.457848837 1 0.736710221 92.69723312
GOTERM_CC_FAT GO:0005746~mitochondrial respiratory chain 5 1.016260163 0.152923811 "SDHA,
UQCRC2, NDUFA9, NDUFV1, NDUFA10" 415 64 12782 2.40625 1 0.539680602 90.0203453
GOTERM_BP_FAT GO:0015980~energy derivation by oxidation of organic compounds 8 1.62601626
0.173478867 "SDHA, UQCRC2, SDHB, NDUFA9, NDUFV1, GNAS, SUCLA2, NDUFA10" 430 144 13528
1.747803618 1 0.785800752 95.86171305
GOTERM_BP_FAT GO:0006119~oxidative phosphorylation 6 1.219512195 0.200036546 "UQCRC2,
MSH2, NDUFA9, NDUFV1, NDUFA10, ATP6V1D" 430 98 13528 1.926150925 1 0.8203822
97.60268824
GOTERM_CC_FAT GO:0044455~mitochondrial membrane part 7 1.422764228 0.219234508 "SDHA,
UQCRC2, NDUFA9, NDUFV1, TOMM40, TIMM50, NDUFA10" 415 125 12782 1.7248 1 0.681178514
96.78250859
GOTERM_CC_FAT GO:0070469~respiratory chain 5 1.016260163 0.225005925 "SDHA, UQCRC2,
NDUFA9, NDUFV1, NDUFA10" 415 75 12782 2.053333333 1 0.687622551 97.09749605
GOTERM_BP_FAT GO:0022900~electron transport chain 6 1.219512195 0.294904772 "SDHA, UQCRC2,
SDHB, NDUFA9, NDUFV1, NDUFA10" 430 114 13528 1.655813953 1 0.917370604 99.70938636
GOTERM_BP_FAT "GO:0006120~mitochondrial electron transport, NADH to ubiquinone" 3 0.609756098
0.386474949 "NDUFA9, NDUFV1, NDUFA10" 430 42 13528 2.24717608 1 0.962834945
99.97159379
GOTERM_MF_FAT GO:0003954~NADH dehydrogenase activity 3 0.609756098 0.392201703
"NDUFA9, NDUFV1, NDUFA10" 408 43 12983 2.220075239 1 0.945444454 99.91967751
GOTERM_MF_FAT GO:0050136~NADH dehydrogenase (quinone) activity 3 0.609756098 0.392201703
"NDUFA9, NDUFV1, NDUFA10" 408 43 12983 2.220075239 1 0.945444454 99.91967751
GOTERM_MF_FAT GO:0008137~NADH dehydrogenase (ubiquinone) activity 3 0.609756098 0.392201703
"NDUFA9, NDUFV1, NDUFA10" 408 43 12983 2.220075239 1 0.945444454 99.91967751
GOTERM_CC_FAT GO:0030964~NADH dehydrogenase complex 3 0.609756098 0.396656277
"NDUFA9, NDUFV1, NDUFA10" 415 42 12782 2.2 1 0.892231895 99.91028311
GOTERM_CC_FAT GO:0045271~respiratory chain complex I 3 0.609756098 0.396656277 "NDUFA9,
NDUFV1, NDUFA10" 415 42 12782 2.2 1 0.892231895 99.91028311
GOTERM_CC_FAT GO:0005747~mitochondrial respiratory chain complex I 3 0.609756098 0.396656277
"NDUFA9, NDUFV1, NDUFA10" 415 42 12782 2.2 1 0.892231895 99.91028311
GOTERM_CC_FAT GO:0031966~mitochondrial membrane 15 3.048780488 0.402159818 "UQCRC2, GPD2,
NDUFA9, HK2, CHCHD3, TOMM40, TIMM50, NDUFA10, SDHA, SDHB, NDUFV1, CSDE1, HSPD1, PMPCB,

TOMM34" 415 394 12782 1.172588832 1 0.891148718 99.92100288
GOTERM_CC_FAT GO:0005743~mitochondrial inner membrane 12 2.43902439 0.40517156 "SDHA, UQCRC2, GPD2, SDHB, NDUFA9, NDUFV1, CHCHD3, CSDE1, TIMM50, HSPD1, NDUFA10, PMPCB" 415 306 12782 1.207843137 1 0.890839424 99.92635326
GOTERM_BP_FAT GO:0006091~generation of precursor metabolites and energy 12 2.43902439 0.407516337 "SDHA, UQCRC2, SDHB, MSH2, NDUFA9, NDUFV1, HK2, GNAS, DLAT, SUCLA2, NDUFA10, ATP6V1D" 430 313 13528 1.206152017 1 0.968373978 99.9841486
GOTERM_MF_FAT "GO:0016655~oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" 3 0.609756098 0.457320172 "NDUFA9, NDUFV1, NDUFA10" 408 49 12983 1.948229292 1 0.966774615 99.98413698
GOTERM_MF_FAT "GO:0016651~oxidoreductase activity, acting on NADH or NADPH"4 0.81300813 0.484929008 "GSR, NDUFA9, NDUFV1, NDUFA10" 408 83 12983 1.533545948 1 0.972982809 99.99248716
GOTERM_CC_FAT GO:0005740~mitochondrial envelope 15 3.048780488 0.489867933 "UQCRC2, GPD2, NDUFA9, HK2, CHCHD3, TOMM40, TIMM50, NDUFA10, SDHA, SDHB, NDUFV1, CSDE1, HSPD1, PMPCB, TOMM34" 415 419 12782 1.102625298 1 0.936009678 99.99127398
GOTERM_BP_FAT GO:0042775~mitochondrial ATP synthesis coupled electron transport 3 0.609756098 0.534178694 "NDUFA9, NDUFV1, NDUFA10" 430 56 13528 1.68538206 1 0.988076491 99.99971557
GOTERM_BP_FAT GO:0042773~ATP synthesis coupled electron transport 3 0.609756098 0.534178694 "NDUFA9, NDUFV1, NDUFA10" 430 56 13528 1.68538206 1 0.988076491 99.99971557
GOTERM_CC_FAT GO:0031090~organelle membrane33 6.707317073 0.7587133 "UQCRC2, VAPB, HK2, CHCHD3, CBX3, RER1, TIMM50, SUMO1, MRPL19, CSDE1, PCYT1A, RAB21, TOMM34, GPD2, SPTLC1, SPTLC2, NDUFA9, TOMM40, NUP85, NDUFA10, ATP6V1D, SDHA, SDHB, BNIP1, NDUFV1, PCNA, GNAS, TMPO, HSPD1, MATR3, LRPPRC, PMPCB, GOLGB1" 415 1096 12782 0.927372263 1 0.993950855 99.99999973
GOTERM_BP_FAT GO:0055114~oxidation reduction 12 2.43902439 0.992562445 "SDHA, UQCRC2, GPD2, OGFOD1, SDHB, GSR, NDUFA9, NDUFV1, RRM1, NDUFA10, TECR, HIBADH" 430 639 13528 0.590806857 1 0.999999996 100

Annotation Cluster 56 Enrichment Score: 0.5465532336128925
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0016575~histone deacetylation 3 0.609756098 0.099785944 "HDAC2, HDAC1, RBM14" 430 17 13528 5.551846785 1 0.622870887 82.74773677
GOTERM_BP_FAT GO:0006476~protein amino acid deacetylation 3 0.609756098 0.153149367 "HDAC2, HDAC1, RBM14" 430 22 13528 4.290063425 1 0.752016906 93.78813963
GOTERM_BP_FAT GO:0016569~covalent chromatin modification 5 1.016260163 0.569730695 "HDAC2, HDAC1, ACTL6A, RBM14, SMARCA4" 430 126 13528 1.248431155 1 0.991346866 99.99992456
GOTERM_BP_FAT GO:0016570~histone modification 4 0.81300813 0.748053865 "HDAC2, HDAC1, ACTL6A, RBM14"430 122 13528 1.03149066 1 0.999099685 99.99999999

Annotation Cluster 57 Enrichment Score: 0.5452273326108682
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0017038~protein import 8 1.62601626 0.122984018 "NUP98, NUP205, TOMM40, NOP58, RANBP2, TPR, AIP, TOMM34" 430 131 13528 1.921249778 1 0.687340138 88.84894869
GOTERM_BP_FAT GO:0007005~mitochondrion organization 7 1.422764228 0.273793906 "TFAM, TOMM40, TIMM50, DNAJA3, AIP, DAP3, TOMM34" 430 138 13528 1.595820694 1 0.903259452 99.5241361
GOTERM_BP_FAT GO:0006626~protein targeting to mitochondrion 3 0.609756098 0.293442222 "TOMM40, AIP, TOMM34" 430 34 13528 2.775923393 1 0.917079263 99.69914393
GOTERM_BP_FAT GO:0070585~protein localization in mitochondrion 3 0.609756098 0.293442222 "TOMM40, AIP, TOMM34" 430 34 13528 2.775923393 1 0.917079263 99.69914393

GOTERM_BP_FAT	GO:0006839~mitochondrial transport	3	0.609756098	0.647956239	"TOMM40, AIP, TOMM34"	430	69	13528	1.367846309	1	0.996371988	99.99999736

Annotation Cluster 58	Enrichment Score: 0.46736831546617624
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007569~cell aging	4	0.81300813	0.085824778	"NRAS, MORC3, NPM1, DNAJA3"	430	33	13528	3.813389711	1	0.582517287	77.68639162
GOTERM_BP_FAT	GO:0007568~aging	5	1.016260163	0.462951425	"NRAS, MORC3, MSH2, NPM1, DNAJA3"	430	110	13528	1.430021142	1	0.978604659	99.99693156
GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	5	1.016260163	0.997118885	"RBBP4, MORC3, NPM1, SF1, DNAJA3"	430	361	13528	0.435740514	1	1	100

Annotation Cluster 59	Enrichment Score: 0.4527786796922535
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006541~glutamine metabolic process	3	0.609756098	0.120458357	"GLUL, GMPS, PFAS"	430	19	13528	4.96744186	1	0.681326004	88.29982504
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	3	0.609756098	0.494457257	"GLUL, GMPS, PFAS"	430	52	13528	1.815026834	1	0.982473006	99.99888306
GOTERM_MF_FAT	"GO:0016879~ligase activity, forming carbon-nitrogen bonds"	7	1.422764228	0.735695788	"PRPF19, GLUL, UBE3A, UBR5, GMPS, ATG3, PFAS"	408	231	12983	0.964275104	1	0.99818329	99.99999947

Annotation Cluster 60	Enrichment Score: 0.42020286235938553
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0050662~coenzyme binding	8	1.62601626	0.340254542	"SDHA, GSR, NDUFA9, NDUFV1, HMBS, DLAT, PARP1, HIBADH"	408	181	12983	1.406456505	1	0.922234692	99.74019903
GOTERM_MF_FAT	GO:0048037~cofactor binding	10	2.032520325	0.380525477	"SDHA, GSR, SPTLC1, SPTLC2, NDUFA9, NDUFV1, HMBS, DLAT, PARP1, HIBADH"	408	249	12983	1.277954957	1	0.941100178	99.89453128
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	8	1.62601626	0.423841758	"SDHA, SDHB, GSR, HMBS, DLAT, SUCLA2, HIBADH, NAPRT1"	430	195	13528	1.290685748	1	0.96998654	99.99006367

Annotation Cluster 61	Enrichment Score: 0.3443098050737374
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051101~regulation of DNA binding	6	1.219512195	0.338676823	"SUMO1, HDAC2, NPM1, APEX1, DNAJA3, SMARCA4"	430	121	13528	1.560023064	1	0.942738631	99.9004495
GOTERM_BP_FAT	GO:0051090~regulation of transcription factor activity	5	1.016260163	0.413356148	"SUMO1, HDAC2, NPM1, DNAJA3, SMARCA4"	430	103	13528	1.527207044	1	0.96815964	99.98656747
GOTERM_BP_FAT	GO:0043433~negative regulation of transcription factor activity	3	0.609756098	0.420046652	"SUMO1, HDAC2, DNAJA3"	430	45	13528	2.097364341	1	0.969576102	99.98891111
GOTERM_BP_FAT	GO:0043392~negative regulation of DNA binding	3	0.609756098	0.484196279	"SUMO1, HDAC2, DNAJA3"	430	51	13528	1.850615595	1	0.981685743	99.9984372
GOTERM_BP_FAT	GO:0051098~regulation of binding	6	1.219512195	0.536489361	"SUMO1, HDAC2, NPM1, APEX1, DNAJA3, SMARCA4"	430	153	13528	1.23374373	1	0.98822462	99.99973826
GOTERM_BP_FAT	GO:0051100~negative regulation of binding	3	0.609756098	0.562537143	"SUMO1, HDAC2, DNAJA3"	430	59	13528	1.599684667	1	0.990657111	99.99990046

Annotation Cluster 62	Enrichment Score: 0.3343074475379571
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic process	3	0.609756098
0.131156219	"NT5E, GMPS, PFAS"	430	20	13528	4.719069767	1	0.708216033	90.46431509
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic process	3	0.609756098
0.131156219	"NT5E, GMPS, PFAS"	430	20	13528	4.719069767	1	0.708216033	90.46431509
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	3	0.609756098
0.187294611	"NT5E, GMPS, PFAS"	430	25	13528	3.775255814	1	0.805095079	96.87790568
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	8	1.62601626	0.376955577	"MSH2,
DTYMK, RRM1, NT5E, GMPS, ATP6V1D, PFAS, NAPRT1"	430	186	13528	1.353138285	1	0.959889257
99.96325585
GOTERM_BP_FAT	"GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process"	8
1.62601626	0.413433149	"MSH2, DTYMK, RRM1, NT5E, GMPS, ATP6V1D, PFAS, NAPRT1"	430	193
13528	1.30406073	1	0.967735769	99.98659691
GOTERM_BP_FAT	"GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process"	8
1.62601626	0.413433149	"MSH2, DTYMK, RRM1, NT5E, GMPS, ATP6V1D, PFAS, NAPRT1"	430	193
13528	1.30406073	1	0.967735769	99.98659691
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	11	2.235772358	0.584227848
"GLUL, MSH2, HMBS, DTYMK, RRM1, SUCLA2, NT5E, GMPS, ATP6V1D, PFAS, NAPRT1"	430	325	13528
1.064815742	1	0.992482122	99.99995746
GOTERM_BP_FAT	GO:0009123~nucleoside monophosphate metabolic process	3	0.609756098
0.623803942	"NT5E, GMPS, PFAS"	430	66	13528	1.430021142	1	0.995267418	99.99999201
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	5	1.016260163	0.695037184
"MSH2, NT5E, GMPS, ATP6V1D, PFAS"	430	148	13528	1.062853551	1	0.998014523	99.99999976
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	6	1.219512195	0.707161722
"NUDT1, MSH2, NT5E, GMPS, ATP6V1D, PFAS"	430	186	13528	1.014853713	1	0.998289465
99.99999988
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	4	0.81300813	0.818055151
"NT5E, GMPS, ATP6V1D, PFAS"	430	138	13528	0.91189754	1	0.999756351	100
GOTERM_BP_FAT	GO:0009259~ribonucleotide metabolic process	4	0.81300813	0.849653541	"NT5E,
GMPS, ATP6V1D, PFAS"	430	147	13528	0.856067078	1	0.999879944	100
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	3	0.609756098	0.889710951
"GMPS, ATP6V1D, PFAS"	430	117	13528	0.806678593	1	0.99996267	100
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	3	0.609756098	0.907948819	"GMPS,
ATP6V1D, PFAS"	430	124	13528	0.761140285	1	0.999980418	100

Annotation Cluster 63	Enrichment Score: 0.33232238084780624
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0008219~cell death	25	5.081300813	0.422966531	"MSH2, VAPB, KIAA1967,
PRKDC, SCRIB, SMNDC1, FXR1, CTNNBL1, SLTM, NRAS, SYNE1, RAD21, BNIP1, TARDBP, SPTBN2,
MFSD10, CDK11B, ACIN1, HSPD1, DNAJA3, PUF60, API5, LUC7L3, DAP3, CCAR1"	430	719	13528
1.093896562	1	0.970121399	99.98980832
GOTERM_BP_FAT	GO:0016265~death	25	5.081300813	0.427217151	"MSH2, VAPB, KIAA1967, PRKDC,
SCRIB, SMNDC1, FXR1, CTNNBL1, SLTM, NRAS, SYNE1, RAD21, BNIP1, TARDBP, SPTBN2, MFSD10,
CDK11B, ACIN1, HSPD1, DNAJA3, PUF60, API5, LUC7L3, DAP3, CCAR1"	430	724	13528	1.086342027
1	0.970672838	99.99099319
GOTERM_BP_FAT	GO:0012501~programmed cell death	21	4.268292683	0.47784917	"MSH2,
KIAA1967, PRKDC, SCRIB, SMNDC1, FXR1, CTNNBL1, SLTM, NRAS, RAD21, BNIP1, MFSD10, CDK11B,
HSPD1, ACIN1, DNAJA3, PUF60, API5, LUC7L3, DAP3, CCAR1"	430	611	13528	1.081292582	1
0.981161114	99.9980827
GOTERM_BP_FAT	GO:0006915~apoptosis	20	4.06504065	0.542581469	"MSH2, KIAA1967, SCRIB,
SMNDC1, FXR1, CTNNBL1, SLTM, NRAS, RAD21, BNIP1, MFSD10, CDK11B, HSPD1, ACIN1, DNAJA3,

PUF60, API5, LUC7L3, DAP3, CCAR1" 430 602 13528 1.045198177 1 0.988726629 99.99979019

Annotation Cluster 64 Enrichment Score: 0.3322190784848886
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0009749~response to glucose stimulus 3 0.609756098 0.420046652 "GLUL, EIF2B3, EIF2B5" 430 45 13528 2.097364341 1 0.969576102 99.98891111
GOTERM_BP_FAT GO:0034284~response to monosaccharide stimulus 3 0.609756098 0.441900663 "GLUL, EIF2B3, EIF2B5" 430 47 13528 2.008114795 1 0.974377489 99.99416501
GOTERM_BP_FAT GO:0009746~response to hexose stimulus 3 0.609756098 0.441900663 "GLUL, EIF2B3, EIF2B5" 430 47 13528 2.008114795 1 0.974377489 99.99416501
GOTERM_BP_FAT GO:0009743~response to carbohydrate stimulus 3 0.609756098 0.571711399 "GLUL, EIF2B3, EIF2B5" 430 60 13528 1.573023256 1 0.991424319 99.99993016

Annotation Cluster 65 Enrichment Score: 0.3110364101780644
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0008584~male gonad development 4 0.81300813 0.227671826 "HMGB2, MSH2, SF1, CSDE1" 430 52 13528 2.420035778 1 0.857631414 98.66801064
GOTERM_BP_FAT GO:0046546~development of primary male sexual characteristics 4 0.81300813 0.340170821 "HMGB2, MSH2, SF1, CSDE1" 430 65 13528 1.936028623 1 0.942915021 99.90414283
GOTERM_BP_FAT GO:0046661~male sex differentiation 4 0.81300813 0.409468224 "HMGB2, MSH2, SF1, CSDE1" 430 73 13528 1.723861102 1 0.968149615 99.98499929
GOTERM_BP_FAT GO:0008406~gonad development 5 1.016260163 0.476862738 "HMGB2, MSH2, SF1, CSDE1, EIF2B5" 430 112 13528 1.40448505 1 0.98123394 99.99802125
GOTERM_BP_FAT GO:0048608~reproductive structure development 5 1.016260163 0.569730695 "HMGB2, MSH2, SF1, CSDE1, EIF2B5" 430 126 13528 1.248431155 1 0.991346866 99.99992456
GOTERM_BP_FAT GO:0045137~development of primary sexual characteristics 5 1.016260163 0.576011836 "HMGB2, MSH2, SF1, CSDE1, EIF2B5" 430 127 13528 1.238600989 1 0.991756947 99.999941
GOTERM_BP_FAT GO:0007548~sex differentiation 5 1.016260163 0.709932106 "HMGB2, MSH2, SF1, CSDE1, EIF2B5" 430 151 13528 1.041737256 1 0.998337128 99.9999999
GOTERM_BP_FAT GO:0003006~reproductive developmental process 6 1.219512195 0.922084951 "HMGB2, MSH2, SF1, CSDE1, PRKDC, EIF2B5" 430 262 13528 0.720468667 1 0.999989524 100

Annotation Cluster 66 Enrichment Score: 0.30837216105451654
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0003924~GTPase activity 10 2.032520325 0.217861422 "RAP2B, GTPBP1, NRAS, NUDT1, GNAQ, EFTUD2, EIF2S3, GNAS, TUBG1, GNL2" 408 211 12983 1.508107983 1 0.804997482 97.03165548
GOTERM_MF_FAT GO:0005525~GTP binding 12 2.43902439 0.621931617 "RAP2B, GTPBP1, NRAS, GNAQ, EFTUD2, EIF2S3, GNAS, DOCK7, TUBG1, GNL2, RAB21, GNL3" 408 372 12983 1.026486401 1 0.992962694 99.99991014
GOTERM_MF_FAT GO:0032561~guanyl ribonucleotide binding 12 2.43902439 0.656589892 "RAP2B, GTPBP1, NRAS, GNAQ, EFTUD2, EIF2S3, GNAS, DOCK7, TUBG1, GNL2, RAB21, GNL3" 408 382 12983 0.999615029 1 0.994897559 99.99997731
GOTERM_MF_FAT GO:0019001~guanyl nucleotide binding 12 2.43902439 0.656589892 "RAP2B, GTPBP1, NRAS, GNAQ, EFTUD2, EIF2S3, GNAS, DOCK7, TUBG1, GNL2, RAB21, GNL3" 408 382 12983 0.999615029 1 0.994897559 99.99997731

Annotation Cluster 67 Enrichment Score: 0.2917079000082014
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0005813~centrosome 10 2.032520325 0.304164386 "DHX9, TCP1, CKAP5, NUDT21, NPM1, C14ORF166, SMEK1, TUBG1, MCM3, APEX1" 415 224 12782 1.375 1 0.805262935 99.34985159
GOTERM_CC_FAT GO:0005815~microtubule organizing center 10 2.032520325 0.435117404 "DHX9, TCP1, CKAP5, NUDT21, NPM1, C14ORF166, SMEK1, TUBG1, MCM3, APEX1" 415 253 12782 1.217391304 1 0.907709092 99.96405516
GOTERM_CC_FAT GO:0015630~microtubule cytoskeleton 19 3.861788618 0.517886434 "TBL1XR1, DHX9, TCP1, CKAP5, CBX3, NUP85, C14ORF166, KLC2, SMEK1, MCM3, SMC3, NUMA1, NPM1, NUDT21, TUBG1, MAP7D1, APEX1, MYH10, ZW10" 415 549 12782 1.065938069 1 0.947592276 99.99601763
GOTERM_CC_FAT GO:0005856~cytoskeleton 43 8.739837398 0.693298396 "KRT6A, CBX3, C14ORF166, ANLN, IGF2BP2, KLC2, PNN, RPA1, NUMA1, GOPC, TGM1, NUDT21, NPM1, TUBG1, TRIP10, APEX1, STAG2, DNAJA3, ZW10, H1F0, DHX9, SYMPK, TBL1XR1, TCP1, CKAP5, KRT13, NUP85, SMEK1, MCM3, SMC3, MPRIP, JUP, SYNE1, KRT16, KRT79, GTF2F2, PSMA3, SPTBN2, RBM39, HNRNPH1, MAP7D1, LRPPRC, MYH10" 415 1381 12782 0.959015206 1 0.988346287 99.99999255
GOTERM_CC_FAT GO:0044430~cytoskeletal part 29 5.894308943 0.732134636 "KRT6A, CBX3, IGF2BP2, ANLN, C14ORF166, KLC2, PNN, NUMA1, GOPC, NUDT21, NPM1, TUBG1, APEX1, DNAJA3, ZW10, DHX9, TBL1XR1, TCP1, CKAP5, KRT13, NUP85, SMEK1, MCM3, SMC3, KRT16, KRT79, SPTBN2, MAP7D1, MYH10" 415 952 12782 0.938235294 1 0.991946981 99.99999886

Annotation Cluster 68 Enrichment Score: 0.2815989834652638
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005913~cell-cell adherens junction 4 0.81300813 0.103197014 "JUP, TJP1, TGM1, SCRIB" 415 35 12782 3.52 1 0.418301258 77.96359728
GOTERM_CC_FAT GO:0030057~desmosome 3 0.609756098 0.135742144 "JUP, DSG3, PNN" 415 20 12782 4.62 1 0.502819876 86.81089472
GOTERM_CC_FAT GO:0043296~apical junction complex 5 1.016260163 0.399832442 "JUP, SYMPK, TJP1, DSG3, PNN" 415 99 12782 1.555555556 1 0.892013909 99.91662362
GOTERM_CC_FAT GO:0016327~apicolateral plasma membrane 5 1.016260163 0.42181925 "JUP, SYMPK, TJP1, DSG3, PNN" 415 102 12782 1.509803922 1 0.900795993 99.95034502
GOTERM_CC_FAT GO:0005911~cell-cell junction 7 1.422764228 0.583033894 "JUP, SYMPK, TJP1, DSG3, TGM1, SCRIB, PNN" 415 190 12782 1.134736842 1 0.9686737 99.99946956
GOTERM_CC_FAT GO:0070161~anchoring junction 6 1.219512195 0.659002973 "JUP, TJP1, DSG3, TGM1, SCRIB, PNN" 415 172 12782 1.074418605 1 0.985251091 99.99996752
GOTERM_CC_FAT GO:0005912~adherens junction 4 0.81300813 0.882655587 "JUP, TJP1, TGM1, SCRIB" 415 155 12782 0.79483871 1 0.999274818 100
GOTERM_CC_FAT GO:0030054~cell junction 8 1.62601626 0.998181301 "JUP, SYMPK, TJP1, DSG3, TGM1, GOPC, SCRIB, PNN" 415 518 12782 0.475675676 1 0.999999988 100
GOTERM_BP_FAT GO:0016337~cell-cell adhesion 3 0.609756098 0.998721214 "JUP, DSG3, SCRIB" 430 276 13528 0.341961577 1 1 100
GOTERM_BP_FAT GO:0007155~cell adhesion 6 1.219512195 0.99999856 "JUP, SYMPK, DSG3, C22ORF28, SCRIB, PNN" 430 700 13528 0.26966113 1 1 100
GOTERM_BP_FAT GO:0022610~biological adhesion 6 1.219512195 0.9999986 "JUP, SYMPK, DSG3, C22ORF28, SCRIB, PNN" 430 701 13528 0.269276449 1 1 100

Annotation Cluster 69 Enrichment Score: 0.2571162182818813
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0009166~nucleotide catabolic process 3 0.609756098 0.484196279 "NUDT1, UPP1, NT5E" 430 51 13528 1.850615595 1 0.981685743 99.9984372
GOTERM_BP_FAT "GO:0034656~nucleobase, nucleoside and nucleotide catabolic process" 3 0.609756098 0.553223104 "NUDT1, UPP1, NT5E" 430 58 13528 1.627265437 1 0.98981603 99.99985844
GOTERM_BP_FAT "GO:0034655~nucleobase, nucleoside, nucleotide and nucleic acid catabolic process" 3 0.609756098 0.553223104 "NUDT1, UPP1, NT5E" 430 58 13528 1.627265437 1 0.98981603

99.99985844
GOTERM_BP_FAT GO:0044270~nitrogen compound catabolic process 3 0.609756098 0.631994154 "NUDT1, UPP1, NT5E" 430 67 13528 1.408677543 1 0.995643398 99.99999447

Annotation Cluster 70 Enrichment Score: 0.2458817472738897
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0030010~establishment of cell polarity 3 0.609756098 0.131156219 "DOCK7, SCRIB, ZW10" 430 20 13528 4.719069767 1 0.708216033 90.46431509
GOTERM_BP_FAT GO:0007163~establishment or maintenance of cell polarity 3 0.609756098 0.463293069 "DOCK7, SCRIB, ZW10" 430 49 13528 1.926150925 1 0.978365894 99.99696403
GOTERM_BP_FAT GO:0000904~cell morphogenesis involved in differentiation 4 0.81300813 0.984948743 "TRIM28, C22ORF28, DOCK7, MYH10" 430 244 13528 0.51574533 1 0.999999957 100
GOTERM_BP_FAT GO:0000902~cell morphogenesis 6 1.219512195 0.98930893 "TRIM28, C22ORF28, DOCK7, SCRIB, MYH10, ZW10" 430 356 13528 0.530232558 1 0.999999984 100
GOTERM_BP_FAT GO:0032989~cellular component morphogenesis 6 1.219512195 0.995866249 "TRIM28, C22ORF28, DOCK7, SCRIB, MYH10, ZW10" 430 397 13528 0.475473024 1 0.999999999 100

Annotation Cluster 71 Enrichment Score: 0.1925230588332424
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0010639~negative regulation of organelle organization 4 0.81300813 0.484535651 "NPM1, SPTBN2, DNMT1, TPR" 430 82 13528 1.534656835 1 0.981477508 99.9984543
GOTERM_BP_FAT GO:0051129~negative regulation of cellular component organization 5 1.016260163 0.663638944 "HMGB1, NPM1, SPTBN2, DNMT1, TPR" 430 142 13528 1.107762856 1 0.997045965 99.99999877
GOTERM_BP_FAT GO:0033043~regulation of organelle organization 6 1.219512195 0.822570677 "NPM1, SPTBN2, DNMT1, RCC1, TPR, CDK13" 430 217 13528 0.869874612 1 0.999778796 100

Annotation Cluster 72 Enrichment Score: 0.19011619585001183
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0043069~negative regulation of programmed cell death 15 3.048780488 0.250388462 "XRCC5, HMGB1, MSH2, ADNP, NRAS, SON, PSMC5, AKT1S1, BNIP1, HDAC1, NPM1, HSPD1, DNAJA3, API5, HSPA9" 430 359 13528 1.314504113 1 0.885163504 99.1913361
GOTERM_BP_FAT GO:0060548~negative regulation of cell death 15 3.048780488 0.254541353 "XRCC5, HMGB1, MSH2, ADNP, NRAS, SON, PSMC5, AKT1S1, BNIP1, HDAC1, NPM1, HSPD1, DNAJA3, API5, HSPA9" 430 360 13528 1.310852713 1 0.888698215 99.26305111
GOTERM_BP_FAT GO:0043066~negative regulation of apoptosis 14 2.845528455 0.333148565 "XRCC5, HMGB1, MSH2, ADNP, NRAS, SON, AKT1S1, HDAC1, BNIP1, NPM1, HSPD1, DNAJA3, API5, HSPA9" 430 354 13528 1.244199185 1 0.940830651 99.88558646
GOTERM_BP_FAT GO:0012501~programmed cell death 21 4.268292683 0.47784917 "MSH2, KIAA1967, PRKDC, SCRIB, SMNDC1, FXR1, CTNNBL1, SLTM, NRAS, RAD21, BNIP1, MFSD10, CDK11B, HSPD1, ACIN1, DNAJA3, PUF60, API5, LUC7L3, DAP3, CCAR1" 430 611 13528 1.081292582 1 0.981161114 99.9980827
GOTERM_BP_FAT GO:0006916~anti-apoptosis 8 1.62601626 0.479806322 "HMGB1, SON, AKT1S1, BNIP1, HDAC1, NPM1, API5, HSPA9" 430 206 13528 1.221765636 1 0.981302437 99.99819936
GOTERM_BP_FAT GO:0043067~regulation of programmed cell death 21 4.268292683 0.905559535 "XRCC5, HMGB1, MSH2, ADNP, PRKDC, RPS6, SCRIB, SMNDC1, CTNNBL1, NRAS, SON, PSMC5, AKT1S1, BNIP1, HDAC1, NPM1, HSPD1, DNAJA3, API5, DAP3, HSPA9" 430 812 13528 0.813632719 1 0.999979326 100
GOTERM_BP_FAT GO:0010941~regulation of cell death 21 4.268292683 0.908689543 "XRCC5, HMGB1, MSH2, ADNP, PRKDC, RPS6, SCRIB, SMNDC1, CTNNBL1, NRAS, SON, PSMC5, AKT1S1, BNIP1, HDAC1, NPM1, HSPD1, DNAJA3, API5, DAP3, HSPA9" 430 815 13528 0.810637751 1 0.999980525 100

GOTERM_BP_FAT GO:0042981~regulation of apoptosis 20 4.06504065 0.931874198 "XRCC5, HMGB1, MSH2, ADNP, PRKDC, RPS6, SCRIB, SMNDC1, CTNNBL1, NRAS, SON, AKT1S1, BNIP1, HDAC1, NPM1, HSPD1, DNAJA3, API5, DAP3, HSPA9" 430 804 13528 0.782598635 1 0.999993211 100

GOTERM_BP_FAT GO:0043065~positive regulation of apoptosis 9 1.829268293 0.965741684 "BNIP1, PRKDC, HSPD1, RPS6, DNAJA3, SCRIB, CTNNBL1, DAP3, SMNDC1" 430 430 13528 0.658474851 1 0.999999337 100

GOTERM_BP_FAT GO:0043068~positive regulation of programmed cell death 9 1.829268293 0.967549829 "BNIP1, PRKDC, HSPD1, RPS6, DNAJA3, SCRIB, CTNNBL1, DAP3, SMNDC1" 430 433 13528 0.65391267 1 0.999999408 100

GOTERM_BP_FAT GO:0010942~positive regulation of cell death 9 1.829268293 0.968706871 "BNIP1, PRKDC, HSPD1, RPS6, DNAJA3, SCRIB, CTNNBL1, DAP3, SMNDC1" 430 435 13528 0.650906175 1 0.999999471 100

GOTERM_BP_FAT GO:0006917~induction of apoptosis 3 0.609756098 0.999655927 "BNIP1, DAP3, SMNDC1" 430 320 13528 0.29494186 1 1 100

GOTERM_BP_FAT GO:0012502~induction of programmed cell death 3 0.609756098 0.999666127 "BNIP1, DAP3, SMNDC1" 430 321 13528 0.294023038 1 1 100

Annotation Cluster 73 Enrichment Score: 0.18782768583458614

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0016049~cell growth 4 0.81300813 0.305209732 "NPM1, NOP58, DDX5, XRN2" 430 61 13528 2.062981319 1 0.922976722 99.77278692

GOTERM_BP_FAT GO:0040007~growth 6 1.219512195 0.693640212 "PRPF19, NPM1, NOP58, DDX5, XRN2, SMARCA4" 430 183 13528 1.03149066 1 0.99800799 99.99999974

GOTERM_BP_FAT GO:0008361~regulation of cell size 5 1.016260163 0.895987391 "AKT1S1, NPM1, NOP58, DDX5, XRN2" 430 206 13528 0.763603522 1 0.999970646 100

GOTERM_BP_FAT GO:0032535~regulation of cellular component size 6 1.219512195 0.934662286 "AKT1S1, NPM1, SPTBN2, NOP58, DDX5, XRN2" 430 271 13528 0.696541663 1 0.999993964 100

Annotation Cluster 74 Enrichment Score: 0.18499839471995924

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0070647~protein modification by small protein conjugation or removal 7 1.422764228 0.397246243 "USP7, PRPF19, SUMO1, TRIM33, UBE3A, SAE1, ATG3" 430 160 13528 1.376395349 1 0.96604918 99.97887348

GOTERM_BP_FAT GO:0032446~protein modification by small protein conjugation 6 1.219512195 0.408167281 "PRPF19, SUMO1, TRIM33, UBE3A, SAE1, ATG3" 430 132 13528 1.430021142 1 0.968146482 99.98443722

GOTERM_BP_FAT GO:0016567~protein ubiquitination 5 1.016260163 0.524377975 "PRPF19, TRIM33, UBE3A, SAE1, ATG3" 430 119 13528 1.321868282 1 0.986969209 99.99959717

GOTERM_MF_FAT "GO:0016879~ligase activity, forming carbon-nitrogen bonds" 7 1.422764228 0.735695788 "PRPF19, GLUL, UBE3A, UBR5, GMPS, ATG3, PFAS" 408 231 12983 0.964275104 1 0.99818329 99.99999947

GOTERM_MF_FAT GO:0019787~small conjugating protein ligase activity 4 0.81300813 0.896764421 "PRPF19, UBE3A, UBR5, ATG3" 408 166 12983 0.766772974 1 0.999949222 100

GOTERM_MF_FAT GO:0004842~ubiquitin-protein ligase activity 3 0.609756098 0.947599869 "PRPF19, UBE3A, UBR5" 408 147 12983 0.649409764 1 0.999995841 100

GOTERM_MF_FAT GO:0016881~acid-amino acid ligase activity 4 0.81300813 0.953821652 "PRPF19, UBE3A, UBR5, ATG3" 408 201 12983 0.633255292 1 0.999996594 100

Annotation Cluster 75 Enrichment Score: 0.1485329872737835

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0031968~organelle outer membrane 4 0.81300813 0.659626187 "HK2,

TOMM40, LRPPRC, TOMM34" 415 104 12782 1.184615385 1 0.984724697 99.99996833
GOTERM_CC_FAT GO:0019867~outer membrane 4 0.81300813 0.684520534 "HK2, TOMM40,
LRPPRC, TOMM34" 415 108 12782 1.140740741 1 0.987579893 99.99998897
GOTERM_CC_FAT GO:0005741~mitochondrial outer membrane 3 0.609756098 0.79381019 "HK2,
TOMM40, TOMM34" 415 90 12782 1.026666667 1 0.996187293 99.99999997

Annotation Cluster 76 Enrichment Score: 0.13393442733250602
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0043414~biopolymer methylation 3 0.609756098 0.647956239 "GATAD2A,
DNMT1, FTSJ3" 430 69 13528 1.367846309 1 0.996371988 99.99999736
GOTERM_BP_FAT GO:0032259~methylation 3 0.609756098 0.699513631 "GATAD2A, DNMT1,
FTSJ3" 430 76 13528 1.241860465 1 0.998123809 99.99999981
GOTERM_BP_FAT GO:0006730~one-carbon metabolic process 3 0.609756098 0.874691408 "GATAD2A,
DNMT1, FTSJ3" 430 112 13528 0.84269103 1 0.999936338 100

Annotation Cluster 77 Enrichment Score: 0.1217598098419647
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0004722~protein serine/threonine phosphatase activity 3 0.609756098 0.414327925
"PPM1G, TIMM50, PPP5C" 408 45 12983 2.121405229 1 0.952676425 99.95275906
GOTERM_BP_FAT GO:0006470~protein amino acid dephosphorylation 4 0.81300813 0.798177103
"PPM1G, TIMM50, PTPN1, PPP5C" 430 133 13528 0.946179402 1 0.999642509 100
GOTERM_BP_FAT GO:0016311~dephosphorylation 4 0.81300813 0.870826777 "PPM1G, TIMM50,
PTPN1, PPP5C" 430 154 13528 0.817154938 1 0.999930704 100
GOTERM_MF_FAT GO:0004721~phosphoprotein phosphatase activity 4 0.81300813 0.894451329
"PPM1G, TIMM50, PTPN1, PPP5C" 408 165 12983 0.771420083 1 0.999948883 100
GOTERM_MF_FAT GO:0016791~phosphatase activity 5 1.016260163 0.955584269 "PPM1G, TIMM50,
PTPN1, NT5E, PPP5C" 408 249 12983 0.638977479 1 0.999996765 100

Annotation Cluster 78 Enrichment Score: 0.11562086476555054
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0006007~glucose catabolic process 3 0.609756098 0.553223104 "HK2, DLAT,
HIBADH" 430 58 13528 1.627265437 1 0.98981603 99.99985844
GOTERM_BP_FAT GO:0019320~hexose catabolic process 3 0.609756098 0.647956239 "HK2, DLAT,
HIBADH" 430 69 13528 1.367846309 1 0.996371988 99.99999736
GOTERM_BP_FAT GO:0046365~monosaccharide catabolic process 3 0.609756098 0.663365034 "HK2,
DLAT, HIBADH" 430 71 13528 1.329315427 1 0.997091241 99.99999875
GOTERM_BP_FAT GO:0046164~alcohol catabolic process 3 0.609756098 0.73238686 "HK2, DLAT,
HIBADH" 430 81 13528 1.165202412 1 0.998828442 99.99999997
GOTERM_BP_FAT GO:0044275~cellular carbohydrate catabolic process 3 0.609756098 0.756441897
"HK2, DLAT, HIBADH" 430 85 13528 1.110369357 1 0.999224429 99.99999999
GOTERM_BP_FAT GO:0016052~carbohydrate catabolic process 3 0.609756098 0.864797992 "HK2,
DLAT, HIBADH" 430 109 13528 0.865884361 1 0.999921134 100
GOTERM_BP_FAT GO:0006006~glucose metabolic process 4 0.81300813 0.867972185 "GPD2, HK2,
DLAT, HIBADH" 430 153 13528 0.82249582 1 0.999927462 100
GOTERM_BP_FAT GO:0019318~hexose metabolic process 4 0.81300813 0.945788004 "GPD2, HK2,
DLAT, HIBADH" 430 192 13528 0.655426357 1 0.999997049 100
GOTERM_BP_FAT GO:0005996~monosaccharide metabolic process 4 0.81300813 0.973830238 "GPD2,
HK2, DLAT, HIBADH" 430 222 13528 0.566855227 1 0.999999682 100

Annotation Cluster 79 Enrichment Score: 0.09648772620953627
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni

Benjamini FDR
GOTERM_BP_FAT GO:0032869~cellular response to insulin stimulus 3 0.609756098 0.64004472
"PRKDC, PTPN1, PARP1" 430 68 13528 1.387961696 1 0.995987286 99.99999618
GOTERM_BP_FAT GO:0043434~response to peptide hormone stimulus 5 1.016260163 0.72429101
"PRKDC, PTPN1, PARP1, EIF2B3, EIF2B5" 430 154 13528 1.021443673 1 0.998664315 99.99999996
GOTERM_BP_FAT GO:0010033~response to organic substance 21 4.268292683 0.764493999 "HMGB2,
MSH2, VAPB, RBM3, PRKDC, DEK, XRCC1, VARS, SRRT, GLUL, HDAC2, GNAS, PTPN1, HSPD1, SUPT5H,
RBM14, PARP1, EIF2B3, DNAJA3, PPP5C, EIF2B5" 430 721 13528 0.916324227 1 0.999330436 100
GOTERM_BP_FAT GO:0032870~cellular response to hormone stimulus 4 0.81300813 0.798177103
"PRKDC, GNAS, PTPN1, PARP1" 430 133 13528 0.946179402 1 0.999642509 100
GOTERM_BP_FAT GO:0032868~response to insulin stimulus 3 0.609756098 0.830686076 "PRKDC,
PTPN1, PARP1" 430 100 13528 0.943813953 1 0.999814279 100
GOTERM_BP_FAT GO:0009719~response to endogenous stimulus 9 1.829268293 0.946784916 "HMGB2,
MSH2, PRKDC, GNAS, PTPN1, PARP1, RBM14, EIF2B3, EIF2B5" 430 405 13528 0.699121447 1
0.99999708 100
GOTERM_BP_FAT GO:0009725~response to hormone stimulus 8 1.62601626 0.94907579 "HMGB2,
PRKDC, GNAS, PTPN1, PARP1, RBM14, EIF2B3, EIF2B5" 430 367 13528 0.685786706 1 0.999997411
100

Annotation Cluster 80 Enrichment Score: 0.08401533979438376
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0017016~Ras GTPase binding 3 0.609756098 0.783643819 "RANBP3, DOCK7,
RANBP2" 408 91 12983 1.049046542 1 0.999190504 99.99999997
GOTERM_MF_FAT GO:0031267~small GTPase binding 3 0.609756098 0.830030731 "RANBP3,
DOCK7, RANBP2" 408 101 12983 0.945180547 1 0.999691665 100
GOTERM_MF_FAT GO:0051020~GTPase binding 3 0.609756098 0.860480626 "RANBP3, DOCK7,
RANBP2" 408 109 12983 0.875809498 1 0.999851803 100

Annotation Cluster 81 Enrichment Score: 0.07769331200692134
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0035113~embryonic appendage morphogenesis 3 0.609756098 0.767754943
"GNAQ, GNAS, SMARCA4" 430 87 13528 1.084843625 1 0.99934597 100
GOTERM_BP_FAT GO:0030326~embryonic limb morphogenesis 3 0.609756098 0.767754943 "GNAQ,
GNAS, SMARCA4" 430 87 13528 1.084843625 1 0.99934597 100
GOTERM_BP_FAT GO:0035107~appendage morphogenesis 3 0.609756098 0.826451204 "GNAQ,
GNAS, SMARCA4" 430 99 13528 0.953347428 1 0.999796089 100
GOTERM_BP_FAT GO:0035108~limb morphogenesis 3 0.609756098 0.826451204 "GNAQ, GNAS,
SMARCA4" 430 99 13528 0.953347428 1 0.999796089 100
GOTERM_BP_FAT GO:0060173~limb development 3 0.609756098 0.842837741 "GNAQ, GNAS,
SMARCA4" 430 103 13528 0.916324227 1 0.999859445 100
GOTERM_BP_FAT GO:0048736~appendage development 3 0.609756098 0.842837741 "GNAQ, GNAS,
SMARCA4" 430 103 13528 0.916324227 1 0.999859445 100
GOTERM_BP_FAT GO:0048598~embryonic morphogenesis 3 0.609756098 0.999491697 "GNAQ,
GNAS, SMARCA4" 430 307 13528 0.307431255 1 1 100

Annotation Cluster 82 Enrichment Score: 0.07341007213238859
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0050769~positive regulation of neurogenesis 3 0.609756098 0.562537143 "XRCC5,
PRPF19, XRCC6" 430 59 13528 1.599684667 1 0.990657111 99.99990046
GOTERM_BP_FAT GO:0010720~positive regulation of cell development 3 0.609756098 0.647956239
"XRCC5, PRPF19, XRCC6" 430 69 13528 1.367846309 1 0.996371988 99.99999736

GOTERM_BP_FAT GO:0045597~positive regulation of cell differentiation 5 1.016260163 0.935526038 "XRCC5, PRPF19, XRCC6, GNAS, ACIN1" 430 229 13528 0.686909719 1 0.999994113 100

GOTERM_BP_FAT GO:0060284~regulation of cell development 4 0.81300813 0.960300413 "XRCC5, PRPF19, HDAC1, XRCC6" 430 205 13528 0.613862734 1 0.999998894 100

GOTERM_BP_FAT GO:0050767~regulation of neurogenesis 3 0.609756098 0.970108593 "XRCC5, PRPF19, XRCC6" 430 166 13528 0.568562623 1 0.99999951 100

GOTERM_BP_FAT GO:0051094~positive regulation of developmental process 5 1.016260163 0.978351822 "XRCC5, PRPF19, XRCC6, GNAS, ACIN1" 430 278 13528 0.565835704 1 0.999999835 100

GOTERM_BP_FAT GO:0051960~regulation of nervous system development 3 0.609756098 0.985494517 "XRCC5, PRPF19, XRCC6" 430 192 13528 0.491569767 1 0.999999958 100

Annotation Cluster 83 Enrichment Score: 0.06405611528059532

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0005882~intermediate filament 5 1.016260163 0.848543284 "KRT6A, KRT16, KRT79, KRT13, PNN" 415 183 12782 0.841530055 1 0.99855361 100

GOTERM_CC_FAT GO:0045111~intermediate filament cytoskeleton 5 1.016260163 0.86005288 "KRT6A, KRT16, KRT79, KRT13, PNN" 415 187 12782 0.823529412 1 0.998831691 100

GOTERM_BP_FAT GO:0007398~ectoderm development 5 1.016260163 0.880303643 "KRT6A, KRT16, TGM1, KRT13, SMARCA4" 430 199 13528 0.790463948 1 0.999947043 100

Annotation Cluster 84 Enrichment Score: 0.058175020088527984

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0005938~cell cortex 5 1.016260163 0.700799807 "SPTBN2, ANLN, TRIP10, NCL, MYH10" 415 146 12782 1.054794521 1 0.98890992 99.99999471

GOTERM_CC_FAT GO:0015629~actin cytoskeleton 5 1.016260163 0.976732245 "JUP, SPTBN2, ANLN, DNAJA3, MYH10" 415 269 12782 0.572490706 1 0.999989761 100

GOTERM_MF_FAT GO:0003779~actin binding 6 1.219512195 0.97747451 "SYNE1, SPTBN2, ANLN, LRPPRC, MYH10, MPRIP" 408 326 12983 0.58566402 1 0.999999567 100

Annotation Cluster 85 Enrichment Score: 0.05204333262714007

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0050870~positive regulation of T cell activation 3 0.609756098 0.699513631 "IL18, HSPD1, DNAJA3" 430 76 13528 1.241860465 1 0.998123809 99.99999981

GOTERM_BP_FAT GO:0051251~positive regulation of lymphocyte activation 3 0.609756098 0.817695114 "IL18, HSPD1, DNAJA3" 430 97 13528 0.973004076 1 0.999760256 100

GOTERM_BP_FAT GO:0002696~positive regulation of leukocyte activation 3 0.609756098 0.85419405 "IL18, HSPD1, DNAJA3" 430 106 13528 0.890390522 1 0.999893357 100

GOTERM_BP_FAT GO:0050867~positive regulation of cell activation 3 0.609756098 0.87147002 "IL18, HSPD1, DNAJA3" 430 111 13528 0.850282841 1 0.999930353 100

GOTERM_BP_FAT GO:0050863~regulation of T cell activation 3 0.609756098 0.889710951 "IL18, HSPD1, DNAJA3" 430 117 13528 0.806678593 1 0.99996267 100

GOTERM_BP_FAT GO:0051249~regulation of lymphocyte activation 3 0.609756098 0.951229499 "IL18, HSPD1, DNAJA3" 430 148 13528 0.637712131 1 0.999997774 100

GOTERM_BP_FAT GO:0002694~regulation of leukocyte activation 3 0.609756098 0.970108593 "IL18, HSPD1, DNAJA3" 430 166 13528 0.568562623 1 0.99999951 100

GOTERM_BP_FAT GO:0050865~regulation of cell activation 3 0.609756098 0.976681586 "IL18, HSPD1, DNAJA3" 430 175 13528 0.539322259 1 0.999999786 100

GOTERM_BP_FAT GO:0002684~positive regulation of immune system process 3 0.609756098 0.996106633 "IL18, HSPD1, DNAJA3" 430 238 13528 0.396560485 1 1 100

Annotation Cluster 86 Enrichment Score: 0.050415803277264026

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0030016~myofibril 3 0.609756098 0.879112281 "JUP, SYNE1, FXR1" 415 111
12782 0.832432432 1 0.999246853 100
GOTERM_CC_FAT GO:0044449~contractile fiber part 3 0.609756098 0.885259273 "JUP, SYNE1, FXR1"
415 113 12782 0.817699115 1 0.999283993 100
GOTERM_CC_FAT GO:0043292~contractile fiber 3 0.609756098 0.907063639 "JUP, SYNE1, FXR1"
415 121 12782 0.763636364 1 0.999595187 100

Annotation Cluster 87 Enrichment Score: 0.04798289299090647
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0001819~positive regulation of cytokine production 3 0.609756098 0.783867471
"IL18, POLR3A, HSPD1" 430 90 13528 1.048682171 1 0.999521462 100
GOTERM_BP_FAT GO:0001817~regulation of cytokine production 4 0.81300813 0.929811789 "IL18,
POLR3A, IGF2BP2, HSPD1" 430 181 13528 0.695258898 1 0.999992504 100
GOTERM_BP_FAT GO:0051240~positive regulation of multicellular organismal process 4 0.81300813
0.984948743 "HDAC2, IL18, POLR3A, HSPD1" 430 244 13528 0.51574533 1 0.999999957 100

Annotation Cluster 88 Enrichment Score: 0.03467426510782083
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0006469~negative regulation of protein kinase activity 3 0.609756098 0.767754943
"AKT1S1, HEXIM1, DNAJA3" 430 87 13528 1.084843625 1 0.99934597 100
GOTERM_BP_FAT GO:0033673~negative regulation of kinase activity 3 0.609756098 0.783867471
"AKT1S1, HEXIM1, DNAJA3" 430 90 13528 1.048682171 1 0.999521462 100
GOTERM_BP_FAT GO:0051348~negative regulation of transferase activity 3 0.609756098 0.813170581
"AKT1S1, HEXIM1, DNAJA3" 430 96 13528 0.983139535 1 0.999736503 100
GOTERM_BP_FAT GO:0045859~regulation of protein kinase activity 4 0.81300813 0.998979466
"AKT1S1, HEXIM1, NPM1, DNAJA3" 430 345 13528 0.364759016 1 1 100
GOTERM_BP_FAT GO:0042325~regulation of phosphorylation 6 1.219512195 0.99923355 "MCM7,
AKT1S1, HEXIM1, NPM1, DOCK7, DNAJA3" 430 466 13528 0.405070366 1 1 100
GOTERM_BP_FAT GO:0043549~regulation of kinase activity 4 0.81300813 0.999268309 "AKT1S1,
HEXIM1, NPM1, DNAJA3" 430 357 13528 0.352498209 1 1 100
GOTERM_BP_FAT GO:0051338~regulation of transferase activity 4 0.81300813 0.999518792 "AKT1S1,
HEXIM1, NPM1, DNAJA3" 430 372 13528 0.338284571 1 1 100
GOTERM_BP_FAT GO:0051174~regulation of phosphorus metabolic process 6 1.219512195 0.999525833
"MCM7, AKT1S1, HEXIM1, NPM1, DOCK7, DNAJA3" 430 485 13528 0.38920163 1 1 100
GOTERM_BP_FAT GO:0019220~regulation of phosphate metabolic process 6 1.219512195 0.999525833
"MCM7, AKT1S1, HEXIM1, NPM1, DOCK7, DNAJA3" 430 485 13528 0.38920163 1 1 100

Annotation Cluster 89 Enrichment Score: 0.03229968231140343
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0001508~regulation of action potential 3 0.609756098 0.64004472 "GNAQ, QKI,
EIF2B5" 430 68 13528 1.387961696 1 0.995987286 99.99999618
GOTERM_BP_FAT GO:0042391~regulation of membrane potential 3 0.609756098 0.929162294 "GNAQ,
QKI, EIF2B5" 430 134 13528 0.704338771 1 0.999992446 100
GOTERM_BP_FAT GO:0019725~cellular homeostasis 6 1.219512195 0.99923355 "GSR, GNAQ, NPM1,
QKI, APEX1, EIF2B5" 430 466 13528 0.405070366 1 1 100
GOTERM_BP_FAT GO:0006873~cellular ion homeostasis 3 0.609756098 0.999933204 "GNAQ, QKI,
EIF2B5" 430 374 13528 0.252356672 1 1 100
GOTERM_BP_FAT GO:0055082~cellular chemical homeostasis 3 0.609756098 0.999944419 "GNAQ, QKI,
EIF2B5" 430 380 13528 0.248372093 1 1 100

GOTERM_BP_FAT	GO:0050801~ion homeostasis	3	0.609756098	0.999977233	"GNAQ, QKI, EIF2B5"	430	409	13528	0.230761358	1	1	100
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	4	0.81300813	0.999991612	"GNAQ, QKI, RPS6, EIF2B5"	430	512	13528	0.245784884	1	1	100

Annotation Cluster 90	Enrichment Score: 0.030885986003323433
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	3	0.609756098	0.846709406	"TBC1D5, DOCK7, SCRIB"	430	104	13528	0.907513417	1	0.99987184	100
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	3	0.609756098	0.905527863	"TBC1D5, DOCK7, SCRIB"	430	123	13528	0.767328417	1	0.999979933	100
GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	7	1.422764228	0.959040968	"GNAQ, MSH2, TBC1D5, DOCK7, HSPD1, DNAJA3, SCRIB"	430	337	13528	0.653481471	1	0.999998826	100
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	4	0.81300813	0.9648432	"NRAS, TBC1D5, DOCK7, SCRIB"	430	210	13528	0.599246955	1	0.999999314	100
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transduction	4	0.81300813	0.987733918	"NRAS, TBC1D5, DOCK7, SCRIB"	430	252	13528	0.499372462	1	0.999999976	100

Annotation Cluster 91	Enrichment Score: 0.024816976886804728
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0005085~guanyl-nucleotide exchange factor activity	4	0.81300813	0.859890755	"DOCK7, RCC1, EIF2B3, EIF2B5"	408	152	12983	0.837396801	1	0.999861006	100
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	8	1.62601626	0.972231318	"DIS3, GOPC, TBC1D5, DOCK7, RCC1, EIF2B3, DNAJA3, EIF2B5"	408	404	12983	0.630120365	1	0.99999931	100
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	5	1.016260163	0.974522012	"DIS3, GOPC, TBC1D5, RCC1, DNAJA3"	408	274	12983	0.580676614	1	0.999999448	100
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	8	1.62601626	0.97662436	"DIS3, GOPC, TBC1D5, DOCK7, RCC1, EIF2B3, DNAJA3, EIF2B5"	408	413	12983	0.616388928	1	0.999999556	100

Annotation Cluster 92	Enrichment Score: 0.017518764648265617
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030425~dendrite	4	0.81300813	0.902251073	"NUMA1, GOPC, CAPRIN1, MYH10"	415	163	12782	0.755828221	1	0.999552318	100
GOTERM_CC_FAT	GO:0043005~neuron projection	7	1.422764228	0.967957165	"NUMA1, GOPC, DOCK7, KLC2, CAPRIN1, MYH10, PPP5C"	415	342	12782	0.630409357	1	0.999978895	100
GOTERM_CC_FAT	GO:0043025~cell soma	3	0.609756098	0.974430507	"NUMA1, MYH10, PPP5C"	415	168	12782	0.55	1	0.999988583	100
GOTERM_CC_FAT	GO:0042995~cell projection	8	1.62601626	0.999978179	"NUMA1, GOPC, GNAS, DOCK7, KLC2, CAPRIN1, MYH10, PPP5C"	415	697	12782	0.353515065	1	1	100

Annotation Cluster 93	Enrichment Score: 0.017284578169930148
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007283~spermatogenesis	7	1.422764228	0.929062628	"GSR, HMGB2, MSH2, LIG3, QKI, XRN2, DAZAP1"	430	308	13528	0.715010571	1	0.999992649	100
GOTERM_BP_FAT	GO:0048232~male gamete generation	7	1.422764228	0.929062628	"GSR, HMGB2, MSH2, LIG3, QKI, XRN2, DAZAP1"	430	308	13528	0.715010571	1	0.999992649	100
GOTERM_BP_FAT	GO:0007276~gamete generation	8	1.62601626	0.969733492	"GSR, HMGB2, MSH2, LIG3, PRKDC, QKI, XRN2, DAZAP1"	430	395	13528	0.637173977	1	0.999999503	100
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	10	2.032520325	0.974199418

"GSR, HMGB2, MSH2, HK2, LIG3, PRKDC, QKI, XRN2, EIF2B5, DAZAP1" 430 487 13528 0.646005444 1 0.999999688 100
GOTERM_BP_FAT GO:0048609~reproductive process in a multicellular organism 10 2.032520325 0.974199418 "GSR, HMGB2, MSH2, HK2, LIG3, PRKDC, QKI, XRN2, EIF2B5, DAZAP1" 430 487 13528 0.646005444 1 0.999999688 100
GOTERM_BP_FAT GO:0019953~sexual reproduction 8 1.62601626 0.991412575 "GSR, HMGB2, MSH2, LIG3, PRKDC, QKI, XRN2, DAZAP1" 430 458 13528 0.549527775 1 0.999999993 100

Annotation Cluster 94 Enrichment Score: 0.010186806993021826
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0004674~protein serine/threonine kinase activity 9 1.829268293 0.962668096 "EXOSC10, VRK1, PRPF4B, CSNK2A1, PRKDC, CDK11B, CDK2, NEK7, CDK13" 408 430 12983 0.666022572 1 0.999998004 100
GOTERM_BP_FAT GO:0006796~phosphate metabolic process 23 4.674796748 0.967267328 "UQCRC2, GPD2, PRPF4B, NDUFA9, MSH2, TRIM28, HK2, PRKDC, TIMM50, NDUFA10, ATP6V1D, CDK2, PPM1G, VRK1, CSNK2A1, MORC3, EIF2S1, NDUFV1, CDK11B, PTPN1, PPP5C, CDK13, NEK7" 430 973 13528 0.743669782 1 0.999999409 100
GOTERM_BP_FAT GO:0006793~phosphorus metabolic process 23 4.674796748 0.967267328 "UQCRC2, GPD2, PRPF4B, NDUFA9, MSH2, TRIM28, HK2, PRKDC, TIMM50, NDUFA10, ATP6V1D, CDK2, PPM1G, VRK1, CSNK2A1, MORC3, EIF2S1, NDUFV1, CDK11B, PTPN1, PPP5C, CDK13, NEK7" 430 973 13528 0.743669782 1 0.999999409 100
GOTERM_BP_FAT GO:0016310~phosphorylation 18 3.658536585 0.973155492 "UQCRC2, PRPF4B, NDUFA9, MSH2, TRIM28, HK2, PRKDC, NDUFA10, ATP6V1D, CDK2, VRK1, CSNK2A1, MORC3, EIF2S1, NDUFV1, CDK11B, NEK7, CDK13" 430 800 13528 0.707860465 1 0.999999673 100
GOTERM_MF_FAT GO:0004672~protein kinase activity 11 2.235772358 0.992956358 "EXOSC10, VRK1, PRPF4B, CSNK2A1, TRIM28, PRKDC, CDK11B, CDK2, NEK7, CDK13, POLR2A" 408 606 12983 0.577610335 1 0.999999988 100
GOTERM_BP_FAT GO:0006468~protein amino acid phosphorylation 11 2.235772358 0.998153062 "VRK1, PRPF4B, CSNK2A1, MORC3, EIF2S1, TRIM28, PRKDC, CDK11B, CDK2, NEK7, CDK13" 430 667 13528 0.518838255 1 1 100

Annotation Cluster 95 Enrichment Score: 0.01001899159770136
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0045211~postsynaptic membrane 3 0.609756098 0.936179514 "SYNE1, GOPC, SCRIB" 415 135 12782 0.684444444 1 0.999863215 100
GOTERM_CC_FAT GO:0044456~synapse part 3 0.609756098 0.997364846 "SYNE1, GOPC, SCRIB" 415 246 12782 0.375609756 1 0.999999974 100
GOTERM_CC_FAT GO:0045202~synapse 4 0.81300813 0.999378115 "SYNE1, GOPC, SCRIB, MYH10" 415 355 12782 0.347042254 1 0.999999999 100

Annotation Cluster 96 Enrichment Score: 0.009027176401813195
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0048514~blood vessel morphogenesis 4 0.81300813 0.965691058 "IL18, QKI, NCL, SMARCA4" 430 211 13528 0.596406922 1 0.999999357 100
GOTERM_BP_FAT GO:0001568~blood vessel development 4 0.81300813 0.985327426 "IL18, QKI, NCL, SMARCA4" 430 245 13528 0.513640247 1 0.999999958 100
GOTERM_BP_FAT GO:0001944~vasculature development 4 0.81300813 0.987414931 "IL18, QKI, NCL, SMARCA4" 430 251 13528 0.501361994 1 0.999999974 100

Annotation Cluster 97 Enrichment Score: 0.007859175598607947
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni

Benjamini FDR
GOTERM_CC_FAT GO:0042175~nuclear envelope-endoplasmic reticulum network 6 1.219512195
0.955604504 "SPTLC1, BNIP1, SPTLC2, VAPB, PCYT1A, LRPPRC" 415 284 12782 0.650704225 1
0.999945916 100
GOTERM_CC_FAT GO:0005789~endoplasmic reticulum membrane 5 1.016260163 0.976732245 "SPTLC1,
BNIP1, SPTLC2, VAPB, PCYT1A" 415 269 12782 0.572490706 1 0.999989761 100
GOTERM_CC_FAT GO:0044432~endoplasmic reticulum part 5 1.016260163 0.996616092 "SPTLC1,
BNIP1, SPTLC2, VAPB, PCYT1A" 415 347 12782 0.443804035 1 0.999999952 100
GOTERM_CC_FAT GO:0005783~endoplasmic reticulum 14 2.845528455 0.999957838 "SPTLC1, CHERP,
SPTLC2, VAPB, SRP68, SYNCRIP, TPD52, TECR, BNIP1, PCYT1A, PTPN1, APEX1, RAB21, ZW10" 415 960
12782 0.449166667 1 1 100

Annotation Cluster 98 Enrichment Score: 0.0015676712093502744
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0030036~actin cytoskeleton organization 3 0.609756098 0.994492056 "NRAS,
TRIP10, MYH10" 430 226 13528 0.417616794 1 0.999999999 100
GOTERM_BP_FAT GO:0030029~actin filament-based process 3 0.609756098 0.996431413 "NRAS,
TRIP10, MYH10" 430 241 13528 0.391624047 1 1 100
GOTERM_BP_FAT GO:0016044~membrane organization 5 1.016260163 0.998270547 "NRAS, BNIP1,
TIMM50, TRIP10, MYH10" 430 381 13528 0.412866996 1 1 100

Annotation Cluster 99 Enrichment Score: 0.0013577379156842762
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0016477~cell migration 4 0.81300813 0.993426689 "PRKDC, NUP85, SCRIB,
MYH10" 430 276 13528 0.45594877 1 0.999999997 100
GOTERM_BP_FAT GO:0048870~cell motility 4 0.81300813 0.997120372 "PRKDC, NUP85, SCRIB,
MYH10" 430 307 13528 0.40990834 1 1 100
GOTERM_BP_FAT GO:0051674~localization of cell 4 0.81300813 0.997120372 "PRKDC, NUP85,
SCRIB, MYH10" 430 307 13528 0.40990834 1 1 100
GOTERM_BP_FAT GO:0006928~cell motion 5 1.016260163 0.999857358 "MSH2, PRKDC, NUP85,
SCRIB, MYH10" 430 475 13528 0.331162791 1 1 100

Annotation Cluster 100 Enrichment Score: 3.9402533074832822E-4
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0005626~insoluble fraction 15 3.048780488 0.998646111 "VAPB, XRCC6,
SYNCRIP, TOMM40, AIP, JUP, NRAS, ADRM1, EBNA1BP2, GNAQ, GOPC, GNAS, PTPN1, CPD, NT5E" 415
839 12782 0.550655542 1 0.999999993 100
GOTERM_CC_FAT GO:0005624~membrane fraction 14 2.845528455 0.99893657 "VAPB, XRCC6,
SYNCRIP, TOMM40, AIP, JUP, NRAS, ADRM1, EBNA1BP2, GNAQ, GOPC, GNAS, CPD, NT5E" 415 809
12782 0.533003708 1 0.999999996 100
GOTERM_CC_FAT GO:0000267~cell fraction 19 3.861788618 0.999697018 "DARS, VAPB, XRCC6,
TOMM40, SYNCRIP, AIP, JUP, GSR, NRAS, ADRM1, EBNA1BP2, GNAQ, UBR5, GOPC, GNAS, PCYT1A,
PTPN1, CPD, NT5E" 415 1083 12782 0.540350877 1 1 100

Annotation Cluster 101 Enrichment Score: 5.294398303298274E-5
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0015672~monovalent inorganic cation transport 3 0.609756098 0.999634594
"NDUFA9, ATP6V1D, CDK2" 430 318 13528 0.296796841 1 1 100
GOTERM_BP_FAT GO:0006812~cation transport 3 0.609756098 0.999999752 "NDUFA9, ATP6V1D,
CDK2" 430 553 13528 0.170671601 1 1 100

GOTERM_BP_FAT	GO:0006811~ion transport	4	0.81300813	0.999999997	"NDUFA9, TOMM40, ATP6V1D, CDK2"	430	768	13528	0.163856589	1	1	100

Annotation Cluster 102	Enrichment Score: 1.545047395447076E-5
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0008270~zinc ion binding	48	9.756097561	0.999833735	"UQCRC2, ZC3H4, ZNF207, POLR2A, RPA1, TOE1, MORC3, ZNF326, ZNF185, USP39, U2AF1, GATAD2A, GATAD2B, TCEA1, RANBP2, RBM27, NT5E, EWSR1, CHD4, DNAJA3, DHX57, NUP153, OSGEP, ZC3H18, MTA2, TRIM28, SF1, LIG3, ADNP, POLR3A, MCM2, SF3A2, RAD50, SF3A3, UHRF1, TRIM33, UBR5, EIF2S2, DNMT1, ZC3H11A, YME1L1, CPD, PTPN1, RBM14, PARP1, MATR3, XRN2, PMPCB"	408	2311	12983	0.660931097	1	1	100
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	56	11.38211382	0.999988398	"UQCRC2, METAP2, ZNF207, ZNF185, U2AF1, RANBP2, NT5E, MTA2, LIG3, SF1, ADNP, MCM2, RAD50, OGFOD1, PPM1G, UHRF1, TRIM33, UBR5, EIF2S2, YME1L1, CPD, MATR3, XRN2, PMPCB, PPP5C, ZC3H4, MRE11A, POLR2A, RPA1, TOE1, MORC3, ZNF326, USP39, GATAD2A, GATAD2B, TCEA1, RBM27, EWSR1, CHD4, DNAJA3, FEN1, DHX57, NUP153, OSGEP, ZC3H18, TRIM28, POLR3A, SF3A2, SF3A3, SDHB, NDUFV1, DNMT1, ZC3H11A, PTPN1, RBM14, PARP1"	408	2785	12983	0.639849333	1	1	100
GOTERM_MF_FAT	GO:0046872~metal ion binding	64	13.00813008	1	"UQCRC2, METAP2, TPD52, ZNF207, ZNF185, U2AF1, RANBP2, NT5E, MTA2, LIG3, ADNP, SF1, MCM2, RAD50, OGFOD1, PPM1G, UHRF1, TRIM33, UBR5, EIF2S2, YME1L1, CPD, MATR3, XRN2, PMPCB, NEK7, PPP5C, ZC3H4, MRE11A, POLR2A, RPA1, TOE1, MORC3, ZNF326, USP39, TGM1, GATAD2A, GATAD2B, TCEA1, RBM27, APEX1, EWSR1, CHD4, DNAJA3, FEN1, DHX57, GPD2, NUP153, S100A16, OSGEP, ZC3H18, MSH2, TRIM28, POLR3A, SF3A2, SF3A3, SDHB, DSG3, NDUFV1, DNMT1, ZC3H11A, PTPN1, RBM14, PARP1"	408	4140	12983	0.491920053	1	1	100
GOTERM_MF_FAT	GO:0043169~cation binding	64	13.00813008	1	"UQCRC2, METAP2, TPD52, ZNF207, ZNF185, U2AF1, RANBP2, NT5E, MTA2, LIG3, ADNP, SF1, MCM2, RAD50, OGFOD1, PPM1G, UHRF1, TRIM33, UBR5, EIF2S2, YME1L1, CPD, MATR3, XRN2, PMPCB, NEK7, PPP5C, ZC3H4, MRE11A, POLR2A, RPA1, TOE1, MORC3, ZNF326, USP39, TGM1, GATAD2A, GATAD2B, TCEA1, RBM27, APEX1, EWSR1, CHD4, DNAJA3, FEN1, DHX57, GPD2, NUP153, S100A16, OSGEP, ZC3H18, MSH2, TRIM28, POLR3A, SF3A2, SF3A3, SDHB, DSG3, NDUFV1, DNMT1, ZC3H11A, PTPN1, RBM14, PARP1"	408	4179	12983	0.48732927	1	1	100
GOTERM_MF_FAT	GO:0043167~ion binding	64	13.00813008	1	"UQCRC2, METAP2, TPD52, ZNF207, ZNF185, U2AF1, RANBP2, NT5E, MTA2, LIG3, ADNP, SF1, MCM2, RAD50, OGFOD1, PPM1G, UHRF1, TRIM33, UBR5, EIF2S2, YME1L1, CPD, MATR3, XRN2, PMPCB, NEK7, PPP5C, ZC3H4, MRE11A, POLR2A, RPA1, TOE1, MORC3, ZNF326, USP39, TGM1, GATAD2A, GATAD2B, TCEA1, RBM27, APEX1, EWSR1, CHD4, DNAJA3, FEN1, DHX57, GPD2, NUP153, S100A16, OSGEP, ZC3H18, MSH2, TRIM28, POLR3A, SF3A2, SF3A3, SDHB, DSG3, NDUFV1, DNMT1, ZC3H11A, PTPN1, RBM14, PARP1"	408	4241	12983	0.480204909	1	1	100

Annotation Cluster 103	Enrichment Score: 3.869832311060282E-6
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	5	1.016260163	0.999987445	"GOPC, ANP32E, NAP1L1, HSPD1, RAB21"	415	550	12782	0.28	1	1	100
GOTERM_CC_FAT	GO:0031982~vesicle	7	1.422764228	0.999989231	"GOPC, ANP32E, NAP1L1, GNAS, PTPN1, HSPD1, RAB21"	415	670	12782	0.321791045	1	1	100
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	5	1.016260163	0.999992568	"GOPC, ANP32E, NAP1L1, HSPD1, RAB21"	415	568	12782	0.271126761	1	1	100
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	6	1.219512195	0.999995114	"GOPC, ANP32E, NAP1L1, PTPN1, HSPD1, RAB21"	415	642	12782	0.287850467	1	1	100

Annotation Cluster 104	Enrichment Score: 3.107465222899971E-10
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni

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Benjamini	FDR
GOTERM_CC_FAT	GO:0005615~extracellular space	3	0.609756098	0.999999998	"IL18, ADNP, HSPD1"
415	685	12782	0.134890511	1	1	100
GOTERM_CC_FAT	GO:0044421~extracellular region part	4	0.81300813	1	"IL18, ADNP, HSPD1,
SMC3"	415	960	12782	0.128333333	1	1	100
GOTERM_CC_FAT	GO:0005576~extracellular region	5	1.016260163	1	"IL18, ADNP, GNAS, HSPD1,
SMC3"	415	2010	12782	0.076616915	1	1	100
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Annotation Cluster 1	Enrichment Score: 2.517480899138746
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006928~cell motion	7	2.473498233	8.39E-05	"TUBB, AIMP1, VIM, S100A9, MYH9, S100A2, FN1"	23	475	13528	8.667826087	0.027211799	0.027211799	0.11356924
GOTERM_BP_FAT	GO:0016477~cell migration	5	1.766784452	9.28E-04	"AIMP1, S100A9, MYH9, S100A2, FN1"	23	276	13528	10.65532451	0.263193284	0.059257607	1.250130872
GOTERM_BP_FAT	GO:0048870~cell motility	5	1.766784452	0.001377173	"AIMP1, S100A9, MYH9, S100A2, FN1"	23	307	13528	9.579379691	0.364537572	0.072782443	1.850154379
GOTERM_BP_FAT	GO:0051674~localization of cell	5	1.766784452	0.001377173	"AIMP1, S100A9, MYH9, S100A2, FN1"	23	307	13528	9.579379691	0.364537572	0.072782443	1.850154379
GOTERM_BP_FAT	GO:0050900~leukocyte migration	3	1.060070671	0.003817034	"AIMP1, S100A9, MYH9"	23	57	13528	30.95652174	0.715836907	0.11822706	5.050338624
GOTERM_BP_FAT	GO:0006954~inflammatory response	4	1.413427562	0.015082506	"S100A8, AIMP1, S100A9, FN1"	23	325	13528	7.239063545	0.993261689	0.300324762	18.6117212
GOTERM_BP_FAT	GO:0006952~defense response	5	1.766784452	0.016101533	"TUBB, S100A8, AIMP1, S100A9, FN1"	23	615	13528	4.781901732	0.995206603	0.299551471	19.74542297
GOTERM_BP_FAT	GO:0009611~response to wounding	4	1.413427562	0.052975475	"S100A8, AIMP1, S100A9, FN1"	23	530	13528	4.4390484	0.999999983	0.460710226	52.17304917

Annotation Cluster 2	Enrichment Score: 2.39598383812333
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0044421~extracellular region part	8	2.826855124	0.001109975	"HDLBP, LAD1, AIMP1, RPTN, HSD17B12, RNH1, CALR, FN1"	24	960	12782	4.438194444	0.120875414	0.031694037	1.259061845
GOTERM_CC_FAT	GO:0031012~extracellular matrix	5	1.766784452	0.003076321	"LAD1, RPTN, HSD17B12, CALR, FN1"	24	345	12782	7.718599034	0.300509617	0.068985704	3.454068019
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	4	1.413427562	0.018997809	"LAD1, RPTN, CALR, FN1"	24	320	12782	6.657291667	0.891926963	0.199480831	19.6540113

Annotation Cluster 3	Enrichment Score: 1.9237459940649901
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	6	2.120141343	5.68E-04	"TCHH, TUBB, S100A9, MYH9, DYNC1H1, CALR"	23	436	13528	8.094136418	0.170568599	0.089268755	0.76732207
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	3	1.060070671	0.051557464	"S100A9, MYH9, CALR"	23	226	13528	7.807618315	0.999999973	0.475343499	51.19345725
GOTERM_BP_FAT	GO:0030029~actin filament-based process	3	1.060070671	0.057798112	"S100A9, MYH9, CALR"	23	241	13528	7.321666967	0.999999997	0.47947027	55.37000684

Annotation Cluster 4	Enrichment Score: 1.7200608154070252
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030216~keratinocyte differentiation	3	1.060070671	0.005084887	"TCHH, FLG, CDSN"	23	66	13528	26.73517787	0.813102638	0.141417353	6.674865436
GOTERM_BP_FAT	GO:0009913~epidermal cell differentiation	3	1.060070671	0.00602361	"TCHH, FLG, CDSN"	23	72	13528	24.50724638	0.862998103	0.152654459	7.861041904
GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	3	1.060070671	0.020600854	"TCHH, FLG, CDSN"	23	137	13528	12.87972072	0.99893892	0.331588346	24.57838331
GOTERM_BP_FAT	GO:0008544~epidermis development	3	1.060070671	0.035562525	"TCHH, FLG, CDSN"	23	184	13528	9.58979206	0.999993299	0.404267996	38.77917673
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GOTERM_BP_FAT	GO:0007398~ectoderm development	3	1.060070671	0.041011484	"TCHH, FLG, CDSN"	23	199	13528	8.866943413	0.999998961	0.436761787	43.30369035
GOTERM_BP_FAT	GO:0060429~epithelium development	3	1.060070671	0.051965323	"TCHH, FLG, CDSN"	23	227	13528	7.77322352	0.999999976	0.465823694	51.47710193

Annotation Cluster 5	Enrichment Score: 1.5920208058478782

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005856~cytoskeleton	10	3.533568905	3.90E-04	"TCHH, TUBA8, TUBB, FLG, RPTN, VIM, TUBA4A, MYH9, DYNC1H1, CDSN"	24	1381	12782	3.856504948	0.044230757	0.022365486	0.443943878
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	6	2.120141343	5.68E-04	"TCHH, TUBB, S100A9, MYH9, DYNC1H1, CALR"	23	436	13528	8.094136418	0.170568599	0.089268755	0.76732207
GOTERM_BP_FAT	GO:0007017~microtubule-based process	5	1.766784452	6.70E-04	"TUBA8, TUBB, TUBA4A, MYH9, DYNC1H1"	23	253	13528	11.62399038	0.197926871	0.07088104	0.904315255
GOTERM_BP_FAT	GO:0007018~microtubule-based movement	4	1.413427562	7.78E-04	"TUBA8, TUBB, TUBA4A, DYNC1H1"	23	113	13528	20.82031551	0.226010798	0.06204128	1.0496835
GOTERM_BP_FAT	GO:0043623~cellular protein complex assembly	4	1.413427562	0.002196129	"TUBA8, TUBB, TUBA4A, CALR"	23	162	13528	14.52281267	0.514861627	0.098172112	2.935289943
GOTERM_BP_FAT	GO:0007051~spindle organization	3	1.060070671	0.002395802	"TUBB, MYH9, DYNC1H1"	23	45	13528	39.2115942	0.545775873	0.093936209	3.198170223
GOTERM_BP_FAT	GO:0051258~protein polymerization	3	1.060070671	0.002834752	"TUBA8, TUBB, TUBA4A"	23	49	13528	36.01064774	0.60700472	0.098570169	3.773756347
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	7	2.473498233	0.005644408	"TUBA8, TUBB, FLG, VIM, TUBA4A, MYH9, DYNC1H1"	24	952	12782	3.916053922	0.481391545	0.103658993	6.253748242
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	11	3.886925795	0.009921558	"TCHH, TUBA8, TUBB, FLG, RPTN, VIM, S100A9, TUBA4A, MYH9, DYNC1H1, CDSN"	24	2596	12782	2.25670904	0.685461291	0.152305907	10.75266459
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	11	3.886925795	0.009921558	"TCHH, TUBA8, TUBB, FLG, RPTN, VIM, S100A9, TUBA4A, MYH9, DYNC1H1, CDSN"	24	2596	12782	2.25670904	0.685461291	0.152305907	10.75266459
GOTERM_CC_FAT	GO:0005874~microtubule	4	1.413427562	0.012564171	"TUBA8, TUBB, TUBA4A, DYNC1H1"	24	274	12782	7.774939173	0.7693092	0.167510462	13.43291906
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	4	1.413427562	0.014229981	"TUBA8, TUBB, TUBA4A, CALR"	23	318	13528	7.398414001	0.991042761	0.304215203	17.6518815
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	5	1.766784452	0.015556973	"TUBA8, TUBB, TUBA4A, MYH9, DYNC1H1"	24	549	12782	4.850485732	0.837778622	0.182977096	16.37953566
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	4	1.413427562	0.019347311	"TUBA8, TUBB, TUBA4A, CALR"	23	357	13528	6.5901839	0.99838375	0.330837202	23.2597139
GOTERM_BP_FAT	GO:0000226~microtubule cytoskeleton organization	3	1.060070671	0.023499328	"TUBB, MYH9, DYNC1H1"	23	147	13528	12.00354925	0.999599809	0.35250399	27.54749152
GOTERM_CC_FAT	GO:0005829~cytosol	7	2.473498233	0.026843233	"TUBB, AIMP1, VIM, TUBA4A, MYH9, DYNC1H1, CALR"	24	1330	12782	2.803070175	0.957420006	0.249445337	26.68722281
GOTERM_BP_FAT	GO:0006461~protein complex assembly	4	1.413427562	0.047025155	"TUBA8, TUBB, TUBA4A, CALR"	23	505	13528	4.658803272	0.999999869	0.45637462	47.93641413
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	4	1.413427562	0.047025155	"TUBA8, TUBB, TUBA4A, CALR"	23	505	13528	4.658803272	0.999999869	0.45637462	47.93641413
GOTERM_MF_FAT	GO:0003924~GTPase activity	3	1.060070671	0.061756967	"TUBA8, TUBB,							

TUBA4A" 26 211 12983 7.099708349 0.997501711 0.575150925 50.30617185
GOTERM_BP_FAT GO:0022402~cell cycle process 4 1.413427562 0.06190075 "TUBB, MYH9, DYNC1H1, CALR" 23 565 13528 4.164063101 0.999999999 0.481578672 57.93263054
GOTERM_BP_FAT GO:0065003~macromolecular complex assembly 4 1.413427562 0.091027891 "TUBA8, TUBB, TUBA4A, CALR" 23 665 13528 3.537888199 1 0.592267584 72.56394791
GOTERM_BP_FAT GO:0000279~M phase 3 1.060070671 0.099052136 "TUBB, MYH9, DYNC1H1" 23 329 13528 5.363287961 1 0.614517003 75.67020842
GOTERM_BP_FAT GO:0043933~macromolecular complex subunit organization 4 1.413427562 0.105760526 "TUBA8, TUBB, TUBA4A, CALR" 23 710 13528 3.313655848 1 0.629888343 78.01358244
GOTERM_BP_FAT GO:0007049~cell cycle 4 1.413427562 0.129002518 "TUBB, MYH9, DYNC1H1, CALR" 23 776 13528 3.031824294 1 0.69753674 84.61231224
GOTERM_BP_FAT GO:0022403~cell cycle phase 3 1.060070671 0.144669681 "TUBB, MYH9, DYNC1H1" 23 414 13528 4.262129805 1 0.732398675 87.96763595
GOTERM_MF_FAT GO:0005525~GTP binding 3 1.060070671 0.15990322 "TUBA8, TUBB, TUBA4A" 26 372 12983 4.026985112 0.999999923 0.837945241 85.21228505
GOTERM_MF_FAT GO:0032561~guanyl ribonucleotide binding 3 1.060070671 0.166722363 "TUBA8, TUBB, TUBA4A" 26 382 12983 3.921566653 0.999999964 0.819937435 86.47702871
GOTERM_MF_FAT GO:0019001~guanyl nucleotide binding 3 1.060070671 0.166722363 "TUBA8, TUBB, TUBA4A" 26 382 12983 3.921566653 0.999999964 0.819937435 86.47702871
GOTERM_MF_FAT GO:0000166~nucleotide binding 6 2.120141343 0.439685378 "TUBA8, TUBB, TUBA4A, MYH9, DYNC1H1, GAPDH" 26 2245 12983 1.334555422 1 0.979540252 99.82608919
GOTERM_MF_FAT GO:0032555~purine ribonucleotide binding 5 1.766784452 0.479782043 "TUBA8, TUBB, TUBA4A, MYH9, DYNC1H1" 26 1836 12983 1.359875147 1 0.983349468 99.92298332
GOTERM_MF_FAT GO:0032553~ribonucleotide binding 5 1.766784452 0.479782043 "TUBA8, TUBB, TUBA4A, MYH9, DYNC1H1" 26 1836 12983 1.359875147 1 0.983349468 99.92298332
GOTERM_MF_FAT GO:0017076~purine nucleotide binding 5 1.766784452 0.516169328 "TUBA8, TUBB, TUBA4A, MYH9, DYNC1H1" 26 1918 12983 1.301736585 1 0.985953319 99.96523665

Annotation Cluster 6 Enrichment Score: 1.5496433074108042
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0008201~heparin binding 3 1.060070671 0.016604984 "HSD17B12, CYR61, FN1" 26 103 12983 14.54406273 0.79277971 0.408242062 16.78013587
GOTERM_MF_FAT GO:0005539~glycosaminoglycan binding 3 1.060070671 0.029455396 "HSD17B12, CYR61, FN1" 26 140 12983 10.70027473 0.939819344 0.504704673 27.96202903
GOTERM_MF_FAT GO:0030246~carbohydrate binding 4 1.413427562 0.029654226 "HSD17B12, CALR, CYR61, FN1" 26 354 12983 5.642329422 0.940967285 0.432169715 28.12375734
GOTERM_MF_FAT GO:0030247~polysaccharide binding 3 1.060070671 0.035087043 "HSD17B12, CYR61, FN1" 26 154 12983 9.727522478 0.965175492 0.428546585 32.41713415
GOTERM_MF_FAT GO:0001871~pattern binding 3 1.060070671 0.035087043 "HSD17B12, CYR61, FN1" 26 154 12983 9.727522478 0.965175492 0.428546585 32.41713415

Annotation Cluster 7 Enrichment Score: 1.434939523226183
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0001525~angiogenesis 3 1.060070671 0.023797999 "AIMP1, MYH9, CYR61" 23 148 13528 11.92244418 0.999638124 0.341021058 27.84720667
GOTERM_BP_FAT GO:0007155~cell adhesion 5 1.766784452 0.024698078 "AIMP1, MYH9, CDSN, CYR61, FN1" 23 700 13528 4.201242236 0.999732849 0.337268112 28.7435037
GOTERM_BP_FAT GO:0022610~biological adhesion 5 1.766784452 0.024813173 "AIMP1, MYH9, CDSN, CYR61, FN1" 23 701 13528 4.195249023 0.999743023 0.325405785 28.857368
GOTERM_BP_FAT GO:0048514~blood vessel morphogenesis 3 1.060070671 0.045585342 "AIMP1, MYH9, CYR61" 23 211 13528 8.362662271 0.999999784 0.458821859 46.86032103
GOTERM_BP_FAT GO:0001568~blood vessel development 3 1.060070671 0.059505693 "AIMP1,

MYH9, CYR61" 23 245 13528 7.202129547 0.999999998 0.478527249 56.4536851
GOTERM_BP_FAT GO:0001944~vasculature development 3 1.060070671 0.062100234 "AIMP1, MYH9, CYR61" 23 251 13528 7.029967088 0.999999999 0.472274573 58.05368877

Annotation Cluster 8 Enrichment Score: 1.2538427667470968
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0042330~taxis 3 1.060070671 0.027503918 "AIMP1, S100A9, CYR61" 23 160 13528 11.02826087 0.99989646 0.341025728 31.47180734
GOTERM_BP_FAT GO:0006935~chemotaxis 3 1.060070671 0.027503918 "AIMP1, S100A9, CYR61" 23 160 13528 11.02826087 0.99989646 0.341025728 31.47180734
GOTERM_BP_FAT GO:0007626~locomotory behavior 3 1.060070671 0.072398969 "AIMP1, S100A9, CYR61" 23 274 13528 6.439860362 1 0.516750036 63.88278117
GOTERM_BP_FAT GO:0007610~behavior 3 1.060070671 0.176241196 "AIMP1, S100A9, CYR61" 23 469 13528 3.76230648 1 0.797018915 92.77208792

Annotation Cluster 9 Enrichment Score: 1.0335084876249159
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0016023~cytoplasmic membrane-bounded vesicle 4 1.413427562 0.074126186 "AIMP1, FLG, CTSD, FN1" 24 550 12782 3.873333333 0.999868172 0.525028652 58.46681465
GOTERM_CC_FAT GO:0031988~membrane-bounded vesicle 4 1.413427562 0.079975958 "AIMP1, FLG, CTSD, FN1" 24 568 12782 3.750586854 0.999936802 0.524689653 61.36410138
GOTERM_CC_FAT GO:0031410~cytoplasmic vesicle 4 1.413427562 0.106089269 "AIMP1, FLG, CTSD, FN1" 24 642 12782 3.31827622 0.999997761 0.605145358 72.1821653
GOTERM_CC_FAT GO:0031982~vesicle 4 1.413427562 0.11677866 "AIMP1, FLG, CTSD, FN1" 24 670 12782 3.17960199 0.999999445 0.617230008 75.74971796

Annotation Cluster 10 Enrichment Score: 1.0180209936945734
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007155~cell adhesion 5 1.766784452 0.024698078 "AIMP1, MYH9, CDSN, CYR61, FN1" 23 700 13528 4.201242236 0.999732849 0.337268112 28.7435037
GOTERM_BP_FAT GO:0022610~biological adhesion 5 1.766784452 0.024813173 "AIMP1, MYH9, CDSN, CYR61, FN1" 23 701 13528 4.195249023 0.999743023 0.325405785 28.857368
GOTERM_MF_FAT GO:0042803~protein homodimerization activity 3 1.060070671 0.134566611 "AIMP1, MYH9, CDSN" 26 334 12983 4.485145094 0.999998741 0.816981349 79.51386191
GOTERM_MF_FAT GO:0046983~protein dimerization activity 3 1.060070671 0.280595476 "AIMP1, MYH9, CDSN" 26 542 12983 2.763908601 1 0.940052555 97.30218886
GOTERM_MF_FAT GO:0042802~identical protein binding 3 1.060070671 0.351181477 "AIMP1, MYH9, CDSN" 26 640 12983 2.340685096 1 0.966248062 99.13101382

Annotation Cluster 11 Enrichment Score: 0.891977221951022
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0005509~calcium ion binding 8 2.826855124 0.001350722 "TCHH, S100A8, FLG, RPTN, S100A9, FLG2, CALR, S100A2" 26 919 12983 4.346865322 0.119313594 0.061551064 1.471790005
GOTERM_MF_FAT GO:0046872~metal ion binding 9 3.180212014 0.570085727 "TCHH, S100A8, FLG, RPTN, S100A9, FLG2, ENDOD1, CALR, S100A2" 26 4140 12983 1.085535117 1 0.990606718 99.9904887
GOTERM_MF_FAT GO:0043169~cation binding 9 3.180212014 0.582772979 "TCHH, S100A8, FLG, RPTN, S100A9, FLG2, ENDOD1, CALR, S100A2" 26 4179 12983 1.075404495 1 0.989588808 99.99315257

GOTERM_MF_FAT	GO:0043167~ion binding	9	3.180212014	0.602678435	"TCHH, S100A8, FLG, RPTN, S100A9, FLG2, ENDOD1, CALR, S100A2"	26	4241	12983	1.059682949	1	0.989605383	99.99599471

Annotation Cluster 12	Enrichment Score: 0.4228066813828306
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0015031~protein transport	3	1.060070671	0.353990481	"MYH9, CALR, MVP"	23	762	13528	2.315645327	1	0.969988823	99.73173663
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	3	1.060070671	0.358213143	"MYH9, CALR, MVP"	23	769	13528	2.294566631	1	0.969009536	99.75454776
GOTERM_BP_FAT	GO:0008104~protein localization	3	1.060070671	0.42505669	"MYH9, CALR, MVP"	23	882	13528	2.000591541	1	0.98551722	99.94470368

Annotation Cluster 13	Enrichment Score: 0.1427233412285591
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0043233~organelle lumen	4	1.413427562	0.655629467	"C1QBP, S100A9, CALR, FN1"	24	1820	12782	1.170512821	1	0.997935805	99.99947759
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	4	1.413427562	0.669505469	"C1QBP, S100A9, CALR, FN1"	24	1856	12782	1.147808908	1	0.997792224	99.99967324
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	3	1.060070671	0.849996981	"C1QBP, S100A9, CALR"	24	1779	12782	0.89811692	1	0.999954731	99.99999996

Annotation Cluster 1 Enrichment Score: 16.923845730370257

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0005198~structural molecule activity 49 18.56060606 2.06E-19 "RPL18, RPL17, RPL36A, RPL15, RPL27A, RPL35, RPS26, RPS27, KRT5, RPL7, RPL31, RPS3A, KRT7, RPL9, RPL8, KRT8, KRT1, KRT2, RPL11, RPL10A, RPL4, MRPL3, RPL26, RPL27, RPS9, KRT10, RPL24, RPS4X, CTNNA1, RPL28, CTNNA2, COPG2, KRT18, NUP62, MRPS18B, PKP1, RPL23, RPS16, KRT17, RPL13A, KRT15, RPS14, KRT14, RPS15, RPS13, DSP, MAP7, MRPL47, RPS11" 216 634 12983 4.645453616 8.76E-17 4.38E-17 2.90E-16

GOTERM_CC_FAT GO:0043228~non-membrane-bounded organelle 97 36.74242424 9.06E-17 "RPL18, RPL17, XPO1, MRPS35, RPL36A, HMGN2, PDLIM5, RPL15, STOML2, CBX1, ACSS2, H2AFV, WIBG, H2AFY, RPL11, CLNS1A, TRPA1, FMR1, KRT10, MYH9, CTNNA1, CTNNA2, KRT18, MRPS18B, RPS16, KRT17, KRT15, RPS14, RPS15, KRT14, RPS13, DSP, MRPL47, RPS11, MYO18A, RPS26, RPS27, RPL7, HNRNPF, RPL9, RPL8, NPM3, CLASP2, RPL10A, RPL4, NUDC, GIT1, SRP54, MPHOSPH10, RPS9, NOP14, NUP62, EPS8, PKP1, MAP7, UTP14A, DDX54, RPS3A, NOL6, KIF14, SRPK2, ELP3, MRPL3, SLC25A5, LAS1L, RPS4X, SLC9A3R1, HMGA2, VASP, NOC2L, RUVBL1, WASL, RPL27A, RPL35, CDH1, KLC3, GPHN, KRT5, RPL31, KRT7, KRT8, KRT1, KRT2, AATF, CC2D1A, SSRP1, SHMT2, RRP12, UPF1, RPL26, RPL27, RPL24, RPL28, RPL23, RPL13A, H2AFY2, HIST1H2AJ" 213 2596 12782 2 [Add to Citavi project by ISBN] .2422614784753723 3.39E-14 6.77E-15 1.44E-13

GOTERM_CC_FAT GO:0043232~intracellular non-membrane-bounded organelle 97 36.74242424 9.06E-17 "RPL18, RPL17, XPO1, MRPS35, RPL36A, HMGN2, PDLIM5, RPL15, STOML2, CBX1, ACSS2, H2AFV, WIBG, H2AFY, RPL11, CLNS1A, TRPA1, FMR1, KRT10, MYH9, CTNNA1, CTNNA2, KRT18, MRPS18B, RPS16, KRT17, KRT15, RPS14, RPS15, KRT14, RPS13, DSP, MRPL47, RPS11, MYO18A, RPS26, RPS27, RPL7, HNRNPF, RPL9, RPL8, NPM3, CLASP2, RPL10A, RPL4, NUDC, GIT1, SRP54, MPHOSPH10, RPS9, NOP14, NUP62, EPS8, PKP1, MAP7, UTP14A, DDX54, RPS3A, NOL6, KIF14, SRPK2, ELP3, MRPL3, SLC25A5, LAS1L, RPS4X, SLC9A3R1, HMGA2, VASP, NOC2L, RUVBL1, WASL, RPL27A, RPL35, CDH1, KLC3, GPHN, KRT5, RPL31, KRT7, KRT8, KRT1, KRT2, AATF, CC2D1A, SSRP1, SHMT2, RRP12, UPF1, RPL26, RPL27, RPL24, RPL28, RPL23, RPL13A, H2AFY2, HIST1H2AJ" 213 2596 12782 2 [Add to Citavi project by ISBN] .2422614784753723 3.39E-14 6.77E-15 1.44E-13

Annotation Cluster 2 Enrichment Score: 16.50975535568708

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0006414~translational elongation 29 10.98484848 5.68E-27 "RPL18, RPL17, RPL36A, RPL15, RPL27A, RPL35, RPS26, RPS27, RPL7, RPS3A, RPL31, RPL9, RPL8, RPL11, RPL4, RPL10A, RPL26, RPS9, RPL27, RPL24, RPS4X, RPL28, RPL23, RPS16, RPL13A, RPS14, RPS15, RPS13, RPS11" 225 101 13528 17.26345435 7.90E-24 7.90E-24 9.36E-24

GOTERM_BP_FAT GO:0006412~translation 43 16.28787879 1.68E-25 "RPL18, RPL17, RPL36A, EIF5, RPL15, RPL27A, RPL35, IGF2BP3, DTD1, IARS, RPS26, RPS27, RPL7, RPL31, RPS3A, RPL9, RPL8, RPL11, EIF3J, RPL10A, RPL4, EIF2B4, MARS, MRPL3, AIMP2, RPL26, RPL27, RPS9, RPL24, LRRC47, MRRF, RPS4X, RPL28, EIF4B, MRPS18B, RPL23, RPS16, RPL13A, RPS14, RPS15, RPS13, MRPL47, RPS11" 225 331 13528 7.810728432 2.33E-22 1.16E-22 2.76E-22

GOTERM_MF_FAT GO:0003735~structural constituent of ribosome 32 12.12121212 5.63E-24 "RPL18, RPL17, RPL36A, RPL15, RPL27A, RPL35, RPS26, RPS27, RPL7, RPL31, RPS3A, RPL9, RPL8, RPL11, RPL4, RPL10A, MRPL3, RPL26, RPS9, RPL27, RPL24, RPS4X, RPL28, MRPS18B, RPL23, RPS16, RPL13A, RPS14, RPS15, RPS13, MRPL47, RPS11" 216 168 12983 11.44885362 2.394 [Add to Citavi project by ISBN] 01E-21

GOTERM_CC_FAT GO:0005840~ribosome 34 12.87878788 8.11E-23 "RPL18, MRPS35, RPL17, RPL36A, RPL15, RPL27A, RPL35, RPS26, RPS27, RPL7, RPL31, RPS3A, RPL9, RPL8, RPL11, RPL10A, RPL4, MRPL3, FMR1, RPL26, RPL27, RPS9, RPL24, RPS4X, RPL28, MRPS18B, RPL23, RPS16, RPL13A, RPS14, RPS15, RPS13, MRPL47, RPS11" 213 215 12782 9.489856971 2.47E-20 2.47E-20 1.09E-19

GOTERM_CC_FAT GO:0030529~ribonucleoprotein complex 46 17.42424242 1.21E-20 "RPL18, MRPS35, RPL17, XPO1, RPL36A, RPL15, RPL27A, RPL35, SNRPD1, PATL1, RPS26, RPS27, WDR36, RPL7,

RPL31, RPS3A, RPL9, HNRNPF, RPL8, RPL11, RPL10A, RPL4, NOL6, SRP54, UPF1, MRPL3, FMR1, MPHOSPH10, RPL26, RPL27, RPS9, RPL24, RPS4X, RPL28, PIH1D1, NUP62, MRPS18B, RPL23, RPS16, RPL13A, RPS14, RPS15, RPS13, MRPL47, RPS11, UTP14A" 213 515 12782 5.36006199 3.69E-18 1.85E-18 1.62E-17
GOTERM_CC_FAT GO:0033279~ribosomal subunit 26 9.848484848 3.98E-20 "RPL18, RPL17, MRPS35, RPL35, RPL27A, RPS26, RPS27, RPL7, RPL31, RPS3A, RPL8, RPL11, RPL4, MRPL3, RPL26, RPS9, RPL24, RPS4X, RPL28, MRPS18B, RPS16, RPL13A, RPS14, RPS15, RPS13, RPS11" 213 128 12782 12.18940728 1.22E-17 4.05E-18 5.34E-17
GOTERM_MF_FAT GO:0005198~structural molecule activity 49 18.56060606 2.06E-19 "RPL18, RPL17, RPL36A, RPL15, RPL27A, RPL35, RPS26, RPS27, KRT5, RPL7, RPL31, RPS3A, KRT7, RPL9, RPL8, KRT8, KRT1, KRT2, RPL11, RPL10A, RPL4, MRPL3, RPL26, RPL27, RPS9, KRT10, RPL24, RPS4X, CTNNA1, RPL28, CTNNA2, COPG2, KRT18, NUP62, MRPS18B, PKP1, RPL23, RPS16, KRT17, RPL13A, KRT15, RPS14, KRT14, RPS15, RPS13, DSP, MAP7, MRPL47, RPS11" 216 634 12983 4.645453616 8.76E-17 4.38E-17 2.90E-16
GOTERM_CC_FAT GO:0022626~cytosolic ribosome 21 7.954545455 1.86E-18 "RPL18, RPL35, RPL27A, RPL26, RPS9, RPL24, RPS4X, RPL28, RPS26, RPS27, RPS16, RPL7, RPS3A, RPL31, RPS14, RPS15, RPL8, RPS13, RPL11, RPS11, RPL4" 213 81 12782 15.55798991 5.66E-16 1.41E-16 2.49E-15
GOTERM_MF_FAT GO:0003723~RNA binding 47 17.8030303 1.05E-15 "RPL18, XPO1, RPL36A, PUS1, ZC3HAV1, RPL15, RPL27A, RPL35, SNRPD1, IGF2BP3, PDCD4, RPS26, DDX18, RPL7, RPL31, RPS3A, WIBG, RPL9, HNRNPF, RPL8, PUM1, RPL11, RPL10A, RPL4, MARS, NOL6, SRP54, UPF1, MRPL3, FMR1, RPL26, RPS9, RPL24, LRRC47, RPS4X, RPL28, EIF4B, NOP14, TAF15, RPS16, RPS14, SERBP1, ESRP1, RPS13, RPS11, ESRP2, DDX54" 216 718 12983 3.934546838 4.25E-13 1.42E-13 1.41E-12
GOTERM_CC_FAT GO:0005829~cytosol 61 23.10606061 2.00E-13 "RPL18, XPO1, RPL17, RPL36A, PDLIM5, EIF5, RPL15, SNRPD1, ACSS2, PDCD4, PLCB3, RPS3A, SDPR, PUM1, RPL11, IMPDH2, CLNS1A, BCL10, RAB4A, CORO7, MYH9, RPS4X, VASP, PSME1, RPS16, TACSTD2, RPS14, RPS15, RPS13, RPS11, ANAPC7, PRPS1, CHMP2A, RPL27A, RPL35, ASNS, IARS, RPS26, RPS27, RPL7, RPL31, RPL9, RPL8, EIF3J, RPL4, RPL10A, MARS, CSNK1A1, SHMT1, ACY1, AIMP2, RPL26, RPL27, RPS9, RPL24, RPL28, PPA1, EIF4B, RPL23, RPL13A, RAB38" 213 1330 12782 2.752310353 6.10E-11 1.02E-11 2.68E-10
GOTERM_CC_FAT GO:0044445~cytosolic part 21 7.954545455 7.13E-13 "RPL18, RPL35, RPL27A, RPL26, RPS9, RPL24, RPS4X, RPL28, RPS26, RPS27, RPS16, RPL7, RPS3A, RPL31, RPS14, RPS15, RPL8, RPS13, RPL11, RPS11, RPL4" 213 152 12782 8.290770941 2.17E-10 3.11E-11 9.55E-10
GOTERM_CC_FAT GO:0015934~large ribosomal subunit 14 5.303030303 5.74E-11 "RPL18, RPL17, MRPL3, RPL35, RPL26, RPL27A, RPL24, RPL28, RPL7, RPL31, RPL13A, RPL8, RPL11, RPL4" 213 67 12782 12.53927545 1.75E-08 2.19E-09 7.69E-08
GOTERM_CC_FAT GO:0022625~cytosolic large ribosomal subunit 11 4.166666667 4.02E-10 "RPL18, RPL7, RPL31, RPL8, RPL35, RPL27A, RPL26, RPL11, RPL24, RPL4, RPL28" 213 38 12782 17.37113912 1.23E-07 1.36E-08 5.38E-07
GOTERM_CC_FAT GO:0015935~small ribosomal subunit 12 4.545454545 5.83E-09 "RPS26, MRPS35, RPS27, RPS16, MRPS18B, RPS3A, RPS14, RPS15, RPS13, RPS9, RPS11, RPS4X" 213 63 12782 11.43035994 1.78E-06 1.78E-07 7.81E-06
GOTERM_CC_FAT GO:0022627~cytosolic small ribosomal subunit 10 3.787878788 1.40E-08 "RPS26, RPS27, RPS16, RPS3A, RPS14, RPS15, RPS13, RPS9, RPS11, RPS4X" 213 40 12782 15.00234742 4.28E-06 3.89E-07 1.88E-05

Annotation Cluster 3 Enrichment Score: 5.561760772048757
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005730~nucleolus 32 12.12121212 4.84E-07 "XPO1, RPL36A, RPL35, ACSS2, RPS3A, WIBG, HNRNPF, RPL9, NPM3, AATF, RPL11, CC2D1A, NOL6, SRPK2, ELP3, SRP54, RRP12, FMR1, MPHOSPH10, RPS9, LAS1L, NOC2L, NOP14, NUP62, KRT17, RPL23, RPS14, RPS13, WASL, DDX54, UTP14A, MYO18A" 213 698 12782 2.751146804 1.48E-04 1.23E-05 6.48E-04
GOTERM_CC_FAT GO:0070013~intracellular organelle lumen 57 21.59090909 9.62E-07 "XPO1, MRPS35, GRPEL1, RPL36A, NAA15, SNRPD1, CBX1, ACSS2, RPS3A, WIBG, RPL11, YAP1, HADH, NOL6, SRPK2, ELP3, MRPL3, ACADM, ACO2, SLC25A5, SUCLG2, FMR1, LAS1L, PPP1CB, NOC2L, MRPS18B,

KRT17, RPS14, RPS15, RPS13, RUVBL2, MRPL47, ANAPC7, RUVBL1, WASL, MYO18A, POLR2E, RPL35, DTD1, RPL9, HNRNPF, NPM3, AATF, CC2D1A, HSD17B8, SSRP1, SHMT2, SRP54, RRP12, MPHOSPH10, RPS9, NOP14, NUP62, RPL23, POLD1, DDX54, UTP14A" 213 1779 12782 1.92272918 2.94E-04 2.26E-05 0.00128939
GOTERM_CC_FAT GO:0031974~membrane-enclosed lumen 58 21.96969697 1.66E-06 "XPO1, MRPS35, GRPEL1, RPL36A, NAA15, SNRPD1, CBX1, ACSS2, RPS3A, WIBG, RPL11, YAP1, HADH, NOL6, SRPK2, ELP3, MRPL3, ACADM, ACO2, SLC25A5, SUCLG2, FMR1, LAS1L, PPP1CB, NOC2L, MRPS18B, KRT17, RPS14, RPS15, RPS13, RUVBL2, MRPL47, ANAPC7, RUVBL1, WASL, MYO18A, POLR2E, RPL35, DTD1, RPL9, HNRNPF, NPM3, AATF, CC2D1A, HSD17B8, SSRP1, SHMT2, SRP54, RRP12, MPHOSPH10, AK2, RPS9, NOP14, NUP62, RPL23, POLD1, DDX54, UTP14A" 213 1856 12782 1.875293427 5.05E-04 3.61E-05 0.002220511
GOTERM_CC_FAT GO:0043233~organelle lumen 57 21.59090909 2.00E-06 "XPO1, MRPS35, GRPEL1, RPL36A, NAA15, SNRPD1, CBX1, ACSS2, RPS3A, WIBG, RPL11, YAP1, HADH, NOL6, SRPK2, ELP3, MRPL3, ACADM, ACO2, SLC25A5, SUCLG2, FMR1, LAS1L, PPP1CB, NOC2L, MRPS18B, KRT17, RPS14, RPS15, RPS13, RUVBL2, MRPL47, ANAPC7, RUVBL1, WASL, MYO18A, POLR2E, RPL35, DTD1, RPL9, HNRNPF, NPM3, AATF, CC2D1A, HSD17B8, SSRP1, SHMT2, SRP54, RRP12, MPHOSPH10, RPS9, NOP14, NUP62, RPL23, POLD1, DDX54, UTP14A" 213 1820 12782 1.879414951 6.09E-04 4.06E-05 0.002674507
GOTERM_CC_FAT GO:0031981~nuclear lumen 44 16.66666667 1.01E-04 "XPO1, RPL36A, POLR2E, SNRPD1, NAA15, RPL35, CBX1, ACSS2, RPS3A, WIBG, RPL9, HNRNPF, NPM3, AATF, RPL11, CC2D1A, YAP1, NOL6, SRPK2, SSRP1, ELP3, SRP54, RRP12, FMR1, MPHOSPH10, RPS9, LAS1L, PPP1CB, NOC2L, NOP14, NUP62, RPL23, KRT17, POLD1, RPS14, RPS15, RPS13, RUVBL2, WASL, RUVBL1, ANAPC7, DDX54, UTP14A, MYO18A" 213 1450 12782 1.820974583 0.030275007 0.001706473 0.134942158

Annotation Cluster 4 Enrichment Score: 5.157968690151086
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0022613~ribonucleoprotein complex biogenesis 17 6.439393939 4.95E-08 "CLNS1A, SRPK2, RPL26, MPHOSPH10, SNRPD1, RPL24, NOP14, PIH1D1, WDR36, RPL7, RPS16, RPS14, RPS15, NPM3, RPL11, AATF, UTP14A" 225 180 13528 5.678419753 6.89E-05 2.30E-05 8.16E-05
GOTERM_BP_FAT GO:0042254~ribosome biogenesis 13 4.924242424 8.27E-07 "MPHOSPH10, RPL26, RPL24, NOP14, WDR36, RPL7, RPS16, RPS14, RPS15, NPM3, AATF, RPL11, UTP14A" 225 122 13528 6.406703097 0.001149183 2.87E-04 0.001361793
GOTERM_BP_FAT GO:0006364~rRNA processing 11 4.166666667 2.79E-06 "NOP14, WDR36, RPS16, RPL7, RPS14, RPS15, MPHOSPH10, RPL26, NPM3, RPL11, UTP14A" 225 92 13528 7.188792271 0.003875212 7.76E-04 0.004598365
GOTERM_BP_FAT GO:0016072~rRNA metabolic process 11 4.166666667 4.12E-06 "NOP14, WDR36, RPS16, RPL7, RPS14, RPS15, MPHOSPH10, RPL26, NPM3, RPL11, UTP14A" 225 96 13528 6.889259259 0.005717203 9.55E-04 0.006790291
GOTERM_BP_FAT GO:0034660~ncRNA metabolic process 16 6.060606061 6.65E-06 "PUS1, RPL26, MPHOSPH10, DTD1, NOP14, IARS, WDR36, RPL7, RPS16, RPS14, RPS15, NPM3, RPL11, KIAA0391, UTP14A, MARS" 225 230 13528 4.182570048 0.009203666 0.001320025 0.010950107
GOTERM_BP_FAT GO:0006396~RNA processing 24 9.090909091 3.90E-05 "CLNS1A, SRPK2, RPL36A, POLR2E, PUS1, RPL26, MPHOSPH10, SNRPD1, NOP14, WDR36, RPS16, RPL7, RPS14, HNRNPF, RPS15, ESRP1, NPM3, RPL11, ESRP2, RPL10A, KIAA0391, DDX54, ARL6IP4, UTP14A" 225 547 13528 2.638001219 0.052747284 0.00600295 0.064157839
GOTERM_BP_FAT GO:0034470~ncRNA processing 13 4.924242424 6.64E-05 "NOP14, WDR36, RPS16, PUS1, RPL7, RPS14, RPS15, MPHOSPH10, RPL26, NPM3, RPL11, KIAA0391, UTP14A" 225 187 13528 4.179774213 0.088165313 0.009187194 0.109250457
GOTERM_BP_FAT GO:0042274~ribosomal small subunit biogenesis 4 1.515151515 6.70E-04 "NOP14, RPS16, RPS14, RPS15" 225 11 13528 21.86343434 0.606069688 0.060216188 1.097241417

Annotation Cluster 5 Enrichment Score: 3.692454201451518
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment

Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006417~regulation of translation 12 4.545454545 1.71E-05 "EIF4B, METAP1, UPF1, WIBG, KRT7, EIF5, PUM1, ITGA2, IGF2BP3, RPS4X, FAM129A, EIF2B4" 225 137 13528 5.266374696 0.023456951 0.002962658 0.028107982
GOTERM_BP_FAT GO:0010608~posttranscriptional regulation of gene expression 13 4.924242424 2.07E-04 "METAP1, UPF1, EIF5, ITGA2, IGF2BP3, RPS4X, EIF4B, WIBG, KRT7, SERBP1, PUM1, FAM129A, EIF2B4" 225 211 13528 3.704349658 0.25049538 0.025872404 0.340912414
GOTERM_BP_FAT GO:0032268~regulation of cellular protein metabolic process 18 6.818181818 0.002362604 "BCL10, METAP1, UPF1, EIF5, ITGA2, IGF2BP3, RPS4X, PDCD4, EIF4B, PSME1, PSME2, WIBG, PSMB3, KRT7, PUM1, ANAPC7, FAM129A, EIF2B4" 225 474 13528 2.283206751 0.962668039 0.138818717 3.819144747

Annotation Cluster 6 Enrichment Score: 2.8676371157199765
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005759~mitochondrial matrix 13 4.924242424 4.07E-04 "MRPS35, GRPEL1, SHMT2, ACADM, MRPL3, ACO2, SLC25A5, SUCLG2, DTD1, MRPS18B, MRPL47, HADH, HSD17B8" 213 227 12782 3.436661083 0.11674128 0.006187633 0.543771182
GOTERM_CC_FAT GO:0031980~mitochondrial lumen 13 4.924242424 4.07E-04 "MRPS35, GRPEL1, SHMT2, ACADM, MRPL3, ACO2, SLC25A5, SUCLG2, DTD1, MRPS18B, MRPL47, HADH, HSD17B8" 213 227 12782 3.436661083 0.11674128 0.006187633 0.543771182
GOTERM_CC_FAT GO:0005739~mitochondrion 32 12.12121212 0.002007449 "MRPS35, GRPEL1, STOML2, ACSF2, MTHFD1L, ALDH3A2, NDUFAF2, DTD1, MTHFD1, KIAA0391, HADH, HSD17B8, SHMT1, BSG, SHMT2, ACADM, MRPL3, ACO2, SLC25A5, SUCLG2, SLC25A6, AK2, MRRF, PPA2, DHRS1, LAP3, ALDH7A1, CKMT1A, DHRS4, MRPS18B, DSP, MRPL47" 213 1087 12782 1.766605768 0.458215646 0.024217425 2.656109807
GOTERM_CC_FAT GO:0044429~mitochondrial part 19 7.196969697 0.01018076 "MRPS35, GRPEL1, SHMT2, MRPL3, ACADM, ACO2, SLC25A5, SUCLG2, SLC25A6, STOML2, AK2, ALDH3A2, DTD1, DHRS1, CKMT1A, MRPS18B, MRPL47, HADH, HSD17B8" 213 595 12782 1.916266225 0.955889001 0.109163438 12.81061559

Annotation Cluster 7 Enrichment Score: 2.6846939422344187
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0042257~ribosomal subunit assembly 3 1.136363636 8.10E-04 "RPS14, RPS15, RPL24" 225 3 13528 60.12444444 0.675767217 0.067972862 1.325053194
GOTERM_BP_FAT GO:0022618~ribonucleoprotein complex assembly 7 2.651515152 9.69E-04 "CLNS1A, SRPK2, PIH1D1, RPS14, RPS15, SNRPD1, RPL24" 225 69 13528 6.09958132 0.740005571 0.068444715 1.582754296
GOTERM_BP_FAT GO:0042255~ribosome assembly 3 1.136363636 0.011253414 "RPS14, RPS15, RPL24" 225 10 13528 18.03733333 0.999999853 0.41867524 16.99813128

Annotation Cluster 8 Enrichment Score: 2.2707131662280537
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0005200~structural constituent of cytoskeleton 8 3.03030303 2.18E-04 "KRT17, KRT5, KRT15, KRT14, KRT1, DSP, KRT2, CTNNA2" 216 74 12983 6.497997998 0.088368512 0.015301629 0.305848391
GOTERM_CC_FAT GO:0045095~keratin filament 8 3.03030303 6.37E-04 "KRT18, KRT5, KRT7, KRT8, KRT14, KRT1, KRT2, KRT10" 213 88 12782 5.455399061 0.176620031 0.009211479 0.849967549
GOTERM_CC_FAT GO:0005882~intermediate filament 11 4.166666667 9.51E-04 "KRT18, KRT17, PKP1, KRT5, KRT7, KRT15, KRT8, KRT14, KRT1, KRT2, KRT10" 213 183 12782 3.607121784 0.25190991 0.01310572 1.266711834

GOTERM_BP_FAT GO:0008544~epidermis development 11 4.166666667 9.86E-04 "COL17A1, KRT17, KRT5, COL7A1, KRT15, KRT14, KRT1, DSP, KRT2, KRT10, ALDH3A2" 225 184 13528 3.594396135 0.746061599 0.066237521 1.610221681
GOTERM_CC_FAT GO:0045111~intermediate filament cytoskeleton 11 4.166666667 0.001121172 "KRT18, KRT17, PKP1, KRT5, KRT7, KRT15, KRT8, KRT14, KRT1, KRT2, KRT10" 213 187 12782 3.529964098 0.289757919 0.014765959 1.491607258
GOTERM_BP_FAT GO:0007398~ectoderm development 11 4.166666667 0.001782683 "COL17A1, KRT17, KRT5, COL7A1, KRT15, KRT14, KRT1, DSP, KRT2, KRT10, ALDH3A2" 225 199 13528 3.323461753 0.916268555 0.111394534 2.894600699
GOTERM_CC_FAT GO:0044430~cytoskeletal part 22 8.333333333 0.109866907 "KIF14, KRT10, KLC3, CBX1, MYH9, KRT18, NUP62, KRT17, PKP1, EPS8, KRT5, KRT7, KRT15, KRT14, KRT8, KRT1, KRT2, MAP7, CLASP2, RUVBL1, MYO18A, NUDC" 213 952 12782 1.38677161 1 0.508328338 78.96884648
GOTERM_BP_FAT GO:0060429~epithelium development 6 2.272727273 0.323477539 "BCL10, KRT5, KRT14, DSP, KRT2, VASP" 225 227 13528 1.589192364 1 0.980478022 99.83928394
GOTERM_BP_FAT GO:0030855~epithelial cell differentiation 4 1.515151515 0.396522797 "KRT5, KRT14, DSP, KRT2" 225 137 13528 1.755458232 1 0.991290553 99.97549927

Annotation Cluster 9 Enrichment Score: 2.030428347104485
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0034621~cellular macromolecular complex subunit organization 17 6.439393939 3.02E-04 "CLNS1A, SRPK2, XPO1, SRP54, SNRPD1, RPL24, MRRF, PIH1D1, H2AFV, IPO4, RPS14, RPS15, H2AFY2, H2AFY, WASL, HIST1H2AJ, XPO7" 225 357 13528 2.863068783 0.342955782 0.031791669 0.496190825
GOTERM_BP_FAT GO:0034622~cellular macromolecular complex assembly 15 5.681818182 8.53E-04 "CLNS1A, SRPK2, XPO1, SRP54, SNRPD1, RPL24, PIH1D1, H2AFV, IPO4, RPS14, RPS15, H2AFY2, H2AFY, HIST1H2AJ, XPO7" 225 318 13528 2.8360587 0.694707295 0.063790304 1.395369603
GOTERM_BP_FAT GO:0065003~macromolecular complex assembly 22 8.333333333 0.003461235 "SOAT1, CLNS1A, SRPK2, SHMT1, BCL10, XPO1, SRP54, POLR2E, SNRPD1, CDH1, RPL24, SLC9A3R1, PIH1D1, H2AFV, RPS14, IPO4, RPS15, H2AFY2, H2AFY, WASL, HIST1H2AJ, XPO7" 225 665 13528 1.989079365 0.991928874 0.181932909 5.548021181
GOTERM_BP_FAT GO:0043933~macromolecular complex subunit organization 23 8.712121212 0.003496336 "SOAT1, CLNS1A, SRPK2, XPO1, SHMT1, BCL10, SRP54, POLR2E, SNRPD1, CDH1, RPL24, SLC9A3R1, MRRF, PIH1D1, H2AFV, RPS14, IPO4, RPS15, H2AFY2, H2AFY, WASL, HIST1H2AJ, XPO7" 225 710 13528 1.947693271 0.992314518 0.176948816 5.602773353
GOTERM_BP_FAT GO:0006461~protein complex assembly 10 3.787878788 0.458854977 "BCL10, SHMT1, XPO1, SRP54, POLR2E, IPO4, CDH1, WASL, XPO7, SLC9A3R1" 225 505 13528 1.190583058 1 0.99501629 99.99592867
GOTERM_BP_FAT GO:0070271~protein complex biogenesis 10 3.787878788 0.458854977 "BCL10, SHMT1, XPO1, SRP54, POLR2E, IPO4, CDH1, WASL, XPO7, SLC9A3R1" 225 505 13528 1.190583058 1 0.99501629 99.99592867

Annotation Cluster 10 Enrichment Score: 1.7846170274214415
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005913~cell-cell adherens junction 7 2.651515152 2.11E-05 "ITGA6, PVRL1, DSP, CDH1, MYH9, CDH3, CTNNA2" 213 35 12782 12.00187793 0.006404718 4.02E-04 0.028218324
GOTERM_CC_FAT GO:0070161~anchoring junction 13 4.924242424 2.93E-05 "GIT1, ITGA2, CDH1, MYH9, CTNNA1, CDH3, VASP, CTNNA2, PVRL1, ITGA6, PKP1, PKP3, DSP" 213 172 12782 4.535593405 0.008897636 5.26E-04 0.039248827
GOTERM_CC_FAT GO:0005912~adherens junction 11 4.166666667 2.58E-04 "GIT1, ITGA6, PVRL1, DSP, ITGA2, CDH1, MYH9, CDH3, CTNNA1, VASP, CTNNA2" 213 155 12782 4.25873088 0.075815457 0.00414106 0.345710151
GOTERM_CC_FAT GO:0005911~cell-cell junction 11 4.166666667 0.001264385 "COL17A1, PKP1,

ITGA6, PVRL1, PKP3, SLC2A1, DSP, CDH1, MYH9, CDH3, CTNNA2" 213 190 12782 3.474227823 0.320148875 0.015949826 1.680647305
GOTERM_CC_FAT GO:0016323~basolateral plasma membrane 10 3.787878788 0.006763141 "GIT1, COL17A1, ITGA6, SLC2A1, DSP, ITGA2, CDH1, MAP7, VASP, CTNNA2" 213 203 12782 2.95612757 0.873784543 0.076520189 8.690151716
GOTERM_CC_FAT GO:0030054~cell junction 16 6.060606061 0.025824425 "GIT1, ITGA2, CDH1, MYH9, CDH3, CTNNA1, VASP, CTNNA2, GPHN, COL17A1, PVRL1, ITGA6, PKP1, PKP3, SLC2A1, DSP" 213 518 12782 1.853571882 0.999657739 0.226954477 29.56695455
GOTERM_BP_FAT GO:0007155~cell adhesion 18 6.818181818 0.073424171 "FLRT3, PTPRF, ITGA2, CTNND1, CDH1, MYH9, CDH3, CTNNA1, CTNNA2, LGALS3BP, COL17A1, PVRL1, COL7A1, ITGA6, PKP1, PKP3, CNTN1, AATF" 225 700 13528 1.546057143 1 0.854456869 71.50390291
GOTERM_BP_FAT GO:0022610~biological adhesion 18 6.818181818 0.074175455 "FLRT3, PTPRF, ITGA2, CTNND1, CDH1, MYH9, CDH3, CTNNA1, CTNNA2, LGALS3BP, COL17A1, PVRL1, COL7A1, ITGA6, PKP1, PKP3, CNTN1, AATF" 225 701 13528 1.543851641 1 0.852363318 71.88189128
GOTERM_CC_FAT GO:0030055~cell-substrate junction 5 1.893939394 0.115687671 "GIT1, COL17A1, ITGA2, CDH1, VASP" 213 112 12782 2.67899061 1 0.513792362 80.73840189
GOTERM_CC_FAT GO:0005925~focal adhesion 4 1.515151515 0.239564576 "GIT1, ITGA2, CDH1, VASP" 213 102 12782 2.353309399 1 0.707227951 97.44948516
GOTERM_CC_FAT GO:0005924~cell-substrate adherens junction 4 1.515151515 0.257346912 "GIT1, ITGA2, CDH1, VASP" 213 106 12782 2.264505271 1 0.726475581 98.14237224
GOTERM_BP_FAT GO:0016337~cell-cell adhesion 7 2.651515152 0.310390048 "PTPRF, PVRL1, CTNND1, CDH1, MYH9, CDH3, CTNNA2" 225 276 13528 1.52489533 1 0.980614703 99.7796836
GOTERM_BP_FAT GO:0007156~homophilic cell adhesion 4 1.515151515 0.369573048 "PTPRF, PVRL1, CDH1, CDH3" 225 131 13528 1.835860899 1 0.989413112 99.9497041
GOTERM_BP_FAT GO:0051336~regulation of hydrolase activity 6 2.272727273 0.659871578 "GIT1, ARFGAP2, GNA15, NF1, ITGA2, CDH1" 225 337 13528 1.070464886 1 0.999062401 99.99999805

Annotation Cluster 11 Enrichment Score: 1.4586428292399136
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006563~L-serine metabolic process 3 1.136363636 0.007156533 "SHMT1, SHMT2, PHGDH" 225 8 13528 22.54666667 0.999953838 0.309095444 11.15140125
GOTERM_BP_FAT GO:0006544~glycine metabolic process 3 1.136363636 0.024870972 "SHMT1, SHMT2, PHGDH" 225 15 13528 12.02488889 1 0.653836108 33.94023262
GOTERM_BP_FAT GO:0009069~serine family amino acid metabolic process 3 1.136363636 0.068409624 "SHMT1, SHMT2, PHGDH" 225 26 13528 6.937435897 1 0.838627872 68.85607227
GOTERM_MF_FAT GO:0048037~cofactor binding 8 3.03030303 0.120203203 "SOAT1, SHMT1, SHMT2, SORD, ACADM, PHGDH, ASNS, HADH" 216 249 12983 1.931131935 1 0.959303279 83.50316869

Annotation Cluster 12 Enrichment Score: 1.3340035002618478
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006695~cholesterol biosynthetic process 5 1.893939394 8.22E-04 "EBP, CYP51A1, DHCR7, PRKAA1, FDFT1" 225 26 13528 11.56239316 0.681011545 0.065002839 1.344108198
GOTERM_BP_FAT GO:0016126~sterol biosynthetic process 5 1.893939394 0.002561782 "EBP, CYP51A1, DHCR7, PRKAA1, FDFT1" 225 35 13528 8.589206349 0.971715612 0.143601403 4.13477269
GOTERM_CC_FAT GO:0000267~cell fraction 29 10.98484848 0.012274082 "GALNT3, SORD, GNAI3, CYP51A1, PDLIM5, LEMD3, CTNND1, ASNS, FDFT1, IARS, PLCB3, SLC16A1, VRK2, PVRL1, SLC2A1, HSD17B8, SOAT1, EBP, ACY1, PTPRF, RAB4A, FMR1, CORO7, EPS8, MAPK13, CNTN1, RAB38, SSR3, PRPS1" 213 1083 12782 1.606899631 0.976873113 0.121806441 15.24874717
GOTERM_BP_FAT GO:0006694~steroid biosynthetic process 6 2.272727273 0.013379866 "EBP,

CYP51A1, DHCR7, PRKAA1, HSD17B8, FDFT1" 225 85 13528 4.244078431 0.999999993 0.464266517 19.88842625

GOTERM_BP_FAT GO:0008203~cholesterol metabolic process 6 2.272727273 0.018294688 "SOAT1, EBP, CYP51A1, DHCR7, PRKAA1, FDFT1" 225 92 13528 3.92115942 1 0.563036963 26.21104882

GOTERM_CC_FAT GO:0005626~insoluble fraction 23 8.712121212 0.022082781 "GALNT3, SOAT1, EBP, GNAI3, SORD, PTPRF, CYP51A1, PDLIM5, RAB4A, CTNND1, LEMD3, CORO7, FDFT1, PLCB3, SLC16A1, VRK2, PVRL1, EPS8, SLC2A1, CNTN1, RAB38, SSR3, HSD17B8" 213 839 12782 1.645072661 0.998898109 0.203098553 25.8553099

GOTERM_BP_FAT GO:0016125~sterol metabolic process 6 2.272727273 0.026187887 "SOAT1, EBP, CYP51A1, DHCR7, PRKAA1, FDFT1" 225 101 13528 3.571749175 1 0.662061305 35.39366291

GOTERM_CC_FAT GO:0005624~membrane fraction 22 8.333333333 0.027602364 "GALNT3, SOAT1, EBP, GNAI3, SORD, PTPRF, CYP51A1, PDLIM5, RAB4A, CTNND1, LEMD3, CORO7, FDFT1, SLC16A1, VRK2, PVRL1, EPS8, SLC2A1, CNTN1, RAB38, SSR3, HSD17B8" 213 809 12782 1.631899348 0.999803941 0.227945226 31.26969083

GOTERM_CC_FAT GO:0042598~vesicular fraction 9 3.409090909 0.050742445 "SOAT1, EBP, PTPRF, PVRL1, CYP51A1, RAB4A, RAB38, SSR3, FDFT1" 213 244 12782 2.213461094 0.999999873 0.341618919 50.22387677

GOTERM_BP_FAT GO:0008202~steroid metabolic process 8 3.03030303 0.05114619 "SOAT1, EBP, CYP51A1, OSBPL9, DHCR7, PRKAA1, HSD17B8, FDFT1" 225 202 13528 2.381166117 1 0.795344932 57.86444579

GOTERM_CC_FAT GO:0005792~microsome 8 3.03030303 0.09911999 "SOAT1, EBP, PTPRF, PVRL1, CYP51A1, RAB4A, SSR3, FDFT1" 213 237 12782 2.025633407 1 0.477814396 75.30058116

GOTERM_BP_FAT GO:0008610~lipid biosynthetic process 9 3.409090909 0.168251899 "EBP, CYP51A1, ALOX15B, DHCR7, MBOAT7, PRKAA1, ACSS2, HSD17B8, FDFT1" 225 323 13528 1.675294118 1 0.932492198 95.18181655

GOTERM_CC_FAT GO:0042175~nuclear envelope-endoplasmic reticulum network 8 3.03030303 0.19344337 "SOAT1, OSTC, XPO1, CYP51A1, DHCR7, DAD1, SSR3, FDFT1" 213 284 12782 1.690405343 1 0.670883444 94.38673803

GOTERM_CC_FAT GO:0012505~endomembrane system 17 6.439393939 0.22644171 "SOAT1, OSTC, XPO1, BSG, CYP51A1, CHMP4A, LEMD3, CORO7, FDFT1, COPG2, NUP62, IPO4, DHCR7, DAD1, WASL, XPO7, SSR3" 213 782 12782 1.304551949 1 0.69471694 96.79244008

GOTERM_CC_FAT GO:0005789~endoplasmic reticulum membrane 7 2.651515152 0.289674948 "SOAT1, OSTC, CYP51A1, DHCR7, DAD1, SSR3, FDFT1" 213 269 12782 1.561582631 1 0.751156862 98.97666986

GOTERM_CC_FAT GO:0044432~endoplasmic reticulum part 7 2.651515152 0.518111321 "SOAT1, OSTC, CYP51A1, DHCR7, DAD1, SSR3, FDFT1" 213 347 12782 1.210564057 1 0.918065066 99.9943437

GOTERM_CC_FAT GO:0005783~endoplasmic reticulum 15 5.681818182 0.730601939 "SOAT1, EBP, OSTC, CYP51A1, CNPY2, ALDH3A2, FDFT1, DHRS1, VRK2, PTPLB, DHCR7, DAD1, YIPF5, RAB38, SSR3" 213 960 12782 0.937646714 1 0.980195323 99.99999766

Annotation Cluster 13 Enrichment Score: 1.1982851386375182

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0009113~purine base biosynthetic process 3 1.136363636 0.009101385 "SHMT1, PPAT, PRPS1" 225 9 13528 20.04148148 0.999996976 0.364845752 13.97355971

GOTERM_BP_FAT GO:0046112~nucleobase biosynthetic process 3 1.136363636 0.021789408 "SHMT1, PPAT, PRPS1" 225 14 13528 12.88380952 1 0.615934162 30.41832196

GOTERM_BP_FAT GO:0006144~purine base metabolic process 3 1.136363636 0.021789408 "SHMT1, PPAT, PRPS1" 225 14 13528 12.88380952 1 0.615934162 30.41832196

GOTERM_BP_FAT GO:0009112~nucleobase metabolic process 3 1.136363636 0.054986618 "SHMT1, PPAT, PRPS1" 225 23 13528 7.842318841 1 0.798979641 60.5857811

GOTERM_BP_FAT GO:0046148~pigment biosynthetic process 3 1.136363636 0.135991743 "SHMT1, PPAT, PRPS1" 225 39 13528 4.624957265 1 0.908403087 90.98553169

GOTERM_BP_FAT GO:0042440~pigment metabolic process 3 1.136363636 0.170703383 "SHMT1, PPAT, PRPS1" 225 45 13528 4.008296296 1 0.929691525 95.41034607

GOTERM_BP_FAT "GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process" 6 2.272727273 0.216797581 "MTHFD1, SHMT1, ATP1B3, PPAT, IMPDH2, PRPS1" 225 193 13528 1.869153713 1 0.953114881 98.20970348

GOTERM_BP_FAT "GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process" 6 2.272727273 0.216797581 "MTHFD1, SHMT1, ATP1B3, PPAT, IMPDH2, PRPS1" 225 193 13528 1.869153713 1 0.953114881 98.20970348

Annotation Cluster 14 Enrichment Score: 1.035470843369296

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0004812~aminoacyl-tRNA ligase activity 4 1.515151515 0.042626542 "IARS, LRRC47, DTD1, MARS" 216 47 12983 5.115445232 0.999999991 0.814196696 45.8255119

GOTERM_MF_FAT "GO:0016876~ligase activity, forming aminoacyl-tRNA and related compounds" 4 1.515151515 0.042626542 "IARS, LRRC47, DTD1, MARS" 216 47 12983 5.115445232 0.999999991 0.814196696 45.8255119

GOTERM_MF_FAT "GO:0016875~ligase activity, forming carbon-oxygen bonds" 4 1.515151515 0.042626542 "IARS, LRRC47, DTD1, MARS" 216 47 12983 5.115445232 0.999999991 0.814196696 45.8255119

GOTERM_BP_FAT GO:0006399~tRNA metabolic process 5 1.893939394 0.132279459 "IARS, PUS1, KIAA0391, DTD1, MARS" 225 118 13528 2.547645951 1 0.907092972 90.32629962

GOTERM_BP_FAT GO:0006418~tRNA aminoacylation for protein translation 3 1.136363636 0.176627013 "IARS, DTD1, MARS" 225 46 13528 3.92115942 1 0.929238504 95.92123873

GOTERM_BP_FAT GO:0043039~tRNA aminoacylation 3 1.136363636 0.176627013 "IARS, DTD1, MARS" 225 46 13528 3.92115942 1 0.929238504 95.92123873

GOTERM_BP_FAT GO:0043038~amino acid activation 3 1.136363636 0.176627013 "IARS, DTD1, MARS" 225 46 13528 3.92115942 1 0.929238504 95.92123873

Annotation Cluster 15 Enrichment Score: 1.000055017279598

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0006413~translational initiation 4 1.515151515 0.038201869 "RPS3A, EIF5, EIF3J, EIF2B4" 225 45 13528 5.344395062 1 0.759437499 47.33489032

GOTERM_MF_FAT GO:0003743~translation initiation factor activity 4 1.515151515 0.080197148 "EIF4B, EIF5, EIF3J, EIF2B4" 216 61 12983 3.941408622 1 0.920954637 69.15773141

GOTERM_BP_FAT GO:0006446~regulation of translational initiation 3 1.136363636 0.147384307 "EIF4B, EIF5, EIF2B4" 225 41 13528 4.399349593 1 0.914783533 92.75493711

GOTERM_MF_FAT "GO:0008135~translation factor activity, nucleic acid binding" 4 1.515151515 0.22135287 "EIF4B, EIF5, EIF3J, EIF2B4" 216 98 12983 2.453325775 1 0.980518521 97.04166596

Annotation Cluster 16 Enrichment Score: 0.9962173993216782

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0008652~cellular amino acid biosynthetic process 4 1.515151515 0.052208336 "MTHFD1, SHMT1, PHGDH, ASNS" 225 51 13528 4.715642702 1 0.795216032 58.63423006

GOTERM_BP_FAT GO:0009066~aspartate family amino acid metabolic process 3 1.136363636 0.059347803 "MTHFD1, PHGDH, ASNS" 225 24 13528 7.515555556 1 0.811282567 63.4756816

GOTERM_BP_FAT GO:0016053~organic acid biosynthetic process 6 2.272727273 0.115056673 "MTHFD1, SHMT1, ALOX15B, PHGDH, PRKAA1, ASNS" 225 155 13528 2.327397849 1 0.896207374 86.63072987

GOTERM_BP_FAT GO:0046394~carboxylic acid biosynthetic process 6 2.272727273 0.115056673 "MTHFD1, SHMT1, ALOX15B, PHGDH, PRKAA1, ASNS" 225 155 13528 2.327397849 1 0.896207374 86.63072987

GOTERM_BP_FAT GO:0009309~amine biosynthetic process 4 1.515151515 0.150696864 "MTHFD1, SHMT1, PHGDH, ASNS" 225 81 13528 2.969108368 1 0.915232311 93.20466084

GOTERM_BP_FAT GO:0044271~nitrogen compound biosynthetic process 9 3.409090909 0.170460307 "MTHFD1, SHMT1, GPHN, ATP1B3, PHGDH, ASNS, PPAT, IMPDH2, PRPS1" 225 325 13528 1.664984615 1 0.933191784 95.38814949

Annotation Cluster 17 Enrichment Score: 0.9908277288394629

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0044429~mitochondrial part 19 7.196969697 0.01018076 "MRPS35, GRPEL1, SHMT2, MRPL3, ACADM, ACO2, SLC25A5, SUCLG2, SLC25A6, STOML2, AK2, ALDH3A2, DTD1, DHRS1, CKMT1A, MRPS18B, MRPL47, HADH, HSD17B8" 213 595 12782 1.916266225 0.955889001 0.109163438 12.81061559

GOTERM_CC_FAT GO:0031975~envelope 17 6.439393939 0.054415787 "XPO1, SHMT2, SLC25A5, SLC25A6, STOML2, ITGA2, AK2, LEMD3, ALDH3A2, DHRS1, CKMT1A, NUP62, IPO4, DHCR7, HADH, XPO7, HSD17B8" 213 622 12782 1.640128014 0.999999961 0.354400476 52.74333819

GOTERM_CC_FAT GO:0031967~organelle envelope 16 6.060606061 0.091895275 "XPO1, SHMT2, SLC25A5, SLC25A6, STOML2, AK2, LEMD3, ALDH3A2, DHRS1, CKMT1A, NUP62, IPO4, DHCR7, HADH, XPO7, HSD17B8" 213 620 12782 1.548629411 1 0.465030598 72.51095264

GOTERM_CC_FAT GO:0019866~organelle inner membrane 10 3.787878788 0.098255664 "DHRS1, SHMT2, CKMT1A, SLC25A5, SLC25A6, STOML2, LEMD3, AK2, HADH, ALDH3A2" 213 329 12782 1.823993607 1 0.481686425 74.98122193

GOTERM_CC_FAT GO:0005743~mitochondrial inner membrane 9 3.409090909 0.137095929 "DHRS1, SHMT2, CKMT1A, SLC25A5, SLC25A6, STOML2, AK2, HADH, ALDH3A2" 213 306 12782 1.764982049 1 0.5651827 86.12895858

GOTERM_CC_FAT GO:0031090~organelle membrane 23 8.712121212 0.202409952 "SOAT1, OSTC, BSG, SHMT2, SLC25A5, CYP51A1, CHMP4A, SLC25A6, STOML2, AK2, LEMD3, CORO7, ALDH3A2, FDFT1, DHRS1, CKMT1A, COPG2, NUP62, DHCR7, DAD1, WASL, HADH, SSR3" 213 1096 12782 1.259321134 1 0.671284925 95.16749329

GOTERM_CC_FAT GO:0005740~mitochondrial envelope 10 3.787878788 0.260211004 "DHRS1, SHMT2, CKMT1A, SLC25A5, SLC25A6, STOML2, AK2, HADH, ALDH3A2, HSD17B8" 213 419 12782 1.432205004 1 0.726021242 98.23608616

GOTERM_CC_FAT GO:0031966~mitochondrial membrane 9 3.409090909 0.327823596 "DHRS1, SHMT2, CKMT1A, SLC25A5, SLC25A6, STOML2, AK2, HADH, ALDH3A2" 213 394 12782 1.370772861 1 0.784248229 99.51152197

Annotation Cluster 18 Enrichment Score: 0.9673848509333514

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0008380~RNA splicing 10 3.787878788 0.047065519 "CLNS1A, SRPK2, RPL36A, POLR2E, HNRNPF, SNRPD1, MPHOSPH10, ESRP1, ESRP2, ARL6IP4" 225 284 13528 2.117057903 1 0.789524934 54.78005353

GOTERM_BP_FAT GO:0016071~mRNA metabolic process 11 4.166666667 0.088235031 "CLNS1A, SRPK2, RPL36A, UPF1, POLR2E, WIBG, SERBP1, HNRNPF, SNRPD1, ESRP1, ESRP2" 225 370 13528 1.787483483 1 0.869720306 78.14346488

GOTERM_BP_FAT "GO:0000375~RNA splicing, via transesterification reactions" 6 2.272727273 0.110506507 "CLNS1A, SRPK2, RPL36A, POLR2E, HNRNPF, SNRPD1" 225 153 13528 2.357821351 1 0.892446954 85.45296776

GOTERM_BP_FAT "GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" 6 2.272727273 0.110506507 "CLNS1A, SRPK2, RPL36A, POLR2E, HNRNPF, SNRPD1" 225 153 13528 2.357821351 1 0.892446954 85.45296776

GOTERM_BP_FAT "GO:0000398~nuclear mRNA splicing, via spliceosome" 6 2.272727273 0.110506507 "CLNS1A, SRPK2, RPL36A, POLR2E, HNRNPF, SNRPD1" 225 153 13528 2.357821351 1 0.892446954 85.45296776

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GOTERM_BP_FAT	GO:0006397~mRNA processing	8	3.03030303	0.280016389	"CLNS1A, SRPK2, RPL36A, POLR2E, HNRNPF, SNRPD1, ESRP1, ESRP2"	225	321	13528	1.498428522	1	0.975586531	99.55207467

Annotation Cluster 19	Enrichment Score: 0.934881705740243
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	"GO:0000059~protein import into nucleus, docking"	3	1.136363636	0.031525421	"XPO1, IPO4, XPO7"	225	17	13528	10.61019608	1	0.709697399	40.98253575
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	20	7.575757576	0.052851234	"CHMP2A, XPO1, ARFGAP2, GRPEL1, SRP54, CHMP4A, RAB4A, ITGA2, MYH9, COPG2, KRT18, NUP62, RPL23, IPO4, SYTL4, YIPF5, RPL11, RAB38, XPO7, SSR3"	225	769	13528	1.563704667	1	0.792455939	59.09372869
GOTERM_BP_FAT	GO:0051028~mRNA transport	5	1.893939394	0.056275386	"XPO1, UPF1, NUP62, FMR1, XPO7"	225	87	13528	3.455427842	1	0.800152438	61.46138242
GOTERM_BP_FAT	GO:0006605~protein targeting	8	3.03030303	0.066927812	"XPO1, SRP54, GRPEL1, RPL23, IPO4, RPL11, XPO7, SSR3"	225	215	13528	2.23718863	1	0.837450844	68.03045212
GOTERM_BP_FAT	GO:0051168~nuclear export	4	1.515151515	0.07715018	"XPO1, UPF1, RPS15, XPO7"	225	60	13528	4.008296296	1	0.858848152	73.3327968
GOTERM_BP_FAT	GO:0051236~establishment of RNA localization	5	1.893939394	0.077346702	"XPO1, UPF1, NUP62, FMR1, XPO7"	225	97	13528	3.099198167	1	0.854745201	73.4261294
GOTERM_BP_FAT	GO:0050658~RNA transport	5	1.893939394	0.077346702	"XPO1, UPF1, NUP62, FMR1, XPO7"	225	97	13528	3.099198167	1	0.854745201	73.4261294
GOTERM_BP_FAT	GO:0050657~nucleic acid transport	5	1.893939394	0.077346702	"XPO1, UPF1, NUP62, FMR1, XPO7"	225	97	13528	3.099198167	1	0.854745201	73.4261294
GOTERM_BP_FAT	GO:0015031~protein transport	19	7.196969697	0.081854114	"CHMP2A, XPO1, ARFGAP2, GRPEL1, SRP54, CHMP4A, RAB4A, MYH9, COPG2, KRT18, NUP62, RPL23, IPO4, SYTL4, YIPF5, RPL11, RAB38, XPO7, SSR3"	225	762	13528	1.499165938	1	0.861711028	75.4844242
GOTERM_BP_FAT	GO:0006403~RNA localization	5	1.893939394	0.084340595	"XPO1, UPF1, NUP62, FMR1, XPO7"	225	100	13528	3.006222222	1	0.865712325	76.55479956
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	11	4.166666667	0.092542173	"XPO1, COPG2, SRP54, GRPEL1, KRT18, RPL23, IPO4, SYTL4, RPL11, XPO7, SSR3"	225	374	13528	1.768366013	1	0.874646958	79.78249994
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	6	2.272727273	0.095297911	"XPO1, SRP54, GRPEL1, RPL23, IPO4, XPO7"	225	146	13528	2.47086758	1	0.874785866	80.76982974
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	6	2.272727273	0.117365043	"XPO1, UPF1, RPL23, IPO4, RPS15, XPO7"	225	156	13528	2.312478632	1	0.89805515	87.19339634
GOTERM_BP_FAT	"GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport"	5	1.893939394	0.11799348	"XPO1, UPF1, NUP62, FMR1, XPO7"	225	113	13528	2.660373648	1	0.896328427	87.34268111
GOTERM_BP_FAT	GO:0051169~nuclear transport	6	2.272727273	0.122047432	"XPO1, UPF1, RPL23, IPO4, RPS15, XPO7"	225	158	13528	2.283206751	1	0.895813955	88.26711125
GOTERM_BP_FAT	GO:0046907~intracellular transport	16	6.060606061	0.129934138	"XPO1, GRPEL1, SRP54, UPF1, SLC25A6, MYH9, COPG2, KRT18, RPL23, IPO4, RPS15, SYTL4, PUM1, RPL11, XPO7, SSR3"	225	657	13528	1.464217825	1	0.90552109	89.88675459
GOTERM_CC_FAT	GO:0005643~nuclear pore	4	1.515151515	0.143403996	"XPO1, NUP62, IPO4, XPO7"	213	79	12782	3.03845011	1	0.576149589	87.42752347
GOTERM_BP_FAT	GO:0034613~cellular protein localization	11	4.166666667	0.144201494	"XPO1, COPG2, SRP54, GRPEL1, KRT18, RPL23, IPO4, SYTL4, RPL11, XPO7, SSR3"	225	411	13528	1.609170046	1	0.916919508	92.29661776
GOTERM_BP_FAT	GO:0008104~protein localization	20	7.575757576	0.144368123	"CHMP2A, XPO1, ARFGAP2, GRPEL1, SRP54, CHMP4A, RAB4A, ITGA2, MYH9, COPG2, KRT18, NUP62, RPL23, IPO4, SYTL4, YIPF5, RPL11, RAB38, XPO7, SSR3"	225	882	13528	1.363366087	1	0.914799588	92.3212722
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	11	4.166666667	0.148658241
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"XPO1, COPG2, SRP54, GRPEL1, KRT18, RPL23, IPO4, SYTL4, RPL11, XPO7, SSR3" 225 414 13528 1.597509393 1 0.914423045 92.9311006
GOTERM_BP_FAT GO:0006606~protein import into nucleus 4 1.515151515 0.170683398 "XPO1, RPL23, IPO4, XPO7" 225 86 13528 2.796485788 1 0.931566125 95.40852494
GOTERM_BP_FAT GO:0017038~protein import 5 1.893939394 0.172445872 "XPO1, GRPEL1, RPL23, IPO4, XPO7" 225 131 13528 2.294826124 1 0.929882185 95.56654901
GOTERM_MF_FAT GO:0008565~protein transporter activity 4 1.515151515 0.174790105 "XPO1, RAB4A, IPO4, XPO7" 216 87 12983 2.76351639 1 0.986395644 93.30158242
GOTERM_BP_FAT GO:0051170~nuclear import 4 1.515151515 0.178882777 "XPO1, RPL23, IPO4, XPO7" 225 88 13528 2.732929293 1 0.930034299 96.10134989
GOTERM_BP_FAT GO:0034504~protein localization in nucleus 4 1.515151515 0.204086345 "XPO1, RPL23, IPO4, XPO7" 225 94 13528 2.558486998 1 0.945573104 97.66639079
GOTERM_CC_FAT GO:0046930~pore complex 4 1.515151515 0.20901989 "XPO1, NUP62, IPO4, XPO7" 213 95 12782 2.526711144 1 0.678639858 95.67730494
GOTERM_CC_FAT GO:0005635~nuclear envelope 6 2.272727273 0.252279526 "XPO1, NUP62, DHCR7, IPO4, LEMD3, XPO7" 213 205 12782 1.756372381 1 0.72337528 97.96519443
GOTERM_BP_FAT GO:0043623~cellular protein complex assembly 4 1.515151515 0.505656384 "XPO1, SRP54, IPO4, XPO7" 225 162 13528 1.484554184 1 0.996519676 99.99908162

Annotation Cluster 20 Enrichment Score: 0.8420807051772736
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0004004~ATP-dependent RNA helicase activity 3 1.136363636 0.046633349 "DDX18, UPF1, DDX54" 216 21 12983 8.586640212 0.999999998 0.815729089 48.9300546
GOTERM_MF_FAT GO:0008186~RNA-dependent ATPase activity 3 1.136363636 0.050749992 "DDX18, UPF1, DDX54" 216 22 12983 8.196338384 1 0.817811932 51.94694805
GOTERM_MF_FAT GO:0003724~RNA helicase activity 3 1.136363636 0.08278739 "DDX18, UPF1, DDX54" 216 29 12983 6.217911877 1 0.913572792 70.35762587
GOTERM_MF_FAT GO:0004386~helicase activity 5 1.893939394 0.202452365 "DDX18, UPF1, RUVBL2, RUVBL1, DDX54" 216 140 12983 2.146660053 1 0.984702044 95.85417766
GOTERM_MF_FAT GO:0070035~purine NTP-dependent helicase activity 4 1.515151515 0.22135287 "DDX18, UPF1, RUVBL2, DDX54" 216 98 12983 2.453325775 1 0.980518521 97.04166596
GOTERM_MF_FAT GO:0008026~ATP-dependent helicase activity 4 1.515151515 0.22135287 "DDX18, UPF1, RUVBL2, DDX54" 216 98 12983 2.453325775 1 0.980518521 97.04166596
GOTERM_MF_FAT "GO:0042623~ATPase activity, coupled" 7 2.651515152 0.296325375 "DDX18, UPF1, ATP1B3, RUVBL2, MYH9, DDX54, MYO18A" 216 272 12983 1.546857979 1 0.989177317 99.28819801
GOTERM_MF_FAT GO:0016887~ATPase activity 8 3.03030303 0.31841651 "DDX18, UPF1, ATP1B3, RUVBL2, RUVBL1, MYH9, DDX54, MYO18A" 216 334 12983 1.439676203 1 0.99048419 99.5456034

Annotation Cluster 21 Enrichment Score: 0.826386714371447
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006760~folic acid and derivative metabolic process 3 1.136363636 0.028118405 "MTHFD1, SHMT1, MTHFD1L" 225 16 13528 11.27333333 1 0.677838708 37.47010553
GOTERM_BP_FAT GO:0042558~pteridine and derivative metabolic process 3 1.136363636 0.054986618 "SHMT1, GPHN, MTHFD1L" 225 23 13528 7.842318841 1 0.798979641 60.5857811
GOTERM_BP_FAT GO:0006732~coenzyme metabolic process 6 2.272727273 0.110506507 "MTHFD1, SHMT1, GPHN, ACO2, SUCLG2, MTHFD1L" 225 153 13528 2.357821351 1 0.892446954 85.45296776
GOTERM_BP_FAT GO:0051186~cofactor metabolic process 6 2.272727273 0.222997559 "MTHFD1, SHMT1, GPHN, ACO2, SUCLG2, MTHFD1L" 225 195 13528 1.849982906 1 0.953876523 98.4292641
GOTERM_BP_FAT GO:0006730~one-carbon metabolic process 4 1.515151515 0.283499737 "MTHFD1, SHMT1, SHMT2, MTHFD1L" 225 112 13528 2.147301587 1 0.976175597 99.58644636

GOTERM_BP_FAT	GO:0009108~coenzyme biosynthetic process	3	1.136363636	0.317051542	"MTHFD1, GPHN, MTHFD1L"	225	69	13528	2.61410628	1	0.98085375	99.81222032
GOTERM_BP_FAT	GO:0051188~cofactor biosynthetic process	3	1.136363636	0.479374384	"MTHFD1, GPHN, MTHFD1L"	225	97	13528	1.8595189	1	0.995485743	99.99784541

Annotation Cluster 22	Enrichment Score: 0.8225783727298687
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0008305~integrin complex	3	1.136363636	0.083004994	"ITGA6, ITGA2, MYH9"	213	29	12782	6.207867897	1	0.444183175	68.67856902
GOTERM_CC_FAT	GO:0043235~receptor complex	5	1.893939394	0.126987316	"BCL10, EPS8, ITGA6, ITGA2, MYH9"	213	116	12782	2.586611624	1	0.542290444	83.78675086
GOTERM_BP_FAT	GO:0007229~integrin-mediated signaling pathway	3	1.136363636	0.32314714	"ITGA6, ITGA2, MYH9"	225	70	13528	2.576761905	1	0.980936733	99.83798692

Annotation Cluster 23	Enrichment Score: 0.8143770456967375
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009168~purine ribonucleoside monophosphate biosynthetic process	3	1.136363636	0.035085897	"PPAT, IMPDH2, PRPS1"	225	18	13528	10.02074074	1	0.738617529	44.45461766
GOTERM_BP_FAT	GO:0009127~purine nucleoside monophosphate biosynthetic process	3	1.136363636	0.035085897	"PPAT, IMPDH2, PRPS1"	225	18	13528	10.02074074	1	0.738617529	44.45461766
GOTERM_BP_FAT	GO:0009167~purine ribonucleoside monophosphate metabolic process	3	1.136363636	0.04264351	"PPAT, IMPDH2, PRPS1"	225	20	13528	9.018666667	1	0.771781003	51.19887661
GOTERM_BP_FAT	GO:0009126~purine nucleoside monophosphate metabolic process	3	1.136363636	0.04264351	"PPAT, IMPDH2, PRPS1"	225	20	13528	9.018666667	1	0.771781003	51.19887661
GOTERM_BP_FAT	GO:0009156~ribonucleoside monophosphate biosynthetic process	3	1.136363636	0.054986618	"PPAT, IMPDH2, PRPS1"	225	23	13528	7.842318841	1	0.798979641	60.5857811
GOTERM_BP_FAT	GO:0009161~ribonucleoside monophosphate metabolic process	3	1.136363636	0.063823791	"PPAT, IMPDH2, PRPS1"	225	25	13528	7.214933333	1	0.828459522	66.2338968
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	9	3.409090909	0.170460307	"MTHFD1, SHMT1, GPHN, ATP1B3, PHGDH, ASNS, PPAT, IMPDH2, PRPS1"	225	325	13528	1.664984615	1	0.933191784	95.38814949
GOTERM_BP_FAT	GO:0009124~nucleoside monophosphate biosynthetic process	3	1.136363636	0.200614551	"PPAT, IMPDH2, PRPS1"	225	50	13528	3.607466667	1	0.945456887	97.49304529
GOTERM_BP_FAT	"GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process"	6	2.272727273	0.216797581	"MTHFD1, SHMT1, ATP1B3, PPAT, IMPDH2, PRPS1"	225	193	13528	1.869153713	1	0.953114881	98.20970348
GOTERM_BP_FAT	"GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process"	6	2.272727273	0.216797581	"MTHFD1, SHMT1, ATP1B3, PPAT, IMPDH2, PRPS1"	225	193	13528	1.869153713	1	0.953114881	98.20970348
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	5	1.893939394	0.230276089	"MTHFD1, ATP1B3, PPAT, IMPDH2, PRPS1"	225	148	13528	2.031231231	1	0.957719918	98.65471226
GOTERM_BP_FAT	GO:0009123~nucleoside monophosphate metabolic process	3	1.136363636	0.29869558	"PPAT, IMPDH2, PRPS1"	225	66	13528	2.732929293	1	0.978141846	99.70941598
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	4	1.515151515	0.306117978	"ATP1B3, PPAT, IMPDH2, PRPS1"	225	117	13528	2.055536562	1	0.979910128	99.75610633
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	4	1.515151515	0.337885016	"ATP1B3, PPAT, IMPDH2, PRPS1"	225	124	13528	1.939498208	1	0.983806745	99.88723957
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	5	1.893939394	0.371748062	"MTHFD1, ATP1B3, PPAT, IMPDH2, PRPS1"	225	186	13528	1.616248507	1	0.988742789	99.95248576
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	5	1.893939394	0.371748062	"MTHFD1, ATP1B3, PPAT, IMPDH2, PRPS1"	225	186	13528	1.616248507	1	0.988742789	99.95248576
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	4	1.515151515	0.400986997

"ATP1B3, PPAT, IMPDH2, PRPS1" 225 138 13528 1.74273752 1 0.991338843 99.97831825
GOTERM_BP_FAT GO:0009259~ribonucleotide metabolic process 4 1.515151515 0.440701806 "ATP1B3, PPAT, IMPDH2, PRPS1" 225 147 13528 1.636039305 1 0.994357934 99.99299131

Annotation Cluster 24 Enrichment Score: 0.7861794830826672
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0021782~glial cell development 3 1.136363636 0.068409624 "NF1, PHGDH, EIF2B4" 225 26 13528 6.937435897 1 0.838627872 68.85607227
GOTERM_BP_FAT GO:0010001~glial cell differentiation 3 1.136363636 0.218842567 "NF1, PHGDH, EIF2B4" 225 53 13528 3.40327044 1 0.95207198 98.28512341
GOTERM_BP_FAT GO:0042063~gliogenesis 3 1.136363636 0.292558382 "NF1, PHGDH, EIF2B4" 225 65 13528 2.774974359 1 0.977359739 99.66459814

Annotation Cluster 25 Enrichment Score: 0.7705312764034878
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0000166~nucleotide binding 50 18.93939394 0.022460469 "GRPEL1, GNA15, RPL36A, EIF5, LEMD3, ACSS2, ACSF2, MTHFD1L, MTHFD1, DDX18, KIF14, SRPK2, GBP6, ACADM, SUCLG2, RAB4A, TBRG4, MYH9, MAST4, TAF15, ESRP1, RUVBL2, ESRP2, RUVBL1, MYO18A, PRPS1, SORD, GNAI3, ASNS, IGF2BP3, DTD1, IARS, GPHN, VRK2, HNRNPF, PRKAA1, MARS, CSNK1A1, SRP54, UPF1, AK2, EPHA1, EIF4B, CKMT1A, MAPK13, POLD1, HSPA4L, PHGDH, RAB38, DDX54" 216 2245 12983 1.338674421 0.999935866 0.657925192 27.35939484
GOTERM_MF_FAT GO:0017076~purine nucleotide binding 38 14.39393939 0.178227831 "GRPEL1, GNA15, GNAI3, EIF5, ASNS, ACSS2, ACSF2, MTHFD1L, DTD1, MTHFD1, IARS, VRK2, DDX18, PRKAA1, MARS, CSNK1A1, KIF14, SRPK2, SRP54, GBP6, UPF1, ACADM, SUCLG2, RAB4A, TBRG4, AK2, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, RAB38, DDX54, MYO18A, PRPS1" 216 1918 12983 1.190847913 1 0.984566378 93.68371966
GOTERM_MF_FAT GO:0001883~purine nucleoside binding 32 12.12121212 0.199876788 "GRPEL1, ASNS, ACSS2, ACSF2, MTHFD1L, DTD1, IARS, MTHFD1, VRK2, DDX18, PRKAA1, MARS, CSNK1A1, KIF14, SRPK2, SRP54, UPF1, ACADM, SUCLG2, AK2, TBRG4, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, DDX54, MYO18A, PRPS1" 216 1601 12983 1.201378768 1 0.989033211 95.66176036
GOTERM_MF_FAT GO:0032553~ribonucleotide binding 36 13.63636364 0.207122298 "GNA15, GNAI3, EIF5, ASNS, ACSS2, ACSF2, MTHFD1L, DTD1, MTHFD1, IARS, VRK2, DDX18, PRKAA1, MARS, CSNK1A1, KIF14, SRPK2, SRP54, GBP6, UPF1, SUCLG2, RAB4A, TBRG4, AK2, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, RAB38, DDX54, MYO18A, PRPS1" 216 1836 12983 1.17855846 1 0.983589951 96.18298865
GOTERM_MF_FAT GO:0032555~purine ribonucleotide binding 36 13.63636364 0.207122298 "GNA15, GNAI3, EIF5, ASNS, ACSS2, ACSF2, MTHFD1L, DTD1, MTHFD1, IARS, VRK2, DDX18, PRKAA1, MARS, CSNK1A1, KIF14, SRPK2, SRP54, GBP6, UPF1, SUCLG2, RAB4A, TBRG4, AK2, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, RAB38, DDX54, MYO18A, PRPS1" 216 1836 12983 1.17855846 1 0.983589951 96.18298865
GOTERM_MF_FAT GO:0001882~nucleoside binding 32 12.12121212 0.210948259 "GRPEL1, ASNS, ACSS2, ACSF2, MTHFD1L, DTD1, IARS, MTHFD1, VRK2, DDX18, PRKAA1, MARS, CSNK1A1, KIF14, SRPK2, SRP54, UPF1, ACADM, SUCLG2, AK2, TBRG4, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, DDX54, MYO18A, PRPS1" 216 1612 12983 1.193180774 1 0.982184697 96.43414197
GOTERM_MF_FAT GO:0030554~adenyl nucleotide binding 31 11.74242424 0.234139963 "GRPEL1, ASNS, ACSS2, ACSF2, MTHFD1L, DTD1, IARS, MTHFD1, VRK2, DDX18, PRKAA1, MARS, KIF14, CSNK1A1, SRPK2, UPF1, ACADM, SUCLG2, AK2, TBRG4, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, DDX54, MYO18A, PRPS1" 216 1577 12983 1.181547829 1 0.979946527 97.65653634
GOTERM_MF_FAT GO:0005524~ATP binding 29 10.98484848 0.25020467 "ASNS, ACSS2, MTHFD1L,

ACSF2, DTD1, IARS, MTHFD1, DDX18, VRK2, PRKAA1, MARS, KIF14, CSNK1A1, SRPK2, UPF1, SUCLG2, AK2, TBRG4, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, DDX54, MYO18A, PRPS1" 216 1477 12983 1.180154342 1 0.980702316 98.2609566
GOTERM_MF_FAT GO:0032559~adenyl ribonucleotide binding 29 10.98484848 0.273943623 "ASNS, ACSS2, MTHFD1L, ACSF2, DTD1, IARS, MTHFD1, DDX18, VRK2, PRKAA1, MARS, KIF14, CSNK1A1, SRPK2, UPF1, SUCLG2, AK2, TBRG4, MYH9, EPHA1, MAST4, CKMT1A, MAPK13, HSPA4L, RUVBL2, RUVBL1, DDX54, MYO18A, PRPS1" 216 1497 12983 1.164387417 1 0.985759921 98.89413021

Annotation Cluster 26 Enrichment Score: 0.7398352700315454
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0032268~regulation of cellular protein metabolic process 18 6.818181818 0.002362604 "BCL10, METAP1, UPF1, EIF5, ITGA2, IGF2BP3, RPS4X, PDCD4, EIF4B, PSME1, PSME2, WIBG, PSMB3, KRT7, PUM1, ANAPC7, FAM129A, EIF2B4" 225 474 13528 2.283206751 0.962668039 0.138818717 3.819144747
GOTERM_BP_FAT GO:0032270~positive regulation of cellular protein metabolic process 9 3.409090909 0.040292378 "BCL10, PSME1, PSME2, WIBG, PSMB3, ITGA2, ANAPC7, RPS4X, FAM129A" 225 233 13528 2.322403433 1 0.76048743 49.1879879
GOTERM_BP_FAT GO:0051247~positive regulation of protein metabolic process 9 3.409090909 0.04945272 "BCL10, PSME1, PSME2, WIBG, PSMB3, ITGA2, ANAPC7, RPS4X, FAM129A" 225 243 13528 2.226831276 1 0.798548781 56.60922725
GOTERM_BP_FAT GO:0031398~positive regulation of protein ubiquitination 5 1.893939394 0.050646223 "BCL10, PSME1, PSME2, PSMB3, ANAPC7" 225 84 13528 3.578835979 1 0.79919314 57.49745929
GOTERM_BP_FAT GO:0032269~negative regulation of cellular protein metabolic process 7 2.651515152 0.079064214 "PSME1, PSME2, PSMB3, IGF2BP3, ANAPC7, FAM129A, EIF2B4" 225 180 13528 2.33817284 1 0.856362541 74.22885482
GOTERM_CC_FAT GO:0000502~proteasome complex 4 1.515151515 0.080479411 "PSME1, PSME2, PSMB3, UCHL5" 213 61 12782 3.935041946 1 0.440996341 67.50296164
GOTERM_BP_FAT GO:0031396~regulation of protein ubiquitination 5 1.893939394 0.084340595 "BCL10, PSME1, PSME2, PSMB3, ANAPC7" 225 100 13528 3.006222222 1 0.865712325 76.55479956
GOTERM_BP_FAT GO:0051248~negative regulation of protein metabolic process 7 2.651515152 0.091714551 "PSME1, PSME2, PSMB3, IGF2BP3, ANAPC7, FAM129A, EIF2B4" 225 187 13528 2.250647653 1 0.876222472 79.47680567
GOTERM_BP_FAT GO:0031145~anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process 4 1.515151515 0.092875314 "PSME1, PSME2, PSMB3, ANAPC7" 225 65 13528 3.699965812 1 0.871636643 79.90433909
GOTERM_BP_FAT GO:0051436~negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle 4 1.515151515 0.092875314 "PSME1, PSME2, PSMB3, ANAPC7" 225 65 13528 3.699965812 1 0.871636643 79.90433909
GOTERM_BP_FAT GO:0051444~negative regulation of ubiquitin-protein ligase activity 4 1.515151515 0.09950787 "PSME1, PSME2, PSMB3, ANAPC7" 225 67 13528 3.589519071 1 0.882641095 82.1911462
GOTERM_BP_FAT GO:0051352~negative regulation of ligase activity 4 1.515151515 0.09950787 "PSME1, PSME2, PSMB3, ANAPC7" 225 67 13528 3.589519071 1 0.882641095 82.1911462
GOTERM_BP_FAT GO:0051437~positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle 4 1.515151515 0.102893968 "PSME1, PSME2, PSMB3, ANAPC7" 225 68 13528 3.536732026 1 0.887787485 83.26208735
GOTERM_BP_FAT GO:0006511~ubiquitin-dependent protein catabolic process 8 3.03030303 0.107646865 "ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, USP24, USP15" 225 242 13528 1.98758494 1 0.895815947 84.66363447
GOTERM_BP_FAT GO:0051443~positive regulation of ubiquitin-protein ligase activity 4 1.515151515 0.109801226 "PSME1, PSME2, PSMB3, ANAPC7" 225 70 13528 3.43568254 1 0.897415118 85.26191744
GOTERM_BP_FAT GO:0051439~regulation of ubiquitin-protein ligase activity during mitotic cell cycle 4

1.515151515 0.11332053 "PSME1, PSME2, PSMB3, ANAPC7" 225 71 13528 3.387292645 1 0.895561625 86.1923333

GOTERM_BP_FAT GO:0051351~positive regulation of ligase activity 4 1.515151515 0.120485808 "PSME1, PSME2, PSMB3, ANAPC7" 225 73 13528 3.294490107 1 0.895538441 87.91878796

GOTERM_BP_FAT GO:0031397~negative regulation of protein ubiquitination 4 1.515151515 0.124129897 "PSME1, PSME2, PSMB3, ANAPC7" 225 74 13528 3.24996997 1 0.897142285 88.71694847

GOTERM_BP_FAT GO:0031400~negative regulation of protein modification process 5 1.893939394 0.135219096 "PSME1, PSME2, PSMB3, ANAPC7, FAM129A" 225 119 13528 2.526237162 1 0.909646281 90.85190341

GOTERM_BP_FAT GO:0051438~regulation of ubiquitin-protein ligase activity 4 1.515151515 0.139093763 "PSME1, PSME2, PSMB3, ANAPC7" 225 78 13528 3.083304843 1 0.911140251 91.50378679

GOTERM_BP_FAT GO:0051340~regulation of ligase activity 4 1.515151515 0.150696864 "PSME1, PSME2, PSMB3, ANAPC7" 225 81 13528 2.969108368 1 0.915232311 93.20466084

GOTERM_BP_FAT GO:0043086~negative regulation of catalytic activity 8 3.03030303 0.176527692 "GNAI3, NUP62, PSME1, PSME2, PSMB3, NF1, ANAPC7, PDCD4" 225 277 13528 1.736446049 1 0.930955389 95.91313162

GOTERM_BP_FAT GO:0031401~positive regulation of protein modification process 6 2.272727273 0.201015531 "BCL10, PSME1, PSME2, PSMB3, ANAPC7, FAM129A"225 187 13528 1.92912656 1 0.944328579 97.51366676

GOTERM_BP_FAT GO:0043161~proteasomal ubiquitin-dependent protein catabolic process 4 1.515151515 0.238835446 "PSME1, PSME2, PSMB3, ANAPC7" 225 102 13528 2.357821351 1 0.961999777 98.88090379

GOTERM_BP_FAT GO:0010498~proteasomal protein catabolic process 4 1.515151515 0.238835446 "PSME1, PSME2, PSMB3, ANAPC7" 225 102 13528 2.357821351 1 0.961999777 98.88090379

GOTERM_BP_FAT GO:0044092~negative regulation of molecular function 8 3.03030303 0.317203206 "GNAI3, NUP62, PSME1, PSME2, PSMB3, NF1, ANAPC7, PDCD4" 225 334 13528 1.440106454 1 0.980329477 99.81290563

GOTERM_BP_FAT GO:0031399~regulation of protein modification process 7 2.651515152 0.362092454 "BCL10, PSME1, PSME2, PSMB3, ANAPC7, FAM129A, PDCD4" 225 295 13528 1.426681733 1 0.988478122 99.93892432

GOTERM_BP_FAT GO:0043085~positive regulation of catalytic activity 9 3.409090909 0.634246788 "GNA15, PSME1, PSME2, PSMB3, NF1, ITGA2, PRKAA1, ANAPC7, PPP1CB" 225 520 13528 1.040615385 1 0.998979008 99.99999356

GOTERM_BP_FAT GO:0044093~positive regulation of molecular function 10 3.787878788 0.638972962 "BCL10, GNA15, PSME1, PSME2, PSMB3, NF1, ITGA2, PRKAA1, ANAPC7, PPP1CB" 225 586 13528 1.02601441 1 0.99903351 99.9999948

GOTERM_BP_FAT GO:0010605~negative regulation of macromolecule metabolic process 12 4.545454545 0.676672246 "RPS26, PSME1, PSME2, PSMB3, RPS14, RPS13, AATF, IGF2BP3, ANAPC7, FAM129A, PDCD4, EIF2B4" 225 734 13528 0.982960945 1 0.999227874 99.99999915

GOTERM_BP_FAT GO:0044265~cellular macromolecule catabolic process 11 4.166666667 0.767419715 "ARIH2, UPF1, PSME1, PSME2, WIBG, PSMB3, UCHL5, ANAPC7, MYH9, USP24, USP15" 225 725 13528 0.91223295 1 0.999708927 100

GOTERM_BP_FAT GO:0051603~proteolysis involved in cellular protein catabolic process 9 3.409090909 0.782203393 "ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, MYH9, USP24, USP15" 225 600 13528 0.901866667 1 0.999761481 100

GOTERM_BP_FAT GO:0044257~cellular protein catabolic process 9 3.409090909 0.786777773 "ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, MYH9, USP24, USP15" 225 603 13528 0.897379768 1 0.999773134 100

GOTERM_BP_FAT GO:0030163~protein catabolic process 9 3.409090909 0.814124001 "ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, MYH9, USP24, USP15" 225 622 13528 0.869967846 1 0.99985798 100

GOTERM_BP_FAT GO:0009057~macromolecule catabolic process 11 4.166666667 0.839665848 "ARIH2, UPF1, PSME1, PSME2, WIBG, PSMB3, UCHL5, ANAPC7, MYH9, USP24, USP15" 225 781 13528 0.846823161 1 0.999916351 100

GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	8	3.03030303
0.843354243	"ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, USP24, USP15"	225	574	13528
0.837971351	1	0.999920408	100
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	8	3.03030303
0.843354243	"ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, USP24, USP15"	225	574	13528
0.837971351	1	0.999920408	100
GOTERM_BP_FAT	GO:0006508~proteolysis	14	5.303030303	0.897730958	"METAP1, ACY1, MYH9,
DDI2, LAP3, ARIH2, PSME1, PSME2, PSMB3, UCHL5, KRT1, ANAPC7, USP15, USP24"	225	1054	13528
0.798616909	1	0.999981383	100

Annotation Cluster 27	Enrichment Score: 0.6921054574901059
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_CC_FAT	GO:0000785~chromatin	8	3.03030303	0.048966641	"HMGN2, UPF1, H2AFV,
H2AFY2, H2AFY, HIST1H2AJ, CBX1, HMGA2"	213	200	12782	2.400375587	0.999999776	0.338907437
48.96183891
GOTERM_CC_FAT	GO:0005720~nuclear heterochromatin	3	1.136363636	0.083004994	"H2AFY2, H2AFY,
CBX1"	213	29	12782	6.207867897	1	0.444183175	68.67856902
GOTERM_CC_FAT	GO:0000786~nucleosome	4	1.515151515	0.086740609	"H2AFV, H2AFY2, H2AFY,
HIST1H2AJ"	213	63	12782	3.810119979	1	0.452073809	70.3454315
GOTERM_CC_FAT	GO:0005694~chromosome	12	4.545454545	0.143523075	"NOL6, XPO1, SSRP1,
HMGN2, UPF1, H2AFV, H2AFY2, H2AFY, CLASP2, HIST1H2AJ, CBX1, HMGA2"	213	460	12782
1.565462339	1	0.56992848	87.4509175
GOTERM_CC_FAT	GO:0000792~heterochromatin	3	1.136363636	0.147764962	"H2AFY2, H2AFY,
CBX1"	213	41	12782	4.390930952	1	0.574958047	88.25846385
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	5	1.893939394	0.159657067
"H2AFV, H2AFY2, H2AFY, HIST1H2AJ, CBX1"	225	127	13528	2.367104112	1	0.925713523
94.29332665
GOTERM_BP_FAT	GO:0006334~nucleosome assembly	4	1.515151515	0.162597267	"H2AFV, H2AFY2,
H2AFY, HIST1H2AJ"	225	84	13528	2.863068783	1	0.927487555	94.61327888
GOTERM_CC_FAT	GO:0032993~protein-DNA complex	4	1.515151515	0.171238384	"H2AFV, H2AFY2,
H2AFY, HIST1H2AJ"	213	86	12782	2.791134403	1	0.627563396	91.92344397
GOTERM_BP_FAT	GO:0031497~chromatin assembly	4	1.515151515	0.174769399	"H2AFV, H2AFY2,
H2AFY, HIST1H2AJ"	225	87	13528	2.764342273	1	0.930753631	95.76707991
GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	4	1.515151515	0.191377915	"H2AFV,
H2AFY2, H2AFY, HIST1H2AJ"	225	91	13528	2.642832723	1	0.941523086	96.97111556
GOTERM_CC_FAT	GO:0044427~chromosomal part	10	3.787878788	0.194063954	"XPO1, HMGN2, UPF1,
H2AFV, H2AFY2, H2AFY, CLASP2, HIST1H2AJ, CBX1, HMGA2"	213	386	12782	1.554647401	1
0.666039874	94.44432301
GOTERM_BP_FAT	GO:0034728~nucleosome organization	4	1.515151515	0.199828012	"H2AFV, H2AFY2,
H2AFY, HIST1H2AJ"	225	93	13528	2.585997611	1	0.946244477	97.452128
GOTERM_CC_FAT	GO:0000790~nuclear chromatin	3	1.136363636	0.231628895	"H2AFY2, H2AFY,
CBX1"	213	55	12782	3.273239437	1	0.698635579	97.06890866
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	5	1.893939394	0.282935351	"NOL6, H2AFY2,
H2AFY, CBX1, HMGA2"	213	162	12782	1.852141657	1	0.746098061	98.83866356
GOTERM_BP_FAT	GO:0006325~chromatin organization	9	3.409090909	0.292174273	"HMGN2, H2AFV,
H2AFY2, H2AFY, RUVBL2, HIST1H2AJ, RUVBL1, CBX1, HMGA2"	225	378	13528	1.431534392	1
0.977898307	99.66158762
GOTERM_BP_FAT	GO:0006323~DNA packaging	4	1.515151515	0.306117978	"H2AFV, H2AFY2,
H2AFY, HIST1H2AJ"	225	117	13528	2.055536562	1	0.979910128	99.75610633
GOTERM_BP_FAT	GO:0051276~chromosome organization	9	3.409090909	0.555123399	"HMGN2,
H2AFV, H2AFY2, H2AFY, RUVBL2, HIST1H2AJ, RUVBL1, CBX1, HMGA2"	225	485	13528	1.11571134
1	0.997871084	99.99983811
GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	3	1.136363636	0.603901212	"H2AFY2,

H2AFY, CBX1"	213	122	12782	1.47564073	1	0.948862723	99.99959084
GOTERM_BP_FAT	GO:0016568~chromatin modification	4	1.515151515	0.835697216	"H2AFY2, H2AFY, RUVBL2, RUVBL1"	225	274	13528	0.877729116	1	0.999908373	100

Annotation Cluster 28	Enrichment Score: 0.6619420238819356
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0048770~pigment granule	5	1.893939394	0.060467193	"BSG, ATP1B3, TMEM33, SLC2A1, RAB38"	213	89	12782	3.371314026	0.999999995	0.378482134	56.63797861
GOTERM_CC_FAT	GO:0042470~melanosome	5	1.893939394	0.060467193	"BSG, ATP1B3, TMEM33, SLC2A1, RAB38"	213	89	12782	3.371314026	0.999999995	0.378482134	56.63797861
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	12	4.545454545	0.305285158	"COPG2, BSG, GNAI3, ATP1B3, TMEM33, CHMP4A, RAB4A, SLC2A1, SYTL4, YIPF5, CORO7, RAB38"	213	550	12782	1.309295775	1	0.768183248	99.24014595
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	12	4.545454545	0.342585986	"COPG2, BSG, GNAI3, ATP1B3, TMEM33, CHMP4A, RAB4A, SLC2A1, SYTL4, YIPF5, CORO7, RAB38"	213	568	12782	1.267804007	1	0.793896691	99.63722014
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	12	4.545454545	0.500173818	"COPG2, BSG, GNAI3, ATP1B3, TMEM33, CHMP4A, RAB4A, SLC2A1, SYTL4, YIPF5, CORO7, RAB38"	213	642	12782	1.121670835	1	0.914521265	99.9907707
GOTERM_CC_FAT	GO:0031982~vesicle	12	4.545454545	0.558099982	"COPG2, BSG, GNAI3, ATP1B3, TMEM33, CHMP4A, RAB4A, SLC2A1, SYTL4, YIPF5, CORO7, RAB38"	213	670	12782	1.074795039	1	0.937188016	99.9982278

Annotation Cluster 29	Enrichment Score: 0.6576477269348873
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030057~desmosome	3	1.136363636	0.042765083	"PKP1, PKP3, DSP"	213	20	12782	9.001408451	0.999998376	0.316733602	44.31849484
GOTERM_CC_FAT	GO:0043296~apical junction complex	3	1.136363636	0.491014387	"PKP1, PKP3, DSP"	213	99	12782	1.818466354	1	0.911368041	99.98822877
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	3	1.136363636	0.506842798	"PKP1, PKP3, DSP"	213	102	12782	1.764982049	1	0.913718987	99.99229066

Annotation Cluster 30	Enrichment Score: 0.6466181083736392
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	12	4.545454545	0.044265383	"PSME1, PSME2, PSMB3, POLD1, TBRG4, RPL24, CLASP2, RUVBL1, ANAPC7, HMGA2, PPP1CB, NUDC"	225	370	13528	1.949981982	1	0.776509636	52.54221104
GOTERM_BP_FAT	GO:0022402~cell cycle process	15	5.681818182	0.08685353	"TBRG4, RPL24, MYH9, HMGA2, PPP1CB, PSME1, PSME2, KRT7, POLD1, PSMB3, PHGDH, CLASP2, ANAPC7, RUVBL1, NUDC"	225	565	13528	1.596224189	1	0.869580591	77.59185209
GOTERM_BP_FAT	GO:0007049~cell cycle	18	6.818181818	0.14549177	"UPF1, TBRG4, RPL24, MYH9, HMGA2, PPP1CB, KRT18, PSME1, MAPK13, PSME2, PSMB3, KRT7, POLD1, PHGDH, CLASP2, ANAPC7, RUVBL1, NUDC"	225	776	13528	1.394639175	1	0.914188415	92.48560282
GOTERM_BP_FAT	GO:0022403~cell cycle phase	11	4.166666667	0.148658241	"KRT7, POLD1, TBRG4, RPL24, CLASP2, RUVBL1, ANAPC7, MYH9, HMGA2, PPP1CB, NUDC"	225	414	13528	1.597509393	1	0.914423045	92.9311006
GOTERM_BP_FAT	GO:0051301~cell division	8	3.03030303	0.217325713	"AATF, CLASP2, RUVBL1, ANAPC7, MYH9, HMGA2, PPP1CB, NUDC"	225	295	13528	1.630493409	1	0.952217924	98.22947413
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	6	2.272727273	0.314235681	"RPL24, CLASP2, RUVBL1, ANAPC7, HMGA2, NUDC"	225	224	13528	1.61047619	1	0.980598166	99.79906021

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GOTERM_BP_FAT	GO:0000279~M phase	7	2.651515152	0.461146427	"RPL24, CLASP2, RUVBL1, ANAPC7, MYH9, HMGA2, NUDC"	225	329	13528	1.279243499	1	0.995034616	99.99620337
GOTERM_BP_FAT	GO:0000280~nuclear division	5	1.893939394	0.497371751	"CLASP2, RUVBL1, ANAPC7, HMGA2, NUDC"	225	220	13528	1.366464646	1	0.996148251	99.99879262
GOTERM_BP_FAT	GO:0007067~mitosis	5	1.893939394	0.497371751	"CLASP2, RUVBL1, ANAPC7, HMGA2, NUDC"	225	220	13528	1.366464646	1	0.996148251	99.99879262
GOTERM_BP_FAT	GO:0048285~organelle fission	5	1.893939394	0.527681788	"CLASP2, RUVBL1, ANAPC7, HMGA2, NUDC"	225	229	13528	1.312760796	1	0.997325797	99.99956633

Annotation Cluster 31	Enrichment Score: 0.5691134267905144
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0003924~GTPase activity	7	2.651515152	0.138188194	"SRP54, GBP6, GNA15, GNAI3, RAB4A, EIF5, RAB38"	216	211	12983	1.994053888	1	0.970145079	87.66372851
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	9	3.409090909	0.299727922	"SRP54, GBP6, GNA15, GNAI3, SUCLG2, RAB4A, EIF5, RAB38, PRPS1"	216	382	12983	1.416121291	1	0.988363158	99.33512735
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	9	3.409090909	0.299727922	"SRP54, GBP6, GNA15, GNAI3, SUCLG2, RAB4A, EIF5, RAB38, PRPS1"	216	382	12983	1.416121291	1	0.988363158	99.33512735
GOTERM_MF_FAT	GO:0005525~GTP binding	8	3.03030303	0.426207364	"SRP54, GBP6, GNA15, GNAI3, SUCLG2, RAB4A, EIF5, RAB38"	216	372	12983	1.292612505	1	0.996378987	99.95968893

Annotation Cluster 32	Enrichment Score: 0.5437078888140723
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0051540~metal cluster binding	3	1.136363636	0.200643206	"ELP3, ACO2, PPAT"	216	50	12983	3.606388889	1	0.986783192	95.71986788
GOTERM_MF_FAT	GO:0051536~iron-sulfur cluster binding	3	1.136363636	0.200643206	"ELP3, ACO2, PPAT"	216	50	12983	3.606388889	1	0.986783192	95.71986788
GOTERM_MF_FAT	GO:0005506~iron ion binding	6	2.272727273	0.580801083	"ELP3, ACO2, CYP51A1, ALOX15B, PPP1CB, PPAT"	216	308	12983	1.170905483	1	0.999179628	99.99951354

Annotation Cluster 33	Enrichment Score: 0.5115955033557751
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	4	1.515151515	0.278992283	"MTHFD1, SHMT1, ACADM, DTD1"	225	111	13528	2.166646647	1	0.975931637	99.54146993
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	4	1.515151515	0.278992283	"MTHFD1, SHMT1, ACADM, DTD1"	225	111	13528	2.166646647	1	0.975931637	99.54146993
GOTERM_BP_FAT	GO:0009063~cellular amino acid catabolic process	3	1.136363636	0.310943538	"MTHFD1, SHMT1, DTD1"	225	68	13528	2.65254902	1	0.980195033	99.78257662
GOTERM_BP_FAT	GO:0009310~amine catabolic process	3	1.136363636	0.371323186	"MTHFD1, SHMT1, DTD1"	225	78	13528	2.312478632	1	0.989018583	99.951954

Annotation Cluster 34	Enrichment Score: 0.4130036831644098
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	10	3.787878788	0.297595298	"INF2, EPS8, KRT7, NF1, KRT8, KRT14, MAP7, WASL, MYH9, VASP"	225	436	13528	1.379001019	1	0.978420809	99.70181911
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	6	2.272727273	0.320712093	"INF2, EPS8, NF1, WASL, MYH9, VASP"	225	226	13528	1.596224189	1	0.980791569	99.82812018
GOTERM_BP_FAT	GO:0030029~actin filament-based process	6	2.272727273	0.369909142	"INF2, EPS8,
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NF1, WASL, MYH9, VASP"	225	241	13528	1.496874136	1	0.989125447	99.9501437
GOTERM_MF_FAT	GO:0003779~actin binding	6	2.272727273	0.631173565	"INF2, PDLIM5, SSFA2, WASL, MYH9, VASP"	216	326	12983	1.10625426	1	0.999610301	99.9999197

Annotation Cluster 35	Enrichment Score: 0.3770789961042543
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007163~establishment or maintenance of cell polarity	3	1.136363636	0.194578887	"MAP7, CLASP2, MYH9"	225	49	13528	3.681088435	1	0.942993595	97.16257121
GOTERM_BP_FAT	GO:0031175~neuron projection development	7	2.651515152	0.25106665	"PVRL1, BAIAP2, PHGDH, CDH1, RPL24, VASP, CTNNA2"	225	256	13528	1.644027778	1	0.967763941	99.14286549
GOTERM_BP_FAT	GO:0030030~cell projection organization	9	3.409090909	0.265122229	"ITGA6, PVRL1, BAIAP2, PHGDH, CDH1, RPL24, MYH9, VASP, CTNNA2"	225	368	13528	1.470434783	1	0.970950928	99.37252504
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	6	2.272727273	0.374678013	"PVRL1, BAIAP2, RPL24, MYH9, VASP, CTNNA2"	225	244	13528	1.478469945	1	0.98889783	99.95600502
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	8	3.03030303	0.376851542	"PVRL1, BAIAP2, MAP7, RPL24, CLASP2, MYH9, VASP, CTNNA2"	225	356	13528	1.351111111	1	0.988923597	99.95845591
GOTERM_BP_FAT	GO:0007409~axonogenesis	5	1.893939394	0.398100332	"PVRL1, BAIAP2, RPL24, VASP, CTNNA2"	225	193	13528	1.557628094	1	0.991225721	99.97653259
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	5	1.893939394	0.455204292	"PVRL1, BAIAP2, RPL24, VASP, CTNNA2"	225	209	13528	1.438383838	1	0.995055546	99.99545215
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	5	1.893939394	0.469772211	"PVRL1, BAIAP2, RPL24, VASP, CTNNA2"	225	213	13528	1.411371935	1	0.995379898	99.99708911
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	8	3.03030303	0.488638855	"PVRL1, BAIAP2, MAP7, RPL24, CLASP2, MYH9, VASP, CTNNA2"	225	397	13528	1.211575707	1	0.995846437	99.99839677
GOTERM_BP_FAT	GO:0048666~neuron development	7	2.651515152	0.493135798	"PVRL1, BAIAP2, PHGDH, CDH1, RPL24, VASP, CTNNA2"	225	339	13528	1.241507702	1	0.996008227	99.99861374
GOTERM_BP_FAT	GO:0007411~axon guidance	3	1.136363636	0.531552733	"PVRL1, RPL24, VASP"	225	107	13528	1.685732087	1	0.997407832	99.99962127
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	5	1.893939394	0.581088693	"PVRL1, BAIAP2, RPL24, VASP, CTNNA2"	225	245	13528	1.227029478	1	0.998392632	99.99993985
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	5	1.893939394	0.615812856	"PVRL1, BAIAP2, RPL24, VASP, CTNNA2"	225	256	13528	1.174305556	1	0.998788268	99.99998552
GOTERM_BP_FAT	GO:0030182~neuron differentiation	7	2.651515152	0.736981173	"PVRL1, BAIAP2, PHGDH, CDH1, RPL24, VASP, CTNNA2"	225	438	13528	0.960892948	1	0.99954846	99.99999997

Annotation Cluster 36	Enrichment Score: 0.3640772585754387
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0042803~protein homodimerization activity	8	3.03030303	0.31841651	"SHMT1, GRPEL1, RPL7, PVRL1, ASNS, MYH9, MTHFD1L, PRPS1"	216	334	12983	1.439676203	1	0.99048419	99.5456034
GOTERM_MF_FAT	GO:0046983~protein dimerization activity	11	4.166666667	0.409207796	"SHMT1, GRPEL1, ACY1, RPL7, PVRL1, ITGA2, ASNS, MYH9, MTHFD1L, HSD17B8, PRPS1"	216	542	12983	1.21987324	1	0.996271842	99.93920856
GOTERM_MF_FAT	GO:0042802~identical protein binding	11	4.166666667	0.620624258	"SHMT1, GRPEL1, RPL7, PVRL1, ITGA2, RUVBL2, ASNS, MYH9, MYO18A, MTHFD1L, PRPS1"	216	640	12983	1.03308015	1	0.999578678	99.99988059
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Annotation Cluster 37	Enrichment Score: 0.3430295657933786
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0050803~regulation of synapse structure and activity	3	1.136363636	0.059347803
"PTPRF, PVRL1, CTNNA2"	225	24	13528	7.515555556	1	0.811282567	63.4756816
GOTERM_CC_FAT	GO:0030424~axon	5	1.893939394	0.270895782	"KIAA1598, PVRL1, NF1, ITGA2,
CTNNA2"	213	159	12782	1.887087726	1	0.732869354	98.54844471
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	7	2.651515152	0.310390048	"PTPRF, PVRL1,
CTNND1, CDH1, MYH9, CDH3, CTNNA2"	225	276	13528	1.52489533	1	0.980614703	99.7796836
GOTERM_CC_FAT	GO:0042995~cell projection	13	4.924242424	0.489671492	"KIAA1598, PTPRF,
BAIAP2, NF1, ITGA2, CTNND1, KLC3, MYH9, SLC9A3R1, VASP, CTNNA2, PVRL1, WASL"213	697	12782
1.119256909	1	0.913060599	99.98780584
GOTERM_CC_FAT	GO:0043005~neuron projection	7	2.651515152	0.503759839	"KIAA1598, PTPRF,
PVRL1, NF1, ITGA2, KLC3, CTNNA2"	213	342	12782	1.228262362	1	0.914262111	99.99161939
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	3	1.136363636	0.830505306
"PTPRF, PVRL1, NF1"	225	192	13528	0.939444444	1	0.999902951	100
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	5	1.893939394	0.835461432	"PTPRF,
PVRL1, NF1, EIF2B4, CTNNA2"	225	350	13528	0.858920635	1	0.999910828	100
GOTERM_BP_FAT	GO:0007268~synaptic transmission	3	1.136363636	0.95996699	"PTPRF, PVRL1,
CTNNA2"	225	298	13528	0.605279642	1	0.999999483	100
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	4	1.515151515	0.997621387	"PTPRF, PVRL1,
FGFBP1, CTNNA2"	225	600	13528	0.40082963	1	1	100

Annotation Cluster 38	Enrichment Score: 0.3075240413378717
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0006928~cell motion	11	4.166666667	0.261635168	"SORD, ITGA6, PVRL1,
KRT2, ITGA2, RPL24, CLASP2, WASL, MYH9, VASP, CTNNA2"225	475	13528	1.392355556	1
0.97107211	99.32166993
GOTERM_BP_FAT	GO:0048870~cell motility	6	2.272727273	0.57770693	"SORD, ITGA6, KRT2,
CLASP2, MYH9, CTNNA2"	225	307	13528	1.175070575	1	0.998351342	99.99993133
GOTERM_BP_FAT	GO:0051674~localization of cell	6	2.272727273	0.57770693	"SORD, ITGA6, KRT2,
CLASP2, MYH9, CTNNA2"	225	307	13528	1.175070575	1	0.998351342	99.99993133
GOTERM_BP_FAT	GO:0016477~cell migration	5	1.893939394	0.674205919	"ITGA6, KRT2, CLASP2,
MYH9, CTNNA2"	225	276	13528	1.08921095	1	0.99921575	99.99999904

Annotation Cluster 39	Enrichment Score: 0.2903041271737163
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_MF_FAT	GO:0035257~nuclear hormone receptor binding	3	1.136363636	0.365431592	"NUP62,
DDX54, HSD17B8"	216	77	12983	2.341810967	1	0.992960829	99.83378875
GOTERM_MF_FAT	GO:0051427~hormone receptor binding	3	1.136363636	0.429587343	"NUP62,
DDX54, HSD17B8"	216	88	12983	2.049084596	1	0.996107383	99.96290456
GOTERM_MF_FAT	GO:0008134~transcription factor binding	7	2.651515152	0.857491948	"BCL10,
NUP62, YAP1, DDX54, PPP1R13L, CBFB, HSD17B8"	216	513	12983	0.820166414	1	0.999989877	100

Annotation Cluster 40	Enrichment Score: 0.25495113811226144
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0043407~negative regulation of MAP kinase activity	3	1.136363636	0.119308704
"NUP62, NF1, PDCD4"	225	36	13528	5.01037037	1	0.896072587	87.64983769
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	4	1.515151515	0.414323091	"NUP62,
NF1, PRKAA1, PDCD4"	225	141	13528	1.705657998	1	0.992735201	99.98503338
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GOTERM_BP_FAT	GO:0006469~negative regulation of protein kinase activity	3	1.136363636	0.42381405	"NUP62, NF1, PDCD4"	225	87	13528	2.073256705	1	0.993320874	99.98856288
GOTERM_BP_FAT	GO:0033673~negative regulation of kinase activity	3	1.136363636	0.440812609	"NUP62, NF1, PDCD4"	225	90	13528	2.004148148	1	0.99417899	99.99301414
GOTERM_BP_FAT	GO:0051348~negative regulation of transferase activity	3	1.136363636	0.473964268	"NUP62, NF1, PDCD4"	225	96	13528	1.878888889	1	0.995387644	99.99744567
GOTERM_BP_FAT	GO:0010627~regulation of protein kinase cascade	5	1.893939394	0.593920897	"BCL10, NUP62, NF1, CC2D1A, PDCD4"	225	249	13528	1.207318162	1	0.99853275	99.99996396
GOTERM_BP_FAT	GO:0001666~response to hypoxia	3	1.136363636	0.653898531	"NF1, ITGA2, PRKAA1"	225	134	13528	1.346069652	1	0.999016161	99.9999974
GOTERM_BP_FAT	GO:0070482~response to oxygen levels	3	1.136363636	0.681160816	"NF1, ITGA2, PRKAA1"	225	141	13528	1.279243499	1	0.999245485	99.99999933
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	8	3.03030303	0.69691355	"BCL10, NUP62, NF1, ITGA2, PRKAA1, FAM129A, PDCD4, PPP1CB"	225	485	13528	0.991743414	1	0.999393354	99.99999971
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	8	3.03030303	0.69691355	"BCL10, NUP62, NF1, ITGA2, PRKAA1, FAM129A, PDCD4, PPP1CB"	225	485	13528	0.991743414	1	0.999393354	99.99999971
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	7	2.651515152	0.788469394	"BCL10, NUP62, NF1, PRKAA1, FAM129A, PDCD4, PPP1CB"	225	466	13528	0.903156891	1	0.999768056	100
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	5	1.893939394	0.827135042	"NUP62, NF1, PRKAA1, PDCD4, PPP1CB"	225	345	13528	0.87136876	1	0.999896106	100
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	5	1.893939394	0.846556608	"NUP62, NF1, PRKAA1, PDCD4, PPP1CB"	225	357	13528	0.842079054	1	0.999925814	100
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	5	1.893939394	0.868228695	"NUP62, NF1, PRKAA1, PDCD4, PPP1CB"	225	372	13528	0.808124253	1	0.999950787	100

Annotation Cluster 41	Enrichment Score: 0.24627360904071632
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0021915~neural tube development	3	1.136363636	0.310943538	"BCL10, PHGDH, VASP"	225	68	13528	2.65254902	1	0.980195033	99.78257662
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	6	2.272727273	0.644281929	"BCL10, DAD1, PHGDH, CDH1, MYH9, VASP"	225	331	13528	1.089869084	1	0.999032419	99.99999592
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	6	2.272727273	0.652131579	"BCL10, DAD1, PHGDH, CDH1, MYH9, VASP"	225	334	13528	1.08007984	1	0.999015445	99.99999718
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	3	1.136363636	0.792159886	"DAD1, CDH1, MYH9"	225	176	13528	1.024848485	1	0.999767485	100

Annotation Cluster 42	Enrichment Score: 0.22929872458329784
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	8	3.03030303	0.107646865	"ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, USP24, USP15"	225	242	13528	1.98758494	1	0.895815947	84.66363447
GOTERM_MF_FAT	GO:0004221~ubiquitin thiolesterase activity	3	1.136363636	0.35345684	"UCHL5, USP24, USP15"	216	75	12983	2.404259259	1	0.992384774	99.78377571
GOTERM_MF_FAT	GO:0016790~thiolester hydrolase activity	3	1.136363636	0.506001993	"UCHL5, USP24, USP15"	216	102	12983	1.767837691	1	0.998299824	99.99509786
GOTERM_MF_FAT	GO:0008234~cysteine-type peptidase activity	3	1.136363636	0.681287108	"UCHL5, USP24, USP15"	216	141	12983	1.278861308	1	0.999696321	99.99998971
GOTERM_MF_FAT	"GO:0070011~peptidase activity, acting on L-amino acid peptides"	8	3.03030303	0.809565578	"DDI2, LAP3, METAP1, ACY1, PSMB3, UCHL5, USP24, USP15"	216	549	12983	0.875868583

1	0.999968493	99.99999999
GOTERM_MF_FAT	GO:0008237~metallopeptidase activity	3	1.136363636	0.809927388	"LAP3, METAP1, ACY1"	216	183	12983	0.985352155	1	0.99995812	99.99999999
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	8	3.03030303	0.843354243	"ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, USP24, USP15"	225	574	13528	0.837971351	1	0.999920408	100
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	8	3.03030303	0.843354243	"ARIH2, PSME1, PSME2, PSMB3, UCHL5, ANAPC7, USP24, USP15"	225	574	13528	0.837971351	1	0.999920408	100
GOTERM_MF_FAT	GO:0008233~peptidase activity	8	3.03030303	0.843680261	"DDI2, LAP3, METAP1, ACY1, PSMB3, UCHL5, USP24, USP15"	216	574	12983	0.837720996	1	0.999985023	100
GOTERM_MF_FAT	GO:0004175~endopeptidase activity	3	1.136363636	0.986953069	"DDI2, PSMB3, USP15"	216	375	12983	0.480851852	1	1	100

Annotation Cluster 43	Enrichment Score: 0.20253234965283634
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030099~myeloid cell differentiation	3	1.136363636	0.457533863	"RPS14, MYH9, CBFB"	225	93	13528	1.939498208	1	0.995075499	99.99576192
GOTERM_BP_FAT	GO:0030097~hemopoiesis	5	1.893939394	0.554496784	"EBP, LRRC8A, RPS14, MYH9, CBFB"	225	236	13528	1.273822976	1	0.997919601	99.99983431
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	5	1.893939394	0.627990992	"EBP, LRRC8A, RPS14, MYH9, CBFB"	225	260	13528	1.156239316	1	0.998927998	99.99999148
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	3	1.136363636	0.64166059	"LRRC8A, MYH9, CBFB"	225	131	13528	1.376895674	1	0.999049615	99.9999954
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	4	1.515151515	0.643683558	"LRRC8A, MYH9, CBFB, IMPDH2"	225	199	13528	1.208531547	1	0.999053807	99.99999581
GOTERM_BP_FAT	GO:0002520~immune system development	5	1.893939394	0.674205919	"EBP, LRRC8A, RPS14, MYH9, CBFB"	225	276	13528	1.08921095	1	0.99921575	99.99999904
GOTERM_BP_FAT	GO:0001775~cell activation	5	1.893939394	0.703606329	"LRRC8A, KRT2, MYH9, CBFB, IMPDH2"	225	287	13528	1.047464189	1	0.999435375	99.9999998
GOTERM_BP_FAT	GO:0045321~leukocyte activation	4	1.515151515	0.768007453	"LRRC8A, MYH9, CBFB, IMPDH2"	225	242	13528	0.99379247	1	0.999703493	100

Annotation Cluster 44	Enrichment Score: 0.20140903141121216
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	7	2.651515152	0.535843164	"BCL10, KRT18, NUP62, DAD1, AATF, ASNS, MYO18A"	225	354	13528	1.188901444	1	0.99750547	99.99967451
GOTERM_BP_FAT	GO:0006915~apoptosis	11	4.166666667	0.541833339	"BCL10, CLPTM1L, KRT18, AIMP2, SLC25A6, KRT8, DAD1, TBRG4, AATF, PDCD4, PPP1R13L"	225	602	13528	1.098619417	1	0.997668023	99.99973717
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	7	2.651515152	0.544890538	"BCL10, KRT18, NUP62, DAD1, AATF, ASNS, MYO18A"	225	359	13528	1.172342928	1	0.997709688	99.9997646
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	7	2.651515152	0.551408381	"BCL10, KRT18, NUP62, DAD1, AATF, ASNS, MYO18A"	225	360	13528	1.16908642	1	0.99787983	99.99981436
GOTERM_BP_FAT	GO:0012501~programmed cell death	11	4.166666667	0.560965745	"BCL10, CLPTM1L, KRT18, AIMP2, SLC25A6, KRT8, DAD1, TBRG4, AATF, PDCD4, PPP1R13L"	225	611	13528	1.082436807	1	0.997939812	99.99986977
GOTERM_BP_FAT	GO:0008219~cell death	12	4.545454545	0.650027106	"BCL10, CLPTM1L, KRT18, NUP62, AIMP2, SLC25A6, KRT8, DAD1, TBRG4, AATF, PDCD4, PPP1R13L"	225	719	13528	1.003467779

1 0.999008607 99.99999688

GOTERM_BP_FAT GO:0016265~death 12 4.545454545 0.659037944 "BCL10, CLPTM1L, KRT18, NUP62, AIMP2, SLC25A6, KRT8, DAD1, TBRG4, AATF, PDCD4, PPP1R13L" 225 724 13528 0.996537753 1 0.999077911 99.99999797

GOTERM_BP_FAT GO:0042981~regulation of apoptosis 13 4.924242424 0.686520142 "BCL10, KRT18, NUP62, PTPRF, RPS3A, ALOX15B, NF1, DAD1, CDH1, AATF, RPL11, ASNS, MYO18A" 225 804 13528 0.972161415 1 0.999299131 99.99999949

GOTERM_BP_FAT GO:0043067~regulation of programmed cell death 13 4.924242424 0.699498096 "BCL10, KRT18, NUP62, PTPRF, RPS3A, ALOX15B, NF1, DAD1, CDH1, AATF, RPL11, ASNS, MYO18A" 225 812 13528 0.96258347 1 0.999405357 99.99999975

GOTERM_BP_FAT GO:0010941~regulation of cell death 13 4.924242424 0.704281332 "BCL10, KRT18, NUP62, PTPRF, RPS3A, ALOX15B, NF1, DAD1, CDH1, AATF, RPL11, ASNS, MYO18A" 225 815 13528 0.959040218 1 0.999405411 99.99999981

GOTERM_BP_FAT GO:0006916~anti-apoptosis 3 1.136363636 0.858717634 "DAD1, AATF, MYO18A" 225 206 13528 0.875598706 1 0.999939634 100

Annotation Cluster 45 Enrichment Score: 0.18906511960231515

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0043434~response to peptide hormone stimulus 4 1.515151515 0.47088649 "BSG, BAIAP2, NUDC, EIF2B4" 225 154 13528 1.561673882 1 0.995310695 99.99718819

GOTERM_BP_FAT GO:0032870~cellular response to hormone stimulus 3 1.136363636 0.649856467 "NUP62, BAIAP2, ITGA2" 225 133 13528 1.356190476 1 0.999037627 99.99999686

GOTERM_BP_FAT GO:0009719~response to endogenous stimulus 7 2.651515152 0.665744652 "BSG, NUP62, BAIAP2, ITGA2, ASNS, NUDC, EIF2B4" 225 405 13528 1.039187929 1 0.999134322 99.99999854

GOTERM_BP_FAT GO:0009725~response to hormone stimulus 6 2.272727273 0.731076832 "BSG, NUP62, BAIAP2, ITGA2, NUDC, EIF2B4" 225 367 13528 0.982960945 1 0.999518302 99.99999996

GOTERM_BP_FAT GO:0010033~response to organic substance 11 4.166666667 0.761500195 "BCL10, BSG, NUP62, EPS8, BAIAP2, HSPA4L, ITGA2, CDH1, ASNS, NUDC, EIF2B4" 225 721 13528 0.917293882 1 0.999696223 99.99999999

Annotation Cluster 46 Enrichment Score: 0.182314721137969

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0032318~regulation of Ras GTPase activity 3 1.136363636 0.516274445 "GIT1, ARFGAP2, NF1" 225 104 13528 1.734358974 1 0.996875251 99.99935763

GOTERM_MF_FAT GO:0060589~nucleoside-triphosphatase regulator activity 8 3.03030303 0.529663481 "GIT1, ARFGAP2, GRPEL1, NF1, SYTL4, WASL, SH3BP1, EIF2B4" 216 413 12983 1.164290198 1 0.998742662 99.9975428

GOTERM_BP_FAT GO:0043087~regulation of GTPase activity 3 1.136363636 0.607374732 "GIT1, ARFGAP2, NF1" 225 123 13528 1.466449864 1 0.998680042 99.9999793

GOTERM_BP_FAT GO:0051336~regulation of hydrolase activity 6 2.272727273 0.659871578 "GIT1, ARFGAP2, GNA15, NF1, ITGA2, CDH1" 225 337 13528 1.070464886 1 0.999062401 99.99999805

GOTERM_MF_FAT GO:0030695~GTPase regulator activity 7 2.651515152 0.663668633 "GIT1, ARFGAP2, NF1, SYTL4, WASL, SH3BP1, EIF2B4" 216 404 12983 1.041448937 1 0.99970385 99.99997807

GOTERM_MF_FAT GO:0005083~small GTPase regulator activity 5 1.893939394 0.66884833 "GIT1, ARFGAP2, NF1, SYTL4, WASL" 216 274 12983 1.096833604 1 0.999695942 99.99998237

GOTERM_BP_FAT GO:0046578~regulation of Ras protein signal transduction 4 1.515151515 0.679372197 "GIT1, ARFGAP2, NUP62, NF1" 225 210 13528 1.145227513 1 0.999243471 99.99999926

GOTERM_MF_FAT GO:0005096~GTPase activator activity 4 1.515151515 0.709641802 "GIT1, ARFGAP2, NF1, SH3BP1" 216 220 12983 1.092845118 1 0.999761803 99.99999723

GOTERM_BP_FAT GO:0051056~regulation of small GTPase mediated signal transduction 4 1.515151515

0.791274008 "GIT1, ARFGAP2, NUP62, NF1" 225 252 13528 0.954356261 1 0.999769669 100
GOTERM_MF_FAT GO:0008047~enzyme activator activity 5 1.893939394 0.809660937 "GIT1, BCL10,
ARFGAP2, NF1, SH3BP1" 216 335 12983 0.897111664 1 0.999963499 99.99999999

Annotation Cluster 47 Enrichment Score: 0.17331229802146106
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0010648~negative regulation of cell communication 5 1.893939394 0.59073447
"GNAI3, NUP62, PTPRF, NF1, LEMD3" 225 248 13528 1.21218638 1 0.998499028 99.99995901
GOTERM_BP_FAT GO:0009968~negative regulation of signal transduction 4 1.515151515 0.712359254
"NUP62, PTPRF, NF1, LEMD3" 225 221 13528 1.088225239 1 0.999463494 99.99999988
GOTERM_BP_FAT GO:0008285~negative regulation of cell proliferation 6 2.272727273 0.717747556
"NUP62, PTPRF, KRT5, ALOX15B, NF1, FGFBP1" 225 361 13528 0.999298246 1 0.999488834
99.99999991

Annotation Cluster 48 Enrichment Score: 0.1708980803763945
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0048732~gland development 4 1.515151515 0.387568931 "ALOX15B, NF1,
ITGA2, CDH1" 225 135 13528 1.781465021 1 0.990306974 99.9687768
GOTERM_BP_FAT GO:0030334~regulation of cell migration 3 1.136363636 0.773106962 "ALOX15B,
NF1, ITGA2" 225 169 13528 1.06729783 1 0.999729208 100
GOTERM_BP_FAT GO:0040012~regulation of locomotion 3 1.136363636 0.830505306 "ALOX15B, NF1,
ITGA2" 225 192 13528 0.939444444 1 0.999902951 100
GOTERM_BP_FAT GO:0051270~regulation of cell motion 3 1.136363636 0.832677303 "ALOX15B, NF1,
ITGA2" 225 193 13528 0.934576857 1 0.999906046 100

Annotation Cluster 49 Enrichment Score: 0.17070136353308335
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0043010~camera-type eye development 3 1.136363636 0.531552733 "PVRL1, NF1,
RPL24" 225 107 13528 1.685732087 1 0.997407832 99.99962127
GOTERM_BP_FAT GO:0001654~eye development 3 1.136363636 0.645777187 "PVRL1, NF1, RPL24"
225 132 13528 1.366464646 1 0.999027356 99.9999962
GOTERM_BP_FAT GO:0007423~sensory organ development 3 1.136363636 0.895915097 "PVRL1, NF1,
RPL24" 225 229 13528 0.787656477 1 0.999980491 100

Annotation Cluster 50 Enrichment Score: 0.1655297011387906
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB cascade 3 1.136363636
0.479374384 "BCL10, NUP62, CC2D1A" 225 97 13528 1.8595189 1 0.995485743 99.99784541
GOTERM_BP_FAT GO:0043122~regulation of I-kappaB kinase/NF-kappaB cascade3 1.136363636
0.531552733 "BCL10, NUP62, CC2D1A" 225 107 13528 1.685732087 1 0.997407832 99.99962127
GOTERM_BP_FAT GO:0010627~regulation of protein kinase cascade 5 1.893939394 0.593920897
"BCL10, NUP62, NF1, CC2D1A, PDCD4" 225 249 13528 1.207318162 1 0.99853275 99.99996396
GOTERM_BP_FAT GO:0010740~positive regulation of protein kinase cascade 3 1.136363636 0.767391339
"BCL10, NUP62, CC2D1A" 225 167 13528 1.08007984 1 0.999718136 100
GOTERM_BP_FAT GO:0010647~positive regulation of cell communication 4 1.515151515 0.91282413
"BCL10, NUP62, ITGA2, CC2D1A" 225 329 13528 0.730996285 1 0.999989831 100
GOTERM_BP_FAT GO:0009967~positive regulation of signal transduction 3 1.136363636 0.958226116
"BCL10, NUP62, CC2D1A" 225 295 13528 0.611435028 1 0.999999481 100

Annotation Cluster 51 Enrichment Score: 0.16371037493358656

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0015630~microtubule cytoskeleton 10 3.787878788 0.562531601 "KIF14, KRT18, NUP62, MAP7, KLC3, CLASP2, RUVBL1, CBX1, MYH9, NUDC" 213 549 12782 1.093067207 1 0.937399247 99.99845165
GOTERM_CC_FAT GO:0005813~centrosome 4 1.515151515 0.722079037 "KRT18, NUP62, CLASP2, RUVBL1" 213 224 12782 1.071596244 1 0.979070808 99.99999645
GOTERM_CC_FAT GO:0005815~microtubule organizing center 4 1.515151515 0.79457924 "KRT18, NUP62, CLASP2, RUVBL1" 213 253 12782 0.948765054 1 0.989474776 99.99999994

Annotation Cluster 52 Enrichment Score: 0.16180833383542664
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006974~response to DNA damage stimulus 7 2.651515152 0.58627369 "MRPS35, SSRP1, UPF1, POLD1, RUVBL2, AATF, PPP1CB" 225 373 13528 1.12834078 1 0.998429803 99.999951
GOTERM_BP_FAT GO:0033554~cellular response to stress 10 3.787878788 0.597372006 "MRPS35, SSRP1, UPF1, POLD1, RUVBL2, AATF, ASNS, FAM129A, PPP1CB, EIF2B4" 225 566 13528 1.062269336 1 0.998572784 99.99996868
GOTERM_BP_FAT GO:0006260~DNA replication 4 1.515151515 0.612479519 "SSRP1, UPF1, KRT7, POLD1" 225 190 13528 1.265777778 1 0.998755273 99.99998331
GOTERM_BP_FAT GO:0006259~DNA metabolic process 7 2.651515152 0.848289597 "SSRP1, UPF1, KRT7, POLD1, RUVBL2, RUVBL1, MYO18A" 225 506 13528 0.831761089 1 0.999924941 100
GOTERM_BP_FAT GO:0006281~DNA repair 4 1.515151515 0.853055617 "SSRP1, UPF1, POLD1, RUVBL2" 225 284 13528 0.846823161 1 0.999931488 100

Annotation Cluster 53 Enrichment Score: 0.16091616643531698
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006486~protein amino acid glycosylation 3 1.136363636 0.629085992 "GALNT3, OSTC, DAD1" 225 128 13528 1.409166667 1 0.998913354 99.99999189
GOTERM_BP_FAT GO:0043413~biopolymer glycosylation 3 1.136363636 0.629085992 "GALNT3, OSTC, DAD1" 225 128 13528 1.409166667 1 0.998913354 99.99999189
GOTERM_BP_FAT GO:0070085~glycosylation 3 1.136363636 0.629085992 "GALNT3, OSTC, DAD1" 225 128 13528 1.409166667 1 0.998913354 99.99999189
GOTERM_BP_FAT GO:0009101~glycoprotein biosynthetic process 3 1.136363636 0.740108273 "GALNT3, OSTC, DAD1" 225 158 13528 1.141603376 1 0.999564805 99.99999998
GOTERM_BP_FAT GO:0009100~glycoprotein metabolic process 3 1.136363636 0.851126013 "GALNT3, OSTC, DAD1" 225 202 13528 0.892937294 1 0.999929342 100

Annotation Cluster 54 Enrichment Score: 0.13776164281202655
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0042981~regulation of apoptosis 13 4.924242424 0.686520142 "BCL10, KRT18, NUP62, PTPRF, RPS3A, ALOX15B, NF1, DAD1, CDH1, AATF, RPL11, ASNS, MYO18A" 225 804 13528 0.972161415 1 0.999299131 99.99999949
GOTERM_BP_FAT GO:0043067~regulation of programmed cell death 13 4.924242424 0.699498096 "BCL10, KRT18, NUP62, PTPRF, RPS3A, ALOX15B, NF1, DAD1, CDH1, AATF, RPL11, ASNS, MYO18A" 225 812 13528 0.96258347 1 0.999405357 99.99999975
GOTERM_BP_FAT GO:0010941~regulation of cell death 13 4.924242424 0.704281332 "BCL10, KRT18, NUP62, PTPRF, RPS3A, ALOX15B, NF1, DAD1, CDH1, AATF, RPL11, ASNS, MYO18A" 225 815 13528 0.959040218 1 0.999405411 99.99999981
GOTERM_BP_FAT GO:0043065~positive regulation of apoptosis 7 2.651515152 0.72075784 "BCL10, PTPRF, RPS3A, ALOX15B, NF1, RPL11, AATF" 225 430 13528 0.978770026 1 0.99948828

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99.99999992
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	7	2.651515152	0.726920685	"BCL10, PTPRF, RPS3A, ALOX15B, NF1, RPL11, AATF"	225	433	13528	0.971988709	1	0.99952155	99.99999995
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	7	2.651515152	0.73097653	"BCL10, PTPRF, RPS3A, ALOX15B, NF1, RPL11, AATF"	225	435	13528	0.967519796	1	0.999532499	99.99999996
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	5	1.893939394	0.780188136	"BCL10, RPS3A, ALOX15B, RPL11, AATF"	225	320	13528	0.939444444	1	0.999757237	100
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	5	1.893939394	0.782242996	"BCL10, RPS3A, ALOX15B, RPL11, AATF"	225	321	13528	0.936517826	1	0.999753794	100

Annotation Cluster 55	Enrichment Score: 0.1221976755648286
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	4	1.515151515	0.715225149	"SORD, PRKAA1, PPP1CB, PRPS1"	225	222	13528	1.083323323	1	0.999478128	99.9999999
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	3	1.136363636	0.723805344	"SORD, PRKAA1, PPP1CB"	225	153	13528	1.178910675	1	0.999504723	99.99999994
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	3	1.136363636	0.830505306	"SORD, PRKAA1, PPP1CB"	225	192	13528	0.939444444	1	0.999902951	100

Annotation Cluster 56	Enrichment Score: 0.0917046544852383
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001568~blood vessel development	4	1.515151515	0.775199337	"DHCR7, NF1, NAA15, MYH9"	225	245	13528	0.981623583	1	0.999734174	100
GOTERM_BP_FAT	GO:0001944~vasculature development	4	1.515151515	0.789037322	"DHCR7, NF1, NAA15, MYH9"	225	251	13528	0.958158477	1	0.999763871	100
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	3	1.136363636	0.867710989	"NF1, NAA15, MYH9"	225	211	13528	0.854849921	1	0.999951558	100

Annotation Cluster 57	Enrichment Score: 0.09148857882738487
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0044459~plasma membrane part	37	14.01515152	0.568111002	"CHMP2A, ARFGAP2, GNA15, ATP1B3, CDH1, CDH3, ALDH3A2, GPHN, COL17A1, PVRL1, SDPR, SLC2A1, FLRT3, GIT1, BCL10, EBP, PTPRF, SLC25A5, TRPA1, CNPY2, ITGA2, MYH9, SLC9A3R1, CTNNA1, EPHA1, VASP, CTNNA2, COPG2, PKP1, EPS8, ITGA6, TACSTD2, PKP3, CNTN1, DSP, MAP7, RAB38"	213	2203	12782	1.007874452	1	0.938172828	99.99869626
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	14	5.303030303	0.963647526	"FLRT3, EBP, PTPRF, ATP1B3, SLC25A5, TRPA1, ITGA2, CNPY2, MYH9, EPHA1, COL17A1, EPS8, ITGA6, TACSTD2"	213	1188	12782	0.70718136	1	0.999869769	100
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	14	5.303030303	0.970918672	"FLRT3, EBP, PTPRF, ATP1B3, SLC25A5, TRPA1, ITGA2, CNPY2, MYH9, EPHA1, COL17A1, EPS8, ITGA6, TACSTD2"	213	1215	12782	0.691466218	1	0.999915814	100

Annotation Cluster 58	Enrichment Score: 0.08185993442990334
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	15	5.681818182	0.560699251	"SOAT1, BCL10, NAA15, ITGA2, RPS4X, CBFB, NUP62, PSME1, PSME2, WIBG, PSMB3, AATF, YAP1, ANAPC7, FAM129A"	225	857	13528	1.05235317	1	0.997998759	99.99986846
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	12	4.545454545	0.605088651
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"SOAT1, BCL10, NUP62, WIBG, NAA15, ITGA2, AATF, PRKAA1, YAP1, RPS4X, FAM129A, CBFB" 225 695 13528 1.038119904 1 0.998670261 99.99997722
GOTERM_BP_FAT GO:0010557~positive regulation of macromolecule biosynthetic process 11 4.166666667 0.64744683 "SOAT1, BCL10, NUP62, WIBG, NAA15, ITGA2, AATF, YAP1, RPS4X, FAM129A, CBFB" 225 654 13528 1.011267414 1 0.999025641 99.99999648
GOTERM_MF_FAT GO:0003713~transcription coactivator activity 4 1.515151515 0.691846218 "BCL10, YAP1, CBFB, HSD17B8" 216 214 12983 1.123485635 1 0.999725758 99.9999936
GOTERM_BP_FAT GO:0031328~positive regulation of cellular biosynthetic process 11 4.166666667 0.703643108 "SOAT1, BCL10, NUP62, WIBG, NAA15, ITGA2, AATF, YAP1, RPS4X, FAM129A, CBFB" 225 685 13528 0.965502028 1 0.999416905 99.9999998
GOTERM_MF_FAT GO:0003712~transcription cofactor activity 6 2.272727273 0.722487699 "BCL10, YAP1, DDX54, PPP1R13L, CBFB, HSD17B8" 216 363 12983 0.993495562 1 0.999739939 99.99999853
GOTERM_MF_FAT GO:0008134~transcription factor binding 7 2.651515152 0.857491948 "BCL10, NUP62, YAP1, DDX54, PPP1R13L, CBFB, HSD17B8" 216 513 12983 0.820166414 1 0.999989877 100
GOTERM_MF_FAT GO:0016563~transcription activator activity 5 1.893939394 0.911932668 "BCL10, CDH1, YAP1, CBFB, HSD17B8" 216 410 12983 0.733005872 1 0.999999129 100
GOTERM_BP_FAT "GO:0045893~positive regulation of transcription, DNA-dependent" 5 1.893939394 0.958434706 "BCL10, NAA15, AATF, YAP1, CBFB" 225 477 13528 0.630235267 1 0.999999443 100
GOTERM_BP_FAT GO:0045941~positive regulation of transcription 6 2.272727273 0.959720291 "BCL10, NUP62, NAA15, AATF, YAP1, CBFB" 225 564 13528 0.639621749 1 0.999999493 100
GOTERM_BP_FAT GO:0051254~positive regulation of RNA metabolic process 5 1.893939394 0.960327484 "BCL10, NAA15, AATF, YAP1, CBFB" 225 481 13528 0.624994225 1 0.99999948 100
GOTERM_BP_FAT GO:0010628~positive regulation of gene expression 6 2.272727273 0.966581411 "BCL10, NUP62, NAA15, AATF, YAP1, CBFB" 225 581 13528 0.620906483 1 0.999999708 100
GOTERM_BP_FAT "GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process" 6 2.272727273 0.979428915 "BCL10, NUP62, NAA15, AATF, YAP1, CBFB" 225 624 13528 0.578119658 1 0.999999948 100
GOTERM_BP_FAT GO:0051173~positive regulation of nitrogen compound metabolic process 6 2.272727273 0.983681805 "BCL10, NUP62, NAA15, AATF, YAP1, CBFB" 225 644 13528 0.560165631 1 0.999999979 100
GOTERM_BP_FAT GO:0045944~positive regulation of transcription from RNA polymerase II promoter 3 1.136363636 0.986111359 "AATF, YAP1, CBFB" 225 371 13528 0.486181491 1 0.999999988 100
GOTERM_BP_FAT "GO:0006355~regulation of transcription, DNA-dependent" 13 4.924242424 0.99996348 "ELP3, BCL10, HMGN2, RPS14, NAA15, CNOT2, AATF, TFCP2, RUVBL1, ARNTL2, YAP1, HMGA2, CBFB" 225 1773 13528 0.44084477 1 1 100

Annotation Cluster 59 Enrichment Score: 0.08161564055639785
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0050954~sensory perception of mechanical stimulus 3 1.136363636 0.511109185 "ALDH7A1, TRPA1, ITGA2" 225 103 13528 1.751197411 1 0.996709459 99.9992349
GOTERM_BP_FAT GO:0050953~sensory perception of light stimulus 3 1.136363636 0.876178099 "WDR36, TACSTD2, CDH3" 225 216 13528 0.835061728 1 0.999961018 100
GOTERM_BP_FAT GO:0007601~visual perception 3 1.136363636 0.876178099 "WDR36, TACSTD2, CDH3" 225 216 13528 0.835061728 1 0.999961018 100
GOTERM_BP_FAT GO:0007600~sensory perception 6 2.272727273 0.997891185 "ALDH7A1, WDR36, TACSTD2, TRPA1, ITGA2, CDH3" 225 810 13528 0.445366255 1 1 100
GOTERM_BP_FAT GO:0050890~cognition 7 2.651515152 0.998022055 "ALDH7A1, WDR36, TACSTD2, NF1, TRPA1, ITGA2, CDH3" 225 909 13528 0.463004523 1 1 100

Annotation Cluster 60 Enrichment Score: 0.05977389191451709
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0004672~protein kinase activity 10 3.787878788 0.678504765 "CSNK1A1,

SRPK2, MAST4, VRK2, POLR2E, NUP62, MAPK13, TBRG4, PRKAA1, EPHA1"	216	606	12983
0.99185613	1	0.999718171	99.99998837
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	7	2.651515152	0.721038009
"CSNK1A1, SRPK2, MAST4, VRK2, NUP62, MAPK13, PRKAA1"	216	430	12983	0.978477606	1
0.999763017	99.99999842
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	11	4.166666667	0.965271383	"CSNK1A1,
SRPK2, MAST4, VRK2, PTPRF, MAPK13, PRKAA1, PPP1CB, EPHA1, PPA2, PPA1"	225	973	13528
0.679721366	1	0.999999669	100
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	11	4.166666667	0.965271383	"CSNK1A1,
SRPK2, MAST4, VRK2, PTPRF, MAPK13, PRKAA1, PPP1CB, EPHA1, PPA2, PPA1"	225	973	13528
0.679721366	1	0.999999669	100
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	7	2.651515152	0.967733602
"CSNK1A1, SRPK2, MAST4, VRK2, MAPK13, PRKAA1, EPHA1"	225	667	13528	0.630991171	1
0.999999711	100
GOTERM_BP_FAT	GO:0016310~phosphorylation	7	2.651515152	0.992638017	"CSNK1A1, SRPK2,
MAST4, VRK2, MAPK13, PRKAA1, EPHA1"	225	800	13528	0.526088889	1	0.999999999	100

Annotation Cluster 61	Enrichment Score: 0.05555082082162576
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	"GO:0006351~transcription, DNA-dependent"	4	1.515151515	0.865775049
"POLR2E, TRIM29, NPM3, CBFB"	225	292	13528	0.823622527	1	0.999949763	100
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	4	1.515151515	0.871765725	"POLR2E,
TRIM29, NPM3, CBFB"	225	296	13528	0.812492492	1	0.999955376	100
GOTERM_BP_FAT	GO:0006366~transcription from RNA polymerase II promoter	3	1.136363636
0.90269842	"POLR2E, TRIM29, CBFB"	225	234	13528	0.770826211	1	0.999984753	100

Annotation Cluster 62	Enrichment Score: 0.05302548022942436
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	12	4.545454545
0.676672246	"RPS26, PSME1, PSME2, PSMB3, RPS14, RPS13, AATF, IGF2BP3, ANAPC7, FAM129A, PDCD4,
EIF2B4"	225	734	13528	0.982960945	1	0.999227874	99.99999915
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	6	2.272727273
0.958383949	"RPS14, AATF, PRKAA1, IGF2BP3, PDCD4, EIF2B4"	225	561	13528	0.643042187	1
0.999999465	100
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	6	2.272727273	0.963498167
"RPS14, AATF, PRKAA1, IGF2BP3, PDCD4, EIF2B4"	225	573	13528	0.629575334	1	0.999999607	100
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	5	1.893939394
0.982040254	"RPS14, AATF, IGF2BP3, PDCD4, EIF2B4"	225	547	13528	0.549583587	1	0.999999969
100

Annotation Cluster 63	Enrichment Score: 0.01738312216827029
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	4	1.515151515	0.949698565	"GNA15, NF1,
SLC9A3R1, EIF2B4"	225	374	13528	0.643042187	1	0.999998944	100
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	5	1.893939394	0.952793687	"CLNS1A, GNA15,
NF1, SLC9A3R1, EIF2B4"	225	466	13528	0.645112065	1	0.999999174	100
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	4	1.515151515	0.953340216	"GNA15, NF1,
SLC9A3R1, EIF2B4"	225	380	13528	0.632888889	1	0.99999918	100
GOTERM_BP_FAT	GO:0050801~ion homeostasis	4	1.515151515	0.967728885	"GNA15, NF1,
SLC9A3R1, EIF2B4"	225	409	13528	0.588014127	1	0.999999724	100
GOTERM_BP_FAT	GO:0042592~homeostatic process	8	3.03030303	0.968768645	"CLNS1A, SOAT1,

GNA15, RPS14, NF1, ITGA2, SLC9A3R1, EIF2B4" 225 751 13528 0.640473443 1 0.999999737 100
GOTERM_BP_FAT GO:0048878~chemical homeostasis 5 1.893939394 0.972511896 "SOAT1, GNA15,
NF1, SLC9A3R1, EIF2B4" 225 512 13528 0.587152778 1 0.999999834 100

Annotation Cluster 64 Enrichment Score: 0.015242502007302008
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0005578~proteinaceous extracellular matrix 4 1.515151515 0.903762586 "FLRT3,
COL17A1, LGALS3BP, COL7A1" 213 320 12782 0.750117371 1 0.998482635 100
GOTERM_CC_FAT GO:0031012~extracellular matrix 4 1.515151515 0.928742728 "FLRT3, COL17A1,
LGALS3BP, COL7A1" 213 345 12782 0.69576104 1 0.999248363 100
GOTERM_CC_FAT GO:0044421~extracellular region part 6 2.272727273 0.999727818 "FLRT3,
COL17A1, LGALS3BP, SORD, COL7A1, FGFBP1" 213 960 12782 0.375058685 1 0.999999999 100
GOTERM_CC_FAT GO:0005615~extracellular space 3 1.136363636 0.999898527 "LGALS3BP, SORD,
FGFBP1"213 685 12782 0.262814845 1 1 100
GOTERM_CC_FAT GO:0005576~extracellular region 7 2.651515152 1 "FLRT3, COL17A1, LGALS3BP,
SORD, COL7A1, PVRL1, FGFBP1" 213 2010 12782 0.208987924 1 1 100

Annotation Cluster 65 Enrichment Score: 0.0048671261503787575
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0006357~regulation of transcription from RNA polymerase II promoter 8
3.03030303 0.960357578 "ELP3, RPS14, CNOT2, AATF, TFCP2, RUVBL1, YAP1, CBFB" 225 727 13528
0.661616995 1 0.999999457 100
GOTERM_BP_FAT GO:0051252~regulation of RNA metabolic process 19 7.196969697 0.995702665
"ELP3, BCL10, HMGN2, NAA15, CNOT2, TFCP2, HMGA2, CBFB, RPS26, SERBP1, RPS14, HNRNPF, ESRP1,
RPS13, AATF, ESRP2, YAP1, RUVBL1, ARNTL2" 225 1813 13528 0.630096219 1 1 100
GOTERM_BP_FAT "GO:0006355~regulation of transcription, DNA-dependent" 13 4.924242424
0.99996348 "ELP3, BCL10, HMGN2, RPS14, NAA15, CNOT2, AATF, TFCP2, RUVBL1, ARNTL2, YAP1,
HMGA2, CBFB" 225 1773 13528 0.44084477 1 1 100
GOTERM_BP_FAT GO:0045449~regulation of transcription 23 8.712121212 0.999964815 "ELP3, SSRP1,
BCL10, HMGN2, TADA2B, NAA15, CTNND1, CNOT2, TFCP2, HMGA2, PPP1R13L, PDCD4, CBFB, NUP62,
RPS14, AATF, RUVBL2, WASL, ARNTL2, CC2D1A, YAP1, RUVBL1, DDX54" 225 2601 13528
0.531665599 1 1 100

Annotation Cluster 66 Enrichment Score: 0.004582679427708416
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0051253~negative regulation of RNA metabolic process 3 1.136363636
0.98414091 "RPS26, RPS14, RPS13" 225 362 13528 0.498268877 1 0.99999998 100
GOTERM_BP_FAT "GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid
metabolic process" 4 1.515151515 0.991820074 "RPS26, RPS14, RPS13, PDCD4" 225 512 13528
0.469722222 1 0.999999999 100
GOTERM_BP_FAT GO:0051172~negative regulation of nitrogen compound metabolic process 4
1.515151515 0.992571458 "RPS26, RPS14, RPS13, PDCD4" 225 519 13528 0.463386855 1 0.999999999
100

Annotation Cluster 67 Enrichment Score: 7.059053231878534E-6
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0046914~transition metal ion binding 26 9.848484848 0.999945529 "GALNT3,
ARFGAP2, METAP1, SORD, ZC3HAV1, CYP51A1, PDLIM5, PPAT, IARS, RPS27, ARIH2, LUC7L2, GIT1, ELP3,
UPF1, ACY1, ZC3H15, ACO2, TRIM29, TADA2B, PPP1CB, LAP3, TAF15, ALOX15B, POLD1, SYTL4" 216 2785
12983 0.561137709 1 1 100

GOTERM_MF_FAT	GO:0008270~zinc ion binding	18	6.818181818	0.999991107	"GIT1, ARFGAP2, ACY1, ZC3H15, SORD, UPF1, ZC3HAV1, PDLIM5, TRIM29, TADA2B, LAP3, IARS, ARIH2, RPS27, TAF15, POLD1, SYTL4, LUC7L2"	216	2311	12983	0.468159527	1	1	100

GOTERM_MF_FAT	GO:0046872~metal ion binding	42	15.90909091	0.999992479	"GALNT3, ARFGAP2, METAP1, SORD, ATP1B3, ZC3HAV1, CYP51A1, PDLIM5, CDH1, CDH3, PPAT, FDFT1, EFHD2, IARS, GPHN, PLCB3, ARIH2, RPS27, LUC7L2, PRKAA1, IMPDH2, GIT1, SRPK2, ELP3, ZC3H15, ACY1, UPF1, ACO2, TRIM29, TADA2B, ITGA2, PPP1CB, PPA2, PPA1, LAP3, MAST4, TAF15, ITGA6, ALOX15B, POLD1, SYTL4, PRPS1"	216	4140	12983	0.609775899	1	1	100

GOTERM_MF_FAT	GO:0043167~ion binding	43	16.28787879	0.999994578	"GALNT3, ARFGAP2, METAP1, SORD, ATP1B3, ZC3HAV1, CYP51A1, PDLIM5, CDH1, CDH3, PPAT, FDFT1, EFHD2, IARS, GPHN, PLCB3, ARIH2, RPS27, LUC7L2, PRKAA1, IMPDH2, GIT1, SRPK2, ELP3, ZC3H15, ACY1, UPF1, PTPRF, ACO2, TRIM29, TADA2B, ITGA2, PPP1CB, PPA2, PPA1, LAP3, MAST4, TAF15, ITGA6, ALOX15B, POLD1, SYTL4, PRPS1"	216	4241	12983	0.609426716	1	1	100

GOTERM_MF_FAT	GO:0043169~cation binding	42	15.90909091	0.999995038	"GALNT3, ARFGAP2, METAP1, SORD, ATP1B3, ZC3HAV1, CYP51A1, PDLIM5, CDH1, CDH3, PPAT, FDFT1, EFHD2, IARS, GPHN, PLCB3, ARIH2, RPS27, LUC7L2, PRKAA1, IMPDH2, GIT1, SRPK2, ELP3, ZC3H15, ACY1, UPF1, ACO2, TRIM29, TADA2B, ITGA2, PPP1CB, PPA2, PPA1, LAP3, MAST4, TAF15, ITGA6, ALOX15B, POLD1, SYTL4, PRPS1"	216	4179	12983	0.604085241	1	1	100

Annotation Cluster 1 Enrichment Score: 11.397715250494837

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0006412~translation 42 13.5483871 9.71E-22 "TUFM, NACA, RPS2, KARS, RPS3, RPS25, EIF3B, EIF3G, RPL32, GFM1, EIF3E, EIF3F, EIF3K, RPL10, MRPL37, FAU, EIF3L, RPL12, EIF3M, RPS23, RPS24, RPL36AL, EGFR, RPSA, AIMP1, AARS, DARS2, RPS5, RPS7, EIF4G1, RPS18, RPS19, RPL18A, RPL21, EEF1A1P5, EIF4A1, FARSB, RPS12, RPS4Y1, CARS2, FARSA, EIF2AK2" 264 331 13528 6.502059874 1.66E-18 1.66E-18 1.64E-18

GOTERM_CC_FAT GO:0030529~ribonucleoprotein complex 42 13.5483871 1.20E-15 "PTGES3, SRP14, RBM4, BOP1, RPS2, NUFIP2, STAU1, RPS3, PRMT3, RPS25, TRIM5, MOV10, RPL32, PLRG1, RBM8A, FRG1, PCBP1, PCBP2, RPL10, MRPL37, FAU, RPL12, DDX20, RPS23, HSPA8, RPS24, GEMIN5, RPL36AL, RPSA, RPS5, RPS7, PPIE, PA2G4, RPS18, PPIH, AQR, RPS19, RPL18A, RPL21, RPS12, RPS4Y1, UTP20" 236 515 12782 4.417014974 3.64E-13 1.82E-13 1.63E-12

GOTERM_BP_FAT GO:0006414~translational elongation 21 6.774193548 4.73E-15 "TUFM, RPSA, RPS2, RPS5, RPS3, RPS7, RPS25, RPS18, RPS19, RPL32, RPL18A, GFM1, EEF1A1P5, RPL21, RPS12, RPS4Y1, RPL10, FAU, RPL12, RPS23, RPS24" 264 101 13528 10.65436544 8.19E-12 4.09E-12 8.06E-12

GOTERM_CC_FAT GO:0044445~cytosolic part 22 7.096774194 5.27E-13 "RPSA, IDE, CCT2, CCT6A, CCT3, RPS2, RPS5, RPS3, RPS7, RPS25, RPS18, CCT4, RPS19, RPL32, RPL18A, RPL21, RPS12, RPS4Y1, RPL10, FAU, RPS23, RPS24" 236 152 12782 7.839094558 1.57E-10 5.24E-11 7.04E-10

GOTERM_CC_FAT GO:0022626~cytosolic ribosome 17 5.483870968 1.19E-12 "RPSA, RPS2, RPS5, RPS3, RPS7, RPS25, RPS18, RPS19, RPL32, RPL18A, RPL21, RPS12, RPS4Y1, FAU, RPL10, RPS23, RPS24" 236 81 12782 11.36712701 3.54E-10 8.86E-11 1.59E-09

GOTERM_CC_FAT GO:0022627~cytosolic small ribosomal subunit 13 4.193548387 3.99E-12 "RPSA, RPS2, RPS5, RPS7, RPS3, RPS25, RPS18, RPS19, RPS12, RPS4Y1, FAU, RPS23, RPS24" 236 40 12782 17.60233051 1.19E-09 2.38E-10 5.33E-09

GOTERM_CC_FAT GO:0005840~ribosome 22 7.096774194 4.28E-10 "RPSA, RPS2, RPS5, NUFIP2, RPS3, RPS7, PRMT3, RPS25, RPS18, RPS19, RPL32, RPL18A, RPL21, RPS12, RPS4Y1, RPL10, MRPL37, FAU, RPL12, RPS23, RPL36AL, RPS24" 236 215 12782 5.542057548 1.27E-07 1.82E-08 5.71E-07

GOTERM_CC_FAT GO:0015935~small ribosomal subunit 13 4.193548387 1.31E-09 "RPSA, RPS2, RPS5, RPS7, RPS3, RPS25, RPS18, RPS19, RPS12, RPS4Y1, FAU, RPS23, RPS24" 236 63 12782 11.17608286 3.91E-07 4.35E-08 1.75E-06

GOTERM_CC_FAT GO:0033279~ribosomal subunit 17 5.483870968 1.54E-09 "RPSA, RPS2, RPS5, RPS3, RPS7, RPS25, RPS18, RPS19, RPL32, RPL18A, RPL21, RPS12, RPS4Y1, FAU, RPL10, RPS23, RPS24" 236 128 12782 7.193260064 4.58E-07 4.58E-08 2.05E-06

GOTERM_MF_FAT GO:0003735~structural constituent of ribosome 19 6.129032258 3.79E-09 "RPSA, RPS2, RPS5, RPS3, RPS7, RPS18, RPS19, RPL32, RPL18A, RPL21, RPS12, RPS4Y1, RPL10, FAU, MRPL37, RPL12, RPS23, RPL36AL, RPS24" 251 168 12983 5.849862455 1.83E-06 1.83E-07 5.43E-06

GOTERM_MF_FAT GO:0005198~structural molecule activity 28 9.032258065 9.34E-05 "RPS2, RPS3, KRT9, TUBGCP3, EIF3B, RPL32, PLS1, MRPL37, FAU, RPL10, KRT3, AGRN, RPL12, RPS23, RPL36AL, RPS24, RPSA, G3BP2, RPS5, RPS7, KRT19, RPS18, SMTN, RPS19, RPL18A, RPL21, RPS12, RPS4Y1" 251 634 12983 2.284389257 0.044103307 0.003463636 0.133736015

Annotation Cluster 2 Enrichment Score: 9.739936947184216

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0000166~nucleotide binding 88 28.38709677 1.31E-11 "HSP90AB1, KIF23, LDHB, ATL2, RBM4, IDE, CAD, CCT2, CCT3, HSPH1, KDM1A, ANKRD17, ATAD3B, SLK, NUBP2, RBM8A, NT5C3, DDX21, DDX20, MX1, TOP2B, TOP2A, EGFR, IKBKAP, CDK1, HSP90AA1, PDXK, STK24, RAN, G3BP1, AARS, G3BP2, MINK1, CCT6A, PBK, DARS2, STK3, RFC4, RAB18, TIAL1, EEF1A1P5, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, TUFM, IFIH1, GNAI1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, DDX47, MOV10, CHD7, EIF3B, EIF3G, GFM1, RAC1, SPATA5, HSPA8, ERCC6L, RPS24, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, IDH3B, YTHDC2, DRG1, SMC2, EPHA2, IDH3A, GART, SMC4, TP53RK, PPIE, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 2245 12983 2.027531744 6.34E-09 3.17E-09

1.88E-08

GOTERM_MF_FAT GO:0005524~ATP binding 66 21.29032258 7.60E-11 "HSP90AB1, KIF23, IDE, CAD, CCT2, CCT3, HSPH1, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, TOP2A, EGFR, CDK1, IKBKAP, HSP90AA1, PDXK, STK24, G3BP1, AARS, MINK1, CCT6A, DARS2, PBK, STK3, RFC4, RAB18, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, IFIH1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, MOV10, DDX47, CHD7, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1477 12983 2.311345006 3.67E-08 1.22E-08 1.09E-07

GOTERM_MF_FAT GO:0032559~adenyl ribonucleotide binding 66 21.29032258 1.35E-10 "HSP90AB1, KIF23, IDE, CAD, CCT2, CCT3, HSPH1, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, TOP2A, EGFR, CDK1, IKBKAP, HSP90AA1, PDXK, STK24, G3BP1, AARS, MINK1, CCT6A, DARS2, PBK, STK3, RFC4, RAB18, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, IFIH1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, MOV10, DDX47, CHD7, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1497 12983 2.280465313 6.54E-08 1.63E-08 1.94E-07

GOTERM_MF_FAT GO:0032553~ribonucleotide binding 75 24.19354839 1.50E-10 "HSP90AB1, KIF23, ATL2, IDE, CAD, CCT2, CCT3, HSPH1, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, MX1, TOP2A, EGFR, IKBKAP, CDK1, HSP90AA1, PDXK, RAN, STK24, G3BP1, AARS, MINK1, CCT6A, PBK, DARS2, STK3, RFC4, RAB18, EEF1A1P5, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, TUFM, IFIH1, GNAI1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, DDX47, MOV10, CHD7, GFM1, RAC1, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, DRG1, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1836 12983 2.112953415 7.24E-08 1.45E-08 2.15E-07

GOTERM_MF_FAT GO:0032555~purine ribonucleotide binding 75 24.19354839 1.50E-10 "HSP90AB1, KIF23, ATL2, IDE, CAD, CCT2, CCT3, HSPH1, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, MX1, TOP2A, EGFR, IKBKAP, CDK1, HSP90AA1, PDXK, RAN, STK24, G3BP1, AARS, MINK1, CCT6A, PBK, DARS2, STK3, RFC4, RAB18, EEF1A1P5, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, TUFM, IFIH1, GNAI1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, DDX47, MOV10, CHD7, GFM1, RAC1, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, DRG1, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1836 12983 2.112953415 7.24E-08 1.45E-08 2.15E-07

GOTERM_MF_FAT GO:0001882~nucleoside binding 68 21.93548387 4.25E-10 "HSP90AB1, KIF23, IDE, CAD, CCT2, CCT3, HSPH1, KDM1A, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, TOP2A, EGFR, CDK1, IKBKAP, HSP90AA1, PDXK, STK24, G3BP1, AARS, MINK1, CCT6A, DARS2, PBK, STK3, RFC4, RAB18, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, IFIH1, FKBP4, OAS3, OAS2, BMS1, POLR2B, KARS, SRC, MOV10, DDX47, CHD7, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1612 12983 2.181952092 2.05E-07 3.42E-08 6.09E-07

GOTERM_MF_FAT GO:0017076~purine nucleotide binding 76 24.51612903 4.44E-10 "HSP90AB1, KIF23, ATL2, IDE, CAD, CCT2, CCT3, HSPH1, KDM1A, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, MX1, TOP2A, EGFR, IKBKAP, CDK1, HSP90AA1, PDXK, RAN, STK24, G3BP1, AARS, MINK1, CCT6A, PBK, DARS2, STK3, RFC4, RAB18, EEF1A1P5, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, TUFM, IFIH1, GNAI1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, DDX47, MOV10, CHD7, GFM1, RAC1, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, DRG1, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1918 12983 2.049586846 2.14E-07 3.06E-08 6.36E-07

GOTERM_MF_FAT GO:0030554~adenyl nucleotide binding 67 21.61290323 4.50E-10 "HSP90AB1, KIF23, IDE, CAD, CCT2, CCT3, HSPH1, KDM1A, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, TOP2A, EGFR, CDK1, IKBKAP, HSP90AA1, PDXK, STK24, G3BP1, AARS, MINK1, CCT6A, DARS2, PBK, STK3, RFC4, RAB18, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, IFIH1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, MOV10, DDX47, CHD7, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1577 12983 2.19757874 2.17E-07 2.72E-08 6.45E-07

GOTERM_MF_FAT GO:0001883~purine nucleoside binding 67 21.61290323 8.51E-10 "HSP90AB1,

KIF23, IDE, CAD, CCT2, CCT3, HSPH1, KDM1A, ANKRD17, ATAD3B, SLK, NUBP2, DDX21, DDX20, TOP2B, TOP2A, EGFR, CDK1, IKBKAP, HSP90AA1, PDXK, STK24, G3BP1, AARS, MINK1, CCT6A, DARS2, PBK, STK3, RFC4, RAB18, EIF4A1, FARSB, FARSA, EIF2AK2, PRPS2, IFIH1, FKBP4, OAS3, OAS2, BMS1, KARS, SRC, MOV10, DDX47, CHD7, SPATA5, HSPA8, ERCC6L, TRIP13, CSNK1A1, MSH6, MAP2K1, MAT2A, YTHDC2, SMC2, EPHA2, GART, SMC4, TP53RK, CCT4, PSMC4, CCT8, UBA3, HSPA14, CARS2, PAICS" 251 1601 12983 2.164635649 4.11E-07 4.57E-08 1.22E-06

Annotation Cluster 3 Enrichment Score: 7.613058307393814
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0070013~intracellular organelle lumen 69 22.25806452 1.21E-09 "KIF23, PTGS2, LYAR, RBM4, IDE, CAD, CCT2, MIPEP, RPS2, KDM1A, GTF2E1, PLRG1, RBM8A, MRPL37, DDX21, DDX20, TOP2B, TOP2A, ANAPC1, CDK1, IKBKAP, SP100, STK24, RAN, EXOSC3, POLR1C, DARS2, IFI16, MRTO4, PA2G4, RPS19, RFC4, RCC2, KPNA2, RNF20, TUFM, FKBP4, NOC3L, ERI1, BOP1, BMS1, POLR2B, KARS, RPS25, DDX47, SET, FRG1, EIF3E, EIF3L, WDHD1, NSUN2, GEMIN5, PDCD11, UAP1, SUB1, SMAD3, IDH3B, STAT1, PWP2, IDH3A, RPS7, CTR9, PPIH, GTF2F1, POLDIP2, RRS1, CARS2, UTP20, ADAR" 236 1779 12782 2.100680253 3.59E-07 4.49E-08 1.61E-06
GOTERM_CC_FAT GO:0031974~membrane-enclosed lumen 70 22.58064516 2.85E-09 "KIF23, PTGS2, LYAR, RBM4, IDE, CAD, CCT2, MIPEP, RPS2, KDM1A, GTF2E1, PLRG1, RBM8A, MRPL37, DDX21, DDX20, TOP2B, TOP2A, ANAPC1, IKBKAP, CDK1, SP100, STK24, RAN, EXOSC3, POLR1C, DARS2, IFI16, MRTO4, PA2G4, RPS19, RFC4, RCC2, KPNA2, RNF20, TUFM, FKBP4, NOC3L, PNPT1, ERI1, BOP1, BMS1, POLR2B, KARS, RPS25, DDX47, SET, FRG1, EIF3E, EIF3L, WDHD1, NSUN2, GEMIN5, PDCD11, UAP1, SUB1, SMAD3, IDH3B, STAT1, PWP2, IDH3A, RPS7, CTR9, PPIH, GTF2F1, POLDIP2, RRS1, CARS2, UTP20, ADAR" 236 1856 12782 2.042710769 8.50E-07 7.73E-08 3.81E-06
GOTERM_CC_FAT GO:0043233~organelle lumen 69 22.25806452 3.17E-09 "KIF23, PTGS2, LYAR, RBM4, IDE, CAD, CCT2, MIPEP, RPS2, KDM1A, GTF2E1, PLRG1, RBM8A, MRPL37, DDX21, DDX20, TOP2B, TOP2A, ANAPC1, CDK1, IKBKAP, SP100, STK24, RAN, EXOSC3, POLR1C, DARS2, IFI16, MRTO4, PA2G4, RPS19, RFC4, RCC2, KPNA2, RNF20, TUFM, FKBP4, NOC3L, ERI1, BOP1, BMS1, POLR2B, KARS, RPS25, DDX47, SET, FRG1, EIF3E, EIF3L, WDHD1, NSUN2, GEMIN5, PDCD11, UAP1, SUB1, SMAD3, IDH3B, STAT1, PWP2, IDH3A, RPS7, CTR9, PPIH, GTF2F1, POLDIP2, RRS1, CARS2, UTP20, ADAR" 236 1820 12782 2.053357236 9.45E-07 7.88E-08 4.23E-06
GOTERM_CC_FAT GO:0031981~nuclear lumen 58 18.70967742 1.56E-08 "KIF23, LYAR, RBM4, CAD, CCT2, RPS2, KDM1A, GTF2E1, PLRG1, RBM8A, DDX21, DDX20, TOP2B, TOP2A, ANAPC1, CDK1, IKBKAP, SP100, RAN, STK24, EXOSC3, POLR1C, IFI16, MRTO4, PA2G4, RFC4, RPS19, RCC2, KPNA2, RNF20, FKBP4, NOC3L, ERI1, BOP1, BMS1, POLR2B, RPS25, DDX47, SET, FRG1, EIF3E, EIF3L, WDHD1, NSUN2, GEMIN5, PDCD11, UAP1, SUB1, SMAD3, STAT1, PWP2, RPS7, CTR9, PPIH, GTF2F1, RRS1, UTP20, ADAR" 236 1450 12782 2.166440678 4.64E-06 3.57E-07 2.08E-05
GOTERM_CC_FAT GO:0005730~nucleolus 37 11.93548387 1.70E-08 "FKBP4, LYAR, RBM4, NOC3L, ERI1, CCT2, BOP1, RPS2, BMS1, RPS25, DDX47, FRG1, EIF3L, DDX21, TOP2B, WDHD1, NSUN2, TOP2A, IKBKAP, PDCD11, UAP1, SP100, SUB1, EXOSC3, POLR1C, IFI16, STAT1, PWP2, MRTO4, RPS7, PA2G4, RPS19, RCC2, RRS1, UTP20, RNF20, ADAR" 236 698 12782 2.870999466 5.06E-06 3.61E-07 2.26E-05
GOTERM_CC_FAT GO:0005654~nucleoplasm 34 10.96774194 7.27E-05 "KIF23, RBM4, NOC3L, BOP1, RPS2, POLR2B, GTF2E1, KDM1A, SET, PLRG1, FRG1, RBM8A, EIF3E, EIF3L, DDX20, WDHD1, TOP2B, TOP2A, GEMIN5, ANAPC1, CDK1, IKBKAP, SP100, SUB1, STK24, RAN, SMAD3, POLR1C, IFI16, CTR9, PPIH, RFC4, GTF2F1, KPNA2" 236 882 12782 2.087839656 0.021436151 0.001353411 0.097023766

Annotation Cluster 4 Enrichment Score: 4.8129354527998265
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005852~eukaryotic translation initiation factor 3 complex 7 2.258064516 1.58E-07 "EIF3B, EIF3G, EIF3E, EIF3F, EIF3K, EIF3L, EIF3M" 236 15 12782 25.27514124 4.70E-05 3.14E-06 2.11E-04
GOTERM_BP_FAT GO:0006413~translational initiation 9 2.903225806 2.12E-06 "EIF3B, EIF3G,

EIF3E, EIF3F, EIF3K, EIF3L, RPS5, EIF3M, RPS3" 264 45 13528 10.24848485 0.003631628 5.20E-04 0.003581848
GOTERM_MF_FAT "GO:0008135~translation factor activity, nucleic acid binding" 12 3.870967742 2.77E-06 "TUFM, EIF4G1, EIF3B, EIF3G, GFM1, EIF3E, EEF1A1P5, EIF4A1, EIF3F, EIF3K, EIF3L, EIF3M" 251 98 12983 6.333685666 0.001337351 1.22E-04 0.00397043
GOTERM_MF_FAT GO:0003743~translation initiation factor activity 9 2.903225806 2.06E-05 "EIF4G1, EIF3B, EIF3G, EIF3E, EIF4A1, EIF3F, EIF3K, EIF3L, EIF3M" 251 61 12983 7.631572072 0.009906245 8.29E-04 0.029533509
GOTERM_BP_FAT GO:0006446~regulation of translational initiation 4 1.290322581 0.045045963 "EIF4G1, EIF3B, EIF3E, EIF3K" 264 41 13528 4.999260902 1 0.557328257 54.07870036

Annotation Cluster 5 Enrichment Score: 4.329935970662983
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0022613~ribonucleoprotein complex biogenesis 16 5.161290323 2.32E-06 "PDCD11, EXOSC3, ERI1, BOP1, BMS1, MRTO4, RPS7, PA2G4, RPS19, FRG1, PRMT5, WDR77, RRS1, DDX20, GEMIN5, RPS24" 264 180 13528 4.554882155 0.003975917 4.98E-04 0.003922089
GOTERM_BP_FAT GO:0034660~ncRNA metabolic process 18 5.806451613 2.58E-06 "PDCD11, ELAC2, AIMP1, AARS, EXOSC3, ERI1, DARS2, BOP1, KARS, RPS7, PA2G4, RPS19, FRG1, FARSB, CARS2, FARSA, NSUN2, RPS24" 264 230 13528 4.01027668 0.004419242 4.92E-04 0.004360372
GOTERM_BP_FAT GO:0042254~ribosome biogenesis 12 3.870967742 2.54E-05 "PDCD11, PA2G4, RPS19, FRG1, RRS1, EXOSC3, ERI1, BOP1, BMS1, MRTO4, RPS7, RPS24" 264 122 13528 5.04023845 0.042630246 0.003106991 0.042881935
GOTERM_BP_FAT GO:0034470~ncRNA processing 13 4.193548387 2.96E-04 "PDCD11, ELAC2, AARS, SMAD3, ERI1, EXOSC3, BOP1, RPS7, PA2G4, RPS19, FRG1, NSUN2, RPS24" 264 187 13528 3.562307568 0.398627504 0.026410286 0.499416496
GOTERM_BP_FAT GO:0006364~rRNA processing 9 2.903225806 4.17E-04 "PDCD11, PA2G4, RPS19, FRG1, EXOSC3, ERI1, BOP1, RPS7, RPS24" 264 92 13528 5.01284585 0.511116288 0.032005298 0.702075413
GOTERM_BP_FAT GO:0016072~rRNA metabolic process 9 2.903225806 5.56E-04 "PDCD11, PA2G4, RPS19, FRG1, EXOSC3, ERI1, BOP1, RPS7, RPS24" 264 96 13528 4.803977273 0.614746387 0.032356454 0.934690659

Annotation Cluster 6 Enrichment Score: 4.251495103296995
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0065003~macromolecular complex assembly 32 10.32258065 5.63E-06 "ATL2, FKBP4, IDE, TP63, HPRT1, BMS1, POLR2B, SRC, GTF2E1, TRIM5, RANBP9, SET, CSE1L, PRMT5, RAC1, WDR77, AGRN, DDX20, GEMIN5, IKBKAP, HSP90AA1, MAP2K1, SMAD3, TRIM22, TUBGCP2, PPIH, PSMG1, IPO7, HIST2H2BE, RRM2, GTF2F1, SURF1" 264 665 13528 2.465800866 0.0096106 8.78E-04 0.009507122
GOTERM_BP_FAT GO:0006461~protein complex assembly 26 8.387096774 1.77E-05 "ATL2, FKBP4, IDE, TP63, HPRT1, SRC, POLR2B, GTF2E1, TRIM5, RANBP9, CSE1L, RAC1, AGRN, GEMIN5, IKBKAP, HSP90AA1, MAP2K1, SMAD3, TRIM22, TUBGCP2, PPIH, PSMG1, IPO7, GTF2F1, RRM2, SURF1" 264 505 13528 2.638223822 0.029939861 0.002529895 0.029922137
GOTERM_BP_FAT GO:0070271~protein complex biogenesis 26 8.387096774 1.77E-05 "ATL2, FKBP4, IDE, TP63, HPRT1, SRC, POLR2B, GTF2E1, TRIM5, RANBP9, CSE1L, RAC1, AGRN, GEMIN5, IKBKAP, HSP90AA1, MAP2K1, SMAD3, TRIM22, TUBGCP2, PPIH, PSMG1, IPO7, GTF2F1, RRM2, SURF1" 264 505 13528 2.638223822 0.029939861 0.002529895 0.029922137
GOTERM_BP_FAT GO:0043933~macromolecular complex subunit organization 32 10.32258065 2.05E-05 "ATL2, FKBP4, IDE, TP63, HPRT1, BMS1, POLR2B, SRC, GTF2E1, TRIM5, RANBP9, SET, CSE1L, PRMT5, RAC1, WDR77, AGRN, DDX20, GEMIN5, IKBKAP, HSP90AA1, MAP2K1, SMAD3, TRIM22, TUBGCP2, PPIH, PSMG1, IPO7, HIST2H2BE, RRM2, GTF2F1, SURF1" 264 710 13528 2.309517712 0.034507981 0.002697696 0.034567795

GOTERM_BP_FAT GO:0034622~cellular macromolecular complex assembly 17 5.483870968 5.00E-04 "HSP90AA1, FKBP4, SMAD3, BMS1, SRC, PSMG1, SET, CSE1L, IPO7, HIST2H2BE, PRMT5, WDR77, RAC1, DDX20, AGRN, SURF1, GEMIN5" 264 318 13528 2.739374881 0.57560402 0.032427514 0.840269132
GOTERM_BP_FAT GO:0034621~cellular macromolecular complex subunit organization 17 5.483870968 0.001711631 "HSP90AA1, FKBP4, SMAD3, BMS1, SRC, PSMG1, SET, CSE1L, IPO7, HIST2H2BE, PRMT5, WDR77, RAC1, DDX20, AGRN, SURF1, GEMIN5" 264 357 13528 2.44011544 0.947026428 0.069150448 2.851046225

Annotation Cluster 7 Enrichment Score: 3.43436592037114
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0000278~mitotic cell cycle 24 7.741935484 9.27E-07 "EGFR, ANAPC1, KIF23, PPP6C, CDK1, MAP2K1, RAN, PBK, ITGB1, SMC2, SMC4, PSMB6, PSMC4, RCC2, PSMA5, NCAPG, CDC123, UBA3, RRS1, PSME3, PSMD5, KPNA2, PSMD7, ERCC6L" 264 370 13528 3.323832924 0.001589291 3.98E-04 0.001565919
GOTERM_BP_FAT GO:0022402~cell cycle process 30 9.677419355 1.78E-06 "KIF23, PPP6C, ITGB1, PSMB6, MACF1, NCAPG, CDC123, RANBP1, PSMD5, PSMD7, TRIP13, ERCC6L, ANAPC1, EGFR, MSH6, CDK1, MAP2K1, RAN, SMAD3, PBK, SMC2, SMC4, PA2G4, RCC2, PSMC4, PSMA5, RRS1, PSME3, KPNA2, ARAP1" 264 565 13528 2.720836685 0.003047975 6.10E-04 0.003005325
GOTERM_BP_FAT GO:0007049~cell cycle 36 11.61290323 2.78E-06 "KIF23, PPP6C, RABGAP1, ITGB1, PSMB6, MACF1, NCAPG, CDC123, RANBP1, PSMD5, PSMD7, TRIP13, ERCC6L, ANAPC1, GPS1, EGFR, MSH6, CDK1, MAP2K1, RAN, SMAD3, PCNP, PBK, SMC2, SMC4, NAE1, PA2G4, RCC2, PSMC4, PSMA5, UBA3, RRS1, PSME3, KPNA2, MCTS1, ARAP1" 264 776 13528 2.377225867 0.004752668 4.76E-04 0.004690134
GOTERM_BP_FAT GO:0022403~cell cycle phase 20 6.451612903 4.81E-04 "EGFR, ANAPC1, KIF23, MSH6, CDK1, PPP6C, MAP2K1, RAN, PBK, ITGB1, SMC2, SMC4, RCC2, NCAPG, CDC123, RRS1, RANBP1, KPNA2, TRIP13, ERCC6L" 264 414 13528 2.475479432 0.562144852 0.033825801 0.809784872
GOTERM_BP_FAT GO:0000279~M phase 16 5.161290323 0.001986857 "ANAPC1, KIF23, CDK1, MSH6, MAP2K1, RAN, PBK, SMC2, SMC4, RCC2, NCAPG, RRS1, RANBP1, KPNA2, TRIP13, ERCC6L" 264 329 13528 2.49203279 0.966986826 0.076257624 3.302286963
GOTERM_BP_FAT GO:0007067~mitosis 12 3.870967742 0.003871586 "KIF23, ANAPC1, CDK1, MAP2K1, RCC2, NCAPG, RAN, RRS1, PBK, SMC2, ERCC6L, SMC4" 264 220 13528 2.795041322 0.998709411 0.122294579 6.339780179
GOTERM_BP_FAT GO:0000280~nuclear division 12 3.870967742 0.003871586 "KIF23, ANAPC1, CDK1, MAP2K1, RCC2, NCAPG, RAN, RRS1, PBK, SMC2, ERCC6L, SMC4" 264 220 13528 2.795041322 0.998709411 0.122294579 6.339780179
GOTERM_BP_FAT GO:0000087~M phase of mitotic cell cycle 12 3.870967742 0.0044319 "KIF23, ANAPC1, CDK1, MAP2K1, RCC2, NCAPG, RAN, RRS1, PBK, SMC2, ERCC6L, SMC4" 264 224 13528 2.74512987 0.99950828 0.133876971 7.225343767
GOTERM_BP_FAT GO:0048285~organelle fission 12 3.870967742 0.005239186 "KIF23, ANAPC1, CDK1, MAP2K1, RCC2, NCAPG, RAN, RRS1, PBK, SMC2, ERCC6L, SMC4" 264 229 13528 2.685192537 0.999877674 0.151085506 8.487402124
GOTERM_BP_FAT GO:0051301~cell division 12 3.870967742 0.029689324 "KIF23, ANAPC1, CDK1, NOTCH1, ATAD3B, RCC2, NCAPG, RAN, CDC123, SMC2, ERCC6L, SMC4" 264 295 13528 2.084437596 1 0.451751822 39.8832242

Annotation Cluster 8 Enrichment Score: 3.3947829223108625
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0034660~ncRNA metabolic process 18 5.806451613 2.58E-06 "PDCD11, ELAC2, AIMP1, AARS, EXOSC3, ERI1, DARS2, BOP1, KARS, RPS7, PA2G4, RPS19, FRG1, FARSB, CARS2, FARSA, NSUN2, RPS24" 264 230 13528 4.01027668 0.004419242 4.92E-04 0.004360372
GOTERM_BP_FAT GO:0006418~tRNA aminoacylation for protein translation 7 2.258064516 2.49E-04 "AIMP1, AARS, FARSB, CARS2, DARS2, FARSA, KARS" 264 46 13528 7.797760211 0.347330508

0.02478672	0.419197586
GOTERM_BP_FAT	GO:0043039~tRNA aminoacylation	7	2.258064516	2.49E-04	"AIMP1, AARS, FARSB, CARS2, DARS2, FARSA, KARS"	264	46	13528	7.797760211	0.347330508	0.02478672	0.419197586
GOTERM_BP_FAT	GO:0043038~amino acid activation	7	2.258064516	2.49E-04	"AIMP1, AARS, FARSB, CARS2, DARS2, FARSA, KARS"	264	46	13528	7.797760211	0.347330508	0.02478672	0.419197586
GOTERM_MF_FAT	GO:0004812~aminoacyl-tRNA ligase activity	6	1.935483871	0.002017082	"AARS, FARSB, CARS2, DARS2, FARSA, KARS"	251	47	12983	6.603204204	0.622896058	0.052738122	2.852010797
GOTERM_MF_FAT	"GO:0016875~ligase activity, forming carbon-oxygen bonds"	6	1.935483871	0.002017082	"AARS, FARSB, CARS2, DARS2, FARSA, KARS"	251	47	12983	6.603204204	0.622896058	0.052738122	2.852010797
GOTERM_MF_FAT	"GO:0016876~ligase activity, forming aminoacyl-tRNA and related compounds"	6	1.935483871	0.002017082	"AARS, FARSB, CARS2, DARS2, FARSA, KARS"	251	47	12983	6.603204204	0.622896058	0.052738122	2.852010797
GOTERM_BP_FAT	GO:0006399~tRNA metabolic process	9	2.903225806	0.002128902	"ELAC2, AIMP1, AARS, FARSB, CARS2, DARS2, FARSA, NSUN2, KARS"	264	118	13528	3.908320493	0.974137436	0.079710739	3.534402464

Annotation Cluster 9	Enrichment Score: 2.8008789781266716
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006396~RNA processing	30	9.677419355	9.25E-07	"ELAC2, PNPT1, RBM4, ERI1, BOP1, POLR2B, MOV10, PLRG1, RBM8A, FRG1, PRMT5, PCBP1, PCBP2, WDR77, DDX20, NSUN2, GEMIN5, RPS24, PDCD11, AARS, SMAD3, EXOSC3, RPS7, PPIE, PA2G4, PPIH, AQR, RPS19, GTF2F1, ADAR"	264	547	13528	2.810370617	0.001585561	5.29E-04	0.001562241
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	20	6.451612903	1.16E-04	"PNPT1, RBM4, POLR2B, ZFP36L2, PPIE, MOV10, PPIH, AQR, PLRG1, RBM8A, FRG1, PCBP1, EIF3E, GTF2F1, PRMT5, PCBP2, WDR77, DDX20, ADAR, GEMIN5"	264	370	13528	2.76986077	0.179934105	0.013137643	0.195108915
GOTERM_BP_FAT	GO:0006397~mRNA processing	17	5.483870968	5.53E-04	"RBM4, POLR2B, PPIE, PPIH, MOV10, AQR, PLRG1, RBM8A, FRG1, PCBP1, GTF2F1, PRMT5, PCBP2, WDR77, DDX20, ADAR, GEMIN5"	264	321	13528	2.713773246	0.612935046	0.033330548	0.930115669
GOTERM_BP_FAT	GO:0008380~RNA splicing	15	4.838709677	0.001350122	"RBM4, POLR2B, PPIE, PPIH, AQR, PLRG1, RBM8A, FRG1, PCBP1, GTF2F1, PRMT5, PCBP2, WDR77, DDX20, GEMIN5"	264	284	13528	2.706466069	0.901433435	0.057680463	2.255330523
GOTERM_BP_FAT	"GO:0000375~RNA splicing, via transesterification reactions"	9	2.903225806	0.010104454	"RBM8A, PRMT5, GTF2F1, PCBP1, PCBP2, WDR77, DDX20, POLR2B, GEMIN5"	264	153	13528	3.01426025	0.999999973	0.23506026	15.75798331
GOTERM_BP_FAT	"GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile"	9	2.903225806	0.010104454	"RBM8A, PRMT5, GTF2F1, PCBP1, PCBP2, WDR77, DDX20, POLR2B, GEMIN5"	264	153	13528	3.01426025	0.999999973	0.23506026	15.75798331
GOTERM_BP_FAT	"GO:0000398~nuclear mRNA splicing, via spliceosome"	9	2.903225806	0.010104454	"RBM8A, PRMT5, GTF2F1, PCBP1, PCBP2, WDR77, DDX20, POLR2B, GEMIN5"	264	153	13528	3.01426025	0.999999973	0.23506026	15.75798331
GOTERM_BP_FAT	GO:0000387~spliceosomal snRNP biogenesis	4	1.290322581	0.016624762	"PRMT5, WDR77, DDX20, GEMIN5"	264	28	13528	7.32034632	1	0.329224768	24.65255175
GOTERM_BP_FAT	GO:0022618~ribonucleoprotein complex assembly	5	1.612903226	0.045187111	"PRMT5, WDR77, DDX20, BMS1, GEMIN5"	264	69	13528	3.713219148	1	0.554785009	54.19316847

Annotation Cluster 10	Enrichment Score: 2.061925392563929
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0000502~proteasome complex	8	2.580645161	1.22E-04	"PSMB6, PSMC4,

PSMA5, IDE, PSME3, PSMD5, PSMD7, TRIP12" 236 61 12782 7.10308419 0.035627057 0.002131677 0.162377539

GOTERM_BP_FAT GO:0031145~anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process 8 2.580645161 2.58E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 65 13528 6.306759907 0.357402934 0.024269389 0.434444429

GOTERM_BP_FAT GO:0051437~positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle 8 2.580645161 3.42E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 68 13528 6.028520499 0.443526661 0.028881521 0.575399925

GOTERM_BP_FAT GO:0051443~positive regulation of ubiquitin-protein ligase activity 8 2.580645161 4.09E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 70 13528 5.856277056 0.50407607 0.03284528 0.688096717

GOTERM_BP_FAT GO:0051439~regulation of ubiquitin-protein ligase activity during mitotic cell cycle 8 2.580645161 4.46E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 71 13528 5.773794281 0.534830111 0.032728637 0.750672026

GOTERM_BP_FAT GO:0051351~positive regulation of ligase activity 8 2.580645161 5.29E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 73 13528 5.615608136 0.596416474 0.033047942 0.889346006

GOTERM_BP_FAT GO:0051438~regulation of ubiquitin-protein ligase activity 8 2.580645161 7.90E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 78 13528 5.255633256 0.74214003 0.044172626 1.325492799

GOTERM_BP_FAT GO:0032269~negative regulation of cellular protein metabolic process 12 3.870967742 7.92E-04 "ANAPC1, HSP90AB1, SRP14, SET, PSMB6, PSMC4, PSMA5, EIF3E, IDE, PSME3, PSMD5, PSMD7" 264 180 13528 3.416161616 0.743053519 0.042888208 1.328940352

GOTERM_BP_FAT GO:0010498~proteasomal protein catabolic process 9 2.903225806 8.32E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PCNP, PSME3, PSMD5, PSMD7" 264 102 13528 4.521390374 0.760178016 0.043639719 1.395918344

GOTERM_BP_FAT GO:0043161~proteasomal ubiquitin-dependent protein catabolic process 9 2.903225806 8.32E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PCNP, PSME3, PSMD5, PSMD7" 264 102 13528 4.521390374 0.760178016 0.043639719 1.395918344

GOTERM_BP_FAT GO:0032268~regulation of cellular protein metabolic process 21 6.774193548 9.86E-04 "EGFR, HSP90AB1, ANAPC1, SRP14, CDK1, IDE, RPS5, EIF4G1, PA2G4, PSMB6, EIF3B, SET, PSMC4, PACSIN3, PSMA5, RBM8A, EIF3E, EIF3K, PSME3, PSMD5, PSMD7" 264 474 13528 2.270233985 0.815971452 0.047211032 1.652650701

GOTERM_BP_FAT GO:0051340~regulation of ligase activity 8 2.580645161 9.90E-04 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 81 13528 5.060980172 0.81700368 0.046079268 1.658096807

GOTERM_BP_FAT GO:0051248~negative regulation of protein metabolic process 12 3.870967742 0.00108206 "ANAPC1, HSP90AB1, SRP14, SET, PSMB6, PSMC4, PSMA5, EIF3E, IDE, PSME3, PSMD5, PSMD7" 264 187 13528 3.288283909 0.843818677 0.048943777 1.811386017

GOTERM_BP_FAT GO:0031398~positive regulation of protein ubiquitination 8 2.580645161 0.00122733 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 84 13528 4.88023088 0.878296128 0.053917383 2.052207402

GOTERM_BP_FAT GO:0051436~negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle 7 2.258064516 0.001613301 "ANAPC1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 65 13528 5.518414918 0.937278138 0.06688435 2.689351334

GOTERM_BP_FAT GO:0051352~negative regulation of ligase activity 7 2.258064516 0.001887372 "ANAPC1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 67 13528 5.353686115 0.960832226 0.074240224 3.139406626

GOTERM_BP_FAT GO:0051444~negative regulation of ubiquitin-protein ligase activity 7 2.258064516 0.001887372 "ANAPC1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 67 13528 5.353686115 0.960832226 0.074240224 3.139406626

GOTERM_BP_FAT GO:0031397~negative regulation of protein ubiquitination 7 2.258064516 0.00313042 "ANAPC1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 74 13528 4.847256347 0.995378758 0.110319883 5.156162356

GOTERM_BP_FAT GO:0031396~regulation of protein ubiquitination 8 2.580645161 0.003338505 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 100 13528 4.099393939 0.996769489 0.114872631 5.489879916

GOTERM_BP_FAT GO:0006511~ubiquitin-dependent protein catabolic process 12 3.870967742 0.007789921 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, USP10, PCNP, PSME3, PSMD5, RNF20, PSMD7, FBXO7" 264 242 13528 2.540946657 0.999998503 0.206452395 12.36974102

GOTERM_BP_FAT GO:0031400~negative regulation of protein modification process 8 2.580645161 0.008575339 "ANAPC1, SET, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 119 13528 3.444868857 0.999999615 0.215048404 13.53362912

GOTERM_BP_FAT GO:0044265~cellular macromolecule catabolic process 22 7.096774194 0.044756181 "ANAPC1, CDK1, PNPT1, IDE, PCNP, OAS2, NAE1, ZFP36L2, TRIM5, PSMB6, PSMC4, PSMA5, RBM8A, EIF3E, UBA3, USP10, PSME3, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 725 13528 1.554942529 1 0.558684566 53.84284946

GOTERM_BP_FAT GO:0044092~negative regulation of molecular function 12 3.870967742 0.062239281 "ANAPC1, GPS1, KDM1A, SP100, PSMB6, PSMC4, GNAI1, PSMA5, PSME3, PSMD5, PSMD7, RPS3" 264 334 13528 1.841045182 1 0.639560913 66.20999688

GOTERM_BP_FAT GO:0031401~positive regulation of protein modification process 8 2.580645161 0.072541547 "ANAPC1, CDK1, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 187 13528 2.192189272 1 0.677906098 71.95963586

GOTERM_BP_FAT GO:0009057~macromolecule catabolic process 22 7.096774194 0.082510375 "ANAPC1, CDK1, PNPT1, IDE, PCNP, OAS2, NAE1, ZFP36L2, TRIM5, PSMB6, PSMC4, PSMA5, RBM8A, EIF3E, UBA3, USP10, PSME3, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 781 13528 1.44344857 1 0.704929661 76.63640704

GOTERM_BP_FAT GO:0043085~positive regulation of catalytic activity 16 5.161290323 0.082765703 "EGFR, ANAPC1, CDK1, MSH6, MAP2K1, SMAD3, STAT1, RPS3, PSMB6, PSMC4, PSMA5, RAC1, PSME3, PSMD5, PSMD7, ARAP1" 264 520 13528 1.576689977 1 0.703126643 76.74594502

GOTERM_BP_FAT GO:0032270~positive regulation of cellular protein metabolic process 9 2.903225806 0.084586745 "ANAPC1, CDK1, PSMB6, PACSIN3, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 233 13528 1.979321108 1 0.70546218 77.51329183

GOTERM_BP_FAT GO:0051247~positive regulation of protein metabolic process 9 2.903225806 0.101765902 "ANAPC1, CDK1, PSMB6, PACSIN3, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 243 13528 1.897867565 1 0.75201975 83.66925353

GOTERM_BP_FAT GO:0044093~positive regulation of molecular function 17 5.483870968 0.108221621 "EGFR, ANAPC1, CDK1, MSH6, SP100, MAP2K1, SMAD3, STAT1, RPS3, PSMB6, PSMC4, PSMA5, RAC1, PSME3, PSMD5, PSMD7, ARAP1" 264 586 13528 1.486554969 1 0.764101399 85.54181758

GOTERM_BP_FAT GO:0031399~regulation of protein modification process 10 3.225806452 0.122417312 "EGFR, ANAPC1, CDK1, SET, PSMB6, PSMC4, PSMA5, PSME3, PSMD5, PSMD7" 264 295 13528 1.73703133 1 0.786580308 88.97325039

GOTERM_BP_FAT GO:0051603~proteolysis involved in cellular protein catabolic process 17 5.483870968 0.125955286 "ANAPC1, CDK1, IDE, PCNP, NAE1, TRIM5, PSMB6, PSMC4, PSMA5, UBA3, PSME3, USP10, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 600 13528 1.451868687 1 0.787651891 89.7002799

GOTERM_BP_FAT GO:0044257~cellular protein catabolic process 17 5.483870968 0.128840256 "ANAPC1, CDK1, IDE, PCNP, NAE1, TRIM5, PSMB6, PSMC4, PSMA5, UBA3, PSME3, USP10, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 603 13528 1.44464546 1 0.786917776 90.25948791

GOTERM_BP_FAT GO:0043632~modification-dependent macromolecule catabolic process 16 5.161290323 0.150962676 "ANAPC1, CDK1, PCNP, NAE1, TRIM5, PSMB6, PSMC4, PSMA5, UBA3, PSME3, USP10, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 574 13528 1.428360258 1 0.817497303 93.69093703

GOTERM_BP_FAT GO:0019941~modification-dependent protein catabolic process 16 5.161290323 0.150962676 "ANAPC1, CDK1, PCNP, NAE1, TRIM5, PSMB6, PSMC4, PSMA5, UBA3, PSME3, USP10, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 574 13528 1.428360258 1 0.817497303 93.69093703

GOTERM_BP_FAT GO:0030163~protein catabolic process 17 5.483870968 0.153996099 "ANAPC1, CDK1, IDE, PCNP, NAE1, TRIM5, PSMB6, PSMC4, PSMA5, UBA3, PSME3, USP10, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 622 13528 1.400516418 1 0.820463259 94.06091797

GOTERM_BP_FAT GO:0010604~positive regulation of macromolecule metabolic process 22 7.096774194

0.16328834 "ANAPC1, CDK1, CNBP, SP100, MAP2K1, RAN, RBM4, SMAD3, TP63, PAWR, NOTCH1, PSMB6, PSMC4, PACSIN3, PSMA5, GTF2F1, SOX15, PSME3, AGRN, PSMD5, PSMD7, RNF20" 264 857 13528 1.315441462 1 0.832700614 95.07130312
GOTERM_BP_FAT GO:0043086~negative regulation of catalytic activity 9 2.903225806 0.172879319 "ANAPC1, GPS1, PSMB6, PSMC4, GNAI1, PSMA5, PSME3, PSMD5, PSMD7" 264 277 13528 1.664916311 1 0.842686883 95.94311732
GOTERM_BP_FAT GO:0006508~proteolysis 19 6.129032258 0.751248868 "ANAPC1, CDK1, IDE, PCNP, MIPEP, PWP2, NAE1, TRIM5, PSMB6, PSMC4, PSMA5, UBA3, PSME3, USP10, PSMD5, PSMD7, RNF20, TRIP12, FBXO7" 264 1054 13528 0.923724915 1 0.99862787 99.99999999

Annotation Cluster 11 Enrichment Score: 1.9176800325023733
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0016604~nuclear body 10 3.225806452 0.003886086 "PPIH, SP100, PLRG1, FRG1, RBM8A, EIF3E, NOC3L, DDX20, CTR9, GEMIN5" 236 168 12782 3.223870056 0.686610852 0.056364659 5.065018866
GOTERM_CC_FAT GO:0005681~spliceosome 8 2.580645161 0.010997464 "PPIE, PPIH, AQR, PLRG1, FRG1, RBM8A, DDX20, GEMIN5" 236 132 12782 3.282485876 0.962946713 0.139111969 13.72434072
GOTERM_CC_FAT GO:0016607~nuclear speck 6 1.935483871 0.041319491 "PPIH, PLRG1, FRG1, RBM8A, NOC3L, CTR9" 236 103 12782 3.155010696 0.999996542 0.342401642 43.06783352

Annotation Cluster 12 Enrichment Score: 1.7334019011063682
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0003755~peptidyl-prolyl cis-trans isomerase activity 5 1.612903226 0.005382417 "PPIE, PPIH, FKBP4, PPID, FKBP11" 251 37 12983 6.989878325 0.926224535 0.102923118 7.442519395
GOTERM_MF_FAT GO:0016859~cis-trans isomerase activity 5 1.612903226 0.006505539 "PPIE, PPIH, FKBP4, PPID, FKBP11" 251 39 12983 6.631423026 0.957252325 0.118471211 8.929048999
GOTERM_MF_FAT GO:0016018~cyclosporin A binding 3 0.967741935 0.007276033 "PPIE, PPIH, PPID" 251 7 12983 22.16789983 0.970612072 0.122462837 9.935974536
GOTERM_MF_FAT GO:0008144~drug binding 5 1.612903226 0.023911168 "PPIE, PPIH, FKBP4, PPID, TOP2A" 251 57 12983 4.537289439 0.999991618 0.283934184 29.30666505
GOTERM_MF_FAT GO:0042277~peptide binding 6 1.935483871 0.353373877 "PPIE, SRP14, PPIH, PPID, IDE, KPNA2" 251 203 12983 1.528820678 1 0.908642435 99.80653958

Annotation Cluster 13 Enrichment Score: 1.6600228560382928
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0046983~protein dimerization activity 21 6.774193548 0.004115615 "EGFR, SP100, HSP90AA1, PDXK, GGCT, AIMP1, IDE, SMAD3, POLR1C, BCL2L1, HPRT1, SMC2, ITGB1, STK3, SMC4, NAE1, TRIM5, UBA3, GALE, TOP2B, TOP2A" 251 542 12983 2.004109025 0.863570017 0.086564851 5.738745478
GOTERM_MF_FAT GO:0042802~identical protein binding 21 6.774193548 0.022635272 "EGFR, LDHB, SP100, HSP90AA1, PDXK, GGCT, ATL2, AIMP1, IDE, SMAD3, TP63, BCL2L1, HPRT1, ITGB1, TRIM5, PSME3, GALE, TRIP6, PAICS, TOP2A, TRIP13" 251 640 12983 1.697229831 0.999984247 0.277652616 27.9708412
GOTERM_MF_FAT GO:0042803~protein homodimerization activity 11 3.548387097 0.112385686 "TRIM5, PDXK, SP100, HSP90AA1, GGCT, AIMP1, IDE, SMAD3, GALE, HPRT1, TOP2A" 251 334 12983 1.703521244 1 0.662590524 81.88512489

Annotation Cluster 14 Enrichment Score: 1.657175170711187
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0004386~helicase activity 10 3.225806452 0.00154564 "MOV10, IFIH1,

DDX47, CHD7, G3BP1, EIF4A1, YTHDC2, DDX21, DDX20, ERCC6L" 251 140 12983 3.694649972 0.526271816 0.048588022 2.192283994

GOTERM_MF_FAT GO:0004004~ATP-dependent RNA helicase activity 4 1.290322581 0.007259935 "DDX47, G3BP1, DDX21, DDX20" 251 21 12983 9.852399924 0.970381004 0.126597876 9.915043967

GOTERM_MF_FAT GO:0008186~RNA-dependent ATPase activity 4 1.290322581 0.008288281 "DDX47, G3BP1, DDX21, DDX20" 251 22 12983 9.404563564 0.982045638 0.13373867 11.24310243

GOTERM_MF_FAT GO:0003724~RNA helicase activity 4 1.290322581 0.017820584 "DDX47, G3BP1, DDX21, DDX20" 251 29 12983 7.134496497 0.99983089 0.237692291 22.71562029

GOTERM_MF_FAT GO:0016887~ATPase activity 13 4.193548387 0.028593446 "MSH6, ATP1B1, DDX47, RFC4, PSMC4, EIF4A1, CCT8, G3BP1, IDE, DDX21, DDX20, TOP2A, HSPA8" 251 334 12983 2.01325238 0.999999178 0.308391294 34.0139448

GOTERM_MF_FAT "GO:0042623~ATPase activity, coupled" 10 3.225806452 0.080312725 "ATP1B1, DDX47, RFC4, CCT8, G3BP1, EIF4A1, DDX21, DDX20, TOP2A, HSPA8" 251 272 12983 1.901658074 1 0.576995679 69.87337262

GOTERM_MF_FAT GO:0070035~purine NTP-dependent helicase activity 5 1.612903226 0.120520285 "DDX47, G3BP1, EIF4A1, DDX21, DDX20" 251 98 12983 2.639035694 1 0.676256279 84.12419301

GOTERM_MF_FAT GO:0008026~ATP-dependent helicase activity 5 1.612903226 0.120520285 "DDX47, G3BP1, EIF4A1, DDX21, DDX20" 251 98 12983 2.639035694 1 0.676256279 84.12419301

Annotation Cluster 15 Enrichment Score: 1.591857503333551

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0048770~pigment granule 9 2.903225806 2.27E-04 "HSP90AB1, SLC1A5, HSP90AA1, CCT4, RAN, RAC1, FASN, ITGB1, HSPA8" 236 89 12782 5.47695677 0.065494292 0.003558786 0.302981332

GOTERM_CC_FAT GO:0042470~melanosome 9 2.903225806 2.27E-04 "HSP90AB1, SLC1A5, HSP90AA1, CCT4, RAN, RAC1, FASN, ITGB1, HSPA8" 236 89 12782 5.47695677 0.065494292 0.003558786 0.302981332

GOTERM_CC_FAT GO:0016023~cytoplasmic membrane-bounded vesicle 14 4.516129032 0.213754508 "EGFR, HSP90AB1, TF, HSP90AA1, AIMP1, RAN, ITGB1, SLC1A5, NOTCH1, CCT4, RAC1, FASN, HSPA8, ARHGDIB" 236 550 12782 1.378644068 1 0.754680516 95.9657276

GOTERM_CC_FAT GO:0031988~membrane-bounded vesicle 14 4.516129032 0.247208479 "EGFR, HSP90AB1, TF, HSP90AA1, AIMP1, RAN, ITGB1, SLC1A5, NOTCH1, CCT4, RAC1, FASN, HSPA8, ARHGDIB" 236 568 12782 1.334954643 1 0.797424857 97.74221451

GOTERM_CC_FAT GO:0031410~cytoplasmic vesicle 15 4.838709677 0.294609402 "EGFR, HSP90AB1, TF, HSP90AA1, AIMP1, RAN, ITGB1, AGTRAP, SLC1A5, NOTCH1, CCT4, RAC1, FASN, HSPA8, ARHGDIB" 236 642 12782 1.265444321 1 0.828429994 99.05239258

GOTERM_CC_FAT GO:0031982~vesicle 15 4.838709677 0.349544181 "EGFR, HSP90AB1, TF, HSP90AA1, AIMP1, RAN, ITGB1, AGTRAP, SLC1A5, NOTCH1, CCT4, RAC1, FASN, HSPA8, ARHGDIB" 236 670 12782 1.212560081 1 0.869235288 99.67895084

Annotation Cluster 16 Enrichment Score: 1.586068908170852

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0000796~condensin complex 3 0.967741935 0.004808561 "NCAPG, SMC2, SMC4" 236 6 12782 27.08050847 0.762219538 0.066113488 6.231966988

GOTERM_BP_FAT GO:0006323~DNA packaging 8 2.580645161 0.007842632 "SET, HIST2H2BE, NCAPG, NAA10, HAT1, TOP2A, SMC2, SMC4" 264 117 13528 3.503755504 0.999998633 0.204565425 12.448312

GOTERM_BP_FAT GO:0030261~chromosome condensation 4 1.290322581 0.012179866 "NCAPG, TOP2A, SMC2, SMC4" 264 25 13528 8.198787879 0.999999999 0.262574468 18.69100244

GOTERM_BP_FAT GO:0007076~mitotic chromosome condensation 3 0.967741935 0.02550099 "NCAPG, SMC2, SMC4" 264 13 13528 11.82517483 1 0.429235411 35.34834018

GOTERM_BP_FAT GO:0000070~mitotic sister chromatid segregation 4 1.290322581 0.032363003

"NCAPG, RRS1, SMC2, SMC4" 264 36 13528 5.693602694 1 0.46950168 42.61977681
GOTERM_BP_FAT GO:0000819~sister chromatid segregation 4 1.290322581 0.034727068 "NCAPG,
RRS1, SMC2, SMC4" 264 37 13528 5.53972154 1 0.490082798 44.94139324
GOTERM_BP_FAT GO:0007059~chromosome segregation 5 1.612903226 0.072897804 "NCAPG, RRS1,
TOP2A, SMC2, SMC4" 264 81 13528 3.163112608 1 0.676575723 72.14094336
GOTERM_CC_FAT GO:0000793~condensed chromosome 5 1.612903226 0.213471954 "NCAPG, RRS1,
SMC2, ERCC6L, SMC4" 236 129 12782 2.099264223 1 0.767848147 95.94633064

Annotation Cluster 17 Enrichment Score: 1.5577394365757766
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0030235~nitric-oxide synthase regulator activity 3 0.967741935 0.00355425
"EGFR, HSP90AB1, HSP90AA1" 251 5 12983 31.03505976 0.820891046 0.082394802 4.974454604
GOTERM_BP_FAT GO:0045429~positive regulation of nitric oxide biosynthetic process 3 0.967741935
0.062051302 "EGFR, HSP90AB1, HSP90AA1" 264 21 13528 7.32034632 1 0.641833198 66.09544953
GOTERM_BP_FAT GO:0045428~regulation of nitric oxide biosynthetic process 3 0.967741935
0.096223859 "EGFR, HSP90AB1, HSP90AA1" 264 27 13528 5.693602694 1 0.739475826 81.88200369

Annotation Cluster 18 Enrichment Score: 1.3315148334392213
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0046112~nucleobase biosynthetic process 5 1.612903226 1.20E-04 "UMPS, CAD,
HPRT1, PAICS, GART" 264 14 13528 18.3008658 0.185825062 0.012766559 0.202192643
GOTERM_BP_FAT GO:0009112~nucleobase metabolic process 5 1.612903226 9.24E-04 "UMPS, CAD,
HPRT1, PAICS, GART" 264 23 13528 11.13965744 0.795087003 0.045552501 1.54851421
GOTERM_BP_FAT GO:0009156~ribonucleoside monophosphate biosynthetic process 4 1.290322581
0.009649395 "UMPS, PAICS, PRPS2, GART" 264 23 13528 8.911725955 0.99999994 0.23199077
15.10171433
GOTERM_BP_FAT GO:0009161~ribonucleoside monophosphate metabolic process 4 1.290322581
0.012179866 "UMPS, PAICS, PRPS2, GART" 264 25 13528 8.198787879 0.999999999 0.262574468
18.69100244
GOTERM_BP_FAT GO:0009113~purine base biosynthetic process 3 0.967741935 0.012386568 "HPRT1,
PAICS, GART" 264 9 13528 17.08080808 0.999999999 0.259970433 18.9777981
GOTERM_BP_FAT GO:0009165~nucleotide biosynthetic process 9 2.903225806 0.028977224 "ATP1B1,
UMPS, RRM2, CAD, HPRT1, PAICS, MON2, PRPS2, GART" 264 186 13528 2.479472141 1 0.451385528
39.1339391
GOTERM_BP_FAT GO:0006144~purine base metabolic process 3 0.967741935 0.029375155 "HPRT1,
PAICS, GART" 264 14 13528 10.98051948 1 0.452047351 39.5537256
GOTERM_BP_FAT "GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process" 9
2.903225806 0.034939833 "ATP1B1, UMPS, RRM2, CAD, HPRT1, PAICS, MON2, PRPS2, GART" 264 193
13528 2.389543099 1 0.488424587 45.14594544
GOTERM_BP_FAT "GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process" 9
2.903225806 0.034939833 "ATP1B1, UMPS, RRM2, CAD, HPRT1, PAICS, MON2, PRPS2, GART" 264 193
13528 2.389543099 1 0.488424587 45.14594544
GOTERM_BP_FAT GO:0009259~ribonucleotide metabolic process 7 2.258064516 0.067289196 "ATP1B1,
UMPS, NUDT5, PAICS, MON2, PRPS2, GART" 264 147 13528 2.44011544 1 0.662457594
69.15437309
GOTERM_BP_FAT GO:0009124~nucleoside monophosphate biosynthetic process 4 1.290322581
0.073073605 "UMPS, PAICS, PRPS2, GART" 264 50 13528 4.099393939 1 0.674327522 72.23000556
GOTERM_BP_FAT GO:0009260~ribonucleotide biosynthetic process 6 1.935483871 0.094306538 "ATP1B1,
UMPS, PAICS, MON2, PRPS2, GART" 264 124 13528 2.479472141 1 0.737531448 81.22197178
GOTERM_BP_FAT GO:0009123~nucleoside monophosphate metabolic process 4 1.290322581
0.136981998 "UMPS, PAICS, PRPS2, GART" 264 66 13528 3.105601469 1 0.797915982 91.68757425
GOTERM_BP_FAT GO:0046148~pigment biosynthetic process 3 0.967741935 0.175271705 "HPRT1,

PAICS, GART"	264	39	13528	3.941724942	1	0.842175576	96.13675717
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	10	3.225806452	0.181171669	"ATP1B1, UMPS, MAT2A, RRM2, CAD, HPRT1, PAICS, MON2, PRPS2, GART"	264	325	13528	1.576689977	1	0.849515986	96.57779837
GOTERM_BP_FAT	GO:0042440~pigment metabolic process	3	0.967741935	0.217776989	"HPRT1, PAICS, GART"	264	45	13528	3.416161616	1	0.889792994	98.41896599
GOTERM_BP_FAT	GO:0006164~purine nucleotide biosynthetic process	5	1.612903226	0.32484263	"ATP1B1, HPRT1, PAICS, MON2, GART"	264	148	13528	1.731162981	1	0.949249457	99.8682986
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	4	1.290322581	0.39822882	"ATP1B1, PAICS, MON2, GART"	264	117	13528	1.751877752	1	0.973060256	99.9811283
GOTERM_BP_FAT	GO:0006163~purine nucleotide metabolic process	5	1.612903226	0.487632818	"ATP1B1, HPRT1, PAICS, MON2, GART"	264	186	13528	1.377484523	1	0.985017825	99.99875139
GOTERM_BP_FAT	GO:0009150~purine ribonucleotide metabolic process	4	1.290322581	0.504667732	"ATP1B1, PAICS, MON2, GART"	264	138	13528	1.485287659	1	0.985840368	99.99929452

Annotation Cluster 19	Enrichment Score: 1.3017160253422817
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033365~protein localization in organelle	10	3.225806452	0.002209085	"COG3, SRP14, PPIH, CSE1L, MACF1, IPO7, RAN, KPNA6, MIPEP, KPNA2"	264	146	13528	3.509755085	0.977466939	0.080829655	3.665197641
GOTERM_BP_FAT	GO:0006913~nucleocytoplasmic transport	10	3.225806452	0.003449733	"PPIH, AAAS, SET, CSE1L, XPO5, IPO7, RAN, ANP32A, KPNA6, KPNA2"	264	156	13528	3.284770785	0.997332251	0.11615111	5.667808807
GOTERM_BP_FAT	GO:0051169~nuclear transport	10	3.225806452	0.003753277	"PPIH, AAAS, SET, CSE1L, XPO5, IPO7, RAN, ANP32A, KPNA6, KPNA2"	264	158	13528	3.243191408	0.998417864	0.121008094	6.151780342
GOTERM_BP_FAT	GO:0046907~intracellular transport	23	7.419354839	0.009235408	"SRP14, HSP90AA1, ATL2, MAP2K1, RAN, XPO5, BCL2L1, MIPEP, MON2, COG3, PPIH, COG5, KIAA1279, SET, AAAS, CSE1L, MACF1, IPO7, ANP32A, KPNA6, RANBP1, KPNA2, HSPA8"	264	657	13528	1.793874821	0.999999877	0.226361262	14.50050269
GOTERM_CC_FAT	GO:0005643~nuclear pore	6	1.935483871	0.015082724	"AAAS, CSE1L, IPO7, RAN, KPNA6, KPNA2"	236	79	12782	4.113494958	0.989207376	0.159861205	18.36230113
GOTERM_BP_FAT	GO:0006605~protein targeting	10	3.225806452	0.02477892	"SRP14, PPIH, CSE1L, MACF1, XPO5, IPO7, RAN, KPNA6, MIPEP, KPNA2"	264	215	13528	2.383368569	1	0.428131894	34.5347171
GOTERM_BP_FAT	GO:0006606~protein import into nucleus	6	1.935483871	0.026033846	"PPIH, CSE1L, IPO7, RAN, KPNA6, KPNA2"	264	86	13528	3.575052854	1	0.431920515	35.94264744
GOTERM_MF_FAT	GO:0008565~protein transporter activity	6	1.935483871	0.026221107	"COG3, CSE1L, XPO5, IPO7, KPNA6, KPNA2"	251	87	12983	3.567248248	0.999997331	0.293095294	31.66664976
GOTERM_BP_FAT	GO:0051170~nuclear import	6	1.935483871	0.028396461	"PPIH, CSE1L, IPO7, RAN, KPNA6, KPNA2"	264	88	13528	3.493801653	1	0.448568717	38.51635374
GOTERM_CC_FAT	GO:0046930~pore complex	6	1.935483871	0.030708094	"AAAS, CSE1L, IPO7, RAN, KPNA6, KPNA2"	236	95	12782	3.420695807	0.999908068	0.282473251	34.05574234
GOTERM_BP_FAT	GO:0034504~protein localization in nucleus	6	1.935483871	0.036281771	"PPIH, CSE1L, IPO7, RAN, KPNA6, KPNA2"	264	94	13528	3.270793037	1	0.49787893	46.41969753
GOTERM_BP_FAT	GO:0017038~protein import	7	2.258064516	0.042719605	"PPIH, CSE1L, IPO7, RAN, KPNA6, MIPEP, KPNA2"	264	131	13528	2.738144807	1	0.545318772	52.15286527
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	13	4.193548387	0.11077098	"EGFR, COG3, SRP14, PPIH, CSE1L, MACF1, XPO5, IPO7, RAN, KPNA6, MIPEP, KPNA2, STAU1"	264	414	13528	1.609061631	1	0.767531022	86.22406696
GOTERM_CC_FAT	GO:0005635~nuclear envelope	7	2.258064516	0.176753999	"AAAS, CSE1L, IPO7, RAN, SMAD3, KPNA6, KPNA2"	236	205	12782	1.849400579	1	0.701062923	92.54629755

GOTERM_BP_FAT GO:0034613~cellular protein localization 12 3.870967742 0.17772858 "EGFR, COG3, SRP14, PPIH, CSE1L, MACF1, XPO5, IPO7, RAN, KPNA6, MIPEP, KPNA2" 264 411 13528 1.496129175 1 0.84501714 96.32654444
GOTERM_BP_FAT GO:0006886~intracellular protein transport 11 3.548387097 0.193658256 "COG3, SRP14, PPIH, CSE1L, MACF1, XPO5, IPO7, RAN, KPNA6, MIPEP, KPNA2" 264 374 13528 1.507130125 1 0.86404124 97.35988242
GOTERM_BP_FAT GO:0015031~protein transport 16 5.161290323 0.517119428 "SRP14, NACA, RAN, XPO5, LIN7C, MIPEP, MON2, COG3, PPIH, COG5, CSE1L, MACF1, RAB18, IPO7, KPNA6, KPNA2" 264 762 13528 1.075956415 1 0.987095249 99.99954102
GOTERM_BP_FAT GO:0045184~establishment of protein localization 16 5.161290323 0.533040325 "SRP14, NACA, RAN, XPO5, LIN7C, MIPEP, MON2, COG3, PPIH, COG5, CSE1L, MACF1, RAB18, IPO7, KPNA6, KPNA2" 264 769 13528 1.066162273 1 0.988050877 99.99973941
GOTERM_BP_FAT GO:0008104~protein localization 18 5.806451613 0.551122937 "EGFR, SRP14, NACA, RAN, XPO5, G3BP2, LIN7C, MIPEP, MON2, COG3, PPIH, COG5, CSE1L, MACF1, RAB18, IPO7, KPNA6, KPNA2" 264 882 13528 1.04576376 1 0.98941969 99.99986623
GOTERM_CC_FAT GO:0012505~endomembrane system 8 2.580645161 0.990929354 "EGFR, AAAS, CSE1L, IPO7, RAN, SMAD3, KPNA6, KPNA2" 236 782 12782 0.5540769 1 0.999998594 100

Annotation Cluster 20 Enrichment Score: 1.2484407936739237
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006730~one-carbon metabolic process 8 2.580645161 0.006213778 "PRMT3, KDM1A, MTHFD2, PRMT1, MAT2A, PRMT5, RNF20, NSUN2" 264 112 13528 3.66017316 0.999977226 0.171005431 9.989494691
GOTERM_BP_FAT GO:0006479~protein amino acid methylation 4 1.290322581 0.03971535 "PRMT3, PRMT1, PRMT5, RNF20" 264 39 13528 5.255633256 1 0.522587948 49.55330397
GOTERM_BP_FAT GO:0008213~protein amino acid alkylation 4 1.290322581 0.03971535 "PRMT3, PRMT1, PRMT5, RNF20" 264 39 13528 5.255633256 1 0.522587948 49.55330397
GOTERM_BP_FAT GO:0043414~biopolymer methylation 5 1.612903226 0.045187111 "PRMT3, PRMT1, PRMT5, RNF20, NSUN2" 264 69 13528 3.713219148 1 0.554785009 54.19316847
GOTERM_BP_FAT GO:0032259~methylation 5 1.612903226 0.060489787 "PRMT3, PRMT1, PRMT5, RNF20, NSUN2" 264 76 13528 3.371212121 1 0.635609696 65.12969867
GOTERM_MF_FAT GO:0008276~protein methyltransferase activity 3 0.967741935 0.250371737 "PRMT3, PRMT1, PRMT5" 251 50 12983 3.103505976 1 0.835962632 98.39121886
GOTERM_MF_FAT GO:0008170~N-methyltransferase activity 3 0.967741935 0.27186921 "PRMT3, PRMT1, PRMT5" 251 53 12983 2.927835827 1 0.859796716 98.93974453

Annotation Cluster 21 Enrichment Score: 1.2475493030942248
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005694~chromosome 17 5.483870968 0.011010582 "PTGES3, MSH6, SP100, RAN, SMC2, SMC4, CHD7, RFC4, RCC2, HIST2H2BE, NCAPG, EIF3E, RRS1, TOP2B, TOP2A, RNF20, ERCC6L" 236 460 12782 2.0016028 0.963092884 0.133635916 13.73961586
GOTERM_CC_FAT GO:0044427~chromosomal part 13 4.193548387 0.053493363 "PTGES3, MSH6, RAN, SMC2, SMC4, CHD7, RFC4, RCC2, NCAPG, HIST2H2BE, EIF3E, TOP2B, ERCC6L" 236 386 12782 1.8240757 0.999999923 0.400689874 51.99732241
GOTERM_CC_FAT GO:0000785~chromatin 6 1.935483871 0.307073192 "MSH6, CHD7, HIST2H2BE, RAN, EIF3E, TOP2B" 236 200 12782 1.624830508 1 0.838286142 99.25308114

Annotation Cluster 22 Enrichment Score: 1.1852342318766527
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0016323~basolateral plasma membrane 10 3.225806452 0.012802191 "EGFR, TF, ATP1B1, SDC1, LIMA1, MACF1, ITGB4, TRIP6, ITGB1, MLF2" 236 203 12782 2.668030392 0.978499605

0.147844991 15.80248966

GOTERM_CC_FAT GO:0070161~anchoring junction 9 2.903225806 0.014216864 "SDC1, LIMA1, DSG2, PKP2, DSC3, TRIP6, ITGB1, MLLT4, MLF2" 236 172 12782 2.834006701 0.985976625 0.156909683 17.39900625

GOTERM_CC_FAT GO:0030055~cell-substrate junction 6 1.935483871 0.055615189 "SDC1, LIMA1, MACF1, TRIP6, ITGB1, MLF2" 236 112 12782 2.901483051 0.999999961 0.403530997 53.41412988

GOTERM_CC_FAT GO:0005912~adherens junction 7 2.258064516 0.066537736 "SDC1, LIMA1, PKP2, TRIP6, ITGB1, MLLT4, MLF2" 236 155 12782 2.445981411 0.999999999 0.434454341 60.11495789

GOTERM_CC_FAT GO:0005925~focal adhesion 5 1.612903226 0.118561731 "SDC1, LIMA1, TRIP6, ITGB1, MLF2" 236 102 12782 2.654951811 1 0.591564486 81.4499404

GOTERM_CC_FAT GO:0005924~cell-substrate adherens junction 5 1.612903226 0.13125356 "SDC1, LIMA1, TRIP6, ITGB1, MLF2" 236 106 12782 2.55476495 1 0.606145222 84.7152158

GOTERM_CC_FAT GO:0030054~cell junction 11 3.548387097 0.48189808 "SDC1, LIMA1, DSG2, MACF1, PKP2, DSC3, LIN7C, TRIP6, ITGB1, MLLT4, MLF2" 236 518 12782 1.150137426 1 0.939155025 99.98459658

Annotation Cluster 23 Enrichment Score: 1.1848630542284015

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0043065~positive regulation of apoptosis 17 5.483870968 0.010014195 "MSH6, PTGS2, SMAD3, TP63, BCL2L1, IFI16, PAWR, STAT1, STK3, SRC, RPS3, NOTCH1, TIAL1, RAC1, DDX20, MX1, TOP2A" 264 430 13528 2.025863284 0.999999968 0.236392852 15.62819573

GOTERM_BP_FAT GO:0043068~positive regulation of programmed cell death 17 5.483870968 0.010674679 "MSH6, PTGS2, SMAD3, TP63, BCL2L1, IFI16, PAWR, STAT1, STK3, SRC, RPS3, NOTCH1, TIAL1, RAC1, DDX20, MX1, TOP2A" 264 433 13528 2.01182728 0.99999999 0.243362503 16.57360269

GOTERM_BP_FAT GO:0010942~positive regulation of cell death 17 5.483870968 0.011128503 "MSH6, PTGS2, SMAD3, TP63, BCL2L1, IFI16, PAWR, STAT1, STK3, SRC, RPS3, NOTCH1, TIAL1, RAC1, DDX20, MX1, TOP2A" 264 435 13528 2.002577499 0.999999995 0.249077874 17.21741341

GOTERM_BP_FAT GO:0042981~regulation of apoptosis 23 7.419354839 0.066437593 "EGFR, MSH6, CDK1, IFIH1, PTGS2, AARS, SMAD3, TP63, BCL2L1, IFI16, PAWR, STAT1, STK3, SRC, RPS3, NAE1, NOTCH1, TIAL1, RAC1, PSME3, DDX20, MX1, TOP2A" 264 804 13528 1.465890246 1 0.66097073 68.67538559

GOTERM_BP_FAT GO:0043067~regulation of programmed cell death 23 7.419354839 0.072070303 "EGFR, MSH6, CDK1, IFIH1, PTGS2, AARS, SMAD3, TP63, BCL2L1, IFI16, PAWR, STAT1, STK3, SRC, RPS3, NAE1, NOTCH1, TIAL1, RAC1, PSME3, DDX20, MX1, TOP2A" 264 812 13528 1.451447977 1 0.678651285 71.71810251

GOTERM_BP_FAT GO:0010941~regulation of cell death 23 7.419354839 0.074180204 "EGFR, MSH6, CDK1, IFIH1, PTGS2, AARS, SMAD3, TP63, BCL2L1, IFI16, PAWR, STAT1, STK3, SRC, RPS3, NAE1, NOTCH1, TIAL1, RAC1, PSME3, DDX20, MX1, TOP2A" 264 815 13528 1.446105224 1 0.676897081 72.78449867

GOTERM_BP_FAT GO:0006915~apoptosis 17 5.483870968 0.127983103 "GGCT, AIMP1, SMAD3, TP63, BCL2L1, PAWR, STAT1, STK3, RPS3, NAE1, CSE1L, SLK, TIAL1, RAC1, PSME3, EIF2AK2, TOP2A" 264 602 13528 1.447045203 1 0.788892015 90.09639795

GOTERM_BP_FAT GO:0012501~programmed cell death 17 5.483870968 0.139526106 "GGCT, AIMP1, SMAD3, TP63, BCL2L1, PAWR, STAT1, STK3, RPS3, NAE1, CSE1L, SLK, TIAL1, RAC1, PSME3, EIF2AK2, TOP2A" 264 611 13528 1.425730298 1 0.802271101 92.09177112

GOTERM_BP_FAT GO:0008219~cell death 19 6.129032258 0.162004443 "GGCT, AIMP1, SMAD3, TP63, BCL2L1, PAWR, HPRT1, STAT1, STK3, RPS3, NAE1, CSE1L, SLK, ATXN10, TIAL1, RAC1, PSME3, EIF2AK2, TOP2A" 264 719 13528 1.35411135 1 0.831870326 94.94203981

GOTERM_BP_FAT GO:0016265~death 19 6.129032258 0.165995953 "GGCT, AIMP1, SMAD3, TP63, BCL2L1, PAWR, HPRT1, STAT1, STK3, RPS3, NAE1, CSE1L, SLK, ATXN10, TIAL1, RAC1, PSME3, EIF2AK2, TOP2A" 264 724 13528 1.344759752 1 0.834607158 95.3337884

GOTERM_BP_FAT GO:0006917~induction of apoptosis 10 3.225806452 0.171111884 "MSH6, TIAL1, RAC1, SMAD3, TP63, DDX20, IFI16, MX1, STAT1, RPS3" 264 320 13528 1.601325758 1 0.841050214 95.79423568

GOTERM_BP_FAT GO:0012502~induction of programmed cell death 10 3.225806452 0.174206661

"MSH6, TIAL1, RAC1, SMAD3, TP63, DDX20, IFI16, MX1, STAT1, RPS3" 264 321 13528 1.596337204 1 0.843489067 96.05165186

Annotation Cluster 24 Enrichment Score: 1.1835674145319524

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006401~RNA catabolic process	5	1.612903226	0.037546221	"ZFP36L2, RBM8A, EIF3E, PNPT1, OAS2"	264	65	13528	3.941724942	1	0.506245887	47.59439279
GOTERM_BP_FAT	GO:0006402~mRNA catabolic process	4	1.290322581	0.050712437	"ZFP36L2, RBM8A, EIF3E, PNPT1"	264	43	13528	4.766737139	1	0.583156853	58.4689227
GOTERM_BP_FAT	GO:0000956~nuclear-transcribed mRNA catabolic process	3	0.967741935	0.14778047	"ZFP36L2, RBM8A, EIF3E"	264	35	13528	4.392207792	1	0.816012277	93.27956945

Annotation Cluster 25 Enrichment Score: 1.132806518715459

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	"GO:0042770~DNA damage response, signal transduction"	6	1.935483871	0.019715559	"CDK1, MSH6, SP100, TP63, IFI16, NAE1"	264	80	13528	3.843181818	1	0.361951746	28.55287351
GOTERM_MF_FAT	GO:0003690~double-stranded DNA binding	6	1.935483871	0.039279045	"EGFR, MSH6, ANKRD17, SMAD3, TP63, IFI16"	251	97	12983	3.199490697	0.999999996	0.39120118	43.68650852
GOTERM_BP_FAT	"GO:0008630~DNA damage response, signal transduction resulting in induction of apoptosis"	3	0.967741935	0.134398779	"MSH6, TP63, IFI16"	264	33	13528	4.658402204	1	0.795403465	91.25733278
GOTERM_BP_FAT	GO:0008629~induction of apoptosis by intracellular signals	3	0.967741935	0.282753887	"MSH6, TP63, IFI16"	264	54	13528	2.846801347	1	0.933734066	99.63437911

Annotation Cluster 26 Enrichment Score: 1.1243453335393583

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016779~nucleotidyltransferase activity	8	2.580645161	0.010530049	"PTGES3, RPAP1, UAP1, PNPT1, OAS3, POLR1C, OAS2, POLR2B"	251	125	12983	3.310406375	0.993981885	0.156700166	14.0753596
GOTERM_MF_FAT	GO:0003899~DNA-directed RNA polymerase activity	3	0.967741935	0.20057038	"RPAP1, POLR1C, POLR2B"	251	43	12983	3.608727879	1	0.791329216	95.95605349
GOTERM_MF_FAT	GO:0034062~RNA polymerase activity	3	0.967741935	0.20057038	"RPAP1, POLR1C, POLR2B"	251	43	12983	3.608727879	1	0.791329216	95.95605349

Annotation Cluster 27 Enrichment Score: 1.0895419953593255

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0008536~Ran GTPase binding	3	0.967741935	0.021463091	"RANBP9, IPO7, RANBP1"	251	12	12983	12.9312749	0.999971894	0.272078348	26.72294452
GOTERM_MF_FAT	GO:0017016~Ras GTPase binding	5	1.612903226	0.098578943	"RANBP9, MAP2K1, IPO7, DIAPH3, RANBP1"	251	91	12983	2.84203844	1	0.633054496	77.40056784
GOTERM_MF_FAT	GO:0031267~small GTPase binding	5	1.612903226	0.130515559	"RANBP9, MAP2K1, IPO7, DIAPH3, RANBP1"	251	101	12983	2.560648495	1	0.70068178	86.52279884
GOTERM_MF_FAT	GO:0051020~GTPase binding	5	1.612903226	0.158742534	"RANBP9, MAP2K1, IPO7, DIAPH3, RANBP1"	251	109	12983	2.372710991	1	0.734261094	91.60145065

Annotation Cluster 28 Enrichment Score: 1.015395571140834

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	14	4.516129032	0.030682494	"CDK1,							

MSH6, SP100, RBM4, TP63, IFI16, NAE1, RPS3, ANKRD17, RFC4, SLK, TOP2A, MCTS1, TRIP13"264 373 13528 1.923308149 1 0.458983898 40.91377511
GOTERM_BP_FAT GO:0033554~cellular response to stress 18 5.806451613 0.050467943 "GPS1, MSH6, CDK1, SP100, RBM4, AARS, MINK1, TP63, IFI16, RPS3, NAE1, ANKRD17, RFC4, SLK, EIF2AK2, MCTS1, TOP2A, TRIP13" 264 566 13528 1.629617732 1 0.584941712 58.2879471
GOTERM_BP_FAT GO:0006259~DNA metabolic process 15 4.838709677 0.117563866 "PTGES3, MSH6, RAN, RBM4, NAE1, ANKRD17, SET, RFC4, SLK, RRM2, TOP2B, KPNA2, TOP2A, DUT, TRIP13" 264 506 13528 1.519044197 1 0.779203713 87.89708856
GOTERM_BP_FAT GO:0006281~DNA repair 7 2.258064516 0.476691711 "MSH6, ANKRD17, RFC4, SLK, RBM4, TOP2A, TRIP13" 264 284 13528 1.263017499 1 0.983895431 99.99821612

Annotation Cluster 29 Enrichment Score: 1.0013353146822748
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0001836~release of cytochrome c from mitochondria 3 0.967741935 0.062051302 "GGCT, SMAD3, BCL2L1" 264 21 13528 7.32034632 1 0.641833198 66.09544953
GOTERM_BP_FAT GO:0008637~apoptotic mitochondrial changes 3 0.967741935 0.121314908 "GGCT, SMAD3, BCL2L1" 264 31 13528 4.958944282 1 0.787972656 88.73702487
GOTERM_BP_FAT GO:0007005~mitochondrion organization 6 1.935483871 0.131622151 "HSP90AA1, GGCT, GFM1, SMAD3, BCL2L1, MIPEP" 264 138 13528 2.227931489 1 0.79018244 90.77156222

Annotation Cluster 30 Enrichment Score: 0.9475435096207729
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005759~mitochondrial matrix 9 2.903225806 0.058733121 "TUFM, POLDIP2, IDH3B, MRPL37, CARS2, DARS2, MIPEP, IDH3A, KARS" 236 227 12782 2.147353095 0.999999985 0.411698137 55.42600076
GOTERM_CC_FAT GO:0031980~mitochondrial lumen 9 2.903225806 0.058733121 "TUFM, POLDIP2, IDH3B, MRPL37, CARS2, DARS2, MIPEP, IDH3A, KARS" 236 227 12782 2.147353095 0.999999985 0.411698137 55.42600076
GOTERM_CC_FAT GO:0044429~mitochondrial part 16 5.161290323 0.134215473 "TUFM, NDUFB10, PNPT1, IDH3B, DARS2, BCL2L1, MIPEP, IDH3A, MON2, KARS, NDUFA12, POLDIP2, MRPL37, CARS2, AKAP1, SURF1" 236 595 12782 1.456430708 1 0.606880593 85.3964228
GOTERM_CC_FAT GO:0005739~mitochondrion 23 7.419354839 0.350152488 "TUFM, NDUFB10, PNPT1, IDH3B, DARS2, BCL2L1, OAS2, MIPEP, NDUFA12, IDH3A, MON2, KARS, MTHFD2, KIAA1279, PSMC4, GFM1, POLDIP2, MRPL37, CARS2, AKAP1, SURF1, SPATA5, DUT" 236 1087 12782 1.146001279 1 0.865598733 99.68293587

Annotation Cluster 31 Enrichment Score: 0.9063107205147599
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0051259~protein oligomerization 8 2.580645161 0.053269352 "TRIM5, ATL2, MAP2K1, RRM2, IDE, TP63, HPRT1, TRIM22" 264 174 13528 2.355973528 1 0.598062405 60.31782478
GOTERM_BP_FAT GO:0051289~protein homotetramerization 3 0.967741935 0.090211397 "IDE, TP63, HPRT1" 264 26 13528 5.912587413 1 0.723856723 79.73572437
GOTERM_BP_FAT GO:0051262~protein tetramerization 3 0.967741935 0.175271705 "IDE, TP63, HPRT1" 264 39 13528 3.941724942 1 0.842175576 96.13675717
GOTERM_BP_FAT GO:0051260~protein homooligomerization 4 1.290322581 0.28138859 "ATL2, IDE, TP63, HPRT1" 264 95 13528 2.157575758 1 0.93356029 99.62244869

Annotation Cluster 32 Enrichment Score: 0.8910652688958344
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0051276~chromosome organization 17 5.483870968 0.027762354 "PTGES3,

MSH6, RBM4, HAT1, SMC2, SMC4, CTR9, KDM1A, CHD7, SET, NCAPG, HIST2H2BE, PRMT5, RRS1, SOX15, TOP2A, RNF20" 264 485 13528 1.796126211 1 0.449055698 37.83531233
GOTERM_BP_FAT GO:0016570~histone modification 6 1.935483871 0.089481685 "KDM1A, PRMT5, RBM4, HAT1, RNF20, CTR9" 264 122 13528 2.520119225 1 0.723661895 79.45953993
GOTERM_BP_FAT GO:0016569~covalent chromatin modification 6 1.935483871 0.099261994 "KDM1A, PRMT5, RBM4, HAT1, RNF20, CTR9" 264 126 13528 2.44011544 1 0.748203734 82.88335844
GOTERM_BP_FAT GO:0006325~chromatin organization 10 3.225806452 0.320295597 "KDM1A, SET, CHD7, HIST2H2BE, PRMT5, RBM4, SOX15, HAT1, RNF20, CTR9" 264 378 13528 1.355619689 1 0.948661439 99.85249394
GOTERM_BP_FAT GO:0016568~chromatin modification 7 2.258064516 0.443761128 "KDM1A, CHD7, PRMT5, RBM4, HAT1, RNF20, CTR9" 264 274 13528 1.309113028 1 0.980043231 99.99500118

Annotation Cluster 33 Enrichment Score: 0.8776581529113374
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0004518~nuclease activity 7 2.258064516 0.085034659 "ELAC2, SLK, PNPT1, G3BP1, EXOSC3, ERI1, RPS3" 251 158 12983 2.291618337 1 0.583552698 72.01569707
GOTERM_MF_FAT GO:0008408~3'-5' exonuclease activity 3 0.967741935 0.100709291 "PNPT1, EXOSC3, ERI1" 251 28 12983 5.541974957 1 0.634062523 78.15400892
GOTERM_MF_FAT GO:0004527~exonuclease activity 3 0.967741935 0.27186921 "PNPT1, EXOSC3, ERI1" 251 53 12983 2.927835827 1 0.859796716 98.93974453

Annotation Cluster 34 Enrichment Score: 0.8528561361004607
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0003924~GTPase activity 9 2.903225806 0.051737816 "TUFM, RAB18, ATL2, GNAI1, RAN, GFM1, EEF1A1P5, RAC1, MX1" 251 211 12983 2.206283869 1 0.4571536 53.29363924
GOTERM_MF_FAT GO:0005525~GTP binding 11 3.548387097 0.184097333 "TUFM, RAB18, ATL2, GNAI1, RAN, GFM1, FKBP4, EEF1A1P5, RAC1, DRG1, MX1" 251 372 12983 1.529505633 1 0.774392569 94.583167
GOTERM_MF_FAT GO:0019001~guanyl nucleotide binding 11 3.548387097 0.201771551 "TUFM, RAB18, ATL2, GNAI1, RAN, GFM1, FKBP4, EEF1A1P5, RAC1, DRG1, MX1" 251 382 12983 1.489466219 1 0.788807888 96.04226058
GOTERM_MF_FAT GO:0032561~guanyl ribonucleotide binding 11 3.548387097 0.201771551 "TUFM, RAB18, ATL2, GNAI1, RAN, GFM1, FKBP4, EEF1A1P5, RAC1, DRG1, MX1" 251 382 12983 1.489466219 1 0.788807888 96.04226058

Annotation Cluster 35 Enrichment Score: 0.77206580333482
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007010~cytoskeleton organization 17 5.483870968 0.011361284 "KIF23, LIMA1, RAN, DIAPH3, PCM1, ITGB1, TUBGCP2, KRT9, TUBGCP3, KRT19, RANBP9, MACF1, RAC1, RANBP1, KRT3, ARAP1, ARHGDIB"264 436 13528 1.997984431 0.999999997 0.250372178 17.54582905
GOTERM_BP_FAT GO:0000226~microtubule cytoskeleton organization 8 2.580645161 0.024795009 "KIF23, TUBGCP3, RANBP9, MACF1, RAN, RANBP1, PCM1, TUBGCP2" 264 147 13528 2.78870336 1 0.424228813 34.55295077
GOTERM_BP_FAT GO:0007017~microtubule-based process 10 3.225806452 0.059006244 "KIF23, TUBGCP3, RANBP9, MACF1, MAP2K1, RAN, RANBP1, PCM1, KPNA2, TUBGCP2" 264 253 13528 2.025392263 1 0.633195029 64.18824828
GOTERM_CC_FAT GO:0015630~microtubule cytoskeleton 14 4.516129032 0.2135273 "KIF23, CDK1, RABGAP1, MAP2K1, PCM1, TUBGCP2, STAU1, TUBGCP3, RANBP9, MACF1, RCC2, NUBP2, RANBP1,

TOP2A" 236 549 12782 1.381155259 1 0.761067863 95.95013682
GOTERM_CC_FAT GO:0005813~centrosome 7 2.258064516 0.231047159 "TUBGCP3, RABGAP1, NUBP2, RANBP1, PCM1, TUBGCP2, TOP2A" 236 224 12782 1.69253178 1 0.778120313 97.00200687
GOTERM_CC_FAT GO:0044450~microtubule organizing center part 3 0.967741935 0.275218479 "TUBGCP3, PCM1, TOP2A"236 56 12782 2.901483051 1 0.819655819 98.63902493
GOTERM_CC_FAT GO:0005819~spindle 5 1.612903226 0.28545936 "KIF23, TUBGCP3, CDK1, RCC2, TUBGCP2" 236 147 12782 1.842211461 1 0.827478761 98.87449205
GOTERM_CC_FAT GO:0005815~microtubule organizing center 7 2.258064516 0.322961901 "TUBGCP3, RABGAP1, NUBP2, RANBP1, PCM1, TUBGCP2, TOP2A" 236 253 12782 1.498526161 1 0.851234104 99.45199028
GOTERM_CC_FAT GO:0005856~cytoskeleton 28 9.032258065 0.397223938 "KIF23, CTTNBP2NL, LIMA1, RABGAP1, PDLIM2, CCT3, STAU1, KRT9, TUBGCP3, RANBP9, MACF1, NUBP2, KRT3, RANBP1, DDX20, TOP2A, ARHGDIB, CDK1, MAP2K1, PTPN13, DRG1, PCM1, TUBGCP2, KRT19, SMTN, RCC2, PKP2, TMOD3" 236 1381 12782 1.098123443 1 0.894758658 99.8837972
GOTERM_CC_FAT GO:0005874~microtubule 6 1.935483871 0.569691981 "KIF23, TUBGCP3, CDK1, MAP2K1, RCC2, TUBGCP2" 236 274 12782 1.18600767 1 0.968009764 99.99870825
GOTERM_CC_FAT GO:0044430~cytoskeletal part 17 5.483870968 0.68294189 "KIF23, CDK1, LIMA1, RABGAP1, MAP2K1, PCM1, TUBGCP2, STAU1, KRT9, TUBGCP3, KRT19, RANBP9, RCC2, NUBP2, KRT3, RANBP1, TOP2A" 236 952 12782 0.967161017 1 0.986140669 99.9999781

Annotation Cluster 36 Enrichment Score: 0.7325475031193392
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0051329~interphase of mitotic cell cycle 5 1.612903226 0.140829151 "EGFR, PPP6C, CDC123, KPNA2, ITGB1" 264 103 13528 2.487496322 1 0.803476271 92.29156107
GOTERM_BP_FAT GO:0051325~interphase 5 1.612903226 0.15157328 "EGFR, PPP6C, CDC123, KPNA2, ITGB1" 264 106 13528 2.417095483 1 0.816982972 93.76711111
GOTERM_BP_FAT GO:0000082~G1/S transition of mitotic cell cycle 3 0.967741935 0.297195534 "EGFR, PPP6C, ITGB1" 264 56 13528 2.74512987 1 0.939988002 99.74065456

Annotation Cluster 37 Enrichment Score: 0.7042298291401311
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0055002~striated muscle cell development 4 1.290322581 0.080146323 "KRT19, SDC1, AGRN, ITGB1" 264 52 13528 3.941724942 1 0.69697361 75.59889342
GOTERM_BP_FAT GO:0055001~muscle cell development 4 1.290322581 0.095135107 "KRT19, SDC1, AGRN, ITGB1" 264 56 13528 3.66017316 1 0.738006849 81.50993207
GOTERM_BP_FAT GO:0042692~muscle cell differentiation 5 1.612903226 0.209433459 "KRT19, SDC1, SOX15, AGRN, ITGB1" 264 121 13528 2.117455547 1 0.882791363 98.10877898
GOTERM_BP_FAT GO:0051146~striated muscle cell differentiation 4 1.290322581 0.244601961 "KRT19, SDC1, AGRN, ITGB1" 264 88 13528 2.329201102 1 0.91193446 99.12287554
GOTERM_CC_FAT GO:0009986~cell surface 6 1.935483871 0.771117296 "SDC1, IDE, PDLIM2, AGRN, ITGB1, HSPA8" 236 348 12782 0.933810637 1 0.995293047 99.99999972

Annotation Cluster 38 Enrichment Score: 0.6818718203139619
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007548~sex differentiation 8 2.580645161 0.02816955 "SDC1, CHD7, FKBP4, IDE, SOX15, TP63, RQCD1, BCL2L1" 264 151 13528 2.714830423 1 0.449876881 38.27345889
GOTERM_BP_FAT GO:0003006~reproductive developmental process 11 3.548387097 0.032293473 "SDC1, CHD7, PTGS2, RAN, FKBP4, IDE, SOX15, TP63, RQCD1, BCL2L1, TRIP13" 264 262 13528 2.151399491 1 0.472571528 42.55012096
GOTERM_BP_FAT GO:0046661~male sex differentiation 4 1.290322581 0.169357887 "SDC1, FKBP4, SOX15, BCL2L1" 264 73 13528 2.807804068 1 0.839410215 95.64141567

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GOTERM_BP_FAT	GO:0045137~development of primary sexual characteristics	5	1.612903226	0.23414542	"SDC1, CHD7, SOX15, TP63, BCL2L1"	264	127	13528	2.017418277	1	0.904262588	98.89370891
GOTERM_BP_FAT	GO:0008584~male gonad development	3	0.967741935	0.268287228	"SDC1, SOX15, BCL2L1"	264	52	13528	2.956293706	1	0.926701749	99.48777519
GOTERM_BP_FAT	GO:0046546~development of primary male sexual characteristics	3	0.967741935	0.361386411	"SDC1, SOX15, BCL2L1"	264	65	13528	2.365034965	1	0.964701677	99.94853105
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristics	3	0.967741935	0.389250133	"CHD7, TP63, BCL2L1"	264	69	13528	2.227931489	1	0.971787213	99.97576673
GOTERM_BP_FAT	GO:0046660~female sex differentiation	3	0.967741935	0.389250133	"CHD7, TP63, BCL2L1"	264	69	13528	2.227931489	1	0.971787213	99.97576673
GOTERM_BP_FAT	GO:0048608~reproductive structure development	4	1.290322581	0.444858889	"SDC1, SOX15, TP63, BCL2L1"	264	126	13528	1.626743627	1	0.980002485	99.99516517
GOTERM_BP_FAT	GO:0008406~gonad development	3	0.967741935	0.643938513	"SDC1, SOX15, BCL2L1"	264	112	13528	1.372564935	1	0.995772071	99.99999732

Annotation Cluster 39	Enrichment Score: 0.6749169329044443
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0032446~protein modification by small protein conjugation	6	1.935483871	0.114892466	"UBA3, PCNP, RNF20, TRIP12, CTR9, NAE1"	264	132	13528	2.329201102	1	0.775766003	87.26335505
GOTERM_BP_FAT	GO:0070647~protein modification by small protein conjugation or removal	6	1.935483871	0.201167639	"UBA3, PCNP, RNF20, TRIP12, CTR9, NAE1"	264	160	13528	1.921590909	1	0.87252977	97.74569202
GOTERM_BP_FAT	GO:0016567~protein ubiquitination	4	1.290322581	0.408695194	"PCNP, RNF20, TRIP12, CTR9"	264	119	13528	1.722434428	1	0.974725658	99.98596696

Annotation Cluster 40	Enrichment Score: 0.6723092994143586
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	9	2.903225806	0.103830369	"EGFR, NOTCH1, MACF1, MAP2K1, EFNB1, RAC1, HPRT1, PCM1, TOP2B"	264	245	13528	1.882374768	1	0.754152437	84.2915579
GOTERM_BP_FAT	GO:0030030~cell projection organization	12	3.870967742	0.104530927	"EGFR, LIMA1, NOTCH1, MACF1, MAP2K1, ATXN10, EFNB1, RAC1, ITGB4, HPRT1, PCM1, TOP2B"	264	368	13528	1.670948617	1	0.754039756	84.49761172
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	8	2.580645161	0.12163293	"EGFR, NOTCH1, MACF1, MAP2K1, EFNB1, RAC1, HPRT1, TOP2B"	264	213	13528	1.924598094	1	0.786598557	88.80565537
GOTERM_BP_FAT	GO:0031175~neuron projection development	9	2.903225806	0.126244896	"EGFR, NOTCH1, MACF1, MAP2K1, ATXN10, EFNB1, RAC1, HPRT1, TOP2B"	264	256	13528	1.801491477	1	0.786258332	89.75775131
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	9	2.903225806	0.126244896	"EGFR, NOTCH1, MACF1, MAP2K1, EFNB1, RAC1, HPRT1, PCM1, TOP2B"	264	256	13528	1.801491477	1	0.786258332	89.75775131
GOTERM_BP_FAT	GO:0030900~forebrain development	6	1.935483871	0.17452968	"KDM1A, NOTCH1, RAC1, HPRT1, TOP2B, SRC"	264	152	13528	2.022727273	1	0.84244484	96.07764814
GOTERM_BP_FAT	GO:0048666~neuron development	10	3.225806452	0.215219395	"EGFR, NOTCH1, MACF1, MAP2K1, ATXN10, EFNB1, RAC1, AGRN, HPRT1, TOP2B"	264	339	13528	1.511575936	1	0.887807307	98.32937909
GOTERM_BP_FAT	GO:0030182~neuron differentiation	12	3.870967742	0.237693533	"EGFR, DFNA5, NOTCH1, MACF1, MAP2K1, ATXN10, EFNB1, RAC1, AGRN, HPRT1, TOP2B, EPHA2"	264	438	13528	1.403902034	1	0.906967641	98.97713506
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GOTERM_BP_FAT GO:0032989~cellular component morphogenesis 11 3.548387097 0.245998132 "EGFR, KRT19, NOTCH1, MACF1, MAP2K1, EFNB1, RAC1, HPRT1, PCM1, TOP2B, ITGB1" 264 397 13528 1.419815281 1 0.912262665 99.14984974

GOTERM_BP_FAT GO:0048667~cell morphogenesis involved in neuron differentiation 6 1.935483871 0.381691397 "NOTCH1, MACF1, EFNB1, RAC1, HPRT1, TOP2B" 264 209 13528 1.47107438 1 0.971388601 99.97017314

GOTERM_BP_FAT GO:0000902~cell morphogenesis 9 2.903225806 0.38972342 "EGFR, NOTCH1, MACF1, MAP2K1, EFNB1, RAC1, HPRT1, PCM1, TOP2B" 264 356 13528 1.295454545 1 0.971520612 99.97608186

GOTERM_BP_FAT GO:0000904~cell morphogenesis involved in differentiation 6 1.935483871 0.512887586 "NOTCH1, MACF1, EFNB1, RAC1, HPRT1, TOP2B" 264 244 13528 1.260059613 1 0.986808475 99.99946816

GOTERM_BP_FAT GO:0007409~axonogenesis 5 1.612903226 0.516107464 "NOTCH1, MACF1, EFNB1, RAC1, TOP2B" 264 193 13528 1.327523944 1 0.987129488 99.99952451

Annotation Cluster 41 Enrichment Score: 0.6456825242480009

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0001942~hair follicle development 4 1.290322581 0.047837664 "NOTCH1, PTGS2, AARS, TP63" 264 42 13528 4.88023088 1 0.568586605 56.29349939

GOTERM_BP_FAT GO:0022404~molting cycle process 4 1.290322581 0.047837664 "NOTCH1, PTGS2, AARS, TP63" 264 42 13528 4.88023088 1 0.568586605 56.29349939

GOTERM_BP_FAT GO:0022405~hair cycle process 4 1.290322581 0.047837664 "NOTCH1, PTGS2, AARS, TP63" 264 42 13528 4.88023088 1 0.568586605 56.29349939

GOTERM_BP_FAT GO:0042633~hair cycle 4 1.290322581 0.050712437 "NOTCH1, PTGS2, AARS, TP63" 264 43 13528 4.766737139 1 0.583156853 58.4689227

GOTERM_BP_FAT GO:0042303~molting cycle 4 1.290322581 0.050712437 "NOTCH1, PTGS2, AARS, TP63" 264 43 13528 4.766737139 1 0.583156853 58.4689227

GOTERM_BP_FAT GO:0043588~skin development 3 0.967741935 0.10857389 "KRT9, AARS, TP63" 264 29 13528 5.300940439 1 0.762777416 85.63794695

GOTERM_BP_FAT GO:0008544~epidermis development 6 1.935483871 0.287884545 "KRT9, NOTCH1, PTGS2, MAP2K1, AARS, TP63" 264 184 13528 1.670948617 1 0.936680812 99.67611661

GOTERM_BP_FAT GO:0007398~ectoderm development 6 1.935483871 0.343590098 "KRT9, NOTCH1, PTGS2, MAP2K1, AARS, TP63" 264 199 13528 1.544997716 1 0.957849366 99.91813563

GOTERM_BP_FAT GO:0050678~regulation of epithelial cell proliferation 3 0.967741935 0.402981241 "EGFR, NOTCH1, SMAD3" 264 71 13528 2.165172855 1 0.974149034 99.9834929

GOTERM_BP_FAT GO:0048729~tissue morphogenesis 4 1.290322581 0.683613645 "NOTCH1, MACF1, SMAD3, TP63" 264 180 13528 1.138720539 1 0.997332857 99.99999964

GOTERM_BP_FAT GO:0043066~negative regulation of apoptosis 7 2.258064516 0.689717926 "EGFR, CDK1, NOTCH1, AARS, SMAD3, TP63, BCL2L1" 264 354 13528 1.013268276 1 0.9974541 99.99999974

GOTERM_BP_FAT GO:0043069~negative regulation of programmed cell death 7 2.258064516 0.702559865 "EGFR, CDK1, NOTCH1, AARS, SMAD3, TP63, BCL2L1" 264 359 13528 0.999155904 1 0.997630526 99.99999987

GOTERM_BP_FAT GO:0060548~negative regulation of cell death 7 2.258064516 0.705085172 "EGFR, CDK1, NOTCH1, AARS, SMAD3, TP63, BCL2L1" 264 360 13528 0.996380471 1 0.997647806 99.99999989

GOTERM_BP_FAT GO:0045596~negative regulation of cell differentiation 4 1.290322581 0.794842976 "NOTCH1, SMAD3, TP63, ITGB1" 264 216 13528 0.948933782 1 0.999339273 100

GOTERM_BP_FAT GO:0006916~anti-apoptosis 3 0.967741935 0.91256874 "CDK1, TP63, BCL2L1" 264 206 13528 0.746248897 1 0.999975925 100

Annotation Cluster 42 Enrichment Score: 0.64157174122118

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni

Benjamini	FDR

GOTERM_BP_FAT	GO:0034097~response to cytokine stimulus	5	1.612903226	0.067789444	"SP100, PTGS2, BCL2L1, STAT1, SRC"	264	79	13528	3.243191408	1	0.661952429	69.43251794
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	7	2.258064516	0.100804503	"EGFR, SDC1, PTGS2, MAP2K1, BCL2L1, STAT1, NDUFA12"	264	164	13528	2.187176644	1	0.751185035	83.37160495
GOTERM_BP_FAT	GO:0048661~positive regulation of smooth muscle cell proliferation	3	0.967741935	0.121314908	"EGFR, PTGS2, STAT1"	264	31	13528	4.958944282	1	0.787972656	88.73702487
GOTERM_BP_FAT	GO:0048660~regulation of smooth muscle cell proliferation	3	0.967741935	0.224956616	"EGFR, PTGS2, STAT1"	264	46	13528	3.341897233	1	0.897333756	98.64691209
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	3	0.967741935	0.297195534	"SDC1, BCL2L1, STAT1"	264	56	13528	2.74512987	1	0.939988002	99.74065456
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	6	1.935483871	0.366036498	"EGFR, SDC1, PTGS2, BCL2L1, STAT1, GART"	264	205	13528	1.499778271	1	0.966078343	99.95450584
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	4	1.290322581	0.419106657	"TF, PTGS2, BCL2L1, STAT1"	264	121	13528	1.693964438	1	0.976275225	99.98960349
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	3	0.967741935	0.429992007	"SDC1, BCL2L1, STAT1"	264	75	13528	2.04969697	1	0.978191077	99.99244605
GOTERM_BP_FAT	GO:0010038~response to metal ion	4	1.290322581	0.460095269	"EGFR, SDC1, PTGS2, BCL2L1"	264	129	13528	1.58891238	1	0.982307016	99.99697789

Annotation Cluster 43	Enrichment Score: 0.6414717267643266

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	29	9.35483871	4.97E-04	"HSP90AB1, SRP14, XPO5, IDE, ERI1, TP63, HAT1, BCL2L1, PAWR, RPS3, KDM1A, MOV10, PSMB6, SET, EIF3E, SOX15, DDX20, PSMD5, PSMD7, ANAPC1, MSH6, SP100, SMAD3, PA2G4, PSMC4, PSMA5, UBA3, PSME3, ADAR"	264	734	13528	2.024564446	0.573406667	0.033502884	0.835227433
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	15	4.838709677	0.114517401	"SP100, XPO5, SMAD3, TP63, HAT1, ERI1, BCL2L1, PAWR, KDM1A, MOV10, PA2G4, UBA3, SOX15, DDX20, ADAR"	264	504	13528	1.52507215	1	0.777002301	87.17191938
GOTERM_MF_FAT	GO:0016564~transcription repressor activity	10	3.225806452	0.155174859	"KDM1A, SP100, PLRG1, UBA3, SMAD3, TP63, PAWR, DDX20, IFI16, TRIM22"	251	316	12983	1.636870241	1	0.73689	91.07636039
GOTERM_BP_FAT	"GO:0045892~negative regulation of transcription, DNA-dependent"	9	2.903225806	0.38972342	"KDM1A, PA2G4, SP100, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20"	264	356	13528	1.295454545	1	0.971520612	99.97608186
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	9	2.903225806	0.407489163	"KDM1A, PA2G4, SP100, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20"	264	362	13528	1.273982923	1	0.974744668	99.98547579
GOTERM_BP_FAT	"GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process"	12	3.870967742	0.412413671	"KDM1A, MSH6, PA2G4, SP100, UBA3, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20, RPS3"	264	512	13528	1.200994318	1	0.975077544	99.98738484
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	7	2.258064516	0.414241007	"KDM1A, SP100, SMAD3, SOX15, TP63, PAWR, DDX20"	264	266	13528	1.348484848	1	0.975242789	99.98803114
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	12	3.870967742	0.436184132	"KDM1A, MSH6, PA2G4, SP100, UBA3, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20, RPS3"	264	519	13528	1.184795936	1	0.97943895	99.99371826
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	12	3.870967742	0.495344685	"KDM1A, SRP14, PA2G4, SP100, EIF3E, UBA3, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20"	264	547	13528	1.124148247	1	0.985507563	99.99903346
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	12	3.870967742	0.529726796	"KDM1A, SRP14, PA2G4, SP100, EIF3E, UBA3, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20"							

264 561 13528 1.096094636 1 0.98773381 99.99970637
GOTERM_BP_FAT GO:0016481~negative regulation of transcription 10 3.225806452 0.537751047 "KDM1A, PA2G4, SP100, UBA3, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20" 264 459 13528 1.116392685 1 0.988389364 99.99978042
GOTERM_BP_FAT GO:0006357~regulation of transcription from RNA polymerase II promoter 15 4.838709677 0.554101662 "IKBKAP, CNBP, SP100, MAP2K1, SUB1, RBM4, SMAD3, TP63, PAWR, KDM1A, NOTCH1, TIAL1, SOX15, DDX20, AGRN" 264 727 13528 1.057271477 1 0.989500164 99.99988046
GOTERM_BP_FAT GO:0009890~negative regulation of biosynthetic process 12 3.870967742 0.560902082 "KDM1A, SRP14, PA2G4, SP100, EIF3E, UBA3, SMAD3, SOX15, HAT1, TP63, PAWR, DDX20" 264 573 13528 1.073139775 1 0.990224472 99.99990778

Annotation Cluster 44 Enrichment Score: 0.6371161340275194
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006633~fatty acid biosynthetic process 5 1.612903226 0.067789444 "ELOVL1, PTGES3, PTGS2, FASN, FADS2" 264 79 13528 3.243191408 1 0.661952429 69.43251794
GOTERM_BP_FAT GO:0006636~unsaturated fatty acid biosynthetic process 3 0.967741935 0.141055095 "PTGES3, PTGS2, FADS2" 264 34 13528 4.521390374 1 0.802035655 92.32571711
GOTERM_BP_FAT GO:0046394~carboxylic acid biosynthetic process 6 1.935483871 0.184355679 "ELOVL1, PTGES3, PTGS2, MAT2A, FASN, FADS2" 264 155 13528 1.983577713 1 0.851877031 96.79567698
GOTERM_BP_FAT GO:0016053~organic acid biosynthetic process 6 1.935483871 0.184355679 "ELOVL1, PTGES3, PTGS2, MAT2A, FASN, FADS2" 264 155 13528 1.983577713 1 0.851877031 96.79567698
GOTERM_BP_FAT GO:0033559~unsaturated fatty acid metabolic process 3 0.967741935 0.26105104 "PTGES3, PTGS2, FADS2" 264 51 13528 3.01426025 1 0.923347979 99.39518623
GOTERM_BP_FAT GO:0006631~fatty acid metabolic process 5 1.612903226 0.540376021 "ELOVL1, PTGES3, PTGS2, FASN, FADS2" 264 198 13528 1.294000612 1 0.988594454 99.99980055
GOTERM_BP_FAT GO:0008610~lipid biosynthetic process 6 1.935483871 0.756661566 "ELOVL1, PTGES3, CNBP, PTGS2, FASN, FADS2" 264 323 13528 0.951871658 1 0.99871735 100

Annotation Cluster 45 Enrichment Score: 0.6258242869572778
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0010033~response to organic substance 21 6.774193548 0.069814625 "EGFR, HSP90AB1, TF, SP100, HSP90AA1, MAP2K1, MAT2A, PTGS2, RBM4, AARS, SMAD3, BCL2L1, HPRT1, STAT1, SRC, GART, HSPH1, KRT19, SDC1, EIF2AK2, HSPA8" 264 721 13528 1.492497793 1 0.669842953 70.53461619
GOTERM_BP_FAT GO:0006979~response to oxidative stress 7 2.258064516 0.100804503 "EGFR, SDC1, PTGS2, MAP2K1, BCL2L1, STAT1, NDUFA12" 264 164 13528 2.187176644 1 0.751185035 83.37160495
GOTERM_BP_FAT GO:0031960~response to corticosteroid stimulus 4 1.290322581 0.229080263 "SDC1, PTGS2, MAP2K1, SRC" 264 85 13528 2.4114082 1 0.900925414 98.76346277
GOTERM_BP_FAT GO:0009719~response to endogenous stimulus 11 3.548387097 0.26404784 "KRT19, SDC1, PTGS2, MAP2K1, MAT2A, RBM4, AARS, BCL2L1, HPRT1, STAT1, SRC" 264 405 13528 1.391769547 1 0.924991832 99.43529331
GOTERM_BP_FAT GO:0009725~response to hormone stimulus 9 2.903225806 0.420126728 "KRT19, SDC1, PTGS2, MAP2K1, MAT2A, RBM4, BCL2L1, STAT1, SRC" 264 367 13528 1.256626208 1 0.976206134 99.98990748
GOTERM_BP_FAT GO:0051384~response to glucocorticoid stimulus 3 0.967741935 0.449821801 "SDC1, PTGS2, MAP2K1" 264 78 13528 1.970862471 1 0.980576819 99.99584538
GOTERM_BP_FAT GO:0048545~response to steroid hormone stimulus 5 1.612903226 0.517264341 "KRT19, SDC1, PTGS2, MAP2K1, SRC" 264 192 13528 1.334438131 1 0.986922242 99.99954334

Annotation Cluster 46	Enrichment Score: 0.6203695175689001
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_CC_FAT	GO:0070161~anchoring junction	9	2.903225806	0.014216864	"SDC1, LIMA1, DSG2,
PKP2, DSC3, TRIP6, ITGB1, MLLT4, MLF2"	236	172	12782	2.834006701	0.985976625	0.156909683
17.39900625
GOTERM_BP_FAT	GO:0007155~cell adhesion	14	4.516129032	0.608085754	"EGFR, RPSA, AIMP1,
DSG2, PKP2, EFNB1, RAC1, ITGB4, DSC3, ITGA3, TRIP6, ITGB1, MLLT4, SRC"	264	700	13528
1.024848485	1	0.993803303	99.99998647
GOTERM_BP_FAT	GO:0022610~biological adhesion	14	4.516129032	0.610163503	"EGFR, RPSA, AIMP1,
DSG2, PKP2, EFNB1, RAC1, ITGB4, DSC3, ITGA3, TRIP6, ITGB1, MLLT4, SRC"	264	701	13528
1.023386504	1	0.993782785	99.99998763
GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	6	1.935483871	0.625614877	"EGFR, DSG2, PKP2,
DSC3, ITGB1, SRC"	264	276	13528	1.113965744	1	0.994917402	99.99999375

Annotation Cluster 47	Enrichment Score: 0.5775041494455133
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0046822~regulation of nucleocytoplasmic transport	4	1.290322581	0.103028396
"AAAS, G3BP2, SMAD3, TRIP6"	264	58	13528	3.533960293	1	0.753910154	84.05251253
GOTERM_BP_FAT	GO:0042990~regulation of transcription factor import into nucleus	3	0.967741935
0.114898608	"G3BP2, SMAD3, TRIP6"	264	30	13528	5.124242424	1	0.773394861	87.26484731
GOTERM_BP_FAT	GO:0032386~regulation of intracellular transport	4	1.290322581	0.15988721	"AAAS,
G3BP2, SMAD3, TRIP6"	264	71	13528	2.88689714	1	0.829319737	94.72188571
GOTERM_BP_FAT	GO:0042306~regulation of protein import into nucleus	3	0.967741935	0.210618334
"G3BP2, SMAD3, TRIP6"	264	44	13528	3.493801653	1	0.883056807	98.15607261
GOTERM_BP_FAT	GO:0033157~regulation of intracellular protein transport	3	0.967741935	0.275522406
"G3BP2, SMAD3, TRIP6"	264	53	13528	2.90051458	1	0.929874033	99.5668956
GOTERM_BP_FAT	GO:0051223~regulation of protein transport	4	1.290322581	0.382439333	"GAPVD1,
G3BP2, SMAD3, TRIP6"	264	114	13528	1.797979798	1	0.970766658	99.97077652
GOTERM_BP_FAT	GO:0070201~regulation of establishment of protein localization	4	1.290322581
0.419106657	"GAPVD1, G3BP2, SMAD3, TRIP6"	264	121	13528	1.693964438	1	0.976275225
99.98960349
GOTERM_BP_FAT	GO:0032880~regulation of protein localization	4	1.290322581	0.504667732
"GAPVD1, G3BP2, SMAD3, TRIP6"	264	138	13528	1.485287659	1	0.985840368	99.99929452
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	5	1.612903226	0.714219133	"AAAS,
CHD7, G3BP2, SMAD3, TRIP6"	264	248	13528	1.033113392	1	0.997839459	99.99999993

Annotation Cluster 48	Enrichment Score: 0.570689575309221
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0019674~NAD metabolic process	3	0.967741935	0.084316228	"LDHB, IDH3B,
IDH3A"	264	25	13528	6.149090909	1	0.707170833	77.4008285
GOTERM_BP_FAT	GO:0046496~nicotinamide nucleotide metabolic process	3	0.967741935	0.182268203
"LDHB, IDH3B, IDH3A"	264	40	13528	3.843181818	1	0.849849892	96.65435983
GOTERM_BP_FAT	GO:0006769~nicotinamide metabolic process	3	0.967741935	0.182268203	"LDHB,
IDH3B, IDH3A"	264	40	13528	3.843181818	1	0.849849892	96.65435983
GOTERM_BP_FAT	GO:0009820~alkaloid metabolic process	3	0.967741935	0.189305241	"LDHB,
IDH3B, IDH3A"	264	41	13528	3.749445676	1	0.858586392	97.10863477
GOTERM_BP_FAT	GO:0019362~pyridine nucleotide metabolic process	3	0.967741935	0.19637862
"LDHB, IDH3B, IDH3A"	264	42	13528	3.66017316	1	0.86679092	97.50630946
GOTERM_MF_FAT	GO:0051287~NAD or NADH binding	3	0.967741935	0.228929108	"LDHB, IDH3B,
IDH3A"	251	47	12983	3.301602102	1	0.816742608	97.58998155
GOTERM_BP_FAT	GO:0006733~oxidoreduction coenzyme metabolic process	3	0.967741935	0.268287228

"LDHB, IDH3B, IDH3A" 264 52 13528 2.956293706 1 0.926701749 99.48777519
GOTERM_BP_FAT GO:0043603~cellular amide metabolic process 3 0.967741935 0.297195534 "LDHB, IDH3B, IDH3A" 264 56 13528 2.74512987 1 0.939988002 99.74065456
GOTERM_BP_FAT GO:0006732~coenzyme metabolic process 5 1.612903226 0.346930694 "MTHFD2, LDHB, PDXK, IDH3B, IDH3A" 264 153 13528 1.674589028 1 0.958864703 99.92489283
GOTERM_MF_FAT GO:0048037~cofactor binding 7 2.258064516 0.34739531 "KDM1A, LDHB, PDXK, FASN, IDH3B, GALE, IDH3A" 251 249 12983 1.454119266 1 0.906461804 99.77926571
GOTERM_BP_FAT GO:0006091~generation of precursor metabolites and energy 8 2.580645161 0.407480803 "LDHB, NDUFB10, FADS2, IDH3B, SURF1, MON2, IDH3A, NDUFA12" 264 313 13528 1.309710524 1 0.975121646 99.98547233
GOTERM_BP_FAT GO:0019748~secondary metabolic process 3 0.967741935 0.456345247 "LDHB, IDH3B, IDH3A" 264 79 13528 1.945914845 1 0.981767757 99.99660323
GOTERM_MF_FAT GO:0050662~coenzyme binding 5 1.612903226 0.456607154 "KDM1A, LDHB, IDH3B, GALE, IDH3A" 251 181 12983 1.428870155 1 0.95645519 99.98400125
GOTERM_BP_FAT GO:0051186~cofactor metabolic process 5 1.612903226 0.526505295 "MTHFD2, LDHB, PDXK, IDH3B, IDH3A" 264 195 13528 1.313908314 1 0.987611112 99.9996705

Annotation Cluster 49 Enrichment Score: 0.5408018653596457
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0030057~desmosome 3 0.967741935 0.051464087 "DSG2, PKP2, DSC3" 236 20 12782 8.124152542 0.999999855 0.398244329 50.60512052
GOTERM_CC_FAT GO:0043296~apical junction complex 4 1.290322581 0.274108508 "DSG2, PKP2, DSC3, LIN7C" 236 99 12782 2.188323917 1 0.823730324 98.61093652
GOTERM_CC_FAT GO:0016327~apicolateral plasma membrane4 1.290322581 0.289134981 "DSG2, PKP2, DSC3, LIN7C" 236 102 12782 2.123961449 1 0.826822062 98.9493726
GOTERM_CC_FAT GO:0005911~cell-cell junction 5 1.612903226 0.462806141 "DSG2, PKP2, DSC3, LIN7C, MLLT4" 236 190 12782 1.42528992 1 0.931690834 99.97503027
GOTERM_CC_FAT GO:0030054~cell junction 11 3.548387097 0.48189808 "SDC1, LIMA1, DSG2, MACF1, PKP2, DSC3, LIN7C, TRIP6, ITGB1, MLLT4, MLF2" 236 518 12782 1.150137426 1 0.939155025 99.98459658
GOTERM_BP_FAT GO:0016337~cell-cell adhesion 6 1.935483871 0.625614877 "EGFR, DSG2, PKP2, DSC3, ITGB1, SRC" 264 276 13528 1.113965744 1 0.994917402 99.99999375

Annotation Cluster 50 Enrichment Score: 0.5071357911426048
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT "GO:0016591~DNA-directed RNA polymerase II, holoenzyme" 5 1.612903226 0.061953773 "GTF2E1, IKBKAP, GTF2F1, POLR2B, CTR9" 236 81 12782 3.343272651 0.999999995 0.419891471 57.41952045
GOTERM_BP_FAT GO:0006368~RNA elongation from RNA polymerase II promoter 3 0.967741935 0.239364893 "GTF2E1, GTF2F1, POLR2B" 264 48 13528 3.202651515 1 0.9076215 99.01434855
GOTERM_BP_FAT GO:0006354~RNA elongation 3 0.967741935 0.26105104 "GTF2E1, GTF2F1, POLR2B" 264 51 13528 3.01426025 1 0.923347979 99.39518623
GOTERM_BP_FAT GO:0006367~transcription initiation from RNA polymerase II promoter 3 0.967741935 0.382332352 "GTF2E1, GTF2F1, POLR2B" 264 68 13528 2.260695187 1 0.97116978 99.97069093
GOTERM_BP_FAT GO:0006366~transcription from RNA polymerase II promoter 6 1.935483871 0.476363235 "GTF2E1, GTF2F1, BTF3, STAT1, POLR2B, TRIP13" 264 234 13528 1.313908314 1 0.98407782 99.99819712
GOTERM_BP_FAT GO:0006352~transcription initiation 3 0.967741935 0.481986024 "GTF2E1, GTF2F1, POLR2B" 264 83 13528 1.852135816 1 0.984670098 99.99849755
GOTERM_BP_FAT "GO:0006351~transcription, DNA-dependent" 7 2.258064516 0.49873748 "GTF2E1, GTF2F1, BTF3, POLR1C, STAT1, POLR2B, TRIP13" 264 292 13528 1.22841428 1 0.985667731 99.99913751

GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	7	2.258064516	0.517337894	"GTF2E1, GTF2F1, BTF3, POLR1C, STAT1, POLR2B, TRIP13"	264	296	13528	1.211814087	1	0.986736512	99.99954451

Annotation Cluster 51	Enrichment Score: 0.506978048956781
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009060~aerobic respiration	3	0.967741935	0.14778047	"IDH3B, SURF1, IDH3A"	264	35	13528	4.392207792	1	0.816012277	93.27956945
GOTERM_BP_FAT	GO:0045333~cellular respiration	4	1.290322581	0.29200005	"NDUFB10, IDH3B, SURF1, IDH3A"	264	97	13528	2.113089659	1	0.937981529	99.70631126
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	8	2.580645161	0.407480803	"LDHB, NDUFB10, FADS2, IDH3B, SURF1, MON2, IDH3A, NDUFA12"	264	313	13528	1.309710524	1	0.975121646	99.98547233
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	4	1.290322581	0.533311174	"NDUFB10, IDH3B, SURF1, IDH3A"	264	144	13528	1.423400673	1	0.987911522	99.99974195

Annotation Cluster 52	Enrichment Score: 0.4945679060897601
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016407~acetyltransferase activity	4	1.290322581	0.20979641	"NAA50, NAA10, FASN, HAT1"	251	82	12983	2.52317559	1	0.793937428	96.57577223
GOTERM_BP_FAT	GO:0006473~protein amino acid acetylation	3	0.967741935	0.268287228	"NAA50, NAA10, HAT1"	264	52	13528	2.956293706	1	0.926701749	99.48777519
GOTERM_BP_FAT	GO:0043543~protein amino acid acylation	3	0.967741935	0.325927477	"NAA50, NAA10, HAT1"	264	60	13528	2.562121212	1	0.949199589	99.87182644
GOTERM_MF_FAT	GO:0008080~N-acetyltransferase activity	3	0.967741935	0.3847104	"NAA50, NAA10, HAT1"	251	69	12983	2.248917374	1	0.926199317	99.90506342
GOTERM_MF_FAT	GO:0016410~N-acyltransferase activity	3	0.967741935	0.47698807	"NAA50, NAA10, HAT1"	251	83	12983	1.869581913	1	0.962944413	99.99074942

Annotation Cluster 53	Enrichment Score: 0.47405430417549016
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0008305~integrin complex	3	0.967741935	0.098875543	"ITGB4, ITGA3, ITGB1"	236	29	12782	5.602863822	1	0.54865429	75.08824445
GOTERM_CC_FAT	GO:0043235~receptor complex	5	1.612903226	0.165244424	"ITGB4, SMAD3, ITGA3, TRIP6, ITGB1"	236	116	12782	2.334526593	1	0.681834734	91.02850416
GOTERM_BP_FAT	GO:0007160~cell-matrix adhesion	4	1.290322581	0.249813585	"ITGB4, ITGA3, TRIP6, ITGB1"	264	89	13528	2.303030303	1	0.914969282	99.2196394
GOTERM_BP_FAT	GO:0031589~cell-substrate adhesion	4	1.290322581	0.29731661	"ITGB4, ITGA3, TRIP6, ITGB1"	264	98	13528	2.09152752	1	0.939284399	99.7414079
GOTERM_BP_FAT	GO:0007229~integrin-mediated signaling pathway	3	0.967741935	0.396133522	"ITGB4, ITGA3, ITGB1"	264	70	13528	2.196103896	1	0.97320272	99.97998761
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	10	3.225806452	0.999629533	"SLC1A5, ATP1B1, SDC1, EFNB1, ITGB4, FADS2, ITGA3, TRIP6, ITGB1, EPHA2"	236	1188	12782	0.455900816	1	1	100
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	10	3.225806452	0.999742782	"SLC1A5, ATP1B1, SDC1, EFNB1, ITGB4, FADS2, ITGA3, TRIP6, ITGB1, EPHA2"	236	1215	12782	0.445769687	1	1	100

Annotation Cluster 54	Enrichment Score: 0.46563994633855754
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni

Benjamini	FDR
GOTERM_BP_FAT	GO:0051493~regulation of cytoskeleton organization	6	1.935483871	0.125927511
"LIMA1, MACF1, RAC1, SMAD3, RANBP1, ARAP1"	264	136	13528	2.260695187	1	0.789786142
89.6947523
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization	8	2.580645161	0.13040634
"LIMA1, SET, MACF1, PRMT5, RAC1, SMAD3, RANBP1, ARAP1"	264	217	13528	1.889121631	1
0.789037642	90.55096028
GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	4	1.290322581	0.249813585
"LIMA1, RAC1, SMAD3, ARAP1"	264	89	13528	2.303030303	1	0.914969282	99.2196394
GOTERM_BP_FAT	GO:0032970~regulation of actin filament-based process	4	1.290322581	0.265543273
"LIMA1, RAC1, SMAD3, ARAP1"	264	92	13528	2.227931489	1	0.925321369	99.45435817
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	7	2.258064516	0.275356338	"KRT19,
LIMA1, DIAPH3, RAC1, ITGB1, ARAP1, ARHGDIB"	264	226	13528	1.587154733	1	0.930636965
99.56521628
GOTERM_BP_FAT	GO:0051129~negative regulation of cellular component organization	5	1.612903226
0.298479862	"LIMA1, SET, PACSIN3, RAC1, ARAP1"	264	142	13528	1.804310713	1	0.939295557
99.74854163
GOTERM_BP_FAT	GO:0030029~actin filament-based process	7	2.258064516	0.324234616	"KRT19,
LIMA1, DIAPH3, RAC1, ITGB1, ARAP1, ARHGDIB"	264	241	13528	1.488369169	1	0.949572569
99.86628165
GOTERM_BP_FAT	GO:0007015~actin filament organization	3	0.967741935	0.409792075	"LIMA1,
RAC1, ARAP1"	264	72	13528	2.13510101	1	0.974674888	99.98640008
GOTERM_BP_FAT	GO:0010639~negative regulation of organelle organization	3	0.967741935	0.475645163
"LIMA1, SET, ARAP1"	264	82	13528	1.874722838	1	0.984184198	99.99815492
GOTERM_BP_FAT	GO:0010638~positive regulation of organelle organization	3	0.967741935	0.481986024
"RAC1, SMAD3, RANBP1"	264	83	13528	1.852135816	1	0.984670098	99.99849755
GOTERM_BP_FAT	GO:0044087~regulation of cellular component biogenesis	4	1.290322581	0.523865528
"RAC1, SMAD3, AGRN, ARAP1"	264	142	13528	1.44344857	1	0.987390178	99.99963807
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organization	4	1.290322581
0.68722643	"RAC1, SMAD3, RANBP1, ARAP1"	264	181	13528	1.132429265	1	0.997394571
99.9999997
GOTERM_BP_FAT	GO:0032535~regulation of cellular component size	4	1.290322581	0.900823617
"LIMA1, RAC1, SMAD3, TP63"	264	271	13528	0.756345745	1	0.999963354	100

Annotation Cluster 55	Enrichment Score: 0.46467618414092315
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0007265~Ras protein signal transduction	5	1.612903226	0.147957475
"MAP2K1, G3BP1, G3BP2, SRC, ARHGDIB"	264	105	13528	2.44011544	1	0.814497323	93.30309842
GOTERM_BP_FAT	GO:0030155~regulation of cell adhesion	4	1.290322581	0.499806585	"MAP2K1,
SMAD3, SRC, ARHGDIB"	264	137	13528	1.496129175	1	0.98563783	99.99916805
GOTERM_BP_FAT	GO:0007264~small GTPase mediated signal transduction	7	2.258064516	0.545798784
"RAB18, MAP2K1, G3BP1, RAC1, G3BP2, SRC, ARHGDIB"	264	305	13528	1.176055638	1	0.98901999
99.99983677

Annotation Cluster 56	Enrichment Score: 0.4610245138468948
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	7	2.258064516	0.135420639
"EGFR, MSH6, MAP2K1, SMAD3, STAT1, ARAP1, RPS3"	264	179	13528	2.003893685	1	0.795974851
91.42997163
GOTERM_BP_FAT	GO:0006919~activation of caspase activity	3	0.967741935	0.282753887	"SMAD3,
STAT1, RPS3"	264	54	13528	2.846801347	1	0.933734066	99.63437911
GOTERM_BP_FAT	GO:0043280~positive regulation of caspase activity	3	0.967741935	0.318768958

"SMAD3, STAT1, RPS3" 264 59 13528 2.605546995 1 0.94914489 99.84679914

GOTERM_BP_FAT GO:0010952~positive regulation of peptidase activity 3 0.967741935 0.318768958 "SMAD3, STAT1, RPS3" 264 59 13528 2.605546995 1 0.94914489 99.84679914

GOTERM_BP_FAT GO:0043281~regulation of caspase activity 3 0.967741935 0.456345247 "SMAD3, STAT1, RPS3" 264 79 13528 1.945914845 1 0.981767757 99.99660323

GOTERM_BP_FAT GO:0052548~regulation of endopeptidase activity 3 0.967741935 0.475645163 "SMAD3, STAT1, RPS3" 264 82 13528 1.874722838 1 0.984184198 99.99815492

GOTERM_BP_FAT GO:0051336~regulation of hydrolase activity 8 2.580645161 0.484824339 "EGFR, MSH6, RABGAP1, MAP2K1, SMAD3, STAT1, ARAP1, RPS3" 264 337 13528 1.216437371 1 0.98496393 99.99863066

GOTERM_BP_FAT GO:0052547~regulation of peptidase activity 3 0.967741935 0.500722803 "SMAD3, STAT1, RPS3" 264 86 13528 1.787526427 1 0.985581556 99.99919341

Annotation Cluster 57 Enrichment Score: 0.449109567194853

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0004672~protein kinase activity 16 5.161290323 0.192082569 "EGFR, CSNK1A1, CDK1, IKBKAP, MAP2K1, STK24, MINK1, CAD, PBK, STK3, EPHA2, SRC, POLR2B, TP53RK, SLK, EIF2AK2" 251 606 12983 1.365679197 1 0.780197263 95.29526573

GOTERM_BP_FAT GO:0006468~protein amino acid phosphorylation 16 5.161290323 0.312155831 "EGFR, CSNK1A1, CDK1, IKBKAP, MAP2K1, STK24, MINK1, CAD, PBK, STAT1, STK3, EPHA2, SRC, TP53RK, SLK, EIF2AK2" 264 667 13528 1.22920358 1 0.946620255 99.81965575

GOTERM_MF_FAT GO:0004674~protein serine/threonine kinase activity 11 3.548387097 0.31580224 "TP53RK, EGFR, CSNK1A1, CDK1, MAP2K1, SLK, STK24, MINK1, PBK, EIF2AK2, STK3" 251 430 12983 1.323200222 1 0.890130705 99.56539666

GOTERM_BP_FAT GO:0016310~phosphorylation 18 5.806451613 0.384393206 "EGFR, CSNK1A1, CDK1, IKBKAP, NDUFB10, MAP2K1, STK24, MINK1, CAD, PBK, STAT1, STK3, EPHA2, SRC, MON2, TP53RK, SLK, EIF2AK2" 264 800 13528 1.152954545 1 0.971002327 99.97229902

GOTERM_BP_FAT GO:0006796~phosphate metabolic process 20 6.451612903 0.526800454 "EGFR, CSNK1A1, CDK1, PPP6C, IKBKAP, NDUFB10, MAP2K1, STK24, MINK1, PTPN13, CAD, PBK, STAT1, STK3, EPHA2, SRC, MON2, TP53RK, SLK, EIF2AK2" 264 973 13528 1.05328724 1 0.987469868 99.99967395

GOTERM_BP_FAT GO:0006793~phosphorus metabolic process 20 6.451612903 0.526800454 "EGFR, CSNK1A1, CDK1, PPP6C, IKBKAP, NDUFB10, MAP2K1, STK24, MINK1, PTPN13, CAD, PBK, STAT1, STK3, EPHA2, SRC, MON2, TP53RK, SLK, EIF2AK2" 264 973 13528 1.05328724 1 0.987469868 99.99967395

Annotation Cluster 58 Enrichment Score: 0.44380216739058637

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0005643~nuclear pore 6 1.935483871 0.015082724 "AAAS, CSE1L, IPO7, RAN, KPNA6, KPNA2" 236 79 12782 4.113494958 0.989207376 0.159861205 18.36230113

GOTERM_CC_FAT GO:0046930~pore complex 6 1.935483871 0.030708094 "AAAS, CSE1L, IPO7, RAN, KPNA6, KPNA2" 236 95 12782 3.420695807 0.999908068 0.282473251 34.05574234

GOTERM_CC_FAT GO:0005635~nuclear envelope 7 2.258064516 0.176753999 "AAAS, CSE1L, IPO7, RAN, SMAD3, KPNA6, KPNA2" 236 205 12782 1.849400579 1 0.701062923 92.54629755

GOTERM_CC_FAT GO:0031967~organelle envelope 14 4.516129032 0.353374272 "NDUFB10, RAN, PNPT1, SMAD3, BCL2L1, MON2, NDUFA12, AAAS, CSE1L, IPO7, KPNA6, AKAP1, KPNA2, SURF1" 236 620 12782 1.222990705 1 0.864507037 99.70328963

GOTERM_CC_FAT GO:0031975~envelope 14 4.516129032 0.362544634 "NDUFB10, RAN, PNPT1, SMAD3, BCL2L1, MON2, NDUFA12, AAAS, CSE1L, IPO7, KPNA6, AKAP1, KPNA2, SURF1" 236 622 12782 1.219058259 1 0.869063377 99.75479812

GOTERM_CC_FAT GO:0070469~respiratory chain 3 0.967741935 0.402448728 "NDUFB10, SURF1, NDUFA12" 236 75 12782 2.166440678 1 0.895287847 99.89654656

GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	8	2.580645161	0.407480803	"LDHB, NDUFB10, FADS2, IDH3B, SURF1, MON2, IDH3A, NDUFA12"	264	313	13528	1.309710524	1	0.975121646	99.98547233
GOTERM_CC_FAT	GO:0044455~mitochondrial membrane part	3	0.967741935	0.672960554	"NDUFB10, SURF1, MON2"	236	125	12782	1.299864407	1	0.985243003	99.99996687
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	7	2.258064516	0.787190398	"NDUFB10, PNPT1, BCL2L1, AKAP1, SURF1, MON2, NDUFA12"	236	419	12782	0.904837992	1	0.996134145	99.99999989
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	6	1.935483871	0.854683354	"NDUFB10, BCL2L1, AKAP1, SURF1, MON2, NDUFA12"	236	394	12782	0.82478706	1	0.998316035	100
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	5	1.612903226	0.858967258	"NDUFB10, SMAD3, SURF1, MON2, NDUFA12"	236	329	12782	0.823115759	1	0.998362216	100
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	4	1.290322581	0.923455399	"NDUFB10, SURF1, MON2, NDUFA12"	236	306	12782	0.70798715	1	0.999684488	100
GOTERM_CC_FAT	GO:0012505~endomembrane system	8	2.580645161	0.990929354	"EGFR, AAAS, CSE1L, IPO7, RAN, SMAD3, KPNA6, KPNA2"	236	782	12782	0.5540769	1	0.999998594	100
GOTERM_CC_FAT	GO:0031090~organelle membrane	8	2.580645161	0.999870514	"EGFR, NDUFB10, SMAD3, BCL2L1, AKAP1, SURF1, MON2, NDUFA12"	236	1096	12782	0.39533589	1	1	100

Annotation Cluster 59	Enrichment Score: 0.4307434538596526
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	7	2.258064516	0.128362076	"KDM1A, PRMT1, CHD7, PSMC4, BTF3, BCL2L1, ITGB1"	264	176	13528	2.038050964	1	0.787764174	90.16881921
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	7	2.258064516	0.626137864	"KDM1A, PRMT1, CHD7, PSMC4, BTF3, BCL2L1, ITGB1"	264	331	13528	1.083676646	1	0.994871379	99.9999939
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	7	2.258064516	0.634838035	"KDM1A, PRMT1, CHD7, PSMC4, BTF3, BCL2L1, ITGB1"	264	334	13528	1.073943023	1	0.995246929	99.9999959

Annotation Cluster 60	Enrichment Score: 0.39602073736613785
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0003682~chromatin binding	8	2.580645161	0.026059278	"MSH6, NOTCH1, CHD7, RAN, SOX15, TP63, TOP2B, TOP2A"	251	150	12983	2.758671979	0.999997108	0.298310939	31.50373245
GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	3	0.967741935	0.50687138	"NOTCH1, CHD7, TP63"	264	87	13528	1.766980146	1	0.986008352	99.99934568
GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	3	0.967741935	0.50687138	"NOTCH1, CHD7, TP63"	264	87	13528	1.766980146	1	0.986008352	99.99934568
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	3	0.967741935	0.576714911	"NOTCH1, CHD7, TP63"	264	99	13528	1.552800735	1	0.991401212	99.99995035
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	3	0.967741935	0.576714911	"NOTCH1, CHD7, TP63"	264	99	13528	1.552800735	1	0.991401212	99.99995035
GOTERM_BP_FAT	GO:0048736~appendage development	3	0.967741935	0.598339764	"NOTCH1, CHD7, TP63"	264	103	13528	1.492497793	1	0.993139389	99.99997952
GOTERM_BP_FAT	GO:0060173~limb development	3	0.967741935	0.598339764	"NOTCH1, CHD7, TP63"	264	103	13528	1.492497793	1	0.993139389	99.99997952
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	5	1.612903226	0.851643997	"NOTCH1, CHD7, MACF1, SMAD3, TP63"	264	307	13528	0.83456717	1	0.999822131	100

Annotation Cluster 61	Enrichment Score: 0.3949410097697996

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0043433~negative regulation of transcription factor activity 3 0.967741935 0.217776989 "KDM1A, SP100, RPS3" 264 45 13528 3.416161616 1 0.889792994 98.41896599

GOTERM_BP_FAT GO:0043392~negative regulation of DNA binding 3 0.967741935 0.26105104 "KDM1A, SP100, RPS3" 264 51 13528 3.01426025 1 0.923347979 99.39518623

GOTERM_BP_FAT GO:0051100~negative regulation of binding 3 0.967741935 0.318768958 "KDM1A, SP100, RPS3" 264 59 13528 2.605546995 1 0.94914489 99.84679914

GOTERM_BP_FAT GO:0051098~regulation of binding 4 1.290322581 0.574474372 "KDM1A, SP100, SMAD3, RPS3" 264 153 13528 1.339671222 1 0.991280778 99.99994573

GOTERM_BP_FAT GO:0051090~regulation of transcription factor activity 3 0.967741935 0.598339764 "KDM1A, SP100, RPS3" 264 103 13528 1.492497793 1 0.993139389 99.99997952

GOTERM_BP_FAT GO:0051101~regulation of DNA binding 3 0.967741935 0.685365089 "KDM1A, SP100, RPS3" 264 121 13528 1.270473328 1 0.997361399 99.99999967

Annotation Cluster 62 Enrichment Score: 0.37592348735984066

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0008134~transcription factor binding 19 6.129032258 0.010328575 "PDCD11, SP100, SUB1, RAN, RBM4, SMAD3, DRG1, PAWR, TRIM22, RPS3, KDM1A, PLRG1, RAB18, GTF2F1, WDR77, TRIP6, RNF20, TRIP12, TRIP13" 251 513 12983 1.91574443 0.993360003 0.158794042 13.82429785

GOTERM_BP_FAT GO:0016202~regulation of striated muscle tissue development 4 1.290322581 0.073073605 "NOTCH1, SMAD3, SOX15, AGRN" 264 50 13528 4.099393939 1 0.674327522 72.23000556

GOTERM_BP_FAT GO:0048634~regulation of muscle development 4 1.290322581 0.076573674 "NOTCH1, SMAD3, SOX15, AGRN" 264 51 13528 4.019013666 1 0.68276186 73.94838719

GOTERM_BP_FAT GO:0010604~positive regulation of macromolecule metabolic process 22 7.096774194 0.16328834 "ANAPC1, CDK1, CNBP, SP100, MAP2K1, RAN, RBM4, SMAD3, TP63, PAWR, NOTCH1, PSMB6, PSMC4, PACSIN3, PSMA5, GTF2F1, SOX15, PSME3, AGRN, PSMD5, PSMD7, RNF20" 264 857 13528 1.315441462 1 0.832700614 95.07130312

GOTERM_MF_FAT GO:0003712~transcription cofactor activity 11 3.548387097 0.163901306 "SP100, PLRG1, SUB1, RAN, GTF2F1, WDR77, RBM4, PAWR, TRIM22, RNF20, TRIP13" 251 363 12983 1.567427261 1 0.741007367 92.31007088

GOTERM_MF_FAT GO:0003713~transcription coactivator activity 7 2.258064516 0.231540146 "SP100, SUB1, RAN, GTF2F1, WDR77, RBM4, RNF20" 251 214 12983 1.69194251 1 0.816599538 97.70432737

GOTERM_BP_FAT GO:0051173~positive regulation of nitrogen compound metabolic process 16 5.161290323 0.272314074 "EGFR, HSP90AB1, CNBP, SP100, HSP90AA1, MAP2K1, RAN, RBM4, SMAD3, TP63, HPRT1, NOTCH1, GTF2F1, SOX15, AGRN, RNF20" 264 644 13528 1.273103708 1 0.929099371 99.53334682

GOTERM_MF_FAT GO:0016563~transcription activator activity 10 3.225806452 0.392145729 "NOTCH1, SP100, SUB1, RAN, GTF2F1, WDR77, RBM4, SMAD3, TP63, RNF20" 251 410 12983 1.261587795 1 0.928800962 99.92024319

GOTERM_BP_FAT GO:0031328~positive regulation of cellular biosynthetic process 15 4.838709677 0.468007844 "EGFR, HSP90AB1, CNBP, HSP90AA1, SP100, RAN, RBM4, SMAD3, TP63, PAWR, NOTCH1, GTF2F1, SOX15, AGRN, RNF20" 264 685 13528 1.122096881 1 0.983426195 99.99764468

GOTERM_BP_FAT GO:0009891~positive regulation of biosynthetic process 15 4.838709677 0.49733709 "EGFR, HSP90AB1, CNBP, HSP90AA1, SP100, RAN, RBM4, SMAD3, TP63, PAWR, NOTCH1, GTF2F1, SOX15, AGRN, RNF20" 264 695 13528 1.105951602 1 0.985639899 99.99909591

GOTERM_BP_FAT GO:0006357~regulation of transcription from RNA polymerase II promoter 15 4.838709677 0.554101662 "IKBKAP, CNBP, SP100, MAP2K1, SUB1, RBM4, SMAD3, TP63, PAWR, KDM1A, NOTCH1, TIAL1, SOX15, DDX20, AGRN" 264 727 13528 1.057271477 1 0.989500164 99.99988046

GOTERM_BP_FAT GO:0051254~positive regulation of RNA metabolic process 10 3.225806452 0.594387276 "CNBP, NOTCH1, SP100, MAP2K1, RAN, RBM4, SMAD3, SOX15, TP63, AGRN" 264 481 13528 1.065331065 1 0.992875541 99.99997584

GOTERM_BP_FAT GO:0045941~positive regulation of transcription 11 3.548387097 0.662344421 "CNBP,

NOTCH1, SP100, RAN, GTF2F1, RBM4, SMAD3, SOX15, TP63, AGRN, RNF20"	264	564	13528	0.999408983	1	0.996516266	99.99999891
GOTERM_BP_FAT	"GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process"	12	3.870967742	0.673700548	"CNBP, NOTCH1, SP100, MAP2K1, RAN, GTF2F1, RBM4, SMAD3, SOX15, TP63, AGRN, RNF20"	264	624	13528	0.985431235	1	0.996980636	99.99999939
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	11	3.548387097	0.698144867	"CNBP, NOTCH1, SP100, RAN, GTF2F1, RBM4, SMAD3, SOX15, TP63, AGRN, RNF20"	264	581	13528	0.97016638	1	0.997580433	99.99999984
GOTERM_BP_FAT	"GO:0045893~positive regulation of transcription, DNA-dependent"	9	2.903225806	0.714074145	"CNBP, NOTCH1, SP100, RAN, RBM4, SMAD3, SOX15, TP63, AGRN"	264	477	13528	0.966838193	1	0.997871824	99.99999993
GOTERM_BP_FAT	GO:0042060~wound healing	4	1.290322581	0.721668772	"SDC1, NOTCH1, SMAD3, SOX15"	264	191	13528	1.073139775	1	0.99799791	99.99999996
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	12	3.870967742	0.731597689	"CNBP, NOTCH1, SP100, RAN, GTF2F1, RBM4, SMAD3, SOX15, TP63, PAWR, AGRN, RNF20"	264	654	13528	0.940227968	1	0.9982603	99.99999998
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	7	2.258064516	0.73190902	"CNBP, NOTCH1, RBM4, SMAD3, SOX15, TP63, AGRN"	264	371	13528	0.966838193	1	0.998238845	99.99999998
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	27	8.709677419	0.760465073	"CNBP, RBM4, TP63, PAWR, KDM1A, ZFP36L2, GTF2E1, PLRG1, WDR77, BTF3, SOX15, DDX20, TRIP13, IKBKAP, SP100, SUB1, RAN, SMAD3, IFI16, STAT1, TRIM22, NOTCH1, PA2G4, GTF2F1, TIAL1, UBA3, RNF20"	251	1512	12983	0.923662493	1	0.99868887	99.99999987
GOTERM_BP_FAT	GO:0060284~regulation of cell development	3	0.967741935	0.911162413	"NOTCH1, SMAD3, AGRN"	264	205	13528	0.749889135	1	0.999974875	100
GOTERM_BP_FAT	GO:0006350~transcription	30	9.677419355	0.986150327	"CNBP, NACA, RBM4, TP63, PAWR, PTMA, POLR2B, GTF2E1, KDM1A, MOV10, CHD7, PRMT5, ANP32A, BTF3, RQCD1, TRIP13, IKBKAP, SUB1, SMAD3, DRG1, POLR1C, IFI16, STAT1, NOTCH1, RPAP1, PA2G4, PARP14, GTF2F1, DNTTIP2, MCTS1"	264	2101	13528	0.73168621	1	0.999999986	100
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	24	7.741935484	0.99278134	"IKBKAP, CNBP, SP100, MAP2K1, SUB1, RAN, RBM4, SMAD3, TP63, HAT1, IFI16, PAWR, STAT1, TRIM22, KDM1A, ZFP36L2, PA2G4, NOTCH1, RAB18, TIAL1, SOX15, DDX20, AGRN, RNF20"	264	1813	13528	0.67833325	1	0.999999999	100
GOTERM_BP_FAT	GO:0045449~regulation of transcription	37	11.93548387	0.993184865	"CNBP, RBM4, TP63, HAT1, PAWR, RPS3, GTF2E1, KDM1A, MOV10, CHD7, PRMT5, ANP32A, BTF3, RQCD1, SOX15, AGRN, DDX20, IKBKAP, SP100, MAP2K1, SUB1, RAN, SMAD3, IFI16, STAT1, TRIM22, PPIE, PA2G4, NOTCH1, RAB18, TIAL1, PARP14, GTF2F1, UBA3, DNTTIP2, MCTS1, RNF20"	264	2601	13528	0.728938753	1	0.999999999	100
GOTERM_BP_FAT	"GO:0006355~regulation of transcription, DNA-dependent"	23	7.419354839	0.994138729	"IKBKAP, CNBP, SP100, MAP2K1, SUB1, RAN, RBM4, SMAD3, TP63, HAT1, IFI16, PAWR, STAT1, TRIM22, KDM1A, PA2G4, NOTCH1, RAB18, TIAL1, SOX15, DDX20, AGRN, RNF20"	264	1773	13528	0.66473534	1	0.999999999	100
GOTERM_MF_FAT	GO:0003700~transcription factor activity	10	3.225806452	0.996801367	"KDM1A, ZFP36L2, CNBP, PA2G4, NOTCH1, SMAD3, SOX15, TP63, STAT1, TRIM22"	251	975	12983	0.530513842	1	1	100

Annotation Cluster 63	Enrichment Score: 0.3622135686823678
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	"GO:0016879~ligase activity, forming carbon-nitrogen bonds"	8	2.580645161	0.158701614	"UBA3, PPCS, CAD, PAICS, RNF20, TRIP12, FBXO7, GART"	251	231	12983	1.791345441	1	0.739782366	91.59559459
GOTERM_MF_FAT	GO:0016881~acid-amino acid ligase activity	6	1.935483871	0.345567604	"UBA3, PPCS, PAICS, RNF20, TRIP12, FBXO7"	251	201	12983	1.544032824	1	0.907563121	99.77023946

GOTERM_MF_FAT GO:0004842~ubiquitin-protein ligase activity 3 0.967741935 0.778775169 "RNF20, TRIP12, FBXO7" 251 147 12983 1.055614278 1 0.99896565 99.99999996
GOTERM_MF_FAT GO:0019787~small conjugating protein ligase activity 3 0.967741935 0.832950636 "RNF20, TRIP12, FBXO7" 251 166 12983 0.934790957 1 0.999640022 100

Annotation Cluster 64 Enrichment Score: 0.35712916104674236
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0034097~response to cytokine stimulus 5 1.612903226 0.067789444 "SP100, PTGS2, BCL2L1, STAT1, SRC" 264 79 13528 3.243191408 1 0.661952429 69.43251794
GOTERM_BP_FAT GO:0007584~response to nutrient 3 0.967741935 0.759871238 "SP100, PTGS2, STAT1" 264 140 13528 1.098051948 1 0.998772741 100
GOTERM_BP_FAT GO:0009991~response to extracellular stimulus 4 1.290322581 0.804932834 "SP100, RPS19, PTGS2, STAT1" 264 220 13528 0.931680441 1 0.999455034 100
GOTERM_BP_FAT GO:0031667~response to nutrient levels 3 0.967741935 0.899128229 "SP100, PTGS2, STAT1" 264 197 13528 0.780341486 1 0.999961525 100

Annotation Cluster 65 Enrichment Score: 0.3115696658647716
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0051270~regulation of cell motion 9 2.903225806 0.034939833 "EGFR, SP100, RPS19, MAP2K1, RAC1, SMAD3, TRIP6, RNF20, ARAP1" 264 193 13528 2.389543099 1 0.488424587 45.14594544
GOTERM_BP_FAT GO:0051272~positive regulation of cell motion 5 1.612903226 0.123642312 "EGFR, RPS19, MAP2K1, SMAD3, TRIP6" 264 98 13528 2.6144094 1 0.787820824 89.23027535
GOTERM_BP_FAT GO:0030334~regulation of cell migration 6 1.935483871 0.232668317 "EGFR, MAP2K1, RAC1, SMAD3, TRIP6, RNF20" 264 169 13528 1.819257665 1 0.903788462 98.85712525
GOTERM_BP_FAT GO:0030335~positive regulation of cell migration 4 1.290322581 0.249813585 "EGFR, MAP2K1, SMAD3, TRIP6" 264 89 13528 2.303030303 1 0.914969282 99.2196394
GOTERM_BP_FAT GO:0040017~positive regulation of locomotion 4 1.290322581 0.29731661 "EGFR, MAP2K1, SMAD3, TRIP6" 264 98 13528 2.09152752 1 0.939284399 99.7414079
GOTERM_BP_FAT GO:0040012~regulation of locomotion 6 1.935483871 0.319286381 "EGFR, MAP2K1, RAC1, SMAD3, TRIP6, RNF20" 264 192 13528 1.601325758 1 0.948759581 99.84875205
GOTERM_BP_FAT GO:0000165~MAPKKK cascade 4 1.290322581 0.697880163 "EGFR, GPS1, MAP2K1, MINK1"264 184 13528 1.113965744 1 0.997612392 99.99999983
GOTERM_BP_FAT GO:0043405~regulation of MAP kinase activity 3 0.967741935 0.763335517 "EGFR, GPS1, MAP2K1" 264 141 13528 1.090264346 1 0.998810653 100
GOTERM_BP_FAT GO:0033674~positive regulation of kinase activity 3 0.967741935 0.941630639 "EGFR, MAP2K1, RAC1" 264 231 13528 0.665486029 1 0.999995465 100
GOTERM_BP_FAT GO:0051347~positive regulation of transferase activity 3 0.967741935 0.949645423 "EGFR, MAP2K1, RAC1" 264 240 13528 0.640530303 1 0.999997447 100
GOTERM_BP_FAT GO:0043549~regulation of kinase activity 4 1.290322581 0.971599146 "EGFR, GPS1, MAP2K1, RAC1" 264 357 13528 0.574144809 1 0.999999748 100
GOTERM_BP_FAT GO:0051338~regulation of transferase activity 4 1.290322581 0.977414735 "EGFR, GPS1, MAP2K1, RAC1" 264 372 13528 0.550993809 1 0.999999897 100
GOTERM_BP_FAT GO:0019220~regulation of phosphate metabolic process 5 1.612903226 0.986294247 "EGFR, GPS1, MAP2K1, RAC1, SMAD3" 264 485 13528 0.528272415 1 0.999999986 100
GOTERM_BP_FAT GO:0051174~regulation of phosphorus metabolic process 5 1.612903226 0.986294247 "EGFR, GPS1, MAP2K1, RAC1, SMAD3" 264 485 13528 0.528272415 1 0.999999986 100
GOTERM_BP_FAT GO:0045859~regulation of protein kinase activity 3 0.967741935 0.991599974 "EGFR, GPS1, MAP2K1" 264 345 13528 0.445586298 1 0.999999998 100
GOTERM_BP_FAT GO:0042325~regulation of phosphorylation 4 1.290322581 0.99492567 "EGFR, GPS1, MAP2K1, RAC1" 264 466 13528 0.439849135 1 1 100

Annotation Cluster 66	Enrichment Score: 0.3049282717506359
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006928~cell motion	11	3.548387097	0.439818517	"PTGS2, MACF1, PARP9, MAP2K1, AIMP1, EFNB1, RAC1, TOP2B, ITGB1, SRC, ARHGDIB"	264	475	13528	1.186666667	1	0.979705074	99.99436805
GOTERM_BP_FAT	GO:0016477~cell migration	7	2.258064516	0.449021339	"PARP9, AIMP1, EFNB1, RAC1, TOP2B, ITGB1, SRC"	264	276	13528	1.299626702	1	0.9806851	99.99574213
GOTERM_BP_FAT	GO:0051674~localization of cell	7	2.258064516	0.552552072	"PARP9, AIMP1, EFNB1, RAC1, TOP2B, ITGB1, SRC"	264	307	13528	1.168394038	1	0.989451772	99.99987325
GOTERM_BP_FAT	GO:0048870~cell motility	7	2.258064516	0.552552072	"PARP9, AIMP1, EFNB1, RAC1, TOP2B, ITGB1, SRC"	264	307	13528	1.168394038	1	0.989451772	99.99987325

Annotation Cluster 67	Enrichment Score: 0.2883840971123882
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006403~RNA localization	4	1.290322581	0.307965679	"RBM8A, RAN, G3BP2, STAU1"	264	100	13528	2.04969697	1	0.944755571	99.80018119
GOTERM_BP_FAT	GO:0050657~nucleic acid transport	3	0.967741935	0.565589012	"RBM8A, RAN, G3BP2"	264	97	13528	1.584817245	1	0.990654817	99.99992306
GOTERM_BP_FAT	GO:0051236~establishment of RNA localization	3	0.967741935	0.565589012	"RBM8A, RAN, G3BP2"	264	97	13528	1.584817245	1	0.990654817	99.99992306
GOTERM_BP_FAT	GO:0050658~RNA transport	3	0.967741935	0.565589012	"RBM8A, RAN, G3BP2"	264	97	13528	1.584817245	1	0.990654817	99.99992306
GOTERM_BP_FAT	"GO:0015931~nucleobase, nucleoside, nucleotide and nucleic acid transport"	3	0.967741935	0.648745417	"RBM8A, RAN, G3BP2"	264	113	13528	1.360418343	1	0.995997952	99.99999787

Annotation Cluster 68	Enrichment Score: 0.28620230846164385
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046365~monosaccharide catabolic process	3	0.967741935	0.402981241	"LDHB, NUDT5, GALE"	264	71	13528	2.165172855	1	0.974149034	99.9834929
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	3	0.967741935	0.469257641	"LDHB, NUDT5, GALE"	264	81	13528	1.897867565	1	0.983422055	99.99773639
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	3	0.967741935	0.494525388	"LDHB, NUDT5, GALE"	264	85	13528	1.80855615	1	0.985583612	99.99900662
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	3	0.967741935	0.629207619	"LDHB, NUDT5, GALE"	264	109	13528	1.410341952	1	0.995011108	99.99999469
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	5	1.612903226	0.629955264	"LDHB, UAP1, AIMP1, NUDT5, GALE"	264	222	13528	1.154108654	1	0.994982533	99.99999487

Annotation Cluster 69	Enrichment Score: 0.2715832557758869
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0060589~nucleoside-triphosphatase regulator activity	10	3.225806452	0.403353077	"GPS1, GAPVD1, RABGAP1, IPO7, MINK1, RANBP1, AHSA1, ARAP1, ARHGEF10, ARHGDIB"	251	413	12983	1.252423719	1	0.933546727	99.938913
GOTERM_MF_FAT	GO:0005083~small GTPase regulator activity	7	2.258064516	0.433426027	"RABGAP1, IPO7, MINK1, RANBP1, ARAP1, ARHGEF10, ARHGDIB"	251	274	12983	1.32144415	1	0.947697034	99.97088763
GOTERM_MF_FAT	GO:0030695~GTPase regulator activity	9	2.903225806	0.524606052	"GPS1, GAPVD1, RABGAP1, IPO7, MINK1, RANBP1, ARAP1, ARHGEF10, ARHGDIB"	251	404	12983	1.152291823	1	0.976276641	99.99764462

GOTERM_MF_FAT	GO:0005096~GTPase activator activity	5	1.612903226	0.615413182	"GAPVD1, RABGAP1, RANBP1, ARAP1, ARHGDIB"	251	220	12983	1.175570445	1	0.989165063	99.99988707
GOTERM_MF_FAT	GO:0008047~enzyme activator activity	6	1.935483871	0.777111381	"GAPVD1, RABGAP1, RANBP1, AHSA1, ARAP1, ARHGDIB"	251	335	12983	0.926419694	1	0.998997223	99.99999995

Annotation Cluster 70	Enrichment Score: 0.2660054852921242
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	6	1.935483871	0.216406769	"TP53RK, EGFR, MAP2K1, STK24, SRC, EPHA2"	251	166	12983	1.869581913	1	0.800814608	96.9641462
GOTERM_BP_FAT	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	4	1.290322581	0.814603942	"EGFR, AGRN, SRC, EPHA2"	264	224	13528	0.91504329	1	0.999559618	100
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	5	1.612903226	0.903163122	"EGFR, SMAD3, AGRN, SRC, EPHA2"	264	342	13528	0.749158249	1	0.999965232	100

Annotation Cluster 71	Enrichment Score: 0.25260196386632183
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	6	1.935483871	0.343590098	"MSH6, CHD7, SMAD3, MINK1, HPRT1, ITGB1"	264	199	13528	1.544997716	1	0.957849366	99.91813563
GOTERM_BP_FAT	GO:0002521~leukocyte differentiation	4	1.290322581	0.470153577	"CHD7, MINK1, IFI16, ITGB1"	264	131	13528	1.564654175	1	0.983346962	99.99780005
GOTERM_BP_FAT	GO:0001775~cell activation	7	2.258064516	0.487875474	"EGFR, MSH6, CHD7, SMAD3, MINK1, HPRT1, ITGB1"	264	287	13528	1.249815225	1	0.984831394	99.99876133
GOTERM_BP_FAT	GO:0045321~leukocyte activation	6	1.935483871	0.504548617	"MSH6, CHD7, SMAD3, MINK1, HPRT1, ITGB1"	264	242	13528	1.270473328	1	0.986032121	99.99929165
GOTERM_BP_FAT	GO:0030098~lymphocyte differentiation	3	0.967741935	0.598339764	"CHD7, MINK1, ITGB1"	264	103	13528	1.492497793	1	0.993139389	99.99997952
GOTERM_BP_FAT	GO:0002520~immune system development	6	1.935483871	0.625614877	"MSH6, CHD7, RPS19, MINK1, IFI16, ITGB1"	264	276	13528	1.113965744	1	0.994917402	99.99999375
GOTERM_BP_FAT	GO:0030097~hemopoiesis	5	1.612903226	0.677183387	"CHD7, RPS19, MINK1, IFI16, ITGB1"	264	236	13528	1.085644581	1	0.997093089	99.99999949
GOTERM_BP_FAT	GO:0042110~T cell activation	3	0.967741935	0.706629551	"CHD7, SMAD3, MINK1"	264	126	13528	1.22005772	1	0.997667733	99.9999999
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	5	1.612903226	0.748060824	"CHD7, RPS19, MINK1, IFI16, ITGB1"	264	260	13528	0.985431235	1	0.998619951	99.99999999

Annotation Cluster 72	Enrichment Score: 0.22757050621594474
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0031646~positive regulation of neurological system process	3	0.967741935	0.175271705	"EGFR, TF, PTGS2"	264	39	13528	3.941724942	1	0.842175576	96.13675717
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal process	5	1.612903226	0.7022299	"EGFR, TF, CHD7, PTGS2, SMAD3"	264	244	13528	1.050049677	1	0.997700075	99.99999987
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	3	0.967741935	0.783225204	"EGFR, TF, PTGS2"	264	147	13528	1.04576376	1	0.999179704	100
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	3	0.967741935	0.801636991	"EGFR, TF, PTGS2"	264	153	13528	1.004753417	1	0.999423044	100
GOTERM_BP_FAT	GO:0044057~regulation of system process	4	1.290322581	0.942089007	"EGFR, TF, PTGS2, MAP2K1"	264	309	13528	0.663332353	1	0.999995479	100

Annotation Cluster 73	Enrichment Score: 0.22309138942086076
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0051056~regulation of small GTPase mediated signal transduction	6	1.935483871	0.541307006	"GAPVD1, RABGAP1, MAP2K1, RAC1, ARAP1, ARHGEF10"	264	252	13528	1.22005772	1	0.988556385	99.99980726
GOTERM_BP_FAT	GO:0035023~regulation of Rho protein signal transduction	3	0.967741935	0.576714911	"RAC1, ARAP1, ARHGEF10"	264	99	13528	1.552800735	1	0.991401212	99.99995035
GOTERM_BP_FAT	GO:0046578~regulation of Ras protein signal transduction	5	1.612903226	0.586148015	"RABGAP1, MAP2K1, RAC1, ARAP1, ARHGEF10"	264	210	13528	1.22005772	1	0.992289124	99.99996607
GOTERM_BP_FAT	GO:0032318~regulation of Ras GTPase activity	3	0.967741935	0.603615115	"RABGAP1, MAP2K1, ARAP1"	264	104	13528	1.478146853	1	0.993514092	99.99998362
GOTERM_BP_FAT	GO:0043087~regulation of GTPase activity	3	0.967741935	0.694018137	"RABGAP1, MAP2K1, ARAP1"	264	123	13528	1.249815225	1	0.997586237	99.99999979

Annotation Cluster 74	Enrichment Score: 0.2027614770074167
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007498~mesoderm development	3	0.967741935	0.423298526	"MACF1, SMAD3, TP63"	264	74	13528	2.077395577	1	0.976737432	99.99080016
GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	4	1.290322581	0.683613645	"NOTCH1, MACF1, SMAD3, TP63"	264	180	13528	1.138720539	1	0.997332857	99.99999964
GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	5	1.612903226	0.851643997	"NOTCH1, CHD7, MACF1, SMAD3, TP63"	264	307	13528	0.83456717	1	0.999822131	100

Annotation Cluster 75	Enrichment Score: 0.1945872280206682
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048610~reproductive cellular process	5	1.612903226	0.386711576	"SDC1, RAN, BCL2L1, ITGB1, TRIP13"	264	162	13528	1.581556304	1	0.971360155	99.97400873
GOTERM_BP_FAT	GO:0007281~germ cell development	3	0.967741935	0.587631985	"RAN, BCL2L1, TRIP13"	264	101	13528	1.522052205	1	0.992321075	99.99996806
GOTERM_BP_FAT	GO:0007276~gamete generation	8	2.580645161	0.651350648	"KRT9, NOTCH1, PTGS2, RAN, BCL2L1, ITGB1, SPATA5, TRIP13"	264	395	13528	1.03782125	1	0.996085931	99.99999812
GOTERM_BP_FAT	GO:0019953~sexual reproduction	9	2.903225806	0.670905302	"KRT9, NOTCH1, AAAS, PTGS2, RAN, BCL2L1, ITGB1, SPATA5, TRIP13"	264	458	13528	1.006947201	1	0.996898789	99.99999929
GOTERM_BP_FAT	GO:0048232~male gamete generation	6	1.935483871	0.719006603	"KRT9, NOTCH1, RAN, BCL2L1, SPATA5, TRIP13"	264	308	13528	0.998229044	1	0.997939561	99.99999995
GOTERM_BP_FAT	GO:0007283~spermatogenesis	6	1.935483871	0.719006603	"KRT9, NOTCH1, RAN, BCL2L1, SPATA5, TRIP13"	264	308	13528	0.998229044	1	0.997939561	99.99999995
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	9	2.903225806	0.735248035	"EGFR, KRT9, NOTCH1, PTGS2, RAN, BCL2L1, ITGB1, SPATA5, TRIP13"	264	487	13528	0.946985253	1	0.99831203	99.99999998
GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	9	2.903225806	0.735248035	"EGFR, KRT9, NOTCH1, PTGS2, RAN, BCL2L1, ITGB1, SPATA5, TRIP13"	264	487	13528	0.946985253	1	0.99831203	99.99999998

Annotation Cluster 76	Enrichment Score: 0.1920024745148463
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_BP_FAT	GO:0032583~regulation of gene-specific transcription	4	1.290322581	0.485081564	"KDM1A, NOTCH1, SMAD3, RNF20"	264	134	13528	1.529624604	1	0.984778113	99.99864216
GOTERM_BP_FAT	GO:0010551~regulation of specific transcription from RNA polymerase II promoter	3	0.967741935	0.548510576	"KDM1A, NOTCH1, SMAD3"	264	94	13528	1.635396518	1	0.989228049	99.99985246
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	5	1.612903226	0.997683529	"KDM1A, NOTCH1, SMAD3, TP63, STAT1"	251	607	12983	0.426071661	1	1	100

Annotation Cluster 77	Enrichment Score: 0.13838448823648578
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001503~ossification	3	0.967741935	0.658205085	"EGFR, PTGS2, SMAD3"	264	115	13528	1.336758893	1	0.996350616	99.99999866
GOTERM_BP_FAT	GO:0060348~bone development	3	0.967741935	0.694018137	"EGFR, PTGS2, SMAD3"	264	123	13528	1.249815225	1	0.997586237	99.99999979
GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal process	5	1.612903226	0.7022299	"EGFR, TF, CHD7, PTGS2, SMAD3"	264	244	13528	1.050049677	1	0.997700075	99.99999987
GOTERM_BP_FAT	GO:0001501~skeletal system development	5	1.612903226	0.871466458	"EGFR, CHD7, PTGS2, SMAD3, TP63"	264	319	13528	0.803172794	1	0.999904753	100

Annotation Cluster 78	Enrichment Score: 0.1380736110002871
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0016044~membrane organization	9	2.903225806	0.463716212	"EGFR, GAPVD1, HSP90AA1, RAB18, PACSIN3, RAC1, AGRN, BCL2L1, HSPA8"	264	381	13528	1.210450966	1	0.982804837	99.99730247
GOTERM_BP_FAT	GO:0006897~endocytosis	4	1.290322581	0.804932834	"GAPVD1, RAB18, PACSIN3, RAC1"	264	220	13528	0.931680441	1	0.999455034	100
GOTERM_BP_FAT	GO:0010324~membrane invagination	4	1.290322581	0.804932834	"GAPVD1, RAB18, PACSIN3, RAC1"	264	220	13528	0.931680441	1	0.999455034	100
GOTERM_CC_FAT	GO:0009898~internal side of plasma membrane	4	1.290322581	0.933112464	"RAB18, PACSIN3, RAC1, BCL2L1"	236	316	12782	0.685582493	1	0.999753812	100

Annotation Cluster 79	Enrichment Score: 0.11654251431590366
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048511~rhythmic process	3	0.967741935	0.714795053	"EGFR, MAT2A, BCL2L1"	264	128	13528	1.200994318	1	0.997822914	99.99999994
GOTERM_BP_FAT	GO:0009314~response to radiation	4	1.290322581	0.750088737	"EGFR, MSH6, MAT2A, BCL2L1"	264	200	13528	1.024848485	1	0.998622582	99.99999999
GOTERM_BP_FAT	GO:0009416~response to light stimulus	3	0.967741935	0.752811393	"EGFR, MSH6, MAT2A"	264	138	13528	1.113965744	1	0.998643712	99.99999999
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	6	1.935483871	0.846934019	"EGFR, MSH6, MAT2A, RAC1, BCL2L1, STAT1"	264	368	13528	0.835474308	1	0.999799662	100

Annotation Cluster 80	Enrichment Score: 0.11296302993339646
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030425~dendrite	4	1.290322581	0.579588061	"MAP2K1, ATXN10, TP63, STAT1"	236	163	12782	1.32910471	1	0.968030526	99.99905313
GOTERM_CC_FAT	GO:0043005~neuron projection	5	1.612903226	0.878409267	"MAP2K1, ATXN10, TP63, STAT1, STAU1"	236	342	12782	0.791827733	1	0.998831185	100
GOTERM_CC_FAT	GO:0042995~cell projection	10	3.225806452	0.900107894	"SDC1, MAP2K1, ATXN10,

RAC1, TP63, PCM1, STAT1, ITGB1, RPS3, STAU1"236 697 12782 0.777059067 1 0.999326557 100

Annotation Cluster 81 Enrichment Score: 0.09718908570598152
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0000267~cell fraction 21 6.774193548 0.526172779 "LDHB, MAP2K1, PTGS2,
EFNB1, IDE, AARS, OAS3, FADS2, LIN7C, TP63, OAS2, HPRT1, ITGB1, KARS, NAE1, SLC1A5, IPO7, RAC1,
DSC3, FARSB, FARSA" 236 1083 12782 1.050213625 1 0.954561159 99.99532561
GOTERM_CC_FAT GO:0005792~microsome 4 1.290322581 0.815037879 "PTGS2, OAS3, TP63,
OAS2" 236 237 12782 0.914109991 1 0.997305498 99.99999998
GOTERM_CC_FAT GO:0042598~vesicular fraction 4 1.290322581 0.830137858 "PTGS2, OAS3, TP63,
OAS2" 236 244 12782 0.887885524 1 0.997851204 99.99999999
GOTERM_CC_FAT GO:0005626~insoluble fraction 11 3.548387097 0.950078584 "SLC1A5, PTGS2,
RAC1, OAS3, DSC3, FADS2, TP63, LIN7C, OAS2, ITGB1, NAE1" 236 839 12782 0.710096766 1
0.999889915 100
GOTERM_CC_FAT GO:0005624~membrane fraction 10 3.225806452 0.965692042 "SLC1A5, PTGS2,
RAC1, OAS3, DSC3, FADS2, TP63, LIN7C, OAS2, ITGB1" 236 809 12782 0.66948105 1 0.999952281
100

Annotation Cluster 82 Enrichment Score: 0.06530511456409505
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0006935~chemotaxis 3 0.967741935 0.821358167 "MAP2K1, AIMP1, RAC1"
264 160 13528 0.960795455 1 0.999620624 100
GOTERM_BP_FAT GO:0042330~taxis 3 0.967741935 0.821358167 "MAP2K1, AIMP1, RAC1" 264 160
13528 0.960795455 1 0.999620624 100
GOTERM_BP_FAT GO:0007610~behavior 7 2.258064516 0.897706638 "AAAS, CHD7, PTGS2,
MAP2K1, AIMP1, RAC1, HPRT1" 264 469 13528 0.764812302 1 0.999960121 100
GOTERM_BP_FAT GO:0007626~locomotory behavior 4 1.290322581 0.904856989 "CHD7, MAP2K1,
AIMP1, RAC1" 264 274 13528 0.748064587 1 0.999966966 100

Annotation Cluster 83 Enrichment Score: 0.05810413449205857
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0048598~embryonic morphogenesis 5 1.612903226 0.851643997 "NOTCH1,
CHD7, MACF1, SMAD3, TP63" 264 307 13528 0.83456717 1 0.999822131 100
GOTERM_BP_FAT GO:0001501~skeletal system development 5 1.612903226 0.871466458 "EGFR,
CHD7, PTGS2, SMAD3, TP63" 264 319 13528 0.803172794 1 0.999904753 100
GOTERM_BP_FAT GO:0040008~regulation of growth5 1.612903226 0.901942457 "CHD7, SMAD3, TP63,
AGRN, MCTS1" 264 341 13528 0.751355194 1 0.999964215 100

Annotation Cluster 84 Enrichment Score: 0.028992210116657334
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0009611~response to wounding 8 2.580645161 0.894921896 "TF, SDC1,
NOTCH1, MAP2K1, AIMP1, RAC1, SMAD3, SOX15" 264 530 13528 0.773470555 1 0.999956219 100
GOTERM_BP_FAT GO:0045597~positive regulation of cell differentiation3 0.967741935 0.939692251
"NOTCH1, MAP2K1, SMAD3" 264 229 13528 0.671298134 1 0.999994934 100
GOTERM_BP_FAT GO:0051094~positive regulation of developmental process 3 0.967741935 0.973313148
"NOTCH1, MAP2K1, SMAD3" 264 278 13528 0.552975801 1 0.999999799 100

Annotation Cluster 85 Enrichment Score: 0.014303721610134853
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR

GOTERM_MF_FAT GO:0004175~endopeptidase activity 5 1.612903226 0.933682733 "PSMB6, PSMA5, IDE, MIPEP, PWP2" 251 375 12983 0.689667995 1 0.999991716 100

GOTERM_MF_FAT "GO:0070011~peptidase activity, acting on L-amino acid peptides" 6 1.935483871 0.982497515 "PSMB6, PSMA5, IDE, USP10, MIPEP, PWP2" 251 549 12983 0.565301635 1 0.999999952 100

GOTERM_MF_FAT GO:0008233~peptidase activity 6 1.935483871 0.987547622 "PSMB6, PSMA5, IDE, USP10, MIPEP, PWP2" 251 574 12983 0.540680484 1 0.999999986 100

Annotation Cluster 86 Enrichment Score: 3.1675601521453706E-4

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0006812~cation transport 4 1.290322581 0.998813217 "TF, ATP1B1, FKBP4, MON2" 264 553 13528 0.370650447 1 1 100

GOTERM_BP_FAT GO:0030001~metal ion transport 3 0.967741935 0.999026458 "TF, ATP1B1, FKBP4" 264 465 13528 0.330596285 1 1 100

GOTERM_BP_FAT GO:0006811~ion transport 4 1.290322581 0.999973431 "TF, ATP1B1, FKBP4, MON2" 264 768 13528 0.266887626 1 1 100

Annotation Cluster 87 Enrichment Score: 2.3144357435193373E-4

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0046914~transition metal ion binding 37 11.93548387 0.998362984 "PPP6C, TF, IFIH1, LIMA1, CNBP, ELAC2, PTGS2, LYAR, RBM4, IDE, TP63, PDLIM2, CAD, MIPEP, POLR2B, RABGGTA, PRMT3, GTF2E1, TRIM5, ZFP36L2, NUBP2, FASN, PDXK, SP100, MAT2A, FADS2, IDH3B, TRIM22, TRIM61, IDH3A, GART, RRM2, CARS2, TRIP6, RNF20, ARAP1, ADAR" 251 2785 12983 0.687191628 1 1 100

GOTERM_MF_FAT GO:0008270~zinc ion binding 27 8.709677419 0.999626292 "IFIH1, LIMA1, CNBP, ELAC2, LYAR, IDE, RBM4, TP63, PDLIM2, CAD, MIPEP, POLR2B, RABGGTA, PRMT3, ZFP36L2, GTF2E1, TRIM5, FASN, SP100, PDXK, TRIM22, TRIM61, CARS2, TRIP6, RNF20, ARAP1, ADAR" 251 2311 12983 0.604317477 1 1 100

GOTERM_MF_FAT GO:0046872~metal ion binding 57 18.38709677 0.999684497 "ATP1B1, LIMA1, PTGS2, LYAR, RBM4, IDE, TP63, PDLIM2, CAD, MIPEP, PRMT3, MTHFD2, TRIM5, GTF2E1, AASDHPPT, NUBP2, NT5C3, PLS1, PDXK, SP100, NUDT5, STK3, RRM2, FARSB, RNF20, PRPS2, TF, PPP6C, IFIH1, CNBP, ELAC2, ERI1, HPRT1, POLR2B, RABGGTA, ZFP36L2, MACF1, PLCH2, FASN, MSH6, MAT2A, FADS2, IDH3B, ITGA3, STAT1, TRIM22, TRIM61, IDH3A, GART, NOTCH1, DSG2, DSC3, CARS2, TRIP6, ARAP1, DUT, ADAR" 251 4140 12983 0.712157168 1 1 100

GOTERM_MF_FAT GO:0043169~cation binding 57 18.38709677 0.999782093 "ATP1B1, LIMA1, PTGS2, LYAR, RBM4, IDE, TP63, PDLIM2, CAD, MIPEP, PRMT3, MTHFD2, TRIM5, GTF2E1, AASDHPPT, NUBP2, NT5C3, PLS1, PDXK, SP100, NUDT5, STK3, RRM2, FARSB, RNF20, PRPS2, TF, PPP6C, IFIH1, CNBP, ELAC2, ERI1, HPRT1, POLR2B, RABGGTA, ZFP36L2, MACF1, PLCH2, FASN, MSH6, MAT2A, FADS2, IDH3B, ITGA3, STAT1, TRIM22, TRIM61, IDH3A, GART, NOTCH1, DSG2, DSC3, CARS2, TRIP6, ARAP1, DUT, ADAR" 251 4179 12983 0.70551105 1 1 100

GOTERM_MF_FAT GO:0043167~ion binding 57 18.38709677 0.999881033 "ATP1B1, LIMA1, PTGS2, LYAR, RBM4, IDE, TP63, PDLIM2, CAD, MIPEP, PRMT3, MTHFD2, TRIM5, GTF2E1, AASDHPPT, NUBP2, NT5C3, PLS1, PDXK, SP100, NUDT5, STK3, RRM2, FARSB, RNF20, PRPS2, TF, PPP6C, IFIH1, CNBP, ELAC2, ERI1, HPRT1, POLR2B, RABGGTA, ZFP36L2, MACF1, PLCH2, FASN, MSH6, MAT2A, FADS2, IDH3B, ITGA3, STAT1, TRIM22, TRIM61, IDH3A, GART, NOTCH1, DSG2, DSC3, CARS2, TRIP6, ARAP1, DUT, ADAR" 251 4241 12983 0.695197047 1 1 100

Annotation Cluster 88 Enrichment Score: 3.431466855723543E-5

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0005615~extracellular space 4 1.290322581 0.999775776 "EGFR, TF, AIMP1, IDE" 236 685 12782 0.316268712 1 1 100

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GOTERM_CC_FAT	GO:0044421~extracellular region part	5	1.612903226	0.999987212	"EGFR, TF,
AIMP1, IDE, AGRN"	236	960	12782	0.28208863	1	1	100
GOTERM_CC_FAT	GO:0005576~extracellular region	6	1.935483871	1	"EGFR, TF, AIMP1, IDE, AGRN,
TXLNA"	236	2010	12782	0.161674677	1	1	100

Annotation Cluster 89	Enrichment Score: 1.6245134988300134E-5
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0050890~cognition	6	1.935483871	0.999933444	"DFNA5, AAAS, CHD7, PTGS2,
IDH3B, RABGGTA"	264	909	13528	0.338233823	1	1	100
GOTERM_BP_FAT	GO:0050877~neurological system process	9	2.903225806	0.999966647	"DFNA5,
AAAS, CHD7, PTGS2, AARS, IDH3B, LIN7C, AGRN, RABGGTA"	264	1210	13528	0.381141998	1
1	100
GOTERM_BP_FAT	GO:0007600~sensory perception	4	1.290322581	0.999987694	"DFNA5, CHD7,
IDH3B, RABGGTA"	264	810	13528	0.253049009	1	1	100
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Annotation Cluster 1 Enrichment Score: 4.148783723294257
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005884~actin filament 6 4.026845638 3.00E-05 "ACTR3, CALD1, VPS16, TPM1, IQGAP1, LCP1" 115 41 12782 16.26553552 0.007345967 0.001841573 0.038829981
GOTERM_MF_FAT GO:0003779~actin binding 13 8.724832215 8.33E-05 "ACTR3, ACTR2, TWF2, TAGLN, CALD1, CYFIP1, ARPC4, VPS16, MSN, TPM1, PLS3, LCP1, VCL" 128 326 12983 4.04474214 0.027349267 0.013769432 0.112984801
GOTERM_CC_FAT GO:0015629~actin cytoskeleton 11 7.382550336 1.43E-04 "ACTR3, ACTR2, PDLIM7, CLIC4, CALD1, ARPC4, VPS16, TPM1, IQGAP1, LCP1, VCL" 115 269 12782 4.54507839 0.03465614 0.005026028 0.18561615

Annotation Cluster 2 Enrichment Score: 3.1971622736815193
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0015031~protein transport 23 15.43624161 6.93E-06 "VPS29, RAB3GAP2, STX4, AP1M1, YWHAZ, CLTB, EXOC7, AP1G1, SNX5, STAM2, VTA1, ERP29, YWHAB, SNX1, SNX3, OPTN, YWHAG, SNF8, KPNA4, VPS16, SNX12, AP3B1, EXOC6B" 137 762 13528 2.980477805 0.008917286 0.008917286 0.011310541
GOTERM_BP_FAT GO:0045184~establishment of protein localization 23 15.43624161 8.02E-06 "VPS29, RAB3GAP2, STX4, AP1M1, YWHAZ, CLTB, EXOC7, AP1G1, SNX5, STAM2, VTA1, ERP29, YWHAB, SNX1, SNX3, OPTN, YWHAG, SNF8, KPNA4, VPS16, SNX12, AP3B1, EXOC6B" 137 769 13528 2.953347318 0.010302267 0.005164469 0.013076238
GOTERM_BP_FAT GO:0006886~intracellular protein transport 15 10.06711409 2.39E-05 "RAB3GAP2, STX4, YWHAZ, AP1M1, CLTB, AP1G1, STAM2, ERP29, YWHAB, SNX1, OPTN, YWHAG, KPNA4, VPS16, AP3B1" 137 374 13528 3.960341934 0.030397379 0.010236896 0.038973463
GOTERM_BP_FAT GO:0008104~protein localization 23 15.43624161 6.56E-05 "VPS29, RAB3GAP2, STX4, AP1M1, YWHAZ, CLTB, EXOC7, AP1G1, SNX5, STAM2, VTA1, ERP29, YWHAB, SNX1, SNX3, OPTN, YWHAG, SNF8, KPNA4, VPS16, SNX12, AP3B1, EXOC6B" 137 882 13528 2.574970621 0.081237186 0.020959061 0.106935669
GOTERM_BP_FAT GO:0034613~cellular protein localization 15 10.06711409 6.68E-05 "RAB3GAP2, STX4, YWHAZ, AP1M1, CLTB, AP1G1, STAM2, ERP29, YWHAB, SNX1, OPTN, YWHAG, KPNA4, VPS16, AP3B1" 137 411 13528 3.603814801 0.082635641 0.017102178 0.108857161
GOTERM_BP_FAT GO:0070727~cellular macromolecule localization 15 10.06711409 7.22E-05 "RAB3GAP2, STX4, YWHAZ, AP1M1, CLTB, AP1G1, STAM2, ERP29, YWHAB, SNX1, OPTN, YWHAG, KPNA4, VPS16, AP3B1" 137 414 13528 3.577700201 0.08902027 0.015418996 0.117666614
GOTERM_BP_FAT GO:0046907~intracellular transport 18 12.08053691 3.14E-04 "RAB3GAP2, STX4, YWHAZ, AP1M1, CLTB, OPA1, AP1G1, STAM2, ERP29, YWHAB, SNX1, OPTN, TPM1, YWHAG, APOE, KPNA4, VPS16, AP3B1" 137 657 13528 2.705329467 0.333819128 0.056376214 0.511625109
GOTERM_CC_FAT GO:0009898~internal side of plasma membrane 11 7.382550336 5.19E-04 "STOM, AP1M1, CLTB, AP1G1, STAM2, SNX1, VPS16, MSN, VCL, GBP1, AP3B1" 115 316 12782 3.869069895 0.119931849 0.015842655 0.670691911
GOTERM_CC_FAT GO:0031982~vesicle 15 10.06711409 0.002507739 "STX4, YWHAZ, AP1M1, CLTB, AP1G1, GRB2, ERP29, YWHAB, OPTN, STOM, CLIC4, CTSB, AP3B1, FN1, EPN2" 115 670 12782 2.488384166 0.46080538 0.050170918 3.201246655
GOTERM_CC_FAT GO:0031410~cytoplasmic vesicle 14 9.395973154 0.004667327 "STOM, STX4, AP1M1, YWHAZ, CLTB, CLIC4, AP1G1, ERP29, YWHAB, OPTN, CTSB, EPN2, FN1, AP3B1" 115 642 12782 2.423784369 0.683632369 0.084721557 5.881988893
GOTERM_CC_FAT GO:0042470~melanosome 5 3.355704698 0.00819349 "STOM, YWHAZ, ERP29, YWHAB, CTSB" 115 89 12782 6.244259893 0.867861049 0.112239265 10.11224772
GOTERM_CC_FAT GO:0048770~pigment granule 5 3.355704698 0.00819349 "STOM, YWHAZ, ERP29, YWHAB, CTSB" 115 89 12782 6.244259893 0.867861049 0.112239265 10.11224772
GOTERM_CC_FAT GO:0031988~membrane-bounded vesicle 12 8.053691275 0.012457723 "STOM,

STX4, YWHAZ, CLTB, GRB2, AP1G1, ERP29, YWHAB, OPTN, CTSB, EPN2, FN1" 115 568 12782
2.348193509 0.954217293 0.14982055 14.99337272
GOTERM_CC_FAT GO:0016023~cytoplasmic membrane-bounded vesicle 11 7.382550336 0.024989447
"STOM, STX4, YWHAZ, CLTB, AP1G1, ERP29, YWHAB, OPTN, CTSB, EPN2, FN1" 115 550 12782
2.222956522 0.998021701 0.237135383 27.95848264
GOTERM_BP_FAT GO:0006605~protein targeting 6 4.026845638 0.065876988 "YWHAZ, YWHAG,
YWHAB, KPNA4, OPTN, AP3B1" 137 215 13528 2.755661178 1 0.895398001 67.10464644

Annotation Cluster 3 Enrichment Score: 2.506510266395528
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment
Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005856~cytoskeleton 28 18.79194631 6.21E-05 "YWHAZ, PDLIM7, EXOC7,
CALD1, ARPC4, TPM1, IQGAP1, VCL, ACTR3, ACTR2, CTTN, SBDS, BLOC1S2, NDRG1, MSN, VPS16,
TUBA1A, TUBB3, TWF2, TBCE, BICD2, STOM, KRT75, CLIC4, HSPB1, UBXN6, LCP1, CALM1" 115 1381
12782 2.253540283 0.015150864 0.002541234 0.080385217
GOTERM_CC_FAT GO:0015629~actin cytoskeleton 11 7.382550336 1.43E-04 "ACTR3, ACTR2,
PDLIM7, CLIC4, CALD1, ARPC4, VPS16, TPM1, IQGAP1, LCP1, VCL" 115 269 12782 4.54507839
0.03465614 0.005026028 0.18561615
GOTERM_CC_FAT GO:0044430~cytoskeletal part 20 13.42281879 7.18E-04 "YWHAZ, PDLIM7,
EXOC7, CALD1, TBCE, ARPC4, TPM1, IQGAP1, ACTR3, ACTR2, SBDS, KRT75, BLOC1S2, HSPB1, VPS16,
UBXN6, TUBA1A, LCP1, TUBB3, CALM1" 115 952 12782 2.335038363 0.161954322 0.019439967
0.926354197
GOTERM_CC_FAT GO:0043232~intracellular non-membrane-bounded organelle 28 18.79194631 0.21431265
"YWHAZ, PDLIM7, EXOC7, CALD1, ARPC4, TPM1, IQGAP1, VCL, ACTR3, ACTR2, CTTN, SBDS, BLOC1S2,
NDRG1, MSN, VPS16, TUBA1A, TUBB3, TWF2, TBCE, BICD2, STOM, KRT75, CLIC4, HSPB1, UBXN6, LCP1,
CALM1" 115 2596 12782 1.198820929 1 0.702072191 95.60814876
GOTERM_CC_FAT GO:0043228~non-membrane-bounded organelle 28 18.79194631 0.21431265
"YWHAZ, PDLIM7, EXOC7, CALD1, ARPC4, TPM1, IQGAP1, VCL, ACTR3, ACTR2, CTTN, SBDS, BLOC1S2,
NDRG1, MSN, VPS16, TUBA1A, TUBB3, TWF2, TBCE, BICD2, STOM, KRT75, CLIC4, HSPB1, UBXN6, LCP1,
CALM1" 115 2596 12782 1.198820929 1 0.702072191 95.60814876

Annotation Cluster 4 Enrichment Score: 2.458927839317361
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment
Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0016044~membrane organization 12 8.053691275 0.001604631 "AP1M1,
STX4, OPA1, PDLIM7, AP1G1, APOE, ITGAV, SNX1, HSPA4, SNX3, EPN2, AP3B1" 137 381 13528
3.110063797 0.874424524 0.18737443 2.586073865
GOTERM_BP_FAT GO:0016192~vesicle-mediated transport 15 10.06711409 0.001963642 "AP1M1,
STX4, YWHAZ, CLTB, EXOC7, PDLIM7, AP1G1, SNX1, OPTN, SNX3, APOE, ITGAV, AP3B1, EXOC6B, EPN2"
137 576 13528 2.571472019 0.921095658 0.190733167 3.156007687
GOTERM_BP_FAT GO:0010324~membrane invagination 8 5.369127517 0.006806528 "PDLIM7,
AP1G1, APOE, ITGAV, SNX1, SNX3, EPN2, AP3B1" 137 220 13528 3.59071002 0.999852856
0.444714718 10.54459642
GOTERM_BP_FAT GO:0006897~endocytosis 8 5.369127517 0.006806528 "PDLIM7, AP1G1, APOE,
ITGAV, SNX1, SNX3, EPN2, AP3B1" 137 220 13528 3.59071002 0.999852856 0.444714718
10.54459642

Annotation Cluster 5 Enrichment Score: 1.965315800045424
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment
Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006766~vitamin metabolic process 6 4.026845638 9.37E-04 "SCPEP1,
NAMPT, CBR1, GCLC, ALDH1A3, RETSAT" 137 75 13528 7.899562044 0.702123235 0.140482787
1.517700728
GOTERM_BP_FAT GO:0016101~diterpenoid metabolic process 4 2.684563758 0.001519024 "SCPEP1,

ALDH1A3, ADH5, RETSAT" 137 23 13528 17.17296096 0.859713938 0.196059632 2.449708295
GOTERM_BP_FAT GO:0001523~retinoid metabolic process 4 2.684563758 0.001519024 "SCPEP1, ALDH1A3, ADH5, RETSAT" 137 23 13528 17.17296096 0.859713938 0.196059632 2.449708295
GOTERM_BP_FAT GO:0006721~terpenoid metabolic process 4 2.684563758 0.001944031 "SCPEP1, ALDH1A3, ADH5, RETSAT" 137 25 13528 15.79912409 0.919066925 0.20431947 3.124956827
GOTERM_BP_FAT GO:0006775~fat-soluble vitamin metabolic process 4 2.684563758 0.004349362 "SCPEP1, CBR1, ALDH1A3, RETSAT" 137 33 13528 11.9690334 0.996417277 0.351570805 6.864593466
GOTERM_BP_FAT GO:0019748~secondary metabolic process 5 3.355704698 0.008208234 "SCPEP1, NAMPT, ALDH1A3, ADH5, RETSAT" 137 79 13528 6.249653516 0.999976271 0.486009302 12.58227822
GOTERM_BP_FAT GO:0006720~isoprenoid metabolic process 4 2.684563758 0.009744713 "SCPEP1, ALDH1A3, ADH5, RETSAT" 137 44 13528 8.97677505 0.999996799 0.524900133 14.76578864
GOTERM_BP_FAT GO:0034754~cellular hormone metabolic process 4 2.684563758 0.021458366 "SCPEP1, ALDH1A3, COMT, RETSAT" 137 59 13528 6.694544105 1 0.720263927 29.80617391
GOTERM_BP_FAT GO:0006776~vitamin A metabolic process 3 2.013422819 0.022110515 "SCPEP1, ALDH1A3, RETSAT" 137 23 13528 12.87972072 1 0.715200818 30.56553037
GOTERM_BP_FAT GO:0010817~regulation of hormone levels 5 3.355704698 0.065904034 "SCPEP1, YWHAZ, ALDH1A3, COMT, RETSAT" 137 151 13528 3.269686276 1 0.889427955 67.12018177
GOTERM_BP_FAT GO:0042445~hormone metabolic process 4 2.684563758 0.091108939 "SCPEP1, ALDH1A3, COMT, RETSAT" 137 106 13528 3.726208511 1 0.935608491 78.9569092
GOTERM_BP_FAT GO:0055114~oxidation reduction 7 4.697986577 0.625978937 "CBR1, ALDH1A3, ALDH2, ADH5, QDPR, PRDX2, RETSAT" 137 639 13528 1.081708418 1 0.998880304 99.99998924

Annotation Cluster 6 Enrichment Score: 1.3912308150576782
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0030117~membrane coat 5 3.355704698 0.002384874 "AP1M1, CLTB, AP1G1, EPN2, AP3B1" 115 63 12782 8.821256039 0.444218287 0.051997511 3.046633087
GOTERM_CC_FAT GO:0048475~coated membrane 5 3.355704698 0.002384874 "AP1M1, CLTB, AP1G1, EPN2, AP3B1" 115 63 12782 8.821256039 0.444218287 0.051997511 3.046633087
GOTERM_CC_FAT GO:0030118~clathrin coat 4 2.684563758 0.004999275 "AP1M1, CLTB, AP1G1, EPN2" 115 39 12782 11.39977703 0.70855558 0.084298382 6.287913377
GOTERM_CC_FAT GO:0005794~Golgi apparatus 14 9.395973154 0.046611743 "STX4, OSBP, AP1M1, CLTB, AP1G1, GRB2, SNX1, OPTN, BICD2, TMF1, ACTR3, GLA, APOE, AP3B1" 115 872 12782 1.784483446 0.99999205 0.342538431 46.12611559
GOTERM_CC_FAT GO:0000139~Golgi membrane 5 3.355704698 0.084833379 "ACTR3, AP1M1, CLTB, AP1G1, TMF1" 115 186 12782 2.987844787 1 0.483582109 68.29559009
GOTERM_CC_FAT GO:0044431~Golgi apparatus part 6 4.026845638 0.122516907 "ACTR3, AP1M1, STX4, CLTB, AP1G1, TMF1" 115 294 12782 2.268322981 1 0.552370851 81.61394799
GOTERM_CC_FAT GO:0012505~endomembrane system 11 7.382550336 0.159452576 "ACTR3, AP1M1, S100A6, CLTB, HTRA2, GRB2, AP1G1, KPNA4, EPN2, RETSAT, TMF1" 115 782 12782 1.563460469 1 0.629809106 89.46879306
GOTERM_CC_FAT GO:0030136~clathrin-coated vesicle 3 2.013422819 0.329749306 "CLTB, AP1G1, EPN2" 115 132 12782 2.526086957 1 0.822140671 99.43974646
GOTERM_CC_FAT GO:0030135~coated vesicle 3 2.013422819 0.415921409 "CLTB, AP1G1, EPN2" 115 159 12782 2.097128794 1 0.877502851 99.90582456

Annotation Cluster 7 Enrichment Score: 1.2868220681126743
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0030036~actin cytoskeleton organization 7 4.697986577 0.026610222 "PDLIM7, CALD1, ARPC4, CRK, TPM1, PLS3, LCP1" 137 226 13528 3.058458756 1 0.738215977

35.59853762
GOTERM_BP_FAT GO:0007010~cytoskeleton organization 10 6.711409396 0.03188021 "BLOC1S2, PDLIM7, APOE, CALD1, TBCE, ARPC4, CRK, TPM1, PLS3, LCP1" 137 436 13528 2.264782696 1 0.787831313 41.05737124
GOTERM_BP_FAT GO:0030029~actin filament-based process 7 4.697986577 0.03485416 "PDLIM7, CALD1, ARPC4, CRK, TPM1, PLS3, LCP1" 137 241 13528 2.868098252 1 0.805430673 43.94300961
GOTERM_BP_FAT GO:0007015~actin filament organization 4 2.684563758 0.035854888 "CALD1, ARPC4, PLS3, LCP1" 137 72 13528 5.485806975 1 0.803430224 44.88382047
GOTERM_CC_FAT GO:0044463~cell projection part 4 2.684563758 0.34714987 "CALD1, FBXO2, ARPC4, TPM1" 115 234 12782 1.899962839 1 0.831007887 99.60156688

Annotation Cluster 8 Enrichment Score: 1.2602265159625377
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0005543~phospholipid binding 6 4.026845638 0.02990077 "SNX5, APOE, SNX1, SNX3, SNX12, ANXA4" 128 177 12983 3.438294492 0.999959282 0.569326212 33.77491153
GOTERM_MF_FAT GO:0008289~lipid binding 9 6.040268456 0.074171939 "OSBP, SNX5, APOE, ADH5, SNX1, SNX3, SNX12, ANXA4, EPN2" 128 450 12983 2.02859375 1 0.759668174 64.87372993
GOTERM_MF_FAT GO:0035091~phosphoinositide binding 4 2.684563758 0.074713392 "SNX5, SNX1, SNX3, SNX12" 128 100 12983 4.0571875 1 0.743582669 65.15158749

Annotation Cluster 9 Enrichment Score: 1.1459050433758264
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006892~post-Golgi vesicle-mediated transport 4 2.684563758 0.020514716 "AP1M1, STX4, AP1G1, OPTN" 137 58 13528 6.809967279 1 0.737901021 28.69358559
GOTERM_CC_FAT GO:0044431~Golgi apparatus part 6 4.026845638 0.122516907 "ACTR3, AP1M1, STX4, CLTB, AP1G1, TMF1" 115 294 12782 2.268322981 1 0.552370851 81.61394799
GOTERM_BP_FAT GO:0048193~Golgi vesicle transport 4 2.684563758 0.145218963 "AP1M1, STX4, AP1G1, OPTN" 137 131 13528 3.015100017 1 0.965911461 92.26973722

Annotation Cluster 10 Enrichment Score: 1.0965184497609548
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0030336~negative regulation of cell migration 4 2.684563758 0.019594521 "APOE, CLIC4, TPM1, VCL" 137 57 13528 6.929440389 1 0.739630787 27.59272537
GOTERM_BP_FAT GO:0040013~negative regulation of locomotion 4 2.684563758 0.023416065 "APOE, CLIC4, TPM1, VCL" 137 61 13528 6.475050856 1 0.720724933 32.06258814
GOTERM_BP_FAT GO:0051271~negative regulation of cell motion 4 2.684563758 0.025467614 "APOE, CLIC4, TPM1, VCL" 137 63 13528 6.269493686 1 0.736371987 34.3539993
GOTERM_BP_FAT GO:0030334~regulation of cell migration 4 2.684563758 0.241582719 "APOE, CLIC4, TPM1, VCL" 137 169 13528 2.337148534 1 0.984302501 98.90182707
GOTERM_BP_FAT GO:0040012~regulation of locomotion 4 2.684563758 0.304185482 "APOE, CLIC4, TPM1, VCL" 137 192 13528 2.057177616 1 0.987464385 99.7306981
GOTERM_BP_FAT GO:0051270~regulation of cell motion 4 2.684563758 0.30693622 "APOE, CLIC4, TPM1, VCL" 137 193 13528 2.046518664 1 0.987549817 99.74755165

Annotation Cluster 11 Enrichment Score: 1.0507187467605021
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0008234~cysteine-type peptidase activity 6 4.026845638 0.012439149 "CTSZ, UFD1L, USP5, USP47, CTSB, CAPN1" 128 141 12983 4.316156915 0.984520138 0.406089659

15.62735668

GOTERM_MF_FAT GO:0004197~cysteine-type endopeptidase activity 4 2.684563758 0.033446832 "CTSZ, USP5, CTSB, CAPN1" 128 72 12983 5.634982639 0.999987973 0.581638354 36.98674894

GOTERM_CC_FAT GO:0005773~vacuole 6 4.026845638 0.074889321 "CTSZ, STX4, GLA, USP5, VPS16, CTSB" 115 252 12782 2.646376812 0.999999995 0.450314824 63.52978821

GOTERM_MF_FAT "GO:0070011~peptidase activity, acting on L-amino acid peptides" 10 6.711409396 0.089387657 "SCPEP1, DPP3, PREP, CTSZ, HTRA2, UFD1L, USP5, USP47, CTSB, CAPN1" 128 549 12983 1.847535291 1 0.757641888 71.95007829

GOTERM_MF_FAT GO:0008233~peptidase activity 10 6.711409396 0.109749973 "SCPEP1, DPP3, PREP, CTSZ, HTRA2, UFD1L, USP5, USP47, CTSB, CAPN1" 128 574 12983 1.767067726 1 0.800713014 79.36525035

GOTERM_CC_FAT GO:0000323~lytic vacuole 5 3.355704698 0.11976888 "CTSZ, GLA, USP5, VPS16, CTSB" 115 211 12782 2.633834741 1 0.552767713 80.85369695

GOTERM_CC_FAT GO:0005764~lysosome 5 3.355704698 0.11976888 "CTSZ, GLA, USP5, VPS16, CTSB" 115 211 12782 2.633834741 1 0.552767713 80.85369695

GOTERM_BP_FAT GO:0006508~proteolysis 14 9.395973154 0.261090742 "SCPEP1, DPP3, PREP, CTSZ, UFD1L, USP5, FBXO2, HERC4, SKP1, CAPN1, HTRA2, USP47, CTSB, UBXN6" 137 1054 13528 1.311597114 1 0.985725461 99.2821577

GOTERM_MF_FAT GO:0004175~endopeptidase activity 6 4.026845638 0.305354475 "PREP, CTSZ, HTRA2, USP5, CTSB, CAPN1" 128 375 12983 1.622875 1 0.968775875 99.28902538

Annotation Cluster 12 Enrichment Score: 1.0422118691180227

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT "GO:0030674~protein binding, bridging" 4 2.684563758 0.064544692 "GRB2, ARHGAP1, ARPC4, CRK" 128 94 12983 4.316156915 1 0.750588142 59.57753273

GOTERM_MF_FAT GO:0005070~SH3/SH2 adaptor activity 3 2.013422819 0.082934763 "GRB2, ARHGAP1, CRK" 128 49 12983 6.209980867 1 0.74661839 69.12807778

GOTERM_MF_FAT GO:0060090~molecular adaptor activity 3 2.013422819 0.139562022 "GRB2, ARHGAP1, CRK" 128 67 12983 4.541627799 1 0.854149355 87.00475758

Annotation Cluster 13 Enrichment Score: 1.005500695707451

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0019903~protein phosphatase binding 3 2.013422819 0.055617985 "SNX3, IQGAP1, AP3B1" 128 39 12983 7.802283654 0.999999995 0.719276281 54.01488619

GOTERM_MF_FAT GO:0019902~phosphatase binding 3 2.013422819 0.068821839 "SNX3, IQGAP1, AP3B1" 128 44 12983 6.915660511 1 0.752595925 62.01571235

GOTERM_MF_FAT GO:0019899~enzyme binding 8 5.369127517 0.251510656 "STX4, YWHAG, RAB3GAP1, YWHAB, CYFIP1, SNX3, IQGAP1, AP3B1" 128 523 12983 1.551505736 1 0.955484622 98.04113419

Annotation Cluster 14 Enrichment Score: 0.894967739028242

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0007265~Ras protein signal transduction 5 3.355704698 0.021412511 "GRB2, APOE, ARHGAP1, YWHAB, PARK7" 137 105 13528 4.702120264 1 0.735968813 29.75248822

GOTERM_BP_FAT GO:0007264~small GTPase mediated signal transduction 6 4.026845638 0.193304281 "GRB2, APOE, ARHGAP1, YWHAB, IQGAP1, PARK7" 137 305 13528 1.942515257 1 0.97993772 96.99430544

GOTERM_BP_FAT GO:0007242~intracellular signaling cascade 14 9.395973154 0.499100172 "RPS6KA3, APOE, GRB2, TOLLIP, RIPK1, ARHGAP1, YWHAB, PRDX2, SFN, CSK, CRK, PARK7, IQGAP1, TUBB3" 137 1256 13528 1.10065554 1 0.996857478 99.99873714

Annotation Cluster 15	Enrichment Score: 0.8341323146127818
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006887~exocytosis	4	2.684563758	0.109469736	"STX4, YWHAZ, EXOC7, EXOC6B"	137	115	13528	3.434592193	1	0.937583685	84.91640364
GOTERM_BP_FAT	GO:0032940~secretion by cell	5	3.355704698	0.15555694	"STX4, YWHAZ, EXOC7, ERP29, EXOC6B"	137	207	13528	2.385133467	1	0.967066388	93.66165157
GOTERM_BP_FAT	GO:0046903~secretion	6	4.026845638	0.184679885	"STX4, YWHAZ, EXOC7, ERP29, CA2, EXOC6B"	137	300	13528	1.974890511	1	0.978139914	96.42484114

Annotation Cluster 16	Enrichment Score: 0.750193913331748
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0022604~regulation of cell morphogenesis	5	3.355704698	0.04311021	"ACTR3, APOE, NUMB, CYFIP1, FN1"	137	131	13528	3.768875021	1	0.821878968	51.27440422
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	4	2.684563758	0.149933524	"ACTR3, YWHAG, APOE, NUMB"	137	133	13528	2.969760167	1	0.964254256	92.93674045
GOTERM_BP_FAT	GO:0010975~regulation of neuron projection development	3	2.013422819	0.156295672	"ACTR3, APOE, NUMB"	137	70	13528	4.231908238	1	0.965889364	93.75151436
GOTERM_BP_FAT	GO:0010769~regulation of cell morphogenesis involved in differentiation	3	2.013422819	0.18127373	"ACTR3, APOE, NUMB"	137	77	13528	3.847189307	1	0.977631555	96.17320455
GOTERM_BP_FAT	GO:0031344~regulation of cell projection organization	3	2.013422819	0.225252425	"ACTR3, APOE, NUMB"	137	89	13528	3.328467153	1	0.98541056	98.44539644
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	4	2.684563758	0.233570068	"ACTR3, YWHAG, APOE, NUMB"	137	166	13528	2.379386158	1	0.983286155	98.69642065
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	4	2.684563758	0.304185482	"ACTR3, YWHAG, APOE, NUMB"	137	192	13528	2.057177616	1	0.987464385	99.7306981
GOTERM_BP_FAT	GO:0060284~regulation of cell development	4	2.684563758	0.339987416	"ACTR3, YWHAG, APOE, NUMB"	137	205	13528	1.92672245	1	0.990223463	99.88625128

Annotation Cluster 17	Enrichment Score: 0.7201353970104762
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	5	3.355704698	0.083498142	"GCLC, APOE, PRDX2, TPM1, PARK7"	137	164	13528	3.010503828	1	0.927181916	75.89009242
GOTERM_BP_FAT	GO:0003013~circulatory system process	4	2.684563758	0.287712345	"GCLC, APOE, ADH5, TPM1"	137	186	13528	2.123538184	1	0.986963638	99.6055118
GOTERM_BP_FAT	GO:0008015~blood circulation	4	2.684563758	0.287712345	"GCLC, APOE, ADH5, TPM1"	137	186	13528	2.123538184	1	0.986963638	99.6055118

Annotation Cluster 18	Enrichment Score: 0.7146439259985589
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	10	6.711409396	0.056559449	"SBDS, EXOC7, BLOC1S2, TBCE, HSPB1, ARPC4, TUBA1A, UBXN6, TUBB3, CALM1"	115	549	12782	2.024550566	0.999999398	0.38974754	52.9725649
GOTERM_CC_FAT	GO:0005813~centrosome	4	2.684563758	0.322692402	"EXOC7, BLOC1S2, UBXN6, CALM1"	115	224	12782	1.984782609	1	0.819421168	99.35830851
GOTERM_CC_FAT	GO:0005815~microtubule organizing center	4	2.684563758	0.393345613	"EXOC7, BLOC1S2, UBXN6, CALM1"	115	253	12782	1.757277883	1	0.862352837	99.84605824

Annotation Cluster 19	Enrichment Score: 0.665865108581105
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_BP_FAT	GO:0008344~adult locomotory behavior	3	2.013422819	0.102442724	"HTRA2, TBCE, PARK7"	137	54	13528	5.485806975	1	0.942140589	82.85265532
GOTERM_BP_FAT	GO:0030534~adult behavior	3	2.013422819	0.214160144	"HTRA2, TBCE, PARK7"	137	86	13528	3.444576473	1	0.984261817	98.03958837
GOTERM_BP_FAT	GO:0007626~locomotory behavior	5	3.355704698	0.297104858	"TYMP, SBDS, HTRA2, TBCE, PARK7"	137	274	13528	1.801907401	1	0.986391887	99.68232829
GOTERM_BP_FAT	GO:0007610~behavior	7	4.697986577	0.332973788	"TYMP, SBDS, HTRA2, TBCE, COMT, PARK7, APRT"	137	469	13528	1.473798889	1	0.989424919	99.86484107

Annotation Cluster 20	Enrichment Score: 0.6497007043240182
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0009408~response to heat	3	2.013422819	0.108855798	"GCLC, HSPB1, HSPA4"	137	56	13528	5.289885297	1	0.939762892	84.74584677
GOTERM_BP_FAT	GO:0009266~response to temperature stimulus	3	2.013422819	0.203123602	"GCLC, HSPB1, HSPA4"	137	83	13528	3.569079237	1	0.981018106	97.53868382
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	5	3.355704698	0.508494119	"GCLC, HSPB1, HSPA4, CA2, TUBB3"	137	368	13528	1.341637575	1	0.99699694	99.99907272

Annotation Cluster 21	Enrichment Score: 0.6449600075865245
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001501~skeletal system development	7	4.697986577	0.102701514	"RPS6KA3, SBDS, OSTF1, PDLIM7, UFD1L, GFPT1, PAPSS1"	137	319	13528	2.166807771	1	0.939201845	82.933141
GOTERM_BP_FAT	GO:0001503~ossification	3	2.013422819	0.321970441	"SBDS, OSTF1, PDLIM7"	137	115	13528	2.575944145	1	0.988693391	99.82348706
GOTERM_BP_FAT	GO:0060348~bone development	3	2.013422819	0.351339621	"SBDS, OSTF1, PDLIM7"	137	123	13528	2.408403062	1	0.990536458	99.91429355

Annotation Cluster 22	Enrichment Score: 0.6016968852267689
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	8	5.369127517	0.004663299	"GCLC, APOE, PRDX2, NDRG1, CA2, TPM1, PARK7, CALM1"	137	205	13528	3.853444899	0.997616234	0.350376564	7.342557486
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	4	2.684563758	0.039732766	"APOE, PRDX2, TPM1, PARK7"	137	75	13528	5.266374696	1	0.815435323	48.39133782
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	5	3.355704698	0.083498142	"GCLC, APOE, PRDX2, TPM1, PARK7"	137	164	13528	3.010503828	1	0.927181916	75.89009242
GOTERM_BP_FAT	GO:0045454~cell redox homeostasis	3	2.013422819	0.132075578	"GCLC, DNAJC10, PRDX2"	137	63	13528	4.702120264	1	0.957378229	90.08446818
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	5	3.355704698	0.693928663	"GCLC, APOE, DNAJC10, PRDX2, PARK7"	137	466	13528	1.059490617	1	0.999575545	99.99999959
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	3	2.013422819	0.893715914	"GCLC, APOE, PARK7"	137	374	13528	0.792068387	1	0.999998674	100
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	3	2.013422819	0.898829515	"GCLC, APOE, PARK7"	137	380	13528	0.779562044	1	0.999998881	100
GOTERM_BP_FAT	GO:0050801~ion homeostasis	3	2.013422819	0.920485512	"GCLC, APOE, PARK7"	137	409	13528	0.724287473	1	0.999999651	100
GOTERM_BP_FAT	GO:0042592~homeostatic process	5	3.355704698	0.948356856	"GCLC, APOE, DNAJC10, PRDX2, PARK7"	137	751	13528	0.657420277	1	0.999999959	100
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	3	2.013422819	0.967184646	"GCLC, APOE, PARK7"	137	512	13528	0.578581204	1	0.999999996	100

Annotation Cluster 23 Enrichment Score: 0.5937190802192525
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0017016~Ras GTPase binding 3 2.013422819 0.22356312 "STX4, RAB3GAP1, CYFIP1" 128 91 12983 3.343835852 1 0.945283852 96.77793588
GOTERM_MF_FAT GO:0019899~enzyme binding 8 5.369127517 0.251510656 "STX4, YWHAG, RAB3GAP1, YWHAB, CYFIP1, SNX3, IQGAP1, AP3B1" 128 523 12983 1.551505736 1 0.955484622 98.04113419
GOTERM_MF_FAT GO:0031267~small GTPase binding 3 2.013422819 0.259762726 "STX4, RAB3GAP1, CYFIP1" 128 101 12983 3.012762995 1 0.956283896 98.31483269
GOTERM_MF_FAT GO:0051020~GTPase binding 3 2.013422819 0.288795416 "STX4, RAB3GAP1, CYFIP1" 128 109 12983 2.791642775 1 0.964484561 99.02107513

Annotation Cluster 24 Enrichment Score: 0.5827502376847299
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0007017~microtubule-based process 7 4.697986577 0.042524433 "OPA1, BLOC1S2, TBCE, ARPC4, TUBA1A, BICD2, TUBB3" 137 253 13528 2.732061972 1 0.827006051 50.78546054
GOTERM_BP_FAT GO:0051258~protein polymerization 3 2.013422819 0.086909594 "ARPC4, TUBA1A, TUBB3" 137 49 13528 6.045583197 1 0.930730672 77.31327386
GOTERM_BP_FAT GO:0043623~cellular protein complex assembly 4 2.684563758 0.222966366 "HSPA4, ARPC4, TUBA1A, TUBB3" 137 162 13528 2.438136433 1 0.985490063 98.36884007
GOTERM_CC_FAT GO:0005874~microtubule 5 3.355704698 0.228627124 "TBCE, ARPC4, TUBA1A, TUBB3, CALM1" 115 274 12782 2.028245002 1 0.721169249 96.53922839
GOTERM_BP_FAT GO:0006461~protein complex assembly 8 5.369127517 0.245761173 "STOM, STX4, GRB2, YWHAB, HSPA4, ARPC4, TUBA1A, TUBB3" 137 505 13528 1.564269712 1 0.984831713 98.99648251
GOTERM_BP_FAT GO:0070271~protein complex biogenesis 8 5.369127517 0.245761173 "STOM, STX4, GRB2, YWHAB, HSPA4, ARPC4, TUBA1A, TUBB3" 137 505 13528 1.564269712 1 0.984831713 98.99648251
GOTERM_BP_FAT GO:0065003~macromolecular complex assembly 9 6.040268456 0.353020799 "STOM, STX4, GRB2, APOE, YWHAB, HSPA4, ARPC4, TUBA1A, TUBB3" 137 665 13528 1.336392075 1 0.990433651 99.91784663
GOTERM_BP_FAT GO:0043933~macromolecular complex subunit organization 9 6.040268456 0.422397548 "STOM, STX4, GRB2, APOE, YWHAB, HSPA4, ARPC4, TUBA1A, TUBB3" 137 710 13528 1.251691169 1 0.994968738 99.98709035
GOTERM_BP_FAT GO:0051259~protein oligomerization 3 2.013422819 0.524512238 "STOM, GRB2, YWHAB" 137 174 13528 1.70249182 1 0.997434965 99.99945994
GOTERM_BP_FAT GO:0034622~cellular macromolecular complex assembly 4 2.684563758 0.623682616 "HSPA4, ARPC4, TUBA1A, TUBB3" 137 318 13528 1.242069504 1 0.998873582 99.99998811
GOTERM_BP_FAT GO:0034621~cellular macromolecular complex subunit organization 4 2.684563758 0.700497414 "HSPA4, ARPC4, TUBA1A, TUBB3" 137 357 13528 1.106381239 1 0.999601388 99.99999971

Annotation Cluster 25 Enrichment Score: 0.5804301070410901
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0051099~positive regulation of binding 3 2.013422819 0.184891073 "CALD1, RIPK1, CALM1" 137 78 13528 3.797866367 1 0.977022934 96.43992
GOTERM_BP_FAT GO:0051098~regulation of binding 4 2.684563758 0.199500742 "CALD1, RIPK1, PRDX2, CALM1" 137 153 13528 2.581556223 1 0.981555553 97.34962104
GOTERM_BP_FAT GO:0051101~regulation of DNA binding 3 2.013422819 0.344033644 "RIPK1, PRDX2, CALM1" 137 121 13528 2.448211377 1 0.990496761 99.89710977

GOTERM_BP_FAT GO:0044093~positive regulation of molecular function 8 5.369127517 0.375680106 "APOE, CALD1, RIPK1, YWHAB, PRDX2, SKP1, TPM1, CALM1" 137 586 13528 1.34804813 1 0.992018001 99.95407875

Annotation Cluster 26 Enrichment Score: 0.5774516720559246
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0032989~cellular component morphogenesis 8 5.369127517 0.105572527 "S100A6, OPA1, NUMB, TBCE, CYFIP1, ARPC4, TPM1, FN1" 137 397 13528 1.989814117 1 0.937470803 83.80257646
GOTERM_BP_FAT GO:0032990~cell part morphogenesis 6 4.026845638 0.115946695 "S100A6, OPA1, NUMB, TBCE, CYFIP1, ARPC4" 137 256 13528 2.314324818 1 0.941765355 86.60996417
GOTERM_BP_FAT GO:0030030~cell projection organization 7 4.697986577 0.166303604 "S100A6, NUMB, TBCE, CYFIP1, ARPC4, TPM1, VCL" 137 368 13528 1.878292606 1 0.970025647 94.85691958
GOTERM_BP_FAT GO:0000904~cell morphogenesis involved in differentiation 5 3.355704698 0.230746284 "S100A6, NUMB, TBCE, CYFIP1, FN1" 137 244 13528 2.023453392 1 0.98397118 98.61581121
GOTERM_BP_FAT GO:0048858~cell projection morphogenesis 5 3.355704698 0.232898522 "S100A6, NUMB, TBCE, CYFIP1, ARPC4" 137 245 13528 2.015194399 1 0.983871705 98.67765985
GOTERM_BP_FAT GO:0000902~cell morphogenesis 6 4.026845638 0.288011107 "S100A6, NUMB, TBCE, CYFIP1, ARPC4, FN1" 137 356 13528 1.664233577 1 0.986469077 99.60820273
GOTERM_BP_FAT GO:0007409~axonogenesis 4 2.684563758 0.30693622 "S100A6, NUMB, TBCE, CYFIP1" 137 193 13528 2.046518664 1 0.987549817 99.74755165
GOTERM_BP_FAT GO:0048667~cell morphogenesis involved in neuron differentiation 4 2.684563758 0.350996181 "S100A6, NUMB, TBCE, CYFIP1" 137 209 13528 1.889847379 1 0.990847461 99.91355018
GOTERM_BP_FAT GO:0048812~neuron projection morphogenesis 4 2.684563758 0.361986472 "S100A6, NUMB, TBCE, CYFIP1" 137 213 13528 1.854357287 1 0.991427322 99.93457439
GOTERM_BP_FAT GO:0048666~neuron development 5 3.355704698 0.444955255 "S100A6, HTRA2, NUMB, TBCE, CYFIP1" 137 339 13528 1.456408931 1 0.994917774 99.99326026
GOTERM_BP_FAT GO:0030182~neuron differentiation 6 4.026845638 0.451082299 "S100A6, HTRA2, NUMB, TBCE, CYFIP1, TUBB3" 137 438 13528 1.352664734 1 0.99486549 99.9943767
GOTERM_BP_FAT GO:0031175~neuron projection development 4 2.684563758 0.477027377 "S100A6, NUMB, TBCE, CYFIP1" 137 256 13528 1.542883212 1 0.995953579 99.99744783

Annotation Cluster 27 Enrichment Score: 0.5632436270884443
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0030016~myofibril 3 2.013422819 0.260505283 "HSPB1, TPM1, VCL" 115 111 12782 3.0039953 1 0.766759222 97.99708629
GOTERM_CC_FAT GO:0044449~contractile fiber part 3 2.013422819 0.267125506 "HSPB1, TPM1, VCL" 115 113 12782 2.950827241 1 0.770127924 98.21739456
GOTERM_CC_FAT GO:0043292~contractile fiber 3 2.013422819 0.293587273 "HSPB1, TPM1, VCL" 115 121 12782 2.755731225 1 0.800747548 98.89311628

Annotation Cluster 28 Enrichment Score: 0.5489707998945155
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0032496~response to lipopolysaccharide 3 2.013422819 0.18127373 "ADH5, PRDX2, COMT" 137 77 13528 3.847189307 1 0.977631555 96.17320455
GOTERM_BP_FAT GO:0002237~response to molecule of bacterial origin 3 2.013422819 0.214160144 "ADH5, PRDX2, COMT" 137 86 13528 3.444576473 1 0.984261817 98.03958837
GOTERM_BP_FAT GO:0009617~response to bacterium 3 2.013422819 0.580783246 "ADH5, PRDX2, COMT" 137 193 13528 1.534888998 1 0.998117182 99.99993082

Annotation Cluster 29	Enrichment Score: 0.5425351974633094

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006916~anti-apoptosis	6	4.026845638	0.05691532	"YWHAZ, GCLC, APOE, HSPB1, PRDX2, ANXA4"	137	206	13528	2.876054142	1	0.885037314	61.55961292
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	14	9.395973154	0.060937236	"YWHAZ, GCLC, BLOC1S2, HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, HSPB1, PRDX2, SFN, CTSB, ANXA4"	137	804	13528	1.719432037	1	0.888692184	64.14865267
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	14	9.395973154	0.064849831	"YWHAZ, GCLC, BLOC1S2, HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, HSPB1, PRDX2, SFN, CTSB, ANXA4"	137	812	13528	1.70249182	1	0.89767868	66.50950189
GOTERM_BP_FAT	GO:0010941~regulation of cell death	14	9.395973154	0.066359534	"YWHAZ, GCLC, BLOC1S2, HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, HSPB1, PRDX2, SFN, CTSB, ANXA4"	137	815	13528	1.696224979	1	0.8851064	67.38079702
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	5	3.355704698	0.083498142	"GCLC, APOE, PRDX2, TPM1, PARK7"	137	164	13528	3.010503828	1	0.927181916	75.89009242
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	7	4.697986577	0.264685831	"HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, SFN"	137	430	13528	1.607469021	1	0.985387884	99.33706572
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	7	4.697986577	0.269812715	"HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, SFN"	137	433	13528	1.596331822	1	0.985477117	99.408583
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	7	4.697986577	0.273244735	"HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, SFN"	137	435	13528	1.588992365	1	0.9857522	99.45233943
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	6	4.026845638	0.284119715	"YWHAZ, GCLC, APOE, HSPB1, PRDX2, ANXA4"	137	354	13528	1.673636026	1	0.987247541	99.57176453
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	6	4.026845638	0.293867105	"YWHAZ, GCLC, APOE, HSPB1, PRDX2, ANXA4"	137	359	13528	1.650326332	1	0.986735079	99.65759333
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	6	4.026845638	0.295823906	"YWHAZ, GCLC, APOE, HSPB1, PRDX2, ANXA4"	137	360	13528	1.645742092	1	0.986641602	99.67275004
GOTERM_BP_FAT	GO:0008219~cell death	9	6.040268456	0.436293639	"OPA1, HTRA2, ENDOG, RIPK1, KIAA0196, YWHAB, HSPB1, SFN, OPTN"	137	719	13528	1.236023268	1	0.995146601	99.99132314
GOTERM_BP_FAT	GO:0016265~death	9	6.040268456	0.444000713	"OPA1, HTRA2, ENDOG, RIPK1, KIAA0196, YWHAB, HSPB1, SFN, OPTN"	137	724	13528	1.227487196	1	0.995025441	99.99306864
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	4	2.684563758	0.627925733	"HTRA2, APOE, RIPK1, SFN"	137	320	13528	1.234306569	1	0.998879993	99.99999012
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	4	2.684563758	0.630035089	"HTRA2, APOE, RIPK1, SFN"	137	321	13528	1.230461378	1	0.998842578	99.999991
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	5	3.355704698	0.693928663	"GCLC, APOE, DNAJC10, PRDX2, PARK7"	137	466	13528	1.059490617	1	0.999575545	99.99999959
GOTERM_BP_FAT	GO:0006915~apoptosis	6	4.026845638	0.729343354	"OPA1, HTRA2, ENDOG, RIPK1, YWHAB, SFN"	137	602	13528	0.984164706	1	0.999745716	99.99999995
GOTERM_BP_FAT	GO:0012501~programmed cell death	6	4.026845638	0.741243961	"OPA1, HTRA2, ENDOG, RIPK1, YWHAB, SFN"	137	611	13528	0.969668009	1	0.999800576	99.99999997
GOTERM_BP_FAT	GO:0040008~regulation of growth	3	2.013422819	0.861091358	"HTRA2, APOE, SFN"	137	341	13528	0.868720166	1	0.999994037	100
GOTERM_BP_FAT	GO:0042592~homeostatic process	5	3.355704698	0.948356856	"GCLC, APOE, DNAJC10, PRDX2, PARK7"	137	751	13528	0.657420277	1	0.999999959	100

Annotation Cluster 30	Enrichment Score: 0.540510263996261
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0007017~microtubule-based process	7	4.697986577	0.042524433	"OPA1,
BLOC1S2, TBCE, ARPC4, TUBA1A, BICD2, TUBB3"	137	253	13528	2.732061972	1	0.827006051
50.78546054
GOTERM_BP_FAT	GO:0007018~microtubule-based movement	4	2.684563758	0.105272133	"OPA1,
TUBA1A, BICD2, TUBB3"	137	113	13528	3.495381435	1	0.940272948	83.71359426
GOTERM_MF_FAT	GO:0003924~GTPase activity	4	2.684563758	0.340841125	"OPA1, TUBA1A,
TUBB3, GBP1"	128	211	12983	1.922837678	1	0.971525641	99.65110322
GOTERM_MF_FAT	GO:0005525~GTP binding	4	2.684563758	0.709616157	"OPA1, TUBA1A, TUBB3,
GBP1"	128	372	12983	1.090641801	1	0.999068935	99.99999488
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	4	2.684563758	0.726449601	"OPA1,
TUBA1A, TUBB3, GBP1"	128	382	12983	1.062090969	1	0.999053009	99.99999772
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	4	2.684563758	0.726449601	"OPA1,
TUBA1A, TUBB3, GBP1"	128	382	12983	1.062090969	1	0.999053009	99.99999772

Annotation Cluster 31	Enrichment Score: 0.5051660104884375
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0006928~cell motion	10	6.711409396	0.050266981	"PVR, ACTR3, ACTR2,
SBDS, CALD1, HSPB1, MSN, TPM1, VCL, FN1"	137	475	13528	2.078832117	1	0.859117055
56.89147761
GOTERM_BP_FAT	GO:0016477~cell migration	4	2.684563758	0.527334031	"PVR, SBDS, MSN, FN1"
137	276	13528	1.43108008	1	0.997462124	99.99950992
GOTERM_BP_FAT	GO:0051674~localization of cell	4	2.684563758	0.599768538	"PVR, SBDS, MSN,
FN1"	137	307	13528	1.286573623	1	0.998497388	99.99996752
GOTERM_BP_FAT	GO:0048870~cell motility	4	2.684563758	0.599768538	"PVR, SBDS, MSN, FN1"
137	307	13528	1.286573623	1	0.998497388	99.99996752

Annotation Cluster 32	Enrichment Score: 0.4886322344284258
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	8	5.369127517
0.200366576	"GCLC, APOE, RIPK1, ITGAV, FBXO2, YWHAB, HSPB1, SKP1"	137	474	13528	1.666574271
1	0.980888154	97.39600653
GOTERM_BP_FAT	GO:0031396~regulation of protein ubiquitination	3	2.013422819	0.26619772	"GCLC,
FBXO2, SKP1"	137	100	13528	2.962335766	1	0.985144914	99.35895779
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	5	3.355704698	0.344923596
"GCLC, RIPK1, FBXO2, YWHAB, SKP1"	137	295	13528	1.673636026	1	0.990260142	99.89936374
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	6	4.026845638	0.603557357
"APOE, RIPK1, YWHAB, PRDX2, SKP1, TPM1"	137	520	13528	1.13935991	1	0.998491562
99.99997219

Annotation Cluster 33	Enrichment Score: 0.47928284549791283
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	6	4.026845638	0.229138285
"BCAT1, NAMPT, QDPR, PAPSS1, CMPK1, APRT"	137	325	13528	1.822975856	1	0.984252738
98.56784106
GOTERM_BP_FAT	"GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process"	4
2.684563758	0.30693622	"NAMPT, PAPSS1, CMPK1, APRT"	137	193	13528	2.046518664	1
0.987549817	99.74755165
GOTERM_BP_FAT	"GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process"	4

2.684563758 0.30693622 "NAMPT, PAPSS1, CMPK1, APRT" 137 193 13528 2.046518664 1
0.987549817 99.74755165
GOTERM_BP_FAT GO:0009165~nucleotide biosynthetic process 3 2.013422819 0.560627866 "NAMPT,
PAPSS1, CMPK1" 137 186 13528 1.592653638 1 0.997924653 99.99985116

Annotation Cluster 34 Enrichment Score: 0.45803190104828073
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0045321~leukocyte activation 6 4.026845638 0.097195369 "YWHAZ, TOLLIP,
CD276, PRDX2, NDRG1, LCP1" 137 242 13528 2.448211377 1 0.936212948 81.14177978
GOTERM_BP_FAT GO:0001775~cell activation 6 4.026845638 0.1629686 "YWHAZ, TOLLIP, CD276,
PRDX2, NDRG1, LCP1" 137 287 13528 2.064345482 1 0.969266556 94.51077359
GOTERM_BP_FAT GO:0002526~acute inflammatory response 3 2.013422819 0.258736754 "YWHAZ,
PRDX2, FN1" 137 98 13528 3.022791598 1 0.985747377 99.24392255
GOTERM_BP_FAT GO:0009611~response to wounding 8 5.369127517 0.284529862 "YWHAZ,
TOLLIP, ITGB6, PRDX2, CTSB, TPM1, FN1, AP3B1" 137 530 13528 1.490483404 1 0.986777233
99.57574993
GOTERM_BP_FAT GO:0042110~T cell activation 3 2.013422819 0.362246523 "CD276, PRDX2, LCP1"
137 126 13528 2.351060132 1 0.9911272 99.93500811
GOTERM_BP_FAT GO:0006954~inflammatory response 5 3.355704698 0.413415991 "YWHAZ,
TOLLIP, ITGB6, PRDX2, FN1" 137 325 13528 1.519146547 1 0.994599372 99.98339473
GOTERM_BP_FAT GO:0046649~lymphocyte activation 3 2.013422819 0.597518145 "CD276, PRDX2,
LCP1" 137 199 13528 1.488610938 1 0.998544686 99.99996441
GOTERM_BP_FAT GO:0006955~immune response 6 4.026845638 0.829682151 "YWHAZ, TOLLIP,
CD276, PRDX2, LCP1, GBP1" 137 690 13528 0.858648048 1 0.999980374 100
GOTERM_BP_FAT GO:0006952~defense response 5 3.355704698 0.871611723 "YWHAZ, TOLLIP,
ITGB6, PRDX2, FN1" 137 615 13528 0.802801021 1 0.999996087 100

Annotation Cluster 35 Enrichment Score: 0.4400917020454357
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0031980~mitochondrial lumen 4 2.684563758 0.330031772 "TST, GSTK1,
GLS, ALDH2" 115 227 12782 1.958552002 1 0.817093174 99.44279828
GOTERM_CC_FAT GO:0005759~mitochondrial matrix 4 2.684563758 0.330031772 "TST, GSTK1,
GLS, ALDH2" 115 227 12782 1.958552002 1 0.817093174 99.44279828
GOTERM_CC_FAT GO:0044429~mitochondrial part 7 4.697986577 0.439150509 "TST, OPA1, HTRA2,
GSTK1, GLS, NIPSNAP1, ALDH2" 115 595 12782 1.307621483 1 0.891700094 99.94433866

Annotation Cluster 36 Enrichment Score: 0.43236683181677044
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0050865~regulation of cell activation 4 2.684563758 0.257740532 "APOE,
CD276, PRDX2, AP3B1" 137 175 13528 2.257017727 1 0.986140236 99.22717237
GOTERM_BP_FAT GO:0050863~regulation of T cell activation 3 2.013422819 0.329347015 "CD276,
PRDX2, AP3B1" 137 117 13528 2.531910911 1 0.989618956 99.85233874
GOTERM_BP_FAT GO:0051249~regulation of lymphocyte activation 3 2.013422819 0.439824729
"CD276, PRDX2, AP3B1" 137 148 13528 2.001578221 1 0.995058465 99.99216862
GOTERM_BP_FAT GO:0002694~regulation of leukocyte activation 3 2.013422819 0.49936325 "CD276,
PRDX2, AP3B1" 137 166 13528 1.784539618 1 0.996753377 99.99874792

Annotation Cluster 37 Enrichment Score: 0.42156065665965475
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0000267~cell fraction 15 10.06711409 0.101290718 "RAB3GAP2, STX4,

YWHAZ, RAB3GAP1, CALD1, ADH5, LSS, COMT, MOGS, CAPN1, CTTN, CLIC4, CYFIP1, HSPB1, CTSB"115 1083 12782 1.539443575 1 0.517980377 74.93899475

GOTERM_CC_FAT GO:0005626~insoluble fraction 8 5.369127517 0.627336017 "STX4, CALD1, HSPB1, CYFIP1, LSS, MOGS, COMT, CAPN1" 115 839 12782 1.059812406 1 0.960742635 99.9997213

GOTERM_CC_FAT GO:0005624~membrane fraction 6 4.026845638 0.855555442 "STX4, CALD1, CYFIP1, LSS, MOGS, COMT" 115 809 12782 0.824334928 1 0.996986275 100

Annotation Cluster 38 Enrichment Score: 0.41521038793358345

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0005099~Ras GTPase activator activity 3 2.013422819 0.22356312 "RAB3GAP1, ARHGAP1, IQGAP1" 128 91 12983 3.343835852 1 0.945283852 96.77793588

GOTERM_MF_FAT GO:0008047~enzyme activator activity 6 4.026845638 0.230811404 "RAB3GAP2, APOE, RAB3GAP1, ARHGAP1, IQGAP1, FN1" 128 335 12983 1.816651119 1 0.945679409 97.16314744

GOTERM_BP_FAT GO:0043087~regulation of GTPase activity 3 2.013422819 0.351339621 "RAB3GAP2, RAB3GAP1, ARHGAP1" 137 123 13528 2.408403062 1 0.990536458 99.91429355

GOTERM_MF_FAT GO:0005096~GTPase activator activity 4 2.684563758 0.364925349 "RAB3GAP2, RAB3GAP1, ARHGAP1, IQGAP1" 128 220 12983 1.844176136 1 0.977169455 99.78950378

GOTERM_BP_FAT GO:0051336~regulation of hydrolase activity 5 3.355704698 0.44047723 "RAB3GAP2, RAB3GAP1, ARHGAP1, SFN, TPM1"137 337 13528 1.465052308 1 0.994924289 99.99231613

GOTERM_MF_FAT GO:0005083~small GTPase regulator activity 4 2.684563758 0.504124509 "STX4, RAB3GAP1, ARHGAP1, IQGAP1" 128 274 12983 1.480725365 1 0.994431252 99.99267975

GOTERM_MF_FAT GO:0030695~GTPase regulator activity 5 3.355704698 0.560971788 "RAB3GAP2, STX4, RAB3GAP1, ARHGAP1, IQGAP1" 128 404 12983 1.255317915 1 0.995840898 99.99859832

GOTERM_MF_FAT GO:0060589~nucleoside-triphosphatase regulator activity 5 3.355704698 0.578530177 "RAB3GAP2, STX4, RAB3GAP1, ARHGAP1, IQGAP1" 128 413 12983 1.227962318 1 0.996452308 99.9991946

Annotation Cluster 39 Enrichment Score: 0.37948341557520776

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0006469~negative regulation of protein kinase activity 3 2.013422819 0.217852037 "YWHAG, APOE, SFN" 137 87 13528 3.40498364 1 0.984656953 98.18456636

GOTERM_BP_FAT GO:0033673~negative regulation of kinase activity 3 2.013422819 0.228959962 "YWHAG, APOE, SFN" 137 90 13528 3.291484185 1 0.98499305 98.56242621

GOTERM_BP_FAT GO:0044092~negative regulation of molecular function 6 4.026845638 0.245871966 "YWHAG, GLA, APOE, PRDX2, SFN, CALM1" 137 334 13528 1.773853752 1 0.984126561 98.99888483

GOTERM_BP_FAT GO:0051348~negative regulation of transferase activity 3 2.013422819 0.251279207 "YWHAG, APOE, SFN" 137 96 13528 3.085766423 1 0.985019709 99.10978335

GOTERM_BP_FAT GO:0043065~positive regulation of apoptosis 7 4.697986577 0.264685831 "HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, SFN"137 430 13528 1.607469021 1 0.985387884 99.33706572

GOTERM_BP_FAT GO:0043068~positive regulation of programmed cell death 7 4.697986577 0.269812715 "HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, SFN" 137 433 13528 1.596331822 1 0.985477117 99.408583

GOTERM_BP_FAT GO:0010942~positive regulation of cell death 7 4.697986577 0.273244735 "HTRA2, APOE, ALDH1A3, ENDOG, RIPK1, YWHAB, SFN"137 435 13528 1.588992365 1 0.9857522 99.45233943

GOTERM_BP_FAT GO:0044093~positive regulation of molecular function 8 5.369127517 0.375680106 "APOE, CALD1, RIPK1, YWHAB, PRDX2, SKP1, TPM1, CALM1" 137 586 13528 1.34804813 1 0.992018001 99.95407875

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GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	3	2.013422819	0.415649722	"APOE, RIPK1, PRDX2"	137	141	13528	2.100947352	1	0.994587507	99.98439685
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	5	3.355704698	0.458324729	"YWHAG, APOE, RIPK1, PRDX2, SFN"	137	345	13528	1.43108008	1	0.994911318	99.99547226
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	5	3.355704698	0.484733738	"YWHAG, APOE, RIPK1, PRDX2, SFN"	137	357	13528	1.382976548	1	0.996299437	99.99799682
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	5	3.355704698	0.517015691	"YWHAG, APOE, RIPK1, PRDX2, SFN"	137	372	13528	1.327211365	1	0.997297863	99.99930292
GOTERM_BP_FAT	GO:0043086~negative regulation of catalytic activity	4	2.684563758	0.529780453	"YWHAG, GLA, APOE, SFN"	137	277	13528	1.425913726	1	0.997473435	99.9995497
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	6	4.026845638	0.541106001	"YWHAG, APOE, RIPK1, YWHAB, PRDX2, SFN"	137	485	13528	1.221581759	1	0.997585492	99.99969748
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	6	4.026845638	0.541106001	"YWHAG, APOE, RIPK1, YWHAB, PRDX2, SFN"	137	485	13528	1.221581759	1	0.997585492	99.99969748
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	6	4.026845638	0.603557357	"APOE, RIPK1, YWHAB, PRDX2, SKP1, TPM1"	137	520	13528	1.13935991	1	0.998491562	99.99997219
GOTERM_BP_FAT	GO:0006917~induction of apoptosis	4	2.684563758	0.627925733	"HTRA2, APOE, RIPK1, SFN"	137	320	13528	1.234306569	1	0.998879993	99.99999012
GOTERM_BP_FAT	GO:0012502~induction of programmed cell death	4	2.684563758	0.630035089	"HTRA2, APOE, RIPK1, SFN"	137	321	13528	1.230461378	1	0.998842578	99.999991
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	5	3.355704698	0.693928663	"YWHAG, APOE, RIPK1, PRDX2, SFN"	137	466	13528	1.059490617	1	0.999575545	99.99999959
GOTERM_BP_FAT	GO:0033554~cellular response to stress	4	2.684563758	0.927912587	"RIPK1, PRDX2, SFN, TPM1"	137	566	13528	0.69784117	1	0.999999759	100

Annotation Cluster 40	Enrichment Score: 0.37409613578183565
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005739~mitochondrion	14	9.395973154	0.170210632	"YWHAZ, OPA1, ADH5, PARK7, TST, HTRA2, CLIC4, ENDOG, RIPK1, GSTK1, GLS, NIPSNAP1, ALDH2, CTSB"	115	1087	12782	1.431526739	1	0.631316043	91.08776655
GOTERM_CC_FAT	GO:0031967~organelle envelope	8	5.369127517	0.316352787	"TST, S100A6, OPA1, HTRA2, GSTK1, NIPSNAP1, KPNA4, RETSAT"	115	620	12782	1.434165498	1	0.823165004	99.2759716
GOTERM_CC_FAT	GO:0031975~envelope	8	5.369127517	0.319238777	"TST, S100A6, OPA1, HTRA2, GSTK1, NIPSNAP1, KPNA4, RETSAT"	115	622	12782	1.429554033	1	0.820926496	99.31459274
GOTERM_CC_FAT	GO:0044429~mitochondrial part	7	4.697986577	0.439150509	"TST, OPA1, HTRA2, GSTK1, GLS, NIPSNAP1, ALDH2"	115	595	12782	1.307621483	1	0.891700094	99.94433866
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	4	2.684563758	0.516415285	"TST, OPA1, GSTK1, NIPSNAP1"	115	306	12782	1.452912759	1	0.924997438	99.99184547
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	5	3.355704698	0.516748603	"TST, OPA1, HTRA2, GSTK1, NIPSNAP1"	115	419	12782	1.326346373	1	0.922358467	99.991918
GOTERM_CC_FAT	GO:0005635~nuclear envelope	3	2.013422819	0.548591687	"S100A6, KPNA4, RETSAT"	115	205	12782	1.626553552	1	0.936444012	99.99665869
GOTERM_CC_FAT	GO:0019866~organelle inner membrane	4	2.684563758	0.565660951	"TST, OPA1, GSTK1, NIPSNAP1"	115	329	12782	1.351341351	1	0.942112873	99.99797236
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	4	2.684563758	0.687327275	"TST, OPA1, GSTK1, NIPSNAP1"	115	394	12782	1.128404326	1	0.974438194	99.99997133

Annotation Cluster 41	Enrichment Score: 0.3675884494308596
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
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Benjamini	FDR
GOTERM_CC_FAT	GO:0043235~receptor complex	4	2.684563758	0.085100334	"TOLLIP, RIPK1,
ITGAV, ITGB6"	115	116	12782	3.832683658	1	0.474556907	68.41521958
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	7	4.697986577	0.960181416	"STOM,
CLCA2, TOLLIP, ITGAV, NUMB, ITGB6, TUBB3"	115	1188	12782	0.654911433	1	0.999901009	100
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	7	4.697986577	0.965939865	"STOM,
CLCA2, TOLLIP, ITGAV, NUMB, ITGB6, TUBB3"	115	1215	12782	0.640357846	1	0.999929238	100

Annotation Cluster 42	Enrichment Score: 0.34869570544926637
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	5	3.355704698
0.226457287	"UFD1L, USP5, FBXO2, USP47, SKP1"	137	242	13528	2.040176148	1	0.984995406
98.48437507
GOTERM_BP_FAT	GO:0006508~proteolysis	14	9.395973154	0.261090742	"SCPEP1, DPP3, PREP,
CTSZ, UFD1L, USP5, FBXO2, HERC4, SKP1, CAPN1, HTRA2, USP47, CTSB, UBXN6"	137	1054	13528
1.311597114	1	0.985725461	99.2821577
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	9	6.040268456	0.445540683
"UFD1L, APOE, USP5, ENDOG, FBXO2, USP47, HERC4, SKP1, UBXN6"	137	725	13528	1.22579411	1
0.994778557	99.9933753
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	7	4.697986577
0.520204837	"UFD1L, USP5, FBXO2, USP47, HERC4, SKP1, UBXN6"	137	574	13528	1.204201531	1
0.997342177	99.99937434
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	7	4.697986577
0.520204837	"UFD1L, USP5, FBXO2, USP47, HERC4, SKP1, UBXN6"	137	574	13528	1.204201531	1
0.997342177	99.99937434
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	9	6.040268456	0.530328233	"UFD1L,
APOE, USP5, ENDOG, FBXO2, USP47, HERC4, SKP1, UBXN6"	137	781	13528	1.137901063	1
0.997403546	99.99955819
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	7	4.697986577
0.56400124	"UFD1L, USP5, FBXO2, USP47, HERC4, SKP1, UBXN6"	137	600	13528	1.152019465	1
0.997895861	99.99986875
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	7	4.697986577	0.568936844	"UFD1L,
USP5, FBXO2, USP47, HERC4, SKP1, UBXN6"	137	603	13528	1.146288025	1	0.997996138	99.999891
GOTERM_BP_FAT	GO:0030163~protein catabolic process	7	4.697986577	0.59956445	"UFD1L, USP5,
FBXO2, USP47, HERC4, SKP1, UBXN6"	137	622	13528	1.111272796	1	0.998545112	99.99996725

Annotation Cluster 43	Enrichment Score: 0.335844731648099964
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0043009~chordate embryonic development	5	3.355704698	0.426985063	"SBDS,
GFPT1, ENDOG, POFUT1, TPM1"	137	331	13528	1.491609147	1	0.994958306	99.98866522
GOTERM_BP_FAT	GO:0009792~embryonic development ending in birth or egg hatching	5	3.355704698
0.433741591	"SBDS, GFPT1, ENDOG, POFUT1, TPM1"137	334	13528	1.47821146	1	0.995128704
99.99065953
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	3	2.013422819	0.530666967	"SBDS,
ENDOG, TPM1"	137	176	13528	1.683145322	1	0.997323313	99.99956336

Annotation Cluster 44	Enrichment Score: 0.33167279289691043
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0015698~inorganic anion transport	3	2.013422819	0.240106385	"TST, CLCA2,
CLIC4"	137	93	13528	3.185307276	1	0.984602774	98.86642515
GOTERM_BP_FAT	GO:0006820~anion transport	3	2.013422819	0.422614963	"TST, CLCA2, CLIC4"	137
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143 13528 2.071563473 1 0.994786412 99.98716941
GOTERM_BP_FAT GO:0006811~ion transport 3 2.013422819 0.996857413 "TST, CLCA2, CLIC4" 137 768 13528 0.385720803 1 1 100

Annotation Cluster 45 Enrichment Score: 0.3282490527866023
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0001505~regulation of neurotransmitter levels 3 2.013422819 0.145809361 "STX4, COMT, PARK7" 137 67 13528 4.421396666 1 0.964493458 92.35639008
GOTERM_BP_FAT GO:0007267~cell-cell signaling 8 5.369127517 0.398905041 "NAMPT, STX4, YWHAZ, GRB2, TOLLIP, APOE, COMT, PARK7" 137 600 13528 1.316593674 1 0.993890529 99.97526011
GOTERM_BP_FAT GO:0007268~synaptic transmission 4 2.684563758 0.579488204 "STX4, APOE, COMT, PARK7" 137 298 13528 1.325429873 1 0.998141248 99.99992725
GOTERM_BP_FAT GO:0019226~transmission of nerve impulse 4 2.684563758 0.687632928 "STX4, APOE, COMT, PARK7" 137 350 13528 1.128508863 1 0.999551427 99.99999943
GOTERM_BP_FAT GO:0050877~neurological system process 7 4.697986577 0.985595108 "STX4, SBDS, OPA1, APOE, TGFBI, COMT, PARK7" 137 1210 13528 0.571249321 1 1 100

Annotation Cluster 46 Enrichment Score: 0.29427065593015556
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0001568~blood vessel development 4 2.684563758 0.448349337 "TYMP, APOE, ITGAV, POFUT1" 137 245 13528 1.612155519 1 0.994825068 99.99390208
GOTERM_BP_FAT GO:0001944~vasculature development 4 2.684563758 0.464072281 "TYMP, APOE, ITGAV, POFUT1" 137 251 13528 1.573617937 1 0.995189902 99.99619551
GOTERM_BP_FAT GO:0048514~blood vessel morphogenesis 3 2.013422819 0.629485705 "TYMP, APOE, POFUT1" 137 211 13528 1.4039506 1 0.998871868 99.99999078

Annotation Cluster 47 Enrichment Score: 0.25651104031010474
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0032268~regulation of cellular protein metabolic process 8 5.369127517 0.200366576 "GCLC, APOE, RIPK1, ITGAV, FBXO2, YWHAB, HSPB1, SKP1" 137 474 13528 1.666574271 1 0.980888154 97.39600653
GOTERM_BP_FAT GO:0032270~positive regulation of cellular protein metabolic process 3 2.013422819 0.682946284 "GCLC, APOE, SKP1" 137 233 13528 1.271388741 1 0.999523955 99.99999927
GOTERM_BP_FAT GO:0051247~positive regulation of protein metabolic process 3 2.013422819 0.705100978 "GCLC, APOE, SKP1" 137 243 13528 1.219068217 1 0.99962495 99.99999978
GOTERM_BP_FAT GO:0010604~positive regulation of macromolecule metabolic process 5 3.355704698 0.976096372 "GCLC, BLOC1S2, APOE, CD276, SKP1" 137 857 13528 0.57610575 1 0.999999999 100

Annotation Cluster 48 Enrichment Score: 0.18765303456451768
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0032268~regulation of cellular protein metabolic process 8 5.369127517 0.200366576 "GCLC, APOE, RIPK1, ITGAV, FBXO2, YWHAB, HSPB1, SKP1" 137 474 13528 1.666574271 1 0.980888154 97.39600653
GOTERM_BP_FAT GO:0032269~negative regulation of cellular protein metabolic process 3 2.013422819 0.54281475 "GCLC, ITGAV, YWHAB" 137 180 13528 1.645742092 1 0.997568091 99.99971535
GOTERM_BP_FAT GO:0051248~negative regulation of protein metabolic process 3 2.013422819 0.563548671 "GCLC, ITGAV, YWHAB" 137 187 13528 1.584136773 1 0.997953717 99.99986651
GOTERM_BP_FAT GO:0009890~negative regulation of biosynthetic process 6 4.026845638 0.688394064 "GCLC, GLA, APOE, ITGAV, YWHAB, CD276" 137 573 13528 1.03397409 1 0.999540874

99.99999945
GOTERM_BP_FAT GO:0051172~negative regulation of nitrogen compound metabolic process 4 2.684563758 0.898278395 "GCLC, GLA, YWHAB, COMT" 137 519 13528 0.761036806 1 0.999998915 100
GOTERM_BP_FAT GO:0010558~negative regulation of macromolecule biosynthetic process 4 2.684563758 0.917028226 "GCLC, ITGAV, YWHAB, CD276" 137 547 13528 0.722080626 1 0.999999581 100
GOTERM_BP_FAT GO:0031327~negative regulation of cellular biosynthetic process 4 2.684563758 0.925181549 "GCLC, GLA, YWHAB, CD276" 137 561 13528 0.704060788 1 0.99999972 100
GOTERM_BP_FAT GO:0010605~negative regulation of macromolecule metabolic process 4 2.684563758 0.980640078 "GCLC, ITGAV, YWHAB, CD276" 137 734 13528 0.538117305 1 1 100

Annotation Cluster 49 Enrichment Score: 0.18587846044221376
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0032555~purine ribonucleotide binding 19 12.75167785 0.534933669 "CARS, OPA1, GCLC, TWF2, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, PAPSS1, CSK, TUBA1A, GUK1, TUBB3, PIP4K2C, GBP1" 128 1836 12983 1.049653629 1 0.995063892 99.99693562
GOTERM_MF_FAT GO:0032553~ribonucleotide binding 19 12.75167785 0.534933669 "CARS, OPA1, GCLC, TWF2, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, PAPSS1, CSK, TUBA1A, GUK1, TUBB3, PIP4K2C, GBP1" 128 1836 12983 1.049653629 1 0.995063892 99.99693562
GOTERM_MF_FAT GO:0032559~adenyl ribonucleotide binding 15 10.06711409 0.612921159 "CARS, GCLC, TWF2, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, CSK, PAPSS1, GUK1, PIP4K2C" 128 1497 12983 1.016329534 1 0.997707386 99.99974639
GOTERM_MF_FAT GO:0017076~purine nucleotide binding 19 12.75167785 0.614275636 "CARS, OPA1, GCLC, TWF2, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, PAPSS1, CSK, TUBA1A, GUK1, TUBB3, PIP4K2C, GBP1" 128 1918 12983 1.004777926 1 0.997484809 99.99975818
GOTERM_MF_FAT GO:0030554~adenyl nucleotide binding 15 10.06711409 0.691669112 "CARS, GCLC, TWF2, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, CSK, PAPSS1, GUK1, PIP4K2C" 128 1577 12983 0.964771917 1 0.999084884 99.99998844
GOTERM_MF_FAT GO:0005524~ATP binding 14 9.395973154 0.698959882 "CARS, GCLC, TWF2, TFG, CMPK1, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, CSK, PAPSS1, GUK1, PIP4K2C" 128 1477 12983 0.961418839 1 0.99910036 99.99999164
GOTERM_MF_FAT GO:0001883~purine nucleoside binding 15 10.06711409 0.713441191 "CARS, GCLC, TWF2, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, CSK, PAPSS1, GUK1, PIP4K2C" 128 1601 12983 0.950309377 1 0.999028291 99.99999572
GOTERM_MF_FAT GO:0001882~nucleoside binding 15 10.06711409 0.72311037 "CARS, GCLC, TWF2, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, CSK, PAPSS1, GUK1, PIP4K2C" 128 1612 12983 0.943824636 1 0.999097301 99.99999731
GOTERM_MF_FAT GO:0000166~nucleotide binding 20 13.42281879 0.790337674 "CARS, OPA1, GCLC, TWF2, ADH5, TFG, CMPK1, APRT, ACTR3, ACTR2, RPS6KA3, RIPK1, HSPA4, PAPSS1, CSK, TUBA1A, GUK1, TUBB3, PIP4K2C, GBP1" 128 2245 12983 0.903605234 1 0.999740731 99.99999994

Annotation Cluster 50 Enrichment Score: 0.15605359220157347
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0031974~membrane-enclosed lumen 18 12.08053691 0.493193623 "OPA1, ERP29, YWHAB, DNAJC10, SKP1, IQGAP1, TST, RPS6KA3, DUSP3, SBDS, HTRA2, GSTK1, GLS, ALDH2, MSN, CALM1, ACAA1, FN1" 115 1856 12782 1.077942279 1 0.9205917 99.98502568
GOTERM_CC_FAT GO:0043233~organelle lumen 16 10.73825503 0.670349659 "ERP29, YWHAB, DNAJC10, SKP1, IQGAP1, TST, DUSP3, SBDS, RPS6KA3, GSTK1, GLS, ALDH2, MSN, CALM1, FN1, ACAA1" 115 1820 12782 0.977123746 1 0.971141423 99.99994312
GOTERM_CC_FAT GO:0070013~intracellular organelle lumen 15 10.06711409 0.733623193 "ERP29, YWHAB, DNAJC10, SKP1, IQGAP1, TST, DUSP3, SBDS, RPS6KA3, GSTK1, GLS, ALDH2, MSN, CALM1, ACAA1" 115 1779 12782 0.937165481 1 0.983743036 99.99999641

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GOTERM_CC_FAT	GO:0031981~nuclear lumen	8	5.369127517	0.979475852	"RPS6KA3, SBDS, 
DUSP3, YWHAB, SKP1, MSN, IQGAP1, CALM1"	115	1450	12782	0.613229385	1	0.999980857	100

Annotation Cluster 51	Enrichment Score: 0.08895035786220294
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	
Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	4	2.684563758	0.723325359	"BCAT1, TPD52L1, 
SKP1, TUBB3"	137	370	13528	1.067508384	1	0.999719201	99.99999992
GOTERM_BP_FAT	GO:0007049~cell cycle	7	4.697986577	0.799373665	"BCAT1, S100A6, SBDS, 
TPD52L1, SKP1, TUBB3, CALM1"	137	776	13528	0.8907367	1	0.999953575	100
GOTERM_BP_FAT	GO:0022402~cell cycle process	5	3.355704698	0.825201627	"BCAT1, SBDS, 
TPD52L1, SKP1, TUBB3"	137	565	13528	0.873845359	1	0.999978132	100
GOTERM_BP_FAT	GO:0022403~cell cycle phase	3	2.013422819	0.923751093	"BCAT1, TPD52L1, 
TUBB3"	137	414	13528	0.71554004	1	0.999999708	100

Annotation Cluster 52	Enrichment Score: 0.08392684060824891
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	
Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005615~extracellular space	6	4.026845638	0.73801071	"PVR, APOE, TGFBI, 
CA2, SFN, FN1"	115	685	12782	0.973557601	1	0.983736205	99.9999971
GOTERM_CC_FAT	GO:0044421~extracellular region part	7	4.697986577	0.866196882	"PVR, STX4, 
APOE, TGFBI, CA2, SFN, FN1"	115	960	12782	0.810452899	1	0.997423844	100
GOTERM_CC_FAT	GO:0005576~extracellular region	15	10.06711409	0.876072802	"SCPEP1, PVR, STX4, 
CLCA2, DNAJC10, SFN, VCL, GLA, APOE, TGFBI, PON2, CA2, CTSB, CALM1, FN1"	115	2010	12782	
0.829461389	1	0.997790603	100

Annotation Cluster 53	Enrichment Score: 0.05178914704135868
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	
Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	4	2.684563758	0.723325359	"RPS6KA3, 
GRB2, RIPK1, PRDX2"	137	370	13528	1.067508384	1	0.999719201	99.99999992
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	5	3.355704698	0.908314903	
"RPS6KA3, RIPK1, TFG, PRDX2, CSK"	137	667	13528	0.740213835	1	0.999999337	100
GOTERM_BP_FAT	GO:0016310~phosphorylation	6	4.026845638	0.910653611	"RPS6KA3, TOLLIP, 
RIPK1, TFG, PRDX2, CSK"	137	800	13528	0.740583942	1	0.999999393	100
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	7	4.697986577	0.932459612	"RPS6KA3, 
DUSP3, TOLLIP, RIPK1, TFG, PRDX2, CSK"	137	973	13528	0.71039227	1	0.999999823	100
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	7	4.697986577	0.932459612	"RPS6KA3, 
DUSP3, TOLLIP, RIPK1, TFG, PRDX2, CSK"	137	973	13528	0.71039227	1	0.999999823	100
GOTERM_MF_FAT	GO:0004672~protein kinase activity	4	2.684563758	0.939900135	"RPS6KA3, RIPK1, 
TFG, CSK"	128	606	12983	0.669502888	1	0.99999931	100

Annotation Cluster 54	Enrichment Score: 0.03744655781956386
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	
Benjamini	FDR
GOTERM_MF_FAT	GO:0003712~transcription cofactor activity	3	2.013422819	0.874305762	"PIR, 
YWHAB, TMF1"	128	363	12983	0.83826188	1	0.999979411	100
GOTERM_MF_FAT	GO:0008134~transcription factor binding	4	2.684563758	0.883093054	"YWHAZ, 
PIR, YWHAB, TMF1"	128	513	12983	0.790874756	1	0.999983232	100
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	4	2.684563758	0.999978165	"PIR, SNF8, 
YWHAB, TMF1"	128	1512	12983	0.268332507	1	1	100

Annotation Cluster 55	Enrichment Score: 0.005404043054166079
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
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Benjamini FDR
GOTERM_BP_FAT GO:0010604~positive regulation of macromolecule metabolic process 5 3.355704698
0.976096372 "GCLC, BLOC1S2, APOE, CD276, SKP1" 137 857 13528 0.57610575 1 0.999999999 100
GOTERM_BP_FAT GO:0031328~positive regulation of cellular biosynthetic process3 2.013422819
0.993149332 "BLOC1S2, APOE, CD276" 137 685 13528 0.432457776 1 1 100
GOTERM_BP_FAT GO:0009891~positive regulation of biosynthetic process 3 2.013422819 0.993757954
"BLOC1S2, APOE, CD276" 137 695 13528 0.426235362 1 1 100

Annotation Cluster 56 Enrichment Score: 7.45214146356533E-4
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0043167~ion binding 29 19.46308725 0.996959502 "DPP3, VPS29, CLCA2,
S100A6, CARS, GCLC, OPA1, CLTB, PDLIM7, USP5, PDLIM4, ADH5, COMT, CSRP1, ANXA4, CAPN1,
RPS6KA3, GLA, CLIC4, APOE, ITGAV, PIR, ENDOG, CALML5, CA2, POFUT1, PLS3, LCP1, CALM1" 128 4241
12983 0.693577208 1 1 100
GOTERM_MF_FAT GO:0043169~cation binding 28 18.79194631 0.997734406 "DPP3, VPS29, CLCA2,
S100A6, CARS, GCLC, OPA1, CLTB, PDLIM7, USP5, PDLIM4, ADH5, COMT, CSRP1, ANXA4, CAPN1,
RPS6KA3, GLA, APOE, ITGAV, PIR, ENDOG, CALML5, CA2, POFUT1, PLS3, LCP1, CALM1" 128 4179
12983 0.679595896 1 1 100
GOTERM_MF_FAT GO:0046872~metal ion binding 27 18.12080537 0.998545241 "DPP3, VPS29, CLCA2,
S100A6, CARS, GCLC, OPA1, CLTB, PDLIM7, USP5, PDLIM4, ADH5, COMT, CSRP1, ANXA4, CAPN1,
RPS6KA3, APOE, ITGAV, PIR, ENDOG, CALML5, CA2, POFUT1, PLS3, LCP1, CALM1"128 4140 12983
0.661497962 1 1 100
GOTERM_MF_FAT GO:0046914~transition metal ion binding 13 8.724832215 0.99990544 "VPS29,
DPP3, S100A6, CARS, PDLIM7, USP5, ENDOG, PIR, PDLIM4, ADH5, CA2, CSRP1, POFUT1"128 2785
12983 0.473459942 1 1 100

Annotation Cluster 1 Enrichment Score: 8.463854279033956

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0015031~protein transport 41 18.72146119 2.17E-13 "BID, COPA, ARFGAP3, PDIA3, RAB5B, SNX4, CALR, KIF13A, COPB2, AP3M1, SEC16A, VPS4B, NECAP2, RAB11B, VPS4A, AP3D1, VPS35, STAM, RAB6A, SAR1A, SEC61A1, AP2M1, SCAMP1, GDI2, MYO6, STXBP1, PRKCI, YIF1A, MAPK1, RAB32, HSP90B1, YWHAH, VCP, ARF3, ARF4, YWHAQ, USO1, SEC13, PDCD6IP, VPS26A, YKT6" 190 762 13528 3.830971129 3.44E-10 3.44E-10 3.63E-10

GOTERM_BP_FAT GO:0008104~protein localization 44 20.0913242 2.87E-13 "BID, COPA, ARFGAP3, PDIA3, RAB5B, SNX4, NEDD8, CALR, KIF13A, COPB2, AP3M1, SEC16A, VPS4B, NECAP2, RAB11B, VPS4A, AP3D1, VPS35, STAM, RAB6A, SAR1A, SEC61A1, AP2M1, SCAMP1, GDI2, MYO6, HSPG2, PRKCI, STXBP1, YIF1A, MAPK1, RAB32, HSP90B1, YWHAH, VCP, ARF3, BAX, ARF4, YWHAQ, USO1, SEC13, PDCD6IP, VPS26A, YKT6" 190 882 13528 3.551927438 4.55E-10 2.27E-10 4.80E-10

GOTERM_BP_FAT GO:0045184~establishment of protein localization 41 18.72146119 2.92E-13 "BID, COPA, ARFGAP3, PDIA3, RAB5B, SNX4, CALR, KIF13A, COPB2, AP3M1, SEC16A, VPS4B, NECAP2, RAB11B, VPS4A, AP3D1, VPS35, STAM, RAB6A, SAR1A, SEC61A1, AP2M1, SCAMP1, GDI2, MYO6, STXBP1, PRKCI, YIF1A, MAPK1, RAB32, HSP90B1, YWHAH, VCP, ARF3, ARF4, YWHAQ, USO1, SEC13, PDCD6IP, VPS26A, YKT6" 190 769 13528 3.79609883 4.62E-10 1.54E-10 4.88E-10

GOTERM_BP_FAT GO:0016192~vesicle-mediated transport 33 15.06849315 1.83E-11 "COPA, ARFGAP3, NRBP1, SNX4, COPB2, APP, AP3M1, ACTR1A, SEC16A, NECAP2, VPS4B, VPS4A, AP3D1, VPS35, RAB6A, CAP1, EHD1, SAR1A, AP2M1, SCAMP1, MYO6, STXBP1, PRKCI, SCRN1, YIF1A, VCP, TFRC, ARF3, ARF4, USO1, SEC13, YKT6, VPS26A" 190 576 13528 4.079166667 2.90E-08 7.25E-09 3.06E-08

GOTERM_BP_FAT GO:0046907~intracellular transport 31 14.15525114 8.84E-09 "BID, COPA, ARFGAP3, NRBP1, PDIA3, CALR, COPB2, APP, AP3M1, VPS4B, VPS4A, AP3D1, VPS35, STAM, PAFAH1B1, EHD1, SAR1A, SEC61A1, AP2M1, SCAMP1, MYO6, PRKCI, MAPK1, YWHAH, VCP, BAX, YWHAQ, USO1, SEC13, YKT6, VPS26A" 190 657 13528 3.359512938 1.40E-05 2.81E-06 1.48E-05

GOTERM_BP_FAT GO:0006886~intracellular protein transport 20 9.132420091 1.23E-06 "BID, COPA, ARFGAP3, MYO6, PDIA3, PRKCI, CALR, MAPK1, COPB2, YWHAH, VCP, AP3M1, YWHAQ, USO1, AP3D1, SEC13, STAM, SAR1A, SEC61A1, AP2M1" 190 374 13528 3.807486631 0.001949468 3.25E-04 0.002058071

GOTERM_BP_FAT GO:0034613~cellular protein localization 21 9.589041096 1.24E-06 "BID, COPA, ARFGAP3, MYO6, PDIA3, PRKCI, CALR, MAPK1, COPB2, YWHAH, VCP, AP3M1, BAX, YWHAQ, USO1, AP3D1, SEC13, STAM, SAR1A, SEC61A1, AP2M1" 190 411 13528 3.637956204 0.001967387 2.81E-04 0.002077007

GOTERM_BP_FAT GO:0070727~cellular macromolecule localization 21 9.589041096 1.39E-06 "BID, COPA, ARFGAP3, MYO6, PDIA3, PRKCI, CALR, MAPK1, COPB2, YWHAH, VCP, AP3M1, BAX, YWHAQ, USO1, AP3D1, SEC13, STAM, SAR1A, SEC61A1, AP2M1" 190 414 13528 3.611594203 0.002201273 2.75E-04 0.002324194

GOTERM_BP_FAT GO:0006605~protein targeting 9 4.109589041 0.010747838 "BID, MAPK1, MYO6, PDIA3, AP3M1, YWHAQ, PRKCI, CALR, SEC61A1" 190 215 13528 2.980465116 0.999999964 0.248466095 16.53613834

Annotation Cluster 2 Enrichment Score: 6.738993698882086

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0031982~vesicle 29 13.24200913 4.09E-08 "SRI, COPA, PDIA3, RAB5B, PTPN23, PDIA6, PRDX1, ANXA7, COPB2, APP, SND1, NECAP2, RAB11B, HSPA5, EHD1, MYOF, THBS2, AP2M1, SCAMP1, MYO6, STXBP1, SPAG9, HSP90B1, PLA2G4A, TFRC, PPIB, PEBP1, PDCD6IP, YKT6" 168 670 12782 3.293159204 1.09E-05 5.44E-06 5.36E-05

GOTERM_CC_FAT GO:0016023~cytoplasmic membrane-bounded vesicle 25 11.41552511 1.95E-07 "COPA, PDIA3, RAB5B, PTPN23, PDIA6, PRDX1, COPB2, APP, SND1, NECAP2, RAB11B, HSPA5, EHD1, THBS2, AP2M1, SCAMP1, MYO6, STXBP1, SPAG9, HSP90B1, PLA2G4A, TFRC, PPIB, PEBP1, PDCD6IP"

168 550 12782 3.458333333 5.18E-05 1.30E-05 2.55E-04

GOTERM_CC_FAT GO:0042470~melanosome 11 5.02283105 2.31E-07 "HSP90B1, PDIA3, PPIB, TFRC, RAB5B, SND1, PEBP1, PDIA6, PDCD6IP, HSPA5, PRDX1" 168 89 12782 9.403558052 6.16E-05 1.23E-05 3.04E-04

GOTERM_CC_FAT GO:0048770~pigment granule 11 5.02283105 2.31E-07 "HSP90B1, PDIA3, PPIB, TFRC, RAB5B, SND1, PEBP1, PDIA6, PDCD6IP, HSPA5, PRDX1" 168 89 12782 9.403558052 6.16E-05 1.23E-05 3.04E-04

GOTERM_CC_FAT GO:0031410~cytoplasmic vesicle 27 12.32876712 2.46E-07 "COPA, PDIA3, RAB5B, PTPN23, PDIA6, PRDX1, COPB2, APP, SND1, NECAP2, RAB11B, HSPA5, EHD1, MYOF, THBS2, AP2M1, SCAMP1, MYO6, STXBP1, SPAG9, HSP90B1, PLA2G4A, TFRC, PPIB, PEBP1, PDCD6IP, YKT6" 168 642 12782 3.199766355 6.54E-05 1.09E-05 3.23E-04

GOTERM_CC_FAT GO:0031988~membrane-bounded vesicle 25 11.41552511 3.51E-07 "COPA, PDIA3, RAB5B, PTPN23, PDIA6, PRDX1, COPB2, APP, SND1, NECAP2, RAB11B, HSPA5, EHD1, THBS2, AP2M1, SCAMP1, MYO6, STXBP1, SPAG9, HSP90B1, PLA2G4A, TFRC, PPIB, PEBP1, PDCD6IP" 168 568 12782 3.348738263 9.34E-05 1.33E-05 4.60E-04

Annotation Cluster 3 Enrichment Score: 4.501806639613005

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0003924~GTPase activity 15 6.849315068 1.59E-06 "DNM1L, RAB5B, TUBB2A, HBS1L, TUBB, GSPT1, ARF3, ARF4, RAB11B, EFTUD1, TUBA4A, TUBB6, RAB6A, EHD1, SAR1A" 183 211 12983 5.043508663 6.78E-04 6.78E-04 0.00223332

GOTERM_MF_FAT GO:0005525~GTP binding 17 7.762557078 6.93E-05 "DNM1L, RAB5B, TUBB2A, HBS1L, DRG2, RAB32, TUBB, GSPT1, ARF3, ARF4, RAB11B, EFTUD1, TUBA4A, TUBB6, RAB6A, EHD1, SAR1A" 183 372 12983 3.242126447 0.029228413 0.00591525 0.097575837

GOTERM_MF_FAT GO:0019001~guanyl nucleotide binding 17 7.762557078 9.46E-05 "DNM1L, RAB5B, TUBB2A, HBS1L, DRG2, RAB32, TUBB, GSPT1, ARF3, ARF4, RAB11B, EFTUD1, TUBA4A, TUBB6, RAB6A, EHD1, SAR1A" 183 382 12983 3.157254027 0.039683304 0.006725972 0.133169584

GOTERM_MF_FAT GO:0032561~guanyl ribonucleotide binding 17 7.762557078 9.46E-05 "DNM1L, RAB5B, TUBB2A, HBS1L, DRG2, RAB32, TUBB, GSPT1, ARF3, ARF4, RAB11B, EFTUD1, TUBA4A, TUBB6, RAB6A, EHD1, SAR1A" 183 382 12983 3.157254027 0.039683304 0.006725972 0.133169584

Annotation Cluster 4 Enrichment Score: 3.9546358331212215

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0043603~cellular amide metabolic process 8 3.652968037 1.21E-05 "TPI1, TP53I3, PGLS, PGD, IDH1, QPRT, ASL, PNP" 190 56 13528 10.17142857 0.018993425 0.001915774 0.020222826

GOTERM_BP_FAT GO:0046496~nicotinamide nucleotide metabolic process 7 3.196347032 1.78E-05 "TPI1, TP53I3, PGLS, PGD, IDH1, QPRT, PNP" 190 40 13528 12.46 0.027774161 0.002557375 0.029703225

GOTERM_BP_FAT GO:0006769~nicotinamide metabolic process 7 3.196347032 1.78E-05 "TPI1, TP53I3, PGLS, PGD, IDH1, QPRT, PNP" 190 40 13528 12.46 0.027774161 0.002557375 0.029703225

GOTERM_BP_FAT GO:0009820~alkaloid metabolic process 7 3.196347032 2.06E-05 "TPI1, TP53I3, PGLS, PGD, IDH1, QPRT, PNP" 190 41 13528 12.15609756 0.032089425 0.002714274 0.034393429

GOTERM_BP_FAT GO:0019362~pyridine nucleotide metabolic process 7 3.196347032 2.37E-05 "TPI1, TP53I3, PGLS, PGD, IDH1, QPRT, PNP" 190 42 13528 11.86666667 0.036914519 0.002889134 0.039662324

GOTERM_BP_FAT GO:0006732~coenzyme metabolic process 11 5.02283105 5.69E-05 "PANK4, ACOT9, GPX1, TPI1, TP53I3, PGLS, PGD, IDH1, GLO1, QPRT, PNP" 190 153 13528 5.118954248 0.086352968 0.005628535 0.095204779

GOTERM_BP_FAT GO:0006739~NADP metabolic process 5 2.283105023 5.89E-05 "TPI1, TP53I3, PGLS, PGD, IDH1" 190 16 13528 22.25 0.089181511 0.005479734 0.098471875

GOTERM_BP_FAT GO:0006733~oxidoreduction coenzyme metabolic process 7 3.196347032 8.20E-05

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"TPI1, TP53I3, PGLS, PGD, IDH1, QPRT, PNP"	190	52	13528	9.584615385	0.121922417	0.00647993
0.137037242
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	12	5.479452055	9.25E-05	"PANK4,
ACOT9, HMOX2, GPX1, TPI1, TP53I3, PGLS, PGD, IDH1, GLO1, QPRT, PNP"	190	195	13528
4.381538462	0.136496379	0.006964075	0.154663708
GOTERM_BP_FAT	GO:0019748~secondary metabolic process	7	3.196347032	8.20E-04	"TPI1, TP53I3,
PGLS, PGD, IDH1, QPRT, PNP"	190	79	13528	6.308860759	0.727683399	0.045394185	1.362562895
GOTERM_BP_FAT	GO:0006098~pentose-phosphate shunt	3	1.369863014	0.006552873	"TPI1, PGLS,
PGD"	190	9	13528	23.73333333	0.99997038	0.175595249	10.41418628
GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	4	1.826484018	0.013780371	"TP53I3,
PGD, IDH1, SPR"	183	36	12983	7.882817243	0.997365375	0.36672294	17.7536336

Annotation Cluster 5	Enrichment Score: 3.5454043457176776
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005788~endoplasmic reticulum lumen	11	5.02283105	8.29E-08	"HYOU1,
MINPP1, HSP90B1, PDIA3, PPIB, DNAJB11, SUMF1, PDIA6, ERAP1, HSPA5, CALR"	168	80	12782
10.46145833	2.21E-05	7.35E-06	1.09E-04
GOTERM_BP_FAT	GO:0006457~protein folding	8	3.652968037	0.012206262	"COPA, HSP90B1, PPIB,
DNAJB11, PDIA6, FKBP15, ERO1L, CALR"	190	177	13528	3.218079096	0.999999997	0.265950352
18.57072312
GOTERM_MF_FAT	GO:0051082~unfolded protein binding	6	2.739726027	0.022833524	"COPA,
HSP90B1, PPIB, DNAJB11, HSPA5, CALR"	183	115	12983	3.701496793	0.99994912	0.405668706
27.77230101

Annotation Cluster 6	Enrichment Score: 3.3501100656177725
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0000166~nucleotide binding	57	26.02739726	5.18E-06	"ABCF3, NRBP1,
RAB5B, TUBB2A, PGD, HBS1L, QARS, KIF13A, TP53I3, ACTR1A, NT5C2, VPS4B, TUBB6, VPS4A, SPR,
RAB6A, DYNC1H1, SAR1A, MYO6, PFKL, PRKCI, PFKP, GAK, PANK4, MAPK1, UBE2O, DHX29, UBE2K,
ASCC3, EFTUD1, TUBA4A, PEBP1, SLC27A4, GNE, STK10, SKIV2L, RIOK2, TUBB, RAB11B, PNPO, IDH1,
HSPA5, ERO1L, EHD1, PIK3R4, DNM1L, SWAP70, MYO1B, DRG2, HYOU1, RAB32, HSP90B1, GSPT1, VCP,
ARF3, ARF4, PGK1"	183	2245	12983	1.801285187	0.002216073	0.001108651	0.007300849
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	49	22.37442922	9.16E-06	"ABCF3, NRBP1,
RAB5B, TUBB2A, HBS1L, QARS, KIF13A, ACTR1A, VPS4B, TUBB6, VPS4A, RAB6A, DYNC1H1, SAR1A,
MYO6, PFKL, PRKCI, PFKP, GAK, PANK4, UBE2O, MAPK1, DHX29, UBE2K, ASCC3, EFTUD1, PEBP1,
TUBA4A, GNE, STK10, SKIV2L, RIOK2, TUBB, RAB11B, HSPA5, EHD1, PIK3R4, DNM1L, MYO1B, SWAP70,
DRG2, HYOU1, RAB32, HSP90B1, GSPT1, VCP, ARF3, ARF4, PGK1"	183	1836	12983	1.893421789
0.003912568	0.001305894	0.012900554
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	49	22.37442922	9.16E-06	"ABCF3,
NRBP1, RAB5B, TUBB2A, HBS1L, QARS, KIF13A, ACTR1A, VPS4B, TUBB6, VPS4A, RAB6A, DYNC1H1,
SAR1A, MYO6, PFKL, PRKCI, PFKP, GAK, PANK4, UBE2O, MAPK1, DHX29, UBE2K, ASCC3, EFTUD1,
PEBP1, TUBA4A, GNE, STK10, SKIV2L, RIOK2, TUBB, RAB11B, HSPA5, EHD1, PIK3R4, DNM1L, MYO1B,
SWAP70, DRG2, HYOU1, RAB32, HSP90B1, GSPT1, VCP, ARF3, ARF4, PGK1"	183	1836	12983
1.893421789	0.003912568	0.001305894	0.012900554
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	50	22.83105023	1.35E-05	"ABCF3,
NRBP1, RAB5B, TUBB2A, HBS1L, QARS, KIF13A, ACTR1A, VPS4B, TUBB6, VPS4A, RAB6A, DYNC1H1,
SAR1A, MYO6, PFKL, PRKCI, PFKP, GAK, PANK4, UBE2O, MAPK1, DHX29, UBE2K, ASCC3, EFTUD1,
TUBA4A, PEBP1, GNE, STK10, SKIV2L, RIOK2, TUBB, RAB11B, HSPA5, ERO1L, EHD1, PIK3R4, DNM1L,
MYO1B, SWAP70, DRG2, HYOU1, RAB32, HSP90B1, GSPT1, VCP, ARF3, ARF4, PGK1"	183	1918	12983
1.849461814	0.005758128	0.001442651	0.019002769
GOTERM_MF_FAT	GO:0005524~ATP binding	33	15.06849315	0.007999881	"ABCF3, NRBP1, GNE,
STK10, SKIV2L, QARS, RIOK2, KIF13A, ACTR1A, VPS4B, VPS4A, HSPA5, DYNC1H1, EHD1, PIK3R4, MYO6,
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PFKL, SWAP70, MYO1B, PFKP, PRKCI, GAK, PANK4, MAPK1, HYOU1, UBE2O, HSP90B1, VCP, DHX29, UBE2K, ASCC3, PEBP1, PGK1" 183 1477 12983 1.585102723 0.967862059 0.349305319 10.69691461

GOTERM_MF_FAT GO:0001882~nucleoside binding 35 15.98173516 0.009295922 "ABCF3, NRBP1, GNE, STK10, SKIV2L, QARS, RIOK2, PNP, KIF13A, ACTR1A, VPS4B, VPS4A, HSPA5, ERO1L, DYNC1H1, EHD1, PIK3R4, MYO6, PFKL, SWAP70, MYO1B, PFKP, PRKCI, GAK, PANK4, MAPK1, UBE2O, HYOU1, HSP90B1, VCP, DHX29, UBE2K, ASCC3, PEBP1, PGK1" 183 1612 12983 1.540376819 0.981634156 0.358624568 12.32633144

GOTERM_MF_FAT GO:0032559~adenyl ribonucleotide binding 33 15.06849315 0.009678479 "ABCF3, NRBP1, GNE, STK10, SKIV2L, QARS, RIOK2, KIF13A, ACTR1A, VPS4B, VPS4A, HSPA5, DYNC1H1, EHD1, PIK3R4, MYO6, PFKL, SWAP70, MYO1B, PFKP, PRKCI, GAK, PANK4, MAPK1, HYOU1, UBE2O, HSP90B1, VCP, DHX29, UBE2K, ASCC3, PEBP1, PGK1" 183 1497 12983 1.563925666 0.984432427 0.340488929 12.80198573

GOTERM_MF_FAT GO:0030554~adenyl nucleotide binding 34 15.52511416 0.011644228 "ABCF3, NRBP1, GNE, STK10, SKIV2L, QARS, RIOK2, KIF13A, ACTR1A, VPS4B, VPS4A, HSPA5, ERO1L, DYNC1H1, EHD1, PIK3R4, MYO6, PFKL, SWAP70, MYO1B, PFKP, PRKCI, GAK, PANK4, MAPK1, UBE2O, HYOU1, HSP90B1, VCP, DHX29, UBE2K, ASCC3, PEBP1, PGK1" 183 1577 12983 1.529576459 0.993348897 0.366011705 15.20853117

GOTERM_MF_FAT GO:0001883~purine nucleoside binding 34 15.52511416 0.014363903 "ABCF3, NRBP1, GNE, STK10, SKIV2L, QARS, RIOK2, KIF13A, ACTR1A, VPS4B, VPS4A, HSPA5, ERO1L, DYNC1H1, EHD1, PIK3R4, MYO6, PFKL, SWAP70, MYO1B, PFKP, PRKCI, GAK, PANK4, MAPK1, UBE2O, HYOU1, HSP90B1, VCP, DHX29, UBE2K, ASCC3, PEBP1, PGK1" 183 1601 12983 1.506647143 0.997954945 0.357449162 18.4364351

Annotation Cluster 7 Enrichment Score: 3.0683687289370956

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT GO:0005856~cytoskeleton 40 18.26484018 2.32E-06 "TUBB2A, GNE, FERMT1, FHL3, FHL2, PNP, KIF13A, PEA15, APP, TUBB, ARPC3, ACTR1A, PPP2CA, TPT1, TUBB6, CLASP1, MICAL1, PAFAH1B1, CAP1, DYNC1H1, MYOF, TWF1, MYO6, MYO1B, TRADD, MAPK1, ARPC1B, IGBP1, TRIM32, CFL1, TUBA4A, PEBP1, FKBP15, PDCD6IP, WDR1, MAPRE1, WDR44, DYNC1I2, ALDH9A1, ACTR10" 168 1381 12782 2.203717113 6.18E-04 6.18E-05 0.003046599

GOTERM_CC_FAT GO:0044430~cytoskeletal part 30 13.69863014 1.48E-05 "TUBB2A, FERMT1, FHL3, KIF13A, PEA15, APP, TUBB, ARPC3, ACTR1A, PPP2CA, TPT1, TUBB6, MICAL1, PAFAH1B1, CLASP1, CAP1, DYNC1H1, MYOF, MYO6, MYO1B, ARPC1B, TRIM32, CFL1, TUBA4A, FKBP15, PDCD6IP, MAPRE1, WDR44, DYNC1I2, ACTR10" 168 952 12782 2.397584034 0.003920485 3.57E-04 0.019369829

GOTERM_CC_FAT GO:0015630~microtubule cytoskeleton 18 8.219178082 8.45E-04 "TUBB2A, KIF13A, PEA15, TUBB, APP, ACTR1A, PPP2CA, TUBA4A, TUBB6, PAFAH1B1, CLASP1, PDCD6IP, MAPRE1, WDR44, DYNC1H1, MYOF, DYNC1I2, ACTR10" 168 549 12782 2.494535519 0.201303328 0.010646447 1.102342892

GOTERM_BP_FAT GO:0007017~microtubule-based process 11 5.02283105 0.002963809 "KIF13A, APP, TUBB, TUBB2A, TUBA4A, TUBB6, PAFAH1B1, CLASP1, DYNC1H1, DYNC1I2, ACTR10" 190 253 13528 3.095652174 0.990973406 0.108472529 4.843797518

GOTERM_CC_FAT GO:0005874~microtubule 11 5.02283105 0.003216362 "KIF13A, TUBB, TUBB2A, TUBA4A, TUBB6, PAFAH1B1, CLASP1, MAPRE1, WDR44, DYNC1H1, DYNC1I2" 168 274 12782 3.054440389 0.575537306 0.036572342 4.137872574

GOTERM_CC_FAT GO:0043228~non-membrane-bounded organelle 45 20.54794521 0.034683691 "TUBB2A, GNE, FHL3, FERMT1, FHL2, PNP, KIF13A, PEA15, APP, CASP3, TUBB, ARPC3, ACTR1A, PPP2CA, TPT1, TUBB6, SLC4A7, CLASP1, PAFAH1B1, MICAL1, CAP1, DYNC1H1, MYOF, TWF1, MYO6, MYO1B, TRADD, MAPK1, ARPC1B, VCP, IGBP1, TRIM32, CFL1, ZNF259, TUBA4A, PEBP1, FKBP15, SEC13, PDCD6IP, WDR1, MAPRE1, WDR44, DYNC1I2, ALDH9A1, ACTR10" 168 2596 12782 1.318855932 0.999916416 0.224133204 37.06368393

GOTERM_CC_FAT GO:0043232~intracellular non-membrane-bounded organelle 45 20.54794521 0.034683691 "TUBB2A, GNE, FHL3, FERMT1, FHL2, PNP, KIF13A, PEA15, APP, CASP3, TUBB, ARPC3,

ACTR1A, PPP2CA, TPT1, TUBB6, SLC4A7, CLASP1, PAFAH1B1, MICAL1, CAP1, DYNC1H1, MYOF, TWF1, MYO6, MYO1B, TRADD, MAPK1, ARPC1B, VCP, IGBP1, TRIM32, CFL1, ZNF259, TUBA4A, PEBP1, FKBP15, SEC13, PDCD6IP, WDR1, MAPRE1, WDR44, DYNC1I2, ALDH9A1, ACTR10" 168 2596 12782 1.318855932 0.999916416 0.224133204 37.06368393

Annotation Cluster 8 Enrichment Score: 3.0033704693371694
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0016044~membrane organization 19 8.675799087 6.56E-06 "SCAMP1, BID, COPA, NPLOC4, DNM1L, MYO6, PRKCI, STXBP1, SNX4, COPB2, APP, TFRC, BAX, NECAP2, USO1, SEC13, PAFAH1B1, CAP1, EHD1" 190 381 13528 3.550656168 0.010348518 0.001155159 0.010970751
GOTERM_BP_FAT GO:0010324~membrane invagination 9 4.109589041 0.012204755 "SCAMP1, APP, MYO6, TFRC, STXBP1, NECAP2, SNX4, CAP1, EHD1" 190 220 13528 2.912727273 0.999999997 0.269573264 18.56864552
GOTERM_BP_FAT GO:0006897~endocytosis 9 4.109589041 0.012204755 "SCAMP1, APP, MYO6, TFRC, STXBP1, NECAP2, SNX4, CAP1, EHD1" 190 220 13528 2.912727273 0.999999997 0.269573264 18.56864552

Annotation Cluster 9 Enrichment Score: 2.663135631700189
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0015629~actin cytoskeleton 14 6.392694064 5.19E-05 "TWF1, MYO6, MYO1B, FHL3, FERMT1, ARPC1B, ARPC3, ACTR1A, TRIM32, CFL1, FKBP15, CAP1, DYNC1I2, ACTR10" 168 269 12782 3.959727385 0.013722108 0.001062291 0.068115369
GOTERM_MF_FAT GO:0008092~cytoskeletal protein binding 16 7.305936073 0.004892857 "TWF1, MYO6, MYO1B, FHL3, CAPN2, SPAG9, ARPC1B, YWHAH, ARPC3, TRIM32, CFL1, CLASP1, PAFAH1B1, WDR1, MAPRE1, CAP1" 183 504 12983 2.252233498 0.877455684 0.259105847 6.675422287
GOTERM_MF_FAT GO:0003779~actin binding 10 4.566210046 0.040318633 "ARPC1B, TWF1, YWHAH, MYO6, ARPC3, MYO1B, CFL1, FHL3, WDR1, CAP1" 183 326 12983 2.176237889 0.999999978 0.550954726 43.99153625

Annotation Cluster 10 Enrichment Score: 2.6606810918976453
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0016052~carbohydrate catabolic process 9 4.109589041 1.43E-04 "TPI1, PGLS, PFKL, AKR1A1, GM2A, PGD, PGAM1, PFKP, PGK1" 190 109 13528 5.878899083 0.202630699 0.010239819 0.2385364
GOTERM_BP_FAT GO:0006007~glucose catabolic process 7 3.196347032 1.52E-04 "TPI1, PGLS, PFKL, PGD, PGAM1, PFKP, PGK1" 190 58 13528 8.593103448 0.214306258 0.010431653 0.254055677
GOTERM_BP_FAT GO:0019320~hexose catabolic process 7 3.196347032 3.97E-04 "TPI1, PGLS, PFKL, PGD, PGAM1, PFKP, PGK1" 190 69 13528 7.223188406 0.467027236 0.02485724 0.661503335
GOTERM_BP_FAT GO:0046365~monosaccharide catabolic process 7 3.196347032 4.63E-04 "TPI1, PGLS, PFKL, PGD, PGAM1, PFKP, PGK1" 190 71 13528 7.01971831 0.520358372 0.027862778 0.771903573
GOTERM_BP_FAT GO:0046164~alcohol catabolic process 7 3.196347032 9.35E-04 "TPI1, PGLS, PFKL, PGD, PGAM1, PFKP, PGK1" 190 81 13528 6.15308642 0.77334696 0.048273742 1.553323673
GOTERM_BP_FAT GO:0044275~cellular carbohydrate catabolic process 7 3.196347032 0.001204034 "TPI1, PGLS, PFKL, PGD, PGAM1, PFKP, PGK1" 190 85 13528 5.863529412 0.852030463 0.05977593 1.995078559
GOTERM_BP_FAT GO:0006096~glycolysis 5 2.283105023 0.004119619 "TPI1, PFKL, PGAM1, PFKP, PGK1" 190 47 13528 7.574468085 0.998565891 0.125074516 6.672262303
GOTERM_BP_FAT GO:0006006~glucose metabolic process 8 3.652968037 0.005690354 "TPI1, PGLS, PFKL, AKR1A1, PGD, PGAM1, PFKP, PGK1" 190 153 13528 3.722875817 0.999882688 0.159746363 9.10422329
GOTERM_BP_FAT GO:0006098~pentose-phosphate shunt 3 1.369863014 0.006552873 "TPI1, PGLS, PGD"

190 9 13528 23.73333333 0.99997038 0.175595249 10.41418628
GOTERM_BP_FAT GO:0005996~monosaccharide metabolic process 9 4.109589041 0.012812859 "TPI1, PGLS, PFKL, AKR1A1, GNE, PGD, PGAM1, PFKP, PGK1" 190 222 13528 2.886486486 0.999999999 0.269958502 19.40315202
GOTERM_BP_FAT GO:0019318~hexose metabolic process8 3.652968037 0.018341243 "TPI1, PGLS, PFKL, AKR1A1, PGD, PGAM1, PFKP, PGK1" 190 192 13528 2.966666667 1 0.354802167 26.62960304
GOTERM_BP_FAT GO:0006091~generation of precursor metabolites and energy 9 4.109589041 0.072753199 "TXNL1, TPI1, PFKL, TXN, PGAM1, PFKP, IDH1, ERO1L, PGK1" 190 313 13528 2.047284345 1 0.634583323 71.73404944

Annotation Cluster 11 Enrichment Score: 2.605934860159704
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005788~endoplasmic reticulum lumen 11 5.02283105 8.29E-08 "HYOU1, MINPP1, HSP90B1, PDIA3, PPIB, DNAJB11, SUMF1, PDIA6, ERAP1, HSPA5, CALR" 168 80 12782 10.46145833 2.21E-05 7.35E-06 1.09E-04
GOTERM_CC_FAT GO:0044432~endoplasmic reticulum part 16 7.305936073 4.95E-05 "MINPP1, PDIA3, PDIA6, CALR, APOL2, HYOU1, HSP90B1, PPIB, DNAJB11, BAX, SUMF1, ERAP1, ERO1L, HSPA5, SEC61A1, NSDHL" 168 347 12782 3.508165226 0.01309203 0.001097604 0.064968036
GOTERM_CC_FAT GO:0005783~endoplasmic reticulum 28 12.78538813 1.19E-04 "COPA, PDIA3, PDIA6, CALR, HMOX2, DNAJB11, SEC16A, ERAP1, ERO1L, HSPA5, DNAJC3, SAR1A, SEC61A1, NSDHL, MINPP1, NPLOC4, DNM1L, YIF1A, APOL2, HYOU1, HSP90B1, VCP, PPIB, BAX, SUMF1, PEBP1, AHCYL1, YKT6" 168 960 12782 2.219097222 0.031130685 0.001858597 0.155838474
GOTERM_CC_FAT GO:0031974~membrane-enclosed lumen 23 10.50228311 0.722859022 "MINPP1, MYO6, PDIA3, PDIA6, QARS, NFKB2, CALR, MAPK1, HYOU1, APP, HSP90B1, CASP3, PPIB, DNAJB11, VCP, CFL1, ZNF259, SUMF1, ERAP1, NLN, HSPA5, THBS2, CUL1" 168 1856 12782 0.942843032 1 0.971436156 99.99999511
GOTERM_CC_FAT GO:0043233~organelle lumen 22 10.0456621 0.763811459 "MINPP1, MYO6, PDIA3, PDIA6, QARS, NFKB2, CALR, MAPK1, HYOU1, APP, HSP90B1, CASP3, PPIB, DNAJB11, VCP, CFL1, ZNF259, SUMF1, ERAP1, HSPA5, THBS2, CUL1" 168 1820 12782 0.919688645 1 0.980100353 99.9999994
GOTERM_CC_FAT GO:0070013~intracellular organelle lumen 20 9.132420091 0.858254441 "MINPP1, MYO6, PDIA3, PDIA6, QARS, NFKB2, CALR, MAPK1, HYOU1, HSP90B1, CASP3, PPIB, DNAJB11, VCP, CFL1, ZNF259, SUMF1, ERAP1, HSPA5, CUL1" 168 1779 12782 0.855349447 1 0.99417412 100

Annotation Cluster 12 Enrichment Score: 2.3003464255556985
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0042981~regulation of apoptosis 27 12.32876712 5.33E-05 "BID, PDIA3, BCAR1, CALR, PRDX1, GPX1, PEA15, APP, CASP3, TUBB, TP53I3, PPP2CA, TPT1, GLO1, HSPA5, CUL1, RASA1, PRKCI, TRADD, PLEKHF1, MAPK1, HSP90B1, PLA2G4A, VCP, GSPT1, BAX, CFL1" 190 804 13528 2.391044776 0.081128846 0.005624746 0.089196907
GOTERM_BP_FAT GO:0043067~regulation of programmed cell death 27 12.32876712 6.29E-05 "BID, PDIA3, BCAR1, CALR, PRDX1, GPX1, PEA15, APP, CASP3, TUBB, TP53I3, PPP2CA, TPT1, GLO1, HSPA5, CUL1, RASA1, PRKCI, TRADD, PLEKHF1, MAPK1, HSP90B1, PLA2G4A, VCP, GSPT1, BAX, CFL1" 190 812 13528 2.367487685 0.094918437 0.005525247 0.105129226
GOTERM_BP_FAT GO:0010941~regulation of cell death 27 12.32876712 6.68E-05 "BID, PDIA3, BCAR1, CALR, PRDX1, GPX1, PEA15, APP, CASP3, TUBB, TP53I3, PPP2CA, TPT1, GLO1, HSPA5, CUL1, RASA1, PRKCI, TRADD, PLEKHF1, MAPK1, HSP90B1, PLA2G4A, VCP, GSPT1, BAX, CFL1" 190 815 13528 2.358773006 0.10057608 0.005563456 0.111735594
GOTERM_BP_FAT GO:0006917~induction of apoptosis 13 5.936073059 0.001789363 "BID, PRDX1, TRADD, PLEKHF1, GPX1, MAPK1, APP, TUBB, CASP3, TP53I3, PPP2CA, BAX, CUL1" 190 320 13528 2.8925 0.941601875 0.082474488 2.951388888
GOTERM_BP_FAT GO:0012502~induction of programmed cell death 13 5.936073059 0.001852718

"BID, PRDX1, TRADD, PLEKHF1, GPX1, MAPK1, APP, TUBB, CASP3, TP53I3, PPP2CA, BAX, CUL1"190 321
13528 2.883489097 0.947194308 0.082868128 3.054370939
GOTERM_BP_FAT GO:0043065~positive regulation of apoptosis 15 6.849315068 0.002886288 "BID,
PDIA3, PRDX1, TRADD, PLEKHF1, MAPK1, GPX1, TUBB, TP53I3, PLA2G4A, APP, CASP3, PPP2CA, BAX,
CUL1" 190 430 13528 2.48372093 0.989788815 0.108283292 4.71996409
GOTERM_BP_FAT GO:0043068~positive regulation of programmed cell death 15 6.849315068 0.003072447
"BID, PDIA3, PRDX1, TRADD, PLEKHF1, MAPK1, GPX1, TUBB, TP53I3, PLA2G4A, APP, CASP3, PPP2CA,
BAX, CUL1" 190 433 13528 2.466512702 0.992406046 0.107293786 5.017085007
GOTERM_BP_FAT GO:0010942~positive regulation of cell death 15 6.849315068 0.003201951 "BID,
PDIA3, PRDX1, TRADD, PLEKHF1, MAPK1, GPX1, TUBB, TP53I3, PLA2G4A, APP, CASP3, PPP2CA, BAX,
CUL1" 190 435 13528 2.455172414 0.993820032 0.10916937 5.223266226
GOTERM_BP_FAT GO:0006916~anti-apoptosis 9 4.109589041 0.00847364 "GPX1, PEA15, HSP90B1,
BAX, CFL1, TPT1, PRKCI, GLO1, HSPA5" 190 206 13528 3.110679612 0.999998624 0.204475381
13.26787639
GOTERM_BP_FAT GO:0043066~negative regulation of apoptosis 11 5.02283105 0.027134181 "GPX1,
PEA15, CASP3, HSP90B1, BAX, CFL1, TPT1, PRKCI, GLO1, HSPA5, RASA1" 190 354 13528 2.212429379
1 0.436772529 36.88146541
GOTERM_BP_FAT GO:0043069~negative regulation of programmed cell death 11 5.02283105
0.029316138 "GPX1, PEA15, CASP3, HSP90B1, BAX, CFL1, TPT1, PRKCI, GLO1, HSPA5, RASA1" 190 359
13528 2.181615599 1 0.449731373 39.2081409
GOTERM_BP_FAT GO:0060548~negative regulation of cell death 11 5.02283105 0.030093076 "GPX1,
PEA15, CASP3, HSP90B1, BAX, CFL1, TPT1, PRKCI, GLO1, HSPA5, RASA1" 190 360 13528 2.175555556
1 0.454338347 40.01695866
GOTERM_BP_FAT GO:0006915~apoptosis 15 6.849315068 0.042915367 "BID, DNM1L, UBE4B,
NCKAP1, TRADD, PLEKHF1, GPX1, PEA15, CASP3, APP, VCP, GSPT1, BAX, PDCD6IP, CUL1" 190 602
13528 1.774086379 1 0.508292791 51.98810058
GOTERM_BP_FAT GO:0012501~programmed cell death 15 6.849315068 0.047535865 "BID, DNM1L,
UBE4B, NCKAP1, TRADD, PLEKHF1, GPX1, PEA15, CASP3, APP, VCP, GSPT1, BAX, PDCD6IP, CUL1" 190
611 13528 1.747954173 1 0.527599884 55.72151764
GOTERM_BP_FAT GO:0008219~cell death 15 6.849315068 0.131290734 "BID, DNM1L, UBE4B,
NCKAP1, TRADD, PLEKHF1, GPX1, PEA15, CASP3, APP, VCP, GSPT1, BAX, PDCD6IP, CUL1" 190 719
13528 1.485396384 1 0.769748122 90.50425792
GOTERM_BP_FAT GO:0016265~death15 6.849315068 0.13648257 "BID, DNM1L, UBE4B, NCKAP1,
TRADD, PLEKHF1, GPX1, PEA15, CASP3, APP, VCP, GSPT1, BAX, PDCD6IP, CUL1" 190 724 13528
1.475138122 1 0.781533186 91.41022622

Annotation Cluster 13 Enrichment Score: 2.226194529256377
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0006767~water-soluble vitamin metabolic process5 2.283105023 0.002276895
"AKR1A1, PNPO, QPRT, PNP, ALDH9A1" 190 40 13528 8.9 0.973090409 0.095546365 3.741214727
GOTERM_BP_FAT GO:0042364~water-soluble vitamin biosynthetic process 4 1.826484018 0.003868815
"AKR1A1, PNPO, QPRT, PNP" 190 23 13528 12.3826087 0.997861905 0.122611245 6.278324458
GOTERM_BP_FAT GO:0009110~vitamin biosynthetic process 4 1.826484018 0.006800109 "AKR1A1,
PNPO, QPRT, PNP" 190 28 13528 10.17142857 0.999980041 0.175721319 10.78639326
GOTERM_BP_FAT GO:0006766~vitamin metabolic process 5 2.283105023 0.02078668 "AKR1A1,
PNPO, QPRT, PNP, ALDH9A1" 190 75 13528 4.746666667 1 0.374514637 29.62778609

Annotation Cluster 14 Enrichment Score: 2.085957017780011
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_CC_FAT GO:0044432~endoplasmic reticulum part 16 7.305936073 4.95E-05 "MINPP1, PDIA3,
PDIA6, CALR, APOL2, HYOU1, HSP90B1, PPIB, DNAJB11, BAX, SUMF1, ERAP1, ERO1L, HSPA5, SEC61A1,
NSDHL" 168 347 12782 3.508165226 0.01309203 0.001097604 0.064968036

GOTERM_CC_FAT GO:0042175~nuclear envelope-endoplasmic reticulum network 8 3.652968037 0.079123205 "APOL2, NPLOC4, HSP90B1, BAX, ERO1L, HSPA5, SEC61A1, NSDHL" 168 284 12782 2.143192488 1 0.366689323 66.08379978
GOTERM_CC_FAT GO:0005789~endoplasmic reticulum membrane 7 3.196347032 0.140880845 "APOL2, HSP90B1, BAX, ERO1L, HSPA5, SEC61A1, NSDHL" 168 269 12782 1.979863693 1 0.484261457 86.35624977

Annotation Cluster 15 Enrichment Score: 1.6668353603115897
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0000267~cell fraction 30 13.69863014 1.52E-04 "BID, COPA, CYB5R2, RAB5B, BCAR1, CALR, ACP1, ANXA7, HMOX2, APP, TPI1, PPP2CA, GGPS1, IDH1, GLO1, PAFAH1B1, ERO1L, PFKL, SLC12A4, PFKP, CAPN2, MAPK1, HSP90B1, PLA2G4A, VCP, BAX, YWHAQ, USO1, PEBP1, RNPEP" 168 1083 12782 2.10757156 0.039634597 0.002244225 0.199236515
GOTERM_CC_FAT GO:0042598~vesicular fraction 8 3.652968037 0.04116726 "HMOX2, COPA, HSP90B1, VCP, USO1, PAFAH1B1, ERO1L, CALR" 168 244 12782 2.494535519 0.999986081 0.238708107 42.38857081
GOTERM_CC_FAT GO:0005626~insoluble fraction 18 8.219178082 0.047346866 "BID, COPA, RAB5B, BCAR1, SLC12A4, CALR, CAPN2, ANXA7, MAPK1, HMOX2, HSP90B1, PLA2G4A, APP, VCP, USO1, PEBP1, PAFAH1B1, ERO1L" 168 839 12782 1.632300358 0.999997507 0.254150344 47.07346113
GOTERM_CC_FAT GO:0005792~microsome 7 3.196347032 0.090741856 "HMOX2, COPA, HSP90B1, VCP, USO1, ERO1L, CALR" 168 237 12782 2.24718706 1 0.391128854 71.28743545
GOTERM_CC_FAT GO:0005624~membrane fraction 15 6.849315068 0.172290125 "BID, COPA, RAB5B, BCAR1, SLC12A4, CALR, HMOX2, PLA2G4A, APP, HSP90B1, VCP, USO1, PEBP1, PAFAH1B1, ERO1L" 168 809 12782 1.410692213 1 0.50758398 91.62949164

Annotation Cluster 16 Enrichment Score: 1.5701995471868462
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0014902~myotube differentiation 3 1.369863014 0.020486952 "CAST, GPX1, CAPN2" 190 16 13528 13.35 1 0.374370238 29.26660475
GOTERM_BP_FAT GO:0042692~muscle cell differentiation 6 2.739726027 0.027361374 "CAST, GPX1, APP, NRD1, CAPN2, CSRP2" 190 121 13528 3.530578512 1 0.435280931 37.12757608
GOTERM_BP_FAT GO:0051146~striated muscle cell differentiation 5 2.283105023 0.034736505 "CAST, GPX1, APP, NRD1, CAPN2" 190 88 13528 4.045454545 1 0.478995466 44.64388223

Annotation Cluster 17 Enrichment Score: 1.4605137156593397
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0030117~membrane coat 6 2.739726027 0.001367557 "COPB2, COPA, AP3M1, NECAP2, AP3D1, AP2M1" 168 63 12782 7.246031746 0.305122078 0.016410184 1.77912813
GOTERM_CC_FAT GO:0048475~coated membrane 6 2.739726027 0.001367557 "COPB2, COPA, AP3M1, NECAP2, AP3D1, AP2M1" 168 63 12782 7.246031746 0.305122078 0.016410184 1.77912813
GOTERM_CC_FAT GO:0044433~cytoplasmic vesicle part 8 3.652968037 0.011429622 "SCAMP1, COPB2, COPA, APP, MYO6, NECAP2, THBS2, AP2M1" 168 187 12782 3.254901961 0.953008453 0.103454916 13.99747293
GOTERM_CC_FAT GO:0030662~coated vesicle membrane 5 2.283105023 0.015222027 "SCAMP1, COPB2, COPA, MYO6, NECAP2" 168 73 12782 5.211187215 0.983095795 0.127162979 18.22617604
GOTERM_CC_FAT GO:0005905~coated pit 4 1.826484018 0.019611674 "APP, MYO6, NECAP2, AP2M1" 168 44 12782 6.916666667 0.994848865 0.147560189 22.88063333
GOTERM_CC_FAT GO:0030659~cytoplasmic vesicle membrane 6 2.739726027 0.035655874 "SCAMP1, COPB2, COPA, MYO6, NECAP2, AP2M1" 168 139 12782 3.284172662 0.999936067 0.22442415 37.89007953
GOTERM_CC_FAT GO:0012506~vesicle membrane 6 2.739726027 0.04799175 "SCAMP1, COPB2,

COPA, MYO6, NECAP2, AP2M1"	168	151	12782	3.023178808	0.999997918	0.252273324	47.541516
GOTERM_CC_FAT	GO:0030135~coated vesicle	6	2.739726027	0.057474011	"SCAMP1, COPB2, COPA, MYO6, NECAP2, PEBP1"	168	159	12782	2.871069182	0.999999855	0.289852747	53.99677956
GOTERM_CC_FAT	GO:0030120~vesicle coat	3	1.369863014	0.087894023	"COPB2, COPA, NECAP2"	168	38	12782	6.006578947	1	0.387027482	70.08512941
GOTERM_CC_FAT	GO:0030118~clathrin coat	3	1.369863014	0.091878165	"AP3M1, NECAP2, AP2M1"	168	39	12782	5.852564103	1	0.389211199	71.7545813
GOTERM_CC_FAT	GO:0030665~clathrin coated vesicle membrane	3	1.369863014	0.152245089	"SCAMP1, MYO6, NECAP2"	168	53	12782	4.306603774	1	0.502100917	88.54294296
GOTERM_CC_FAT	GO:0030136~clathrin-coated vesicle	4	1.826484018	0.248398979	"SCAMP1, MYO6, NECAP2, PEBP1"	168	132	12782	2.305555556	1	0.603981842	97.63820535
GOTERM_CC_FAT	GO:0044431~Golgi apparatus part	5	2.283105023	0.537994646	"SCAMP1, COPB2, COPA, DNM1L, USO1"	168	294	12782	1.29393424	1	0.89014538	99.99601023

Annotation Cluster 18	Enrichment Score: 1.3653263061658008
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	4	1.826484018	0.013780371	"TP53I3, PGD, IDH1, SPR"	183	36	12983	7.882817243	0.997365375	0.36672294	17.7536336
GOTERM_MF_FAT	GO:0050662~coenzyme binding	7	3.196347032	0.04227149	"ACOT7, TP53I3, PGD, PNPO, IDH1, SPR, ERO1L"	183	181	12983	2.743743018	0.999999991	0.537097263	45.5756676
GOTERM_MF_FAT	GO:0048037~cofactor binding	7	3.196347032	0.137629842	"ACOT7, TP53I3, PGD, PNPO, IDH1, SPR, ERO1L"	183	249	12983	1.994447736	1	0.879061736	87.5770601

Annotation Cluster 19	Enrichment Score: 1.3642299945084122
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048193~Golgi vesicle transport	8	3.652968037	0.002419521	"SCAMP1, COPB2, COPA, NRBP1, VCP, SEC13, YKT6, SAR1A"	190	131	13528	4.348091603	0.97854956	0.096162353	3.971131083
GOTERM_BP_FAT	GO:0006903~vesicle targeting	3	1.369863014	0.037344818	"COPB2, COPA, YKT6"	190	22	13528	9.709090909	1	0.484867635	47.09353145
GOTERM_BP_FAT	GO:0051656~establishment of organelle localization	4	1.826484018	0.072029176	"COPB2, COPA, PAFAH1B1, YKT6"	190	69	13528	4.127536232	1	0.633866662	71.36258494
GOTERM_BP_FAT	GO:0051650~establishment of vesicle localization	3	1.369863014	0.07731787	"COPB2, COPA, YKT6"	190	33	13528	6.472727273	1	0.64272288	73.97367393
GOTERM_BP_FAT	GO:0051648~vesicle localization	3	1.369863014	0.094110026	"COPB2, COPA, YKT6"	190	37	13528	5.772972973	1	0.686876211	80.85813736
GOTERM_BP_FAT	GO:0051640~organelle localization	4	1.826484018	0.137795826	"COPB2, COPA, PAFAH1B1, YKT6"	190	92	13528	3.095652174	1	0.780645706	91.62615091

Annotation Cluster 20	Enrichment Score: 1.2945743532693894
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0045454~cell redox homeostasis	7	3.196347032	2.41E-04	"TXNL1, GPX1, PTGES2, PDIA3, TXN, PDIA6, PRDX1"	190	63	13528	7.911111111	0.317634739	0.015798465	0.402281098
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	16	7.305936073	0.002297854	"TXNL1, SRI, PTGES2, PDIA3, SLC12A4, PDIA6, CALR, PRDX1, ANXA7, GPX1, APP, HSP90B1, TFRC, BAX, TXN, TPT1"	190	466	13528	2.444635193	0.97397218	0.093904456	3.775033101
GOTERM_BP_FAT	GO:0051238~sequestering of metal ion	3	1.369863014	0.003893515	"SRI, HSP90B1, CALR"	190	7	13528	30.51428571	0.997944359	0.120937536	6.317190503
GOTERM_BP_FAT	GO:0042592~homeostatic process	19	8.675799087	0.017846597	"TXNL1, SRI, PTGES2, PDIA3, NCDN, SLC12A4, PDIA6, CALR, PRDX1, ANXA7, GPX1, CASP3, PLA2G4A, APP, HSP90B1, TFRC,

BAX, TXN, TPT1" 190 751 13528 1.801331558 1 0.351265741 26.00872606
GOTERM_BP_FAT "GO:0030005~cellular di-, tri-valent inorganic cation homeostasis" 8 3.652968037
0.040498202 "SRI, ANXA7, APP, HSP90B1, TFRC, BAX, TPT1, CALR" 190 227 13528 2.509251101 1
0.49851351 49.91900996
GOTERM_BP_FAT "GO:0055066~di-, tri-valent inorganic cation homeostasis" 8 3.652968037 0.050740093
"SRI, ANXA7, APP, HSP90B1, TFRC, BAX, TPT1, CALR" 190 239 13528 2.383263598 1 0.541192547
58.14837757
GOTERM_BP_FAT GO:0030003~cellular cation homeostasis 8 3.652968037 0.065986314 "SRI, ANXA7,
APP, HSP90B1, TFRC, BAX, TPT1, CALR" 190 254 13528 2.242519685 1 0.616384702 68.07822971
GOTERM_BP_FAT GO:0055080~cation homeostasis 8 3.652968037 0.105832334 "SRI, ANXA7, APP,
HSP90B1, TFRC, BAX, TPT1, CALR"190 286 13528 1.991608392 1 0.720946897 84.60549133
GOTERM_BP_FAT GO:0006874~cellular calcium ion homeostasis 6 2.739726027 0.113713932 "ANXA7,
APP, HSP90B1, BAX, TPT1, CALR" 190 183 13528 2.33442623 1 0.737851642 86.72457743
GOTERM_BP_FAT GO:0055074~calcium ion homeostasis 6 2.739726027 0.123544415 "ANXA7, APP,
HSP90B1, BAX, TPT1, CALR" 190 188 13528 2.272340426 1 0.761287995 88.98408195
GOTERM_BP_FAT GO:0006875~cellular metal ion homeostasis 6 2.739726027 0.139990379 "ANXA7,
APP, HSP90B1, BAX, TPT1, CALR" 190 196 13528 2.179591837 1 0.782049297 91.97562787
GOTERM_BP_FAT GO:0055065~metal ion homeostasis 6 2.739726027 0.159693017 "ANXA7, APP,
HSP90B1, BAX, TPT1, CALR" 190 205 13528 2.083902439 1 0.810301453 94.55441919
GOTERM_BP_FAT GO:0006873~cellular ion homeostasis 8 3.652968037 0.268874594 "SRI, ANXA7,
APP, HSP90B1, TFRC, BAX, TPT1, CALR" 190 374 13528 1.522994652 1 0.912379948 99.46919069
GOTERM_BP_FAT GO:0055082~cellular chemical homeostasis 8 3.652968037 0.281919616 "SRI, ANXA7,
APP, HSP90B1, TFRC, BAX, TPT1, CALR" 190 380 13528 1.498947368 1 0.921896189 99.60721927
GOTERM_BP_FAT GO:0050801~ion homeostasis 8 3.652968037 0.346807299 "SRI, ANXA7, APP,
HSP90B1, TFRC, BAX, TPT1, CALR"190 409 13528 1.392665037 1 0.946961736 99.91943928
GOTERM_BP_FAT GO:0048878~chemical homeostasis 9 4.109589041 0.424642329 "SRI, ANXA7,
APP, PLA2G4A, HSP90B1, TFRC, BAX, TPT1, CALR" 190 512 13528 1.2515625 1 0.970005192
99.99035312

Annotation Cluster 21 Enrichment Score: 1.2922924851222608
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0007018~microtubule-based movement 10 4.566210046 2.87E-05 "KIF13A, APP,
TUBB, TUBB2A, TUBA4A, TUBB6, PAFAH1B1, DYNC1H1, DYNC1I2, ACTR10" 190 113 13528
6.300884956 0.044461495 0.003243316 0.047956058
GOTERM_BP_FAT GO:0007017~microtubule-based process 11 5.02283105 0.002963809 "KIF13A,
APP, TUBB, TUBB2A, TUBA4A, TUBB6, PAFAH1B1, CLASP1, DYNC1H1, DYNC1I2, ACTR10" 190 253
13528 3.095652174 0.990973406 0.108472529 4.843797518
GOTERM_CC_FAT GO:0005874~microtubule 11 5.02283105 0.003216362 "KIF13A, TUBB, TUBB2A,
TUBA4A, TUBB6, PAFAH1B1, CLASP1, MAPRE1, WDR44, DYNC1H1, DYNC1I2" 168 274 12782
3.054440389 0.575537306 0.036572342 4.137872574
GOTERM_BP_FAT GO:0051258~protein polymerization 4 1.826484018 0.030918618 "TUBB, TUBB2A,
TUBA4A, TUBB6" 190 49 13528 5.812244898 1 0.459332422 40.86528215
GOTERM_BP_FAT GO:0051259~protein oligomerization 7 3.196347032 0.0354946 "SPAG9, PFKL,
VCP, BAX, PFKP, PEBP1, QPRT" 190 174 13528 2.864367816 1 0.482541151 45.36663848
GOTERM_BP_FAT GO:0051260~protein homooligomerization 5 2.283105023 0.044042037 "SPAG9, VCP,
BAX, PFKP, PEBP1" 190 95 13528 3.747368421 1 0.510492566 52.92481648
GOTERM_BP_FAT GO:0070271~protein complex biogenesis 12 5.479452055 0.09691409 "SPAG9,
TUBB, PFKL, VCP, TUBB2A, BAX, PFKP, TUBA4A, TUBB6, PEBP1, QPRT, CALR" 190 505 13528
1.691881188 1 0.69011178 81.82549232
GOTERM_BP_FAT GO:0006461~protein complex assembly 12 5.479452055 0.09691409 "SPAG9,
TUBB, PFKL, VCP, TUBB2A, BAX, PFKP, TUBA4A, TUBB6, PEBP1, QPRT, CALR" 190 505 13528
1.691881188 1 0.69011178 81.82549232
GOTERM_BP_FAT GO:0043623~cellular protein complex assembly 5 2.283105023 0.19125118 "TUBB,

TUBB2A, TUBA4A, TUBB6, CALR"	190	162	13528	2.197530864	1	0.84432332	97.12946547
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	12	5.479452055	0.32608752	"SPAG9, TUBB, PFKL, VCP, TUBB2A, BAX, PFKP, TUBA4A, TUBB6, PEBP1, QPRT, CALR"	190	665	13528	1.28481203	1	0.940362601	99.8641739
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	12	5.479452055	0.406452321	"SPAG9, TUBB, PFKL, VCP, TUBB2A, BAX, PFKP, TUBA4A, TUBB6, PEBP1, QPRT, CALR"	190	710	13528	1.203380282	1	0.966313067	99.98376311
GOTERM_MF_FAT	GO:0005198~structural molecule activity	10	4.566210046	0.533231848	"COPB2, COPA, ARPC1B, TUBB, ARPC3, TUBB2A, TUBA4A, TUBB6, COL12A1, THBS2"	183	634	12983	1.119011912	1	0.989210767	99.99781637
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	5	2.283105023	0.652646049	"TUBB, TUBB2A, TUBA4A, TUBB6, CALR"	190	318	13528	1.119496855	1	0.995833038	99.99999792
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	5	2.283105023	0.738944269	"TUBB, TUBB2A, TUBA4A, TUBB6, CALR"	190	357	13528	0.99719888	1	0.998604039	99.99999998

Annotation Cluster 22	Enrichment Score: 1.2704681982270123
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005938~cell cortex	9	4.109589041	6.57E-04	"NRBP1, MYO6, GM2A, CFL1, PRKCI, PAFAH1B1, CLASP1, CAP1, MAPRE1"	168	146	12782	4.690068493	0.160391104	0.008702864	0.858407475
GOTERM_CC_FAT	GO:0044448~cell cortex part	6	2.739726027	0.004585295	"GM2A, CFL1, PRKCI, CLASP1, CAP1, MAPRE1"	168	83	12782	5.5	0.705505023	0.047723393	5.850547311
GOTERM_BP_FAT	GO:0007163~establishment or maintenance of cell polarity	5	2.283105023	0.004789052	"CFL1, PRKCI, PAFAH1B1, CLASP1, CAP1"	190	49	13528	7.265306122	0.99950635	0.141246756	7.716128734
GOTERM_CC_FAT	GO:0030863~cortical cytoskeleton	4	1.826484018	0.0260279	"CFL1, CLASP1, CAP1, MAPRE1"	168	49	12782	6.210884354	0.999101799	0.181622794	29.24504005
GOTERM_BP_FAT	GO:0030010~establishment of cell polarity	3	1.369863014	0.031278507	"CFL1, PRKCI, PAFAH1B1"	190	20	13528	10.68	1	0.459161981	41.2315609
GOTERM_BP_FAT	GO:0030029~actin filament-based process	8	3.652968037	0.05266121	"MYO6, BCAR1, CFL1, FHL3, PRKCI, PAFAH1B1, CAP1, CALR"	190	241	13528	2.363485477	1	0.551511035	59.54285396
GOTERM_BP_FAT	GO:0006928~cell motion	12	5.479452055	0.069727387	"GPX1, ARPC1B, APP, TUBB, ARPC3, BAX, BCAR1, TXN, CFL1, NRD1, PAFAH1B1, CAP1"	190	475	13528	1.798736842	1	0.62459997	70.15091354
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	11	5.02283105	0.085458111	"TUBB, BCAR1, CFL1, FHL3, PRKCI, PAFAH1B1, MICAL1, CLASP1, CAP1, DYNC1H1, CALR"	190	436	13528	1.796330275	1	0.6581344	77.5592497
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	7	3.196347032	0.095939645	"BCAR1, CFL1, FHL3, PRKCI, PAFAH1B1, CAP1, CALR"	190	226	13528	2.205309735	1	0.691550069	81.49465972
GOTERM_BP_FAT	GO:0016477~cell migration	7	3.196347032	0.18972237	"GPX1, BAX, BCAR1, CFL1, NRD1, PAFAH1B1, CAP1"	190	276	13528	1.805797101	1	0.843338351	97.03733596
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	9	4.109589041	0.192242991	"APP, DNM1L, BAX, CFL1, STXBP1, PRKCI, PAFAH1B1, CLASP1, CAP1"	190	397	13528	1.614105793	1	0.844397047	97.1877862
GOTERM_BP_FAT	GO:0048870~cell motility	7	3.196347032	0.259175606	"GPX1, BAX, BCAR1, CFL1, NRD1, PAFAH1B1, CAP1"	190	307	13528	1.623452769	1	0.906247639	99.33827724
GOTERM_BP_FAT	GO:0051674~localization of cell	7	3.196347032	0.259175606	"GPX1, BAX, BCAR1, CFL1, NRD1, PAFAH1B1, CAP1"	190	307	13528	1.623452769	1	0.906247639	99.33827724
GOTERM_BP_FAT	GO:0007015~actin filament organization	3	1.369863014	0.26641712	"BCAR1, CFL1, PRKCI"	190	72	13528	2.966666667	1	0.911124849	99.43854421

GOTERM_BP_FAT GO:0000902~cell morphogenesis 7 3.196347032 0.379966613 "APP, CFL1, STXBP1, PRKCI, PAFAH1B1, CLASP1, CAP1" 190 356 13528 1.4 1 0.959732104 99.96629881

Annotation Cluster 23 Enrichment Score: 1.1603701740128134

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0033043~regulation of organelle organization 8 3.652968037 0.032849977 "ARPC1B, PLA2G4A, ARPC3, CFL1, PEBP1, CLASP1, MAPRE1, RASA1" 190 217 13528 2.624884793 1 0.47178573 42.80608068

GOTERM_BP_FAT GO:0032535~regulation of cellular component size 9 4.109589041 0.036541364 "ARPC1B, APP, ARPC3, NDRG3, PPP2CA, CFL1, CSRP2, VAT1, RASA1" 190 271 13528 2.364575646 1 0.484887911 46.35003319

GOTERM_BP_FAT GO:0043254~regulation of protein complex assembly 5 2.283105023 0.037265877 "ARPC1B, ARPC3, STXBP1, MAPRE1, RASA1" 190 90 13528 3.955555556 1 0.487910932 47.0209122

GOTERM_BP_FAT GO:0051493~regulation of cytoskeleton organization 6 2.739726027 0.042036029 "ARPC1B, ARPC3, CFL1, CLASP1, MAPRE1, RASA1" 190 136 13528 3.141176471 1 0.504493446 51.244871

GOTERM_BP_FAT GO:0008064~regulation of actin polymerization or depolymerization 4 1.826484018 0.053566401 "ARPC1B, ARPC3, CFL1, RASA1" 190 61 13528 4.668852459 1 0.554467468 60.18465192

GOTERM_BP_FAT GO:0030832~regulation of actin filament length 4 1.826484018 0.05794024 "ARPC1B, ARPC3, CFL1, RASA1" 190 63 13528 4.520634921 1 0.577079799 63.15317413

GOTERM_BP_FAT GO:0032271~regulation of protein polymerization 4 1.826484018 0.069582802 "ARPC1B, ARPC3, MAPRE1, RASA1" 190 68 13528 4.188235294 1 0.626965538 70.07321652

GOTERM_BP_FAT GO:0032956~regulation of actin cytoskeleton organization 4 1.826484018 0.128298509 "ARPC1B, ARPC3, CFL1, RASA1" 190 89 13528 3.2 1 0.765852917 89.94207224

GOTERM_BP_FAT GO:0044087~regulation of cellular component biogenesis 5 2.283105023 0.137717239 "ARPC1B, ARPC3, STXBP1, MAPRE1, RASA1" 190 142 13528 2.507042254 1 0.782592 91.61337453

GOTERM_BP_FAT GO:0032970~regulation of actin filament-based process 4 1.826484018 0.137795826 "ARPC1B, ARPC3, CFL1, RASA1" 190 92 13528 3.095652174 1 0.780645706 91.62615091

GOTERM_BP_FAT GO:0030833~regulation of actin filament polymerization 3 1.369863014 0.174122378 "ARPC1B, ARPC3, RASA1" 190 54 13528 3.955555556 1 0.828649469 95.92416904

Annotation Cluster 24 Enrichment Score: 1.154916501073807

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0008637~apoptotic mitochondrial changes 5 2.283105023 8.64E-04 "BID, GPX1, CASP3, DNM1L, BAX" 190 31 13528 11.48387097 0.746287006 0.046193905 1.436150212

GOTERM_BP_FAT GO:0051402~neuron apoptosis 4 1.826484018 0.002205401 "BID, APP, CASP3, BAX" 190 19 13528 14.98947368 0.96985178 0.095204705 3.625771396

GOTERM_BP_FAT GO:0001836~release of cytochrome c from mitochondria 4 1.826484018 0.002965563 "BID, GPX1, CASP3, BAX" 190 21 13528 13.56190476 0.990998568 0.106091363 4.846598999

GOTERM_BP_FAT GO:0008629~induction of apoptosis by intracellular signals 5 2.283105023 0.006773125 "GPX1, TP53I3, CASP3, BAX, CUL1" 190 54 13528 6.592592593 0.999979162 0.17796865 10.74584076

GOTERM_CC_FAT GO:0005635~nuclear envelope 8 3.652968037 0.01825008 "ANXA7, MYO6, SCRN1, SEC13, PAFAH1B1, TAGLN2, MTMR6, MYOF" 168 205 12782 2.969105691 0.992548691 0.141960525 21.46377071

GOTERM_BP_FAT GO:0009628~response to abiotic stimulus 11 5.02283105 0.03400445 "ANXA7, GPX1, APP, PLA2G4A, CASP3, BAX, UBE4B, PEBP1, ERO1L, MYOF, RIC8A" 190 368 13528 2.12826087 1 0.479625432 43.93742924

GOTERM_BP_FAT GO:0009416~response to light stimulus 6 2.739726027 0.044291124 "GPX1, APP, CASP3, BAX, UBE4B, RIC8A" 190 138 13528 3.095652174 1 0.509031321 53.12957544

GOTERM_BP_FAT GO:0009411~response to UV 4 1.826484018 0.049359274 "GPX1, CASP3, BAX, UBE4B" 190 59 13528 4.827118644 1 0.534474799 57.11830637
GOTERM_BP_FAT GO:0007006~mitochondrial membrane organization 3 1.369863014 0.073284246 "BID, DNM1L, BAX" 190 32 13528 6.675 1 0.634284373 72.0036214
GOTERM_CC_FAT GO:0031967~organelle envelope 13 5.936073059 0.112450858 "BID, ANXA7, DNM1L, MYO6, BAX, SCRN1, PEBP1, SEC13, PAFAH1B1, NLN, TAGLN2, MTMR6, MYOF" 168 620 12782 1.595295699 1 0.438383771 79.08756057
GOTERM_CC_FAT GO:0005741~mitochondrial outer membrane 4 1.826484018 0.113527564 "BID, DNM1L, BAX, PEBP1" 168 90 12782 3.381481481 1 0.435830152 79.41791268
GOTERM_CC_FAT GO:0031975~envelope 13 5.936073059 0.11439454 "BID, ANXA7, DNM1L, MYO6, BAX, SCRN1, PEBP1, SEC13, PAFAH1B1, NLN, TAGLN2, MTMR6, MYOF" 168 622 12782 1.590166131 1 0.432732375 79.68040493
GOTERM_BP_FAT GO:0007005~mitochondrion organization 5 2.283105023 0.127837017 "BID, GPX1, CASP3, DNM1L, BAX" 190 138 13528 2.579710145 1 0.766813262 89.85262996
GOTERM_BP_FAT GO:0009314~response to radiation 6 2.739726027 0.148476751 "GPX1, APP, CASP3, BAX, UBE4B, RIC8A" 190 200 13528 2.136 1 0.796730178 93.20218205
GOTERM_CC_FAT GO:0031968~organelle outer membrane 4 1.826484018 0.154986589 "BID, DNM1L, BAX, PEBP1" 168 104 12782 2.926282051 1 0.498000418 89.01954653
GOTERM_CC_FAT GO:0019867~outer membrane 4 1.826484018 0.167605491 "BID, DNM1L, BAX, PEBP1" 168 108 12782 2.817901235 1 0.506981383 90.98627745
GOTERM_BP_FAT GO:0008624~induction of apoptosis by extracellular signals 3 1.369863014 0.465663973 "BID, CASP3, BAX" 190 112 13528 1.907142857 1 0.977816523 99.99720073
GOTERM_BP_FAT GO:0051726~regulation of cell cycle 5 2.283105023 0.68334873 "APP, CASP3, BAX, PEBP1, CALR" 190 331 13528 1.075528701 1 0.997052873 99.99999956
GOTERM_CC_FAT GO:0005740~mitochondrial envelope 5 2.283105023 0.801934702 "BID, DNM1L, BAX, PEBP1, NLN" 168 419 12782 0.907915672 1 0.986525572 99.99999994
GOTERM_CC_FAT GO:0031966~mitochondrial membrane 4 1.826484018 0.892572886 "BID, DNM1L, BAX, PEBP1" 168 394 12782 0.772419628 1 0.996853497 100
GOTERM_CC_FAT GO:0044429~mitochondrial part 6 2.739726027 0.893896219 "BID, DNM1L, BAX, PEBP1, NLN, QARS" 168 595 12782 0.767226891 1 0.996778046 100

Annotation Cluster 25 Enrichment Score: 1.0981811161623007
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006511~ubiquitin-dependent protein catabolic process 10 4.566210046 0.006987495 "NPLOC4, HSP90B1, USP8, VCP, UBE2K, USP9X, TRIM32, UBE4B, NEDD8, CUL1" 190 242 13528 2.94214876 0.999985203 0.177252922 11.06752906
GOTERM_BP_FAT GO:0070647~protein modification by small protein conjugation or removal 7 3.196347032 0.024867062 "VCP, GSPT1, USP9X, TRIM32, UBE4B, NEDD8, UBE3C" 190 160 13528 3.115 1 0.417076992 34.37545344
GOTERM_BP_FAT GO:0044265~cellular macromolecule catabolic process 18 8.219178082 0.025385199 "NPLOC4, USP8, USP9X, UBE4B, RNH1, UFC1, NEDD8, UBE3C, UBE2O, CASP3, HSP90B1, VCP, GSPT1, UBE2K, BAX, TRIM32, ERAP1, CUL1" 190 725 13528 1.767724138 1 0.419429148 34.95630035
GOTERM_BP_FAT GO:0032446~protein modification by small protein conjugation 6 2.739726027 0.037738819 "VCP, GSPT1, TRIM32, UBE4B, NEDD8, UBE3C" 190 132 13528 3.236363636 1 0.484788842 47.45458093
GOTERM_BP_FAT GO:0009057~macromolecule catabolic process 18 8.219178082 0.046298736 "NPLOC4, USP8, USP9X, UBE4B, RNH1, UFC1, NEDD8, UBE3C, UBE2O, CASP3, HSP90B1, VCP, GSPT1, UBE2K, BAX, TRIM32, ERAP1, CUL1" 190 781 13528 1.640973111 1 0.521499543 54.74960138
GOTERM_BP_FAT GO:0051603~proteolysis involved in cellular protein catabolic process 14 6.392694064 0.077842678 "NPLOC4, USP8, USP9X, UBE4B, UFC1, NEDD8, UBE3C, UBE2O, HSP90B1, VCP, UBE2K, TRIM32, ERAP1, CUL1" 190 600 13528 1.661333333 1 0.642360007 74.22019162
GOTERM_BP_FAT GO:0044257~cellular protein catabolic process 14 6.392694064 0.08020721 "NPLOC4, USP8, USP9X, UBE4B, UFC1, NEDD8, UBE3C, UBE2O, HSP90B1, VCP, UBE2K, TRIM32, ERAP1,

CUL1"	190	603	13528	1.653067993	1	0.64510783	75.30390183

GOTERM_BP_FAT	GO:0016567~protein ubiquitination	5	2.283105023	0.085432931	"VCP, GSPT1, TRIM32, UBE4B, UBE3C"	190	119	13528	2.991596639	1	0.66081096	77.5489124

GOTERM_BP_FAT	GO:0030163~protein catabolic process	14	6.392694064	0.096249602	"NPLOC4, USP8, USP9X, UBE4B, UFC1, NEDD8, UBE3C, UBE2O, HSP90B1, VCP, UBE2K, TRIM32, ERAP1, CUL1"	190	622	13528	1.602572347	1	0.690123086	81.60050204

GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	13	5.936073059	0.107083368	"NPLOC4, USP8, USP9X, UBE4B, UFC1, NEDD8, UBE3C, UBE2O, HSP90B1, VCP, UBE2K, TRIM32, CUL1"	190	574	13528	1.612543554	1	0.722822543	84.96183819

GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	13	5.936073059	0.107083368	"NPLOC4, USP8, USP9X, UBE4B, UFC1, NEDD8, UBE3C, UBE2O, HSP90B1, VCP, UBE2K, TRIM32, CUL1"	190	574	13528	1.612543554	1	0.722822543	84.96183819

GOTERM_BP_FAT	GO:0006508~proteolysis	20	9.132420091	0.151156941	"NPLOC4, USP8, USP9X, UBE4B, NRD1, UFC1, NEDD8, UBE3C, CAPN2, UBE2O, CASP3, HSP90B1, VCP, UBE2K, TRIM32, ERAP1, NLN, DPP9, RNPEP, CUL1"	190	1054	13528	1.351043643	1	0.797004575	93.5513633

GOTERM_MF_FAT	GO:0004842~ubiquitin-protein ligase activity	5	2.283105023	0.15173844	"UBE2O, UBE2K, TRIM32, UBE4B, UBE3C"	183	147	12983	2.413107319	1	0.889315731	90.15268149

GOTERM_MF_FAT	GO:0019787~small conjugating protein ligase activity	5	2.283105023	0.204309482	"UBE2O, UBE2K, TRIM32, UBE4B, UBE3C"	183	166	12983	2.136908289	1	0.923780507	96.00102775

GOTERM_MF_FAT	GO:0016881~acid-amino acid ligase activity	5	2.283105023	0.311342754	"UBE2O, UBE2K, TRIM32, UBE4B, UBE3C"	183	201	12983	1.764809831	1	0.966519311	99.47733982

GOTERM_MF_FAT	"GO:0016879~ligase activity, forming carbon-nitrogen bonds"	5	2.283105023	0.405758522	"UBE2O, UBE2K, TRIM32, UBE4B, UBE3C"	183	231	12983	1.535613749	1	0.977076882	99.9345074

Annotation Cluster 26	Enrichment Score: 1.064807289109177

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_BP_FAT	GO:0010033~response to organic substance	19	8.675799087	0.012233494	"PFKL, SKIV2L, BCAR1, PRKCI, FHL2, NEDD8, ASL, MAPK1, CASP3, PLA2G4A, VCP, TFRC, PPP2CA, CFL1, VPS4B, PEBP1, IDH1, ERO1L, DNAJC3"	190	721	13528	1.87628294	0.999999997	0.262899398	18.60826637

GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	9	4.109589041	0.206558587	"MAPK1, PLA2G4A, BCAR1, CFL1, PRKCI, FHL2, PEBP1, IDH1, ASL"	190	405	13528	1.582222222	1	0.855051557	97.91481035

GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	8	3.652968037	0.252920698	"MAPK1, PLA2G4A, BCAR1, PRKCI, FHL2, PEBP1, IDH1, ASL"	190	367	13528	1.552043597	1	0.902106981	99.23835081

Annotation Cluster 27	Enrichment Score: 1.0403233613613052

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR

GOTERM_BP_FAT	GO:0052548~regulation of endopeptidase activity	6	2.739726027	0.00578182	"GPX1, VCP, GSPT1, BAX, NRD1, HSPA5"	190	82	13528	5.209756098	0.999898614	0.159299951	9.243986512

GOTERM_BP_FAT	GO:0052547~regulation of peptidase activity	6	2.739726027	0.00705831	"GPX1, VCP, GSPT1, BAX, NRD1, HSPA5"	190	86	13528	4.96744186	0.999986785	0.176088905	11.17355535

GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	11	5.02283105	0.020151094	"GPX1, GDI2, ARFGAP3, VCP, GM2A, GSPT1, BAX, NRD1, PAFAH1B1, HSPA5, TBC1D9B"	190	337	13528	2.324035608	1	0.373692359	28.8598154

GOTERM_BP_FAT	GO:0043281~regulation of caspase activity	5	2.283105023	0.024624501	"GPX1, VCP, GSPT1, BAX, HSPA5"	190	79	13528	4.506329114	1	0.418235599	34.10186315

GOTERM_BP_FAT	GO:0006919~activation of caspase activity	3	1.369863014	0.174122378	"VCP, GSPT1, BAX"	190	54	13528	3.955555556	1	0.828649469	95.92416904

GOTERM_BP_FAT	GO:0010952~positive regulation of peptidase activity	3	1.369863014	0.199357408

"VCP, GSPT1, BAX" 190 59 13528 3.620338983 1 0.849812728 97.57461366
GOTERM_BP_FAT GO:0043280~positive regulation of caspase activity 3 1.369863014 0.199357408
"VCP, GSPT1, BAX" 190 59 13528 3.620338983 1 0.849812728 97.57461366
GOTERM_BP_FAT GO:0051345~positive regulation of hydrolase activity 4 1.826484018 0.458000604
"VCP, GM2A, GSPT1, BAX" 190 179 13528 1.591061453 1 0.976835958 99.99644783
GOTERM_BP_FAT GO:0043085~positive regulation of catalytic activity 7 3.196347032 0.738948195
"SPAG9, VCP, GM2A, GSPT1, BAX, CAP1, CUL1" 190 520 13528 0.958461538 1 0.998575619
99.99999998
GOTERM_BP_FAT GO:0044093~positive regulation of molecular function 7 3.196347032 0.833173912
"SPAG9, VCP, GM2A, GSPT1, BAX, CAP1, CUL1" 190 586 13528 0.850511945 1 0.99973413 100

Annotation Cluster 28 Enrichment Score: 1.0278407863370669
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT "GO:0008135~translation factor activity, nucleic acid binding" 6 2.739726027
0.012195962 "EIF4G3, GSPT1, DHX29, EIF1AX, HBS1L, EFTUD1" 183 98 12983 4.343593175
0.994762776 0.354457123 15.87281032
GOTERM_MF_FAT GO:0003743~translation initiation factor activity 3 1.369863014 0.210624611 "EIF4G3,
DHX29, EIF1AX" 183 61 12983 3.489115829 1 0.925397538 96.42558752
GOTERM_BP_FAT GO:0006412~translation 7 3.196347032 0.321182926 "EIF4G3, GSPT1, DHX29,
EIF1AX, HBS1L, EFTUD1, QARS" 190 331 13528 1.505740181 1 0.938752223 99.84665766

Annotation Cluster 29 Enrichment Score: 1.0187943105454393
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0010038~response to metal ion 6 2.739726027 0.034700862 "PEF1, GPX1,
PLA2G4A, IMPA1, TFRC, PEBP1" 190 129 13528 3.311627907 1 0.482620233 44.60968099
GOTERM_BP_FAT GO:0010035~response to inorganic substance 7 3.196347032 0.067954172 "PEF1,
GPX1, PLA2G4A, IMPA1, TFRC, PEBP1, PRDX1" 190 205 13528 2.431219512 1 0.621121425
69.18479036
GOTERM_BP_FAT GO:0051592~response to calcium ion 3 1.369863014 0.179128628 "PEF1, PLA2G4A,
PEBP1" 190 55 13528 3.883636364 1 0.831149699 96.3183204
GOTERM_BP_FAT GO:0007568~aging 4 1.826484018 0.199113804 "PLA2G4A, TFRC, PEBP1, CALR"
190 110 13528 2.589090909 1 0.850955778 97.56224014

Annotation Cluster 30 Enrichment Score: 0.9928635508050009
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0007017~microtubule-based process 11 5.02283105 0.002963809 "KIF13A,
APP, TUBB, TUBB2A, TUBA4A, TUBB6, PAFAH1B1, CLASP1, DYNC1H1, DYNC1I2, ACTR10" 190 253
13528 3.095652174 0.990973406 0.108472529 4.843797518
GOTERM_CC_FAT GO:0005874~microtubule 11 5.02283105 0.003216362 "KIF13A, TUBB, TUBB2A,
TUBA4A, TUBB6, PAFAH1B1, CLASP1, MAPRE1, WDR44, DYNC1H1, DYNC1I2" 168 274 12782
3.054440389 0.575537306 0.036572342 4.137872574
GOTERM_CC_FAT GO:0005881~cytoplasmic microtubule 3 1.369863014 0.022633599 "PAFAH1B1,
CLASP1, MAPRE1" 168 18 12782 12.68055556 0.997733948 0.163985486 25.94127297
GOTERM_BP_FAT GO:0048285~organelle fission 8 3.652968037 0.041960394 "TUBB, DNM1L,
TUBB2A, USP9X, BAX, PAFAH1B1, CLASP1, MAPRE1" 190 229 13528 2.487336245 1 0.507462495
51.18043969
GOTERM_BP_FAT GO:0000278~mitotic cell cycle 10 4.566210046 0.075451944 "APP, TUBB, GSPT1,
TUBB2A, USP9X, PAFAH1B1, CLASP1, MAPRE1, DYNC1H1, CUL1" 190 370 13528 1.924324324 1
0.642379094 73.07912604
GOTERM_CC_FAT GO:0005819~spindle 5 2.283105023 0.126426537 "APP, PPP2CA, PAFAH1B1,
CLASP1, MAPRE1" 168 147 12782 2.587868481 1 0.456311702 83.01815551

GOTERM_BP_FAT	GO:0022403~cell cycle phase	10	4.566210046	0.12646377	"APP, TUBB, GSPT1, TUBB2A, USP9X, PAFAH1B1, CLASP1, MAPRE1, DYNC1H1, CUL1"	190	414	13528	1.719806763	1	0.767473166	89.58203593
GOTERM_BP_FAT	GO:0007049~cell cycle	16	7.305936073	0.126581572	"TUBB2A, USP9X, CALR, GAK, MAPK1, TUBB, APP, GSPT1, VPS4B, VPS4A, PAFAH1B1, CLASP1, PDCD6IP, MAPRE1, DYNC1H1, CUL1"	190	776	13528	1.468041237	1	0.765509095	89.60551183
GOTERM_CC_FAT	GO:0005813~centrosome	6	2.739726027	0.171143633	"ACTR1A, PAFAH1B1, CLASP1, PDCD6IP, MAPRE1, MYOF"	168	224	12782	2.037946429	1	0.509971594	91.47611829
GOTERM_BP_FAT	GO:0007067~mitosis	6	2.739726027	0.195003804	"TUBB, TUBB2A, USP9X, PAFAH1B1, CLASP1, MAPRE1"	190	220	13528	1.941818182	1	0.84583572	97.34431685
GOTERM_BP_FAT	GO:0000280~nuclear division	6	2.739726027	0.195003804	"TUBB, TUBB2A, USP9X, PAFAH1B1, CLASP1, MAPRE1"	190	220	13528	1.941818182	1	0.84583572	97.34431685
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	6	2.739726027	0.20496421	"TUBB, TUBB2A, USP9X, PAFAH1B1, CLASP1, MAPRE1"	190	224	13528	1.907142857	1	0.85408787	97.84360281
GOTERM_CC_FAT	GO:0005815~microtubule organizing center	6	2.739726027	0.236265942	"ACTR1A, PAFAH1B1, CLASP1, PDCD6IP, MAPRE1, MYOF"	168	253	12782	1.804347826	1	0.587344319	97.08611157
GOTERM_BP_FAT	GO:0022402~cell cycle process	11	5.02283105	0.266324169	"APP, TUBB, GSPT1, TUBB2A, USP9X, PAFAH1B1, CLASP1, MAPRE1, DYNC1H1, CALR, CUL1"	190	565	13528	1.38619469	1	0.912096063	99.43735302
GOTERM_MF_FAT	GO:0008017~microtubule binding	3	1.369863014	0.267682127	"PAFAH1B1, CLASP1, MAPRE1"	183	72	12983	2.956056466	1	0.964331399	98.75763623
GOTERM_BP_FAT	GO:0000279~M phase	7	3.196347032	0.312034514	"TUBB, TUBB2A, USP9X, PAFAH1B1, CLASP1, MAPRE1, DYNC1H1"	190	329	13528	1.514893617	1	0.93501482	99.80817139
GOTERM_BP_FAT	GO:0000226~microtubule cytoskeleton organization	4	1.826484018	0.338021121	"TUBB, PAFAH1B1, CLASP1, DYNC1H1"	190	147	13528	1.937414966	1	0.944698358	99.89926295
GOTERM_MF_FAT	GO:0015631~tubulin binding	3	1.369863014	0.41029861	"PAFAH1B1, CLASP1, MAPRE1"	183	100	12983	2.128360656	1	0.975415299	99.94121363

Annotation Cluster 31	Enrichment Score: 0.9661691970380952
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0006575~cellular amino acid derivative metabolic process	7	3.196347032	0.029091372	"GPX1, PLA2G4A, SRM, IDH1, PAFAH1B1, GLO1, ALDH9A1"	190	166	13528	3.002409639	1	0.451352591	38.97224587
GOTERM_BP_FAT	GO:0006749~glutathione metabolic process	3	1.369863014	0.057889535	"GPX1, IDH1, GLO1"	190	28	13528	7.628571429	1	0.580076944	63.11998588
GOTERM_BP_FAT	GO:0006518~peptide metabolic process	3	1.369863014	0.169139683	"GPX1, IDH1, GLO1"	190	53	13528	4.030188679	1	0.822481453	95.49273138
GOTERM_BP_FAT	GO:0006790~sulfur metabolic process	3	1.369863014	0.479417014	"GPX1, IDH1, GLO1"	190	115	13528	1.857391304	1	0.979301962	99.99819026

Annotation Cluster 32	Enrichment Score: 0.9069480802465979
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0044270~nitrogen compound catabolic process	4	1.826484018	0.067175109	"HMOX2, NUDT9, VPS4B, PNP"	190	67	13528	4.250746269	1	0.619941126	68.75109425
GOTERM_BP_FAT	GO:0046700~heterocycle catabolic process	4	1.826484018	0.092934215	"HMOX2, NUDT9, VPS4B, PNP"	190	77	13528	3.698701299	1	0.684775291	80.43826918
GOTERM_BP_FAT	"GO:0034656~nucleobase, nucleoside and nucleotide catabolic process"	3	1.369863014	0.194272725	"NUDT9, VPS4B, PNP"	190	58	13528	3.682758621	1	0.846197558	97.30368385
GOTERM_BP_FAT	"GO:0034655~nucleobase, nucleoside, nucleotide and nucleic acid catabolic process"	3	1.369863014	0.194272725	"NUDT9, VPS4B, PNP"	190	58	13528	3.682758621	1	0.846197558

97.30368385

Annotation Cluster 33	Enrichment Score: 0.8897423239051401
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046903~secretion	9	4.109589041	0.059918865	"SCAMP1, COPA, ARFGAP3, PTGES2, MYO6, SCRN1, STXBP1, PRKCI, YKT6"	190	300	13528	2.136	1	0.586401834	64.42654653
GOTERM_BP_FAT	GO:0032940~secretion by cell	6	2.739726027	0.164579445	"SCAMP1, ARFGAP3, MYO6, SCRN1, STXBP1, YKT6"	190	207	13528	2.063768116	1	0.816875063	95.06057051
GOTERM_BP_FAT	GO:0006887~exocytosis	4	1.826484018	0.217187013	"SCAMP1, SCRN1, STXBP1, YKT6"	190	115	13528	2.476521739	1	0.866302773	98.33591369

Annotation Cluster 34	Enrichment Score: 0.8878518793704525
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0010035~response to inorganic substance	7	3.196347032	0.067954172	"PEF1, GPX1, PLA2G4A, IMPA1, TFRC, PEBP1, PRDX1"	190	205	13528	2.431219512	1	0.621121425	69.18479036
GOTERM_BP_FAT	GO:0006979~response to oxidative stress 6	2.739726027	0.07961011	"HMOX2, GPX1, PLA2G4A, PEBP1, IDH1, PRDX1"	190	164	13528	2.604878049	1	0.645126539	75.03435635
GOTERM_BP_FAT	GO:0042542~response to hydrogen peroxide	3	1.369863014	0.184156816	"GPX1, PLA2G4A, PRDX1"	190	56	13528	3.814285714	1	0.838580504	96.67791852
GOTERM_BP_FAT	GO:0000302~response to reactive oxygen species	3	1.369863014	0.281981319	"GPX1, PLA2G4A, PRDX1"	190	75	13528	2.848	1	0.920980242	99.60778345

Annotation Cluster 35	Enrichment Score: 0.8097840373802003
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0033043~regulation of organelle organization 8	3.652968037	0.032849977	"ARPC1B, PLA2G4A, ARPC3, CFL1, PEBP1, CLASP1, MAPRE1, RASA1"	190	217	13528	2.624884793	1	0.47178573	42.80608068
GOTERM_BP_FAT	GO:0010243~response to organic nitrogen 3	1.369863014	0.219840616	"PLA2G4A, CFL1, PEBP1"	190	63	13528	3.39047619	1	0.868607375	98.42779851
GOTERM_BP_FAT	GO:0051130~positive regulation of cellular component organization	5	2.283105023	0.246960728	"PLA2G4A, CFL1, PRKCI, PEBP1, CALR"	190	181	13528	1.966850829	1	0.898073269	99.13007882
GOTERM_BP_FAT	GO:0010638~positive regulation of organelle organization	3	1.369863014	0.323290509	"PLA2G4A, CFL1, PEBP1"	190	83	13528	2.573493976	1	0.939342171	99.85442999

Annotation Cluster 36	Enrichment Score: 0.7895211717850479
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0030018~Z disc	3	1.369863014	0.121110444	"SRI, FHL3, FHL2"	168	46	12782	4.961956522	1	0.446814082	81.61141785
GOTERM_CC_FAT	GO:0030017~sarcomere	4	1.826484018	0.136665625	"SRI, TRIM32, FHL3, FHL2"	168	98	12782	3.105442177	1	0.47873282	85.45153719
GOTERM_CC_FAT	GO:0031674~I band	3	1.369863014	0.161410162	"SRI, FHL3, FHL2"	168	55	12782	4.15	1	0.502857969	90.0654499
GOTERM_CC_FAT	GO:0030016~myofibril	4	1.826484018	0.177261252	"SRI, TRIM32, FHL3, FHL2"	168	111	12782	2.741741742	1	0.513660003	92.26547651
GOTERM_CC_FAT	GO:0044449~contractile fiber part	4	1.826484018	0.183782805	"SRI, TRIM32, FHL3, FHL2"	168	113	12782	2.693215339	1	0.518077295	93.03219344
GOTERM_CC_FAT	GO:0043292~contractile fiber	4	1.826484018	0.210466276	"SRI, TRIM32, FHL3,

FHL2" 168 121 12782 2.515151515 1 0.55795919 95.49451355

Annotation Cluster 37 Enrichment Score: 0.7391532887277924
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0008629~induction of apoptosis by intracellular signals 5 2.283105023
0.006773125 "GPX1, TP53I3, CASP3, BAX, CUL1" 190 54 13528 6.592592593 0.999979162 0.17796865
10.74584076
GOTERM_BP_FAT GO:0042127~regulation of cell proliferation 8 3.652968037 0.928600766 "MAPK1,
GPX1, PLA2G4A, CASP3, BAX, CALR, PNP, CUL1" 190 787 13528 0.723761118 1 0.999988527 100
GOTERM_BP_FAT GO:0008285~negative regulation of cell proliferation 3 1.369863014 0.96365589
"CASP3, BAX, CUL1" 190 361 13528 0.591689751 1 0.999999019 100

Annotation Cluster 38 Enrichment Score: 0.7252695049726395
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0006690~icosanoid metabolic process 3 1.369863014 0.139834107 "PLA2G4A,
PTGES2, RNPEP" 190 47 13528 4.544680851 1 0.783768373 91.95120266
GOTERM_BP_FAT GO:0033559~unsaturated fatty acid metabolic process 3 1.369863014 0.159251641
"PLA2G4A, PTGES2, RNPEP" 190 51 13528 4.188235294 1 0.811252707 94.50637539
GOTERM_BP_FAT GO:0006631~fatty acid metabolic process 5 2.283105023 0.299567334 "PLA2G4A,
TPI1, PTGES2, RNPEP, SLC27A4" 190 198 13528 1.797979798 1 0.930310788 99.74095052

Annotation Cluster 39 Enrichment Score: 0.7125011906549799
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_MF_FAT GO:0004197~cysteine-type endopeptidase activity 5 2.283105023 0.018355936
"CASP3, USP8, PDIA3, USP9X, CAPN2" 183 72 12983 4.926760777 0.999639976 0.3562977
22.96820655
GOTERM_MF_FAT GO:0008234~cysteine-type peptidase activity 5 2.283105023 0.13636687 "CASP3,
USP8, PDIA3, USP9X, CAPN2" 183 141 12983 2.515792737 1 0.885103129 87.31832357
GOTERM_MF_FAT GO:0008233~peptidase activity 11 5.02283105 0.285523461 "APP, CASP3, USP8,
PDIA3, USP9X, NRD1, ERAP1, NLN, DPP9, CAPN2, RNPEP" 183 574 12983 1.359579978 1
0.967486186 99.1222488
GOTERM_MF_FAT "GO:0070011~peptidase activity, acting on L-amino acid peptides" 10 4.566210046
0.363817328 "CASP3, USP8, PDIA3, USP9X, NRD1, ERAP1, NLN, DPP9, CAPN2, RNPEP" 183 549 12983
1.292265122 1 0.974068319 99.82884719
GOTERM_MF_FAT GO:0004175~endopeptidase activity 7 3.196347032 0.429948314 "CASP3, USP8,
PDIA3, USP9X, NRD1, NLN, CAPN2" 183 375 12983 1.324313297 1 0.976682798 99.96352714
GOTERM_MF_FAT GO:0008237~metallopeptidase activity 4 1.826484018 0.474860466 "NRD1, ERAP1,
NLN, RNPEP" 183 183 12983 1.550718146 1 0.982646937 99.98851912

Annotation Cluster 40 Enrichment Score: 0.7050876682028475
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni
Benjamini FDR
GOTERM_BP_FAT GO:0030433~ER-associated protein catabolic process 3 1.369863014 0.043819965
"NPLOC4, HSP90B1, VCP" 190 24 13528 8.9 1 0.512200214 52.74155587
GOTERM_BP_FAT GO:0043161~proteasomal ubiquitin-dependent protein catabolic process 3 1.369863014
0.41834298 "NPLOC4, HSP90B1, VCP" 190 102 13528 2.094117647 1 0.969174207 99.98842578
GOTERM_BP_FAT GO:0010498~proteasomal protein catabolic process 3 1.369863014 0.41834298
"NPLOC4, HSP90B1, VCP" 190 102 13528 2.094117647 1 0.969174207 99.98842578

Annotation Cluster 41 Enrichment Score: 0.7045139396753253
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni

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Benjamini	FDR
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	5	2.283105023	0.123013623	"YWHAH, MYO6, NCDN, STXBP1, PEBP1"	190	136	13528	2.617647059	1	0.762064255	88.87195444
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	5	2.283105023	0.150485224	"YWHAH, MYO6, NCDN, STXBP1, PEBP1"	190	147	13528	2.421768707	1	0.799429184	93.46546983
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	5	2.283105023	0.166341918	"YWHAH, MYO6, NCDN, STXBP1, PEBP1"	190	153	13528	2.326797386	1	0.818656313	95.23201841
GOTERM_BP_FAT	GO:0048167~regulation of synaptic plasticity	3	1.369863014	0.224990678	"YWHAH, MYO6, NCDN"	190	64	13528	3.3375	1	0.874195454	98.5926784
GOTERM_BP_FAT	GO:0044057~regulation of system process	6	2.739726027	0.43332825	"SRI, YWHAH, MYO6, NCDN, STXBP1, PEBP1"	190	309	13528	1.382524272	1	0.971575611	99.99252037

Annotation Cluster 42	Enrichment Score: 0.7027034573129846
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0007517~muscle organ development	7	3.196347032	0.075599969	"SRI, APP, FHL3, HSPG2, NRD1, TAGLN2, CSRP2"	190	211	13528	2.362085308	1	0.640102056	73.1511335
GOTERM_BP_FAT	GO:0043062~extracellular structure organization	6	2.739726027	0.078504376	"APP, MYO6, HSPG2, NRD1, COL12A1, NFKB2"	190	163	13528	2.620858896	1	0.64267272	74.5278816
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	3	1.369863014	0.497415627	"APP, HSPG2, NRD1"	190	119	13528	1.794957983	1	0.981895576	99.99899537
GOTERM_BP_FAT	GO:0060537~muscle tissue development	3	1.369863014	0.523662244	"APP, HSPG2, NRD1"	190	125	13528	1.7088	1	0.985240231	99.9995904

Annotation Cluster 43	Enrichment Score: 0.6507792732959484
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048871~multicellular organismal homeostasis	4	1.826484018	0.116022716	"GPX1, PLA2G4A, NCDN, BAX"	190	85	13528	3.350588235	1	0.742896327	87.29135446
GOTERM_BP_FAT	GO:0001894~tissue homeostasis	3	1.369863014	0.219840616	"PLA2G4A, NCDN, BAX"	190	63	13528	3.39047619	1	0.868607375	98.42779851
GOTERM_BP_FAT	GO:0060249~anatomical structure homeostasis	3	1.369863014	0.43753341	"PLA2G4A, NCDN, BAX"	190	106	13528	2.01509434	1	0.972093866	99.99339657

Annotation Cluster 44	Enrichment Score: 0.6431517890819116
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	5	2.283105023	0.171771731	"TPI1, PTGES2, AKR1A1, ASL, RNPEP"	190	155	13528	2.296774194	1	0.825877988	95.7257134
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	5	2.283105023	0.171771731	"TPI1, PTGES2, AKR1A1, ASL, RNPEP"	190	155	13528	2.296774194	1	0.825877988	95.7257134
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	5	2.283105023	0.299567334	"PLA2G4A, TPI1, PTGES2, RNPEP, SLC27A4"	190	198	13528	1.797979798	1	0.930310788	99.74095052
GOTERM_BP_FAT	GO:0006633~fatty acid biosynthetic process	3	1.369863014	0.302687861	"TPI1, PTGES2, RNPEP"	190	79	13528	2.703797468	1	0.930879716	99.75959387

Annotation Cluster 45	Enrichment Score: 0.6221814777702516
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0016050~vesicle organization	4	1.826484018	0.035987582	"COPB2, COPA, STXBP1, USO1"	190	52	13528	5.476923077	1	0.483434318	45.83186875
GOTERM_CC_FAT	GO:0044431~Golgi apparatus part	5	2.283105023	0.537994646	"SCAMP1, COPB2, COPA, DNM1L, USO1"	168	294	12782	1.29393424	1	0.89014538	99.99601023
GOTERM_CC_FAT	GO:0000139~Golgi membrane	3	1.369863014	0.702303679	"COPB2, COPA, USO1"
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168 186 12782 1.227150538 1 0.966382477 99.99998749

Annotation Cluster 46 Enrichment Score: 0.5904799187686646
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0016791~phosphatase activity 8 3.652968037 0.061297703 "MINPP1, IMPA1, PPP2CA, NT5C2, PGAM1, PTPN23, MTMR6, ACP1" 183 249 12983 2.279368841 1 0.661407512 58.97524932
GOTERM_BP_FAT GO:0006470~protein amino acid dephosphorylation 4 1.826484018 0.284508722 "PPP2CA, PTPN23, MTMR6, ACP1" 190 133 13528 2.141353383 1 0.922132161 99.6302488
GOTERM_BP_FAT GO:0016311~dephosphorylation 4 1.826484018 0.364427133 "PPP2CA, PTPN23, MTMR6, ACP1" 190 154 13528 1.849350649 1 0.953666141 99.94901185
GOTERM_MF_FAT GO:0004721~phosphoprotein phosphatase activity 4 1.826484018 0.408591992 "PPP2CA, PTPN23, MTMR6, ACP1" 183 165 12983 1.719887399 1 0.976406337 99.93877139
GOTERM_MF_FAT GO:0004725~protein tyrosine phosphatase activity 3 1.369863014 0.429694771 "PTPN23, MTMR6, ACP1" 183 104 12983 2.046500631 1 0.977966752 99.96329798

Annotation Cluster 47 Enrichment Score: 0.5533344222112723
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0019900~kinase binding 7 3.196347032 0.040318692 "SPAG9, MAPK1, PFKL, BCAR1, PGAM1, PEBP1, TRADD" 183 179 12983 2.774399365 0.999999978 0.53504871 43.99158445
GOTERM_MF_FAT GO:0019901~protein kinase binding 5 2.283105023 0.15173844 "SPAG9, MAPK1, BCAR1, PGAM1, PEBP1" 183 147 12983 2.413107319 1 0.889315731 90.15268149
GOTERM_BP_FAT GO:0030335~positive regulation of cell migration 3 1.369863014 0.353890903 "SPAG9, MAPK1, BCAR1" 190 89 13528 2.4 1 0.949509278 99.93287082
GOTERM_BP_FAT GO:0051272~positive regulation of cell motion 3 1.369863014 0.398829698 "SPAG9, MAPK1, BCAR1" 190 98 13528 2.179591837 1 0.964386731 99.97989961
GOTERM_BP_FAT GO:0040017~positive regulation of locomotion 3 1.369863014 0.398829698 "SPAG9, MAPK1, BCAR1" 190 98 13528 2.179591837 1 0.964386731 99.97989961
GOTERM_BP_FAT GO:0030334~regulation of cell migration 4 1.826484018 0.421235242 "SPAG9, MAPK1, BCAR1, WDR44" 190 169 13528 1.685207101 1 0.969719539 99.98935174
GOTERM_BP_FAT GO:0040012~regulation of locomotion 4 1.826484018 0.505911234 "SPAG9, MAPK1, BCAR1, WDR44" 190 192 13528 1.483333333 1 0.982856882 99.99924464
GOTERM_BP_FAT GO:0051270~regulation of cell motion 4 1.826484018 0.510128021 "SPAG9, MAPK1, BCAR1, WDR44" 190 193 13528 1.475647668 1 0.983191573 99.99934553

Annotation Cluster 48 Enrichment Score: 0.5376401981183027
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0009725~response to hormone stimulus 8 3.652968037 0.252920698 "MAPK1, PLA2G4A, BCAR1, PRKCI, FHL2, PEBP1, IDH1, ASL" 190 367 13528 1.552043597 1 0.902106981 99.23835081
GOTERM_BP_FAT GO:0048545~response to steroid hormone stimulus 5 2.283105023 0.281706248 "MAPK1, PLA2G4A, PEBP1, IDH1, ASL" 190 192 13528 1.854166667 1 0.922684095 99.60526245
GOTERM_BP_FAT GO:0051384~response to glucocorticoid stimulus 3 1.369863014 0.29751886 "PLA2G4A, PEBP1, ASL" 190 78 13528 2.738461538 1 0.929657785 99.72798197
GOTERM_BP_FAT GO:0031960~response to corticosteroid stimulus 3 1.369863014 0.333536875 "PLA2G4A, PEBP1, ASL" 190 85 13528 2.512941176 1 0.943470906 99.88721955

Annotation Cluster 49 Enrichment Score: 0.5101196434768559
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_CC_FAT GO:0005925~focal adhesion 4 1.826484018 0.148794905 "BCAR1, FERMT1, FHL2,

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GAK"	168	102	12782	2.983660131	1	0.499015592	87.91598238
GOTERM_CC_FAT	GO:0005924~cell-substrate adherens junction	4	1.826484018	0.161258016	"BCAR1,
FERMT1, FHL2, GAK"	168	106	12782	2.871069182	1	0.507734682	90.04178013
GOTERM_CC_FAT	GO:0030055~cell-substrate junction	4	1.826484018	0.180513893	"BCAR1, FERMT1,
FHL2, GAK"	168	112	12782	2.717261905	1	0.515872463	92.65711912
GOTERM_CC_FAT	GO:0005912~adherens junction	4	1.826484018	0.32999487	"BCAR1, FERMT1,
FHL2, GAK"	168	155	12782	1.96344086	1	0.710228542	99.47694316
GOTERM_CC_FAT	GO:0070161~anchoring junction	4	1.826484018	0.390704667	"BCAR1, FERMT1,
FHL2, GAK"	168	172	12782	1.769379845	1	0.772541998	99.84953308
GOTERM_CC_FAT	GO:0016323~basolateral plasma membrane	4	1.826484018	0.496930605	"BCAR1,
FERMT1, FHL2, GAK"	168	203	12782	1.499178982	1	0.865774388	99.98780868
GOTERM_CC_FAT	GO:0030054~cell junction	4	1.826484018	0.968034773	"BCAR1, FERMT1, FHL2,
GAK"	168	518	12782	0.587516088	1	0.999757875	100

Annotation Cluster 50	Enrichment Score: 0.4956367436330972
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0016049~cell growth	3	1.369863014	0.209572914	"APP, CSRP2, VAT1"	190
61	13528	3.501639344	1	0.858133867	98.04343475
GOTERM_BP_FAT	GO:0008361~regulation of cell size	5	2.283105023	0.329190811	"APP, NDRG3,
PPP2CA, CSRP2, VAT1"	190	206	13528	1.72815534	1	0.941554181	99.87426586
GOTERM_BP_FAT	GO:0040007~growth	4	1.826484018	0.472396764	"GPX1, APP, CSRP2, VAT1"
190	183	13528	1.556284153	1	0.978845743	99.99773573

Annotation Cluster 51	Enrichment Score: 0.49469568339589304
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	7	3.196347032	0.181471682	"CAST, APP,
CASP3, RNH1, PEBP1, HSPA5, DNAJC3"	183	270	12983	1.839324023	1	0.913597462	94.04268577
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	4	1.826484018	0.332246434	"CAST,
APP, PEBP1, HSPA5"	183	145	12983	1.957113247	1	0.97061834	99.66142075
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	4	1.826484018	0.363731192	"CAST, APP,
PEBP1, HSPA5"	183	153	12983	1.854780528	1	0.975800223	99.8285205
GOTERM_CC_FAT	GO:0009986~cell surface	6	2.739726027	0.478814758	"APP, GDI2, NRD1, PEBP1,
HSPA5, CALR"	168	348	12782	1.311781609	1	0.854268157	99.98060929

Annotation Cluster 52	Enrichment Score: 0.4894051868511701
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	5	2.283105023	0.295504617	"PLA2G4A,
TFRC, SKIV2L, HSPA5, ASL"	190	197	13528	1.807106599	1	0.929022966	99.71463683
GOTERM_BP_FAT	GO:0007584~response to nutrient	4	1.826484018	0.311227081	"PLA2G4A, TFRC,
SKIV2L, ASL"	190	140	13528	2.034285714	1	0.935277021	99.80437042
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	5	2.283105023	0.369949794
"PLA2G4A, TFRC, SKIV2L, HSPA5, ASL"	190	220	13528	1.618181818	1	0.955741596	99.95593749

Annotation Cluster 53	Enrichment Score: 0.483372908793063
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0050885~neuromuscular process controlling balance	3	1.369863014	0.085587676
"APP, GM2A, PAFAH1B1"	190	35	13528	6.102857143	1	0.65594609	77.61237052
GOTERM_BP_FAT	GO:0007605~sensory perception of sound	4	1.826484018	0.154132398	"GPX1,
CASP3, MYO6, WDR1"	190	97	13528	2.936082474	1	0.801865123	93.9192316
GOTERM_BP_FAT	GO:0050954~sensory perception of mechanical stimulus	4	1.826484018	0.174486433
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					"GPX1, CASP3, MYO6, WDR1"	190	103	13528	2.765048544	1	0.827591603	95.95411861
GOTERM_BP_FAT	GO:0007611~learning or memory	4	1.826484018	0.202699165	"APP, GM2A, PAFAH1B1, RIC8A"	190	111	13528	2.565765766	1	0.8520659	97.73850254
GOTERM_BP_FAT	GO:0050905~neuromuscular process	3	1.369863014	0.214700921	"APP, GM2A, PAFAH1B1"	190	62	13528	3.44516129	1	0.864185515	98.24526892
GOTERM_BP_FAT	GO:0007610~behavior	8	3.652968037	0.483820208	"MAPK1, APP, MYO6, GM2A, PEBP1, PAFAH1B1, ASL, RIC8A"	190	469	13528	1.214498934	1	0.980029818	99.99842997
GOTERM_BP_FAT	GO:0050890~cognition	9	4.109589041	0.94432949	"MAPK1, GPX1, APP, CASP3, MYO6, GM2A, PAFAH1B1, WDR1, RIC8A"	190	909	13528	0.704950495	1	0.999995047	100
GOTERM_BP_FAT	GO:0050877~neurological system process	11	5.02283105	0.978139276	"MAPK1, GPX1, APP, CASP3, MYO6, GM2A, PEBP1, PAFAH1B1, WDR1, ALDH9A1, RIC8A"	190	1210	13528	0.647272727	1	0.999999849	100
GOTERM_BP_FAT	GO:0007600~sensory perception	5	2.283105023	0.996971782	"MAPK1, GPX1, CASP3, MYO6, WDR1"	190	810	13528	0.439506173	1	1	100

Annotation Cluster 54	Enrichment Score: 0.4449378651602865

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0016887~ATPase activity	8	3.652968037	0.189322535	"ABCF3, VCP, DHX29, ASCC3, SKIV2L, VPS4B, VPS4A, DYNC1H1"	183	334	12983	1.699289945	1	0.917528252	94.79890472
GOTERM_MF_FAT	"GO:0042623~ATPase activity, coupled"	6	2.739726027	0.334391696	"DHX29, ASCC3, SKIV2L, VPS4B, VPS4A, DYNC1H1"	183	272	12983	1.56497107	1	0.969327277	99.676424
GOTERM_MF_FAT	GO:0008026~ATP-dependent helicase activity	3	1.369863014	0.400480999	"DHX29, ASCC3, SKIV2L"	183	98	12983	2.171796587	1	0.977073433	99.92582121
GOTERM_MF_FAT	GO:0070035~purine NTP-dependent helicase activity	3	1.369863014	0.400480999	"DHX29, ASCC3, SKIV2L"	183	98	12983	2.171796587	1	0.977073433	99.92582121
GOTERM_MF_FAT	GO:0004386~helicase activity	3	1.369863014	0.587068865	"DHX29, ASCC3, SKIV2L"	183	140	12983	1.520257611	1	0.993997678	99.9996114

Annotation Cluster 55	Enrichment Score: 0.4415422179719263

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005819~spindle	5	2.283105023	0.126426537	"APP, PPP2CA, PAFAH1B1, CLASP1, MAPRE1"	168	147	12782	2.587868481	1	0.456311702	83.01815551
GOTERM_CC_FAT	"GO:0000775~chromosome, centromeric region"	4	1.826484018	0.220687527	"PPP2CA, SEC13, PAFAH1B1, CLASP1"	168	124	12782	2.454301075	1	0.568099752	96.20241073
GOTERM_CC_FAT	GO:0000776~kinetochore	3	1.369863014	0.266457616	"SEC13, PAFAH1B1, CLASP1"	168	77	12782	2.964285714	1	0.629564904	98.28331242
GOTERM_CC_FAT	GO:0044427~chromosomal part	4	1.826484018	0.884347938	"PPP2CA, SEC13, PAFAH1B1, CLASP1"	168	386	12782	0.788428325	1	0.996395451	100
GOTERM_CC_FAT	GO:0005694~chromosome	4	1.826484018	0.942804345	"PPP2CA, SEC13, PAFAH1B1, CLASP1"	168	460	12782	0.661594203	1	0.999130176	100

Annotation Cluster 56	Enrichment Score: 0.40455019043047413

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0008585~female gonad development	3	1.369863014	0.224990678	"PLA2G4A, BAX, IDH1"	190	64	13528	3.3375	1	0.874195454	98.5926784
GOTERM_BP_FAT	GO:0046660~female sex differentiation	3	1.369863014	0.250852699	"PLA2G4A, BAX, IDH1"	190	69	13528	3.095652174	1	0.901083041	99.20230574
GOTERM_BP_FAT	GO:0046545~development of primary female sexual characteristics	3	1.369863014	0.250852699	"PLA2G4A, BAX, IDH1"	190	69	13528	3.095652174	1	0.901083041	99.20230574
GOTERM_BP_FAT	GO:0008406~gonad development	3	1.369863014	0.465663973	"PLA2G4A, BAX, IDH1"	190	112	13528	1.907142857	1	0.977816523	99.99720073

GOTERM_BP_FAT	GO:0003006~reproductive developmental process	5	2.283105023	0.500009558
"PLA2G4A, BAX, PEBP1, IDH1, PAFAH1B1"	190	262	13528	1.358778626	1	0.981907705	99.99907867
GOTERM_BP_FAT	GO:0048608~reproductive structure development3	1.369863014	0.52794697
"PLA2G4A, BAX, IDH1"	190	126	13528	1.695238095	1	0.985546859	99.99964786
GOTERM_BP_FAT	GO:0045137~development of primary sexual characteristics	3	1.369863014
0.53220571	"PLA2G4A, BAX, IDH1"	190	127	13528	1.681889764	1	0.986057155	99.99969739
GOTERM_BP_FAT	GO:0007548~sex differentiation	3	1.369863014	0.626434428	"PLA2G4A, BAX,
IDH1"	190	151	13528	1.414569536	1	0.994608806	99.99999297

Annotation Cluster 57	Enrichment Score: 0.4027522143146813
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0045787~positive regulation of cell cycle	3	1.369863014	0.189205361	"APP,
PEBP1, CALR"	190	57	13528	3.747368421	1	0.844073561	97.00555586
GOTERM_CC_FAT	GO:0009986~cell surface	6	2.739726027	0.478814758	"APP, GDI2, NRD1, PEBP1,
HSPA5, CALR"	168	348	12782	1.311781609	1	0.854268157	99.98060929
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	5	2.283105023	0.68334873	"APP, CASP3,
BAX, PEBP1, CALR"	190	331	13528	1.075528701	1	0.997052873	99.99999956

Annotation Cluster 58	Enrichment Score: 0.382093877680793
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0019637~organophosphate metabolic process	5	2.283105023	0.305586958
"PLAA, PLA2G4A, TPI1, IMPA1, PAFAH1B1"	190	200	13528	1.78	1	0.932133487	99.77577724
GOTERM_BP_FAT	GO:0046486~glycerolipid metabolic process	4	1.826484018	0.39505614	"GPX1,
PLA2G4A, IMPA1, PAFAH1B1"	190	162	13528	1.758024691	1	0.963399593	99.97768165
GOTERM_BP_FAT	GO:0006650~glycerophospholipid metabolic process	3	1.369863014	0.49295291
"PLA2G4A, IMPA1, PAFAH1B1"	190	118	13528	1.810169492	1	0.9812144	99.99883527
GOTERM_BP_FAT	GO:0006644~phospholipid metabolic process	4	1.826484018	0.497766223	"PLAA,
PLA2G4A, IMPA1, PAFAH1B1"	190	190	13528	1.498947368	1	0.981701908	99.99900703

Annotation Cluster 59	Enrichment Score: 0.37414649033381847
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni
Benjamini	FDR
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	18	8.219178082	0.201148068	"MINPP1,
TWF1, NRBP1, IMPA1, STK10, PTPN23, PRKCI, RIOK2, ACP1, GAK, MAPK1, SPAG9, APP, PPP2CA, CFL1,
PGK1, MTMR6, PIK3R4"	190	973	13528	1.317163412	1	0.851136249	97.66377209
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	18	8.219178082	0.201148068	"MINPP1,
TWF1, NRBP1, IMPA1, STK10, PTPN23, PRKCI, RIOK2, ACP1, GAK, MAPK1, SPAG9, APP, PPP2CA, CFL1,
PGK1, MTMR6, PIK3R4"	190	973	13528	1.317163412	1	0.851136249	97.66377209
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	11	5.02283105	0.455796777
"SPAG9, MAPK1, APP, TWF1, NRBP1, STK10, CFL1, PRKCI, PIK3R4, RIOK2, GAK"	190	667	13528
1.174212894	1	0.976593994	99.99619835
GOTERM_BP_FAT	GO:0016310~phosphorylation	12	5.479452055	0.566223632	"SPAG9, MAPK1, APP,
TWF1, NRBP1, STK10, CFL1, PRKCI, PGK1, PIK3R4, RIOK2, GAK"	190	800	13528	1.068	1
0.989619467	99.99991441
GOTERM_MF_FAT	GO:0004674~protein serine/threonine kinase activity	6	2.739726027	0.72507402
"MAPK1, STK10, PRKCI, PIK3R4, RIOK2, GAK"	183	430	12983	0.989935189	1	0.999236316
99.99999874
GOTERM_MF_FAT	GO:0004672~protein kinase activity	8	3.652968037	0.751532455	"MAPK1, TWF1,
NRBP1, STK10, PRKCI, PIK3R4, RIOK2, GAK"	183	606	12983	0.936572346	1	0.999519453
99.9999997

Annotation Cluster 60	Enrichment Score: 0.3674034342976289

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_MF_FAT GO:0008047~enzyme activator activity 8 3.652968037 0.191242244 "PLAA, APP, GDI2, ARFGAP3, GM2A, RASA1, RIC8A, TBC1D9B" 183 335 12983 1.694217437 1 0.91416117 94.96972244

GOTERM_BP_FAT GO:0043087~regulation of GTPase activity 4 1.826484018 0.24675741 "GDI2, ARFGAP3, PAFAH1B1, TBC1D9B" 190 123 13528 2.315447154 1 0.89903356 99.12614161

GOTERM_MF_FAT GO:0005099~Ras GTPase activator activity 3 1.369863014 0.365553106 "GDI2, RASA1, TBC1D9B" 183 91 12983 2.338857863 1 0.972848139 99.8353086

GOTERM_MF_FAT GO:0005096~GTPase activator activity 5 2.283105023 0.37197186 "GDI2, ARFGAP3, RASA1, RIC8A, TBC1D9B" 183 220 12983 1.612394436 1 0.973213861 99.85728565

GOTERM_BP_FAT GO:0032318~regulation of Ras GTPase activity 3 1.369863014 0.427980085 "ARFGAP3, PAFAH1B1, TBC1D9B" 190 104 13528 2.053846154 1 0.970681095 99.99124773

GOTERM_MF_FAT GO:0030695~GTPase regulator activity 7 3.196347032 0.501393677 "GDI2, ARFGAP3, WDR44, DOCK5, RASA1, RIC8A, TBC1D9B" 183 404 12983 1.229251204 1 0.986657962 99.99446884

GOTERM_MF_FAT GO:0060589~nucleoside-triphosphatase regulator activity 7 3.196347032 0.522977935 "GDI2, ARFGAP3, WDR44, DOCK5, RASA1, RIC8A, TBC1D9B" 183 413 12983 1.202463647 1 0.988460804 99.99703444

GOTERM_MF_FAT GO:0005083~small GTPase regulator activity 5 2.283105023 0.537998095 "GDI2, ARFGAP3, WDR44, RASA1, TBC1D9B" 183 274 12983 1.29462327 1 0.989190594 99.99811029

GOTERM_BP_FAT GO:0051056~regulation of small GTPase mediated signal transduction 4 1.826484018 0.687535316 "ARFGAP3, PAFAH1B1, RASA1, TBC1D9B" 190 252 13528 1.13015873 1 0.997140021 99.99999965

GOTERM_BP_FAT GO:0046578~regulation of Ras protein signal transduction 3 1.369863014 0.795224093 "ARFGAP3, PAFAH1B1, TBC1D9B" 190 210 13528 1.017142857 1 0.999426255 100

Annotation Cluster 61 Enrichment Score: 0.33179482130600396

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0002449~lymphocyte mediated immunity 3 1.369863014 0.256039139 "TUBB, SWAP70, PRDX1" 190 70 13528 3.051428571 1 0.904194112 99.28982115

GOTERM_BP_FAT GO:0002443~leukocyte mediated immunity 3 1.369863014 0.338643742 "TUBB, SWAP70, PRDX1" 190 86 13528 2.48372093 1 0.944355612 99.90083616

GOTERM_BP_FAT GO:0002252~immune effector process 3 1.369863014 0.561280757 "TUBB, SWAP70, PRDX1" 190 134 13528 1.594029851 1 0.989296102 99.99989655

GOTERM_BP_FAT GO:0006955~immune response 6 2.739726027 0.967366736 "TUBB, SWAP70, ERAP1, NFKB2, PRDX1, PNP" 190 690 13528 0.619130435 1 0.999999326 100

Annotation Cluster 62 Enrichment Score: 0.3129751412073192

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0001933~negative regulation of protein amino acid phosphorylation 3 1.369863014 0.073284246 "BAX, PPP2CA, PEBP1" 190 32 13528 6.675 1 0.634284373 72.0036214

GOTERM_BP_FAT GO:0042326~negative regulation of phosphorylation 3 1.369863014 0.130334304 "BAX, PPP2CA, PEBP1" 190 45 13528 4.746666667 1 0.769325946 90.32785719

GOTERM_BP_FAT GO:0010563~negative regulation of phosphorus metabolic process 3 1.369863014 0.144639118 "BAX, PPP2CA, PEBP1" 190 48 13528 4.45 1 0.79159063 92.67114665

GOTERM_BP_FAT GO:0045936~negative regulation of phosphate metabolic process 3 1.369863014 0.144639118 "BAX, PPP2CA, PEBP1" 190 48 13528 4.45 1 0.79159063 92.67114665

GOTERM_BP_FAT GO:0032268~regulation of cellular protein metabolic process 9 4.109589041 0.34374078 "MAPK1, EIF4G3, APP, BAX, PPP2CA, NRD1, PEBP1, CALR, CUL1" 190 474 13528 1.351898734 1 0.945911183 99.91287386

GOTERM_BP_FAT GO:0032269~negative regulation of cellular protein metabolic process 4 1.826484018

				0.46162242	"BAX, PPP2CA, PEBP1, CALR"	190	180	13528	1.582222222	1	0.977442186	99.99682469
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	4	1.826484018	0.486674768	"BAX, PPP2CA, PEBP1, CALR"	190	187	13528	1.522994652	1	0.980388958	99.99856905
GOTERM_BP_FAT	GO:0031400~negative regulation of protein modification process	3	1.369863014	0.497415627	"BAX, PPP2CA, PEBP1"	190	119	13528	1.794957983	1	0.981895576	99.99899537
GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	4	1.826484018	0.677064242	"PPP2CA, STXBP1, PEBP1, CALR"	190	248	13528	1.148387097	1	0.99686202	99.99999939
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	5	2.283105023	0.68334873	"APP, CASP3, BAX, PEBP1, CALR"	190	331	13528	1.075528701	1	0.997052873	99.99999956
GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	3	1.369863014	0.699341634	"BAX, PPP2CA, PEBP1"	190	173	13528	1.234682081	1	0.997505798	99.99999981
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	6	2.739726027	0.784340723	"SPAG9, APP, CASP3, BAX, PPP2CA, PEBP1"	190	466	13528	0.916738197	1	0.999313886	100
GOTERM_BP_FAT	GO:0031399~regulation of protein modification process	4	1.826484018	0.784413476	"BAX, PPP2CA, PEBP1, CUL1"	190	295	13528	0.965423729	1	0.999299923	100
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	6	2.739726027	0.812567042	"SPAG9, APP, CASP3, BAX, PPP2CA, PEBP1"	190	485	13528	0.880824742	1	0.999585058	100
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	6	2.739726027	0.812567042	"SPAG9, APP, CASP3, BAX, PPP2CA, PEBP1"	190	485	13528	0.880824742	1	0.999585058	100
GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	3	1.369863014	0.818023611	"PPP2CA, PEBP1, CALR"	190	221	13528	0.966515837	1	0.999629853	100
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	4	1.826484018	0.864572654	"SPAG9, APP, CASP3, PPP2CA"	190	345	13528	0.825507246	1	0.99987122	100
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	4	1.826484018	0.879425715	"SPAG9, APP, CASP3, PPP2CA"	190	357	13528	0.797759104	1	0.999919288	100
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	4	1.826484018	0.895957064	"SPAG9, APP, CASP3, PPP2CA"	190	372	13528	0.765591398	1	0.999950547	100
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	6	2.739726027	0.978580409	"BAX, PPP2CA, SND1, YWHAQ, PEBP1, CALR"	190	734	13528	0.582016349	1	0.999999856	100

Annotation Cluster 63	Enrichment Score: 0.308037587451377

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0048515~spermatid differentiation	3	1.369863014	0.189205361	"BAX, PEBP1, PAFAH1B1"	190	57	13528	3.747368421	1	0.844073561	97.00555586
GOTERM_BP_FAT	GO:0007281~germ cell development	3	1.369863014	0.41349394	"BAX, PEBP1, PAFAH1B1"	190	101	13528	2.114851485	1	0.967936049	99.98670149
GOTERM_BP_FAT	GO:0007276~gamete generation	7	3.196347032	0.476168841	"SPAG9, PLA2G4A, NDRG3, USP9X, BAX, PEBP1, PAFAH1B1"	190	395	13528	1.261772152	1	0.978830788	99.99799182
GOTERM_BP_FAT	GO:0003006~reproductive developmental process	5	2.283105023	0.500009558	"PLA2G4A, BAX, PEBP1, IDH1, PAFAH1B1"	190	262	13528	1.358778626	1	0.981907705	99.99907867
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	8	3.652968037	0.523775844	"APOL2, SPAG9, PLA2G4A, NDRG3, USP9X, BAX, PEBP1, PAFAH1B1"	190	487	13528	1.169609856	1	0.985036547	99.99959203
GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	8	3.652968037	0.523775844	"APOL2, SPAG9, PLA2G4A, NDRG3, USP9X, BAX, PEBP1, PAFAH1B1"	190	487	13528	1.169609856	1	0.985036547	99.99959203
GOTERM_BP_FAT	GO:0019953~sexual reproduction	7	3.196347032	0.621108997	"SPAG9, PLA2G4A, NDRG3, USP9X, BAX, PEBP1, PAFAH1B1"	190	458	13528	1.088209607	1	0.994287965	99.99999109
GOTERM_BP_FAT	GO:0007283~spermatogenesis	5	2.283105023	0.627732236	"SPAG9, NDRG3, BAX, PEBP1, PAFAH1B1"	190	308	13528	1.155844156	1	0.994614132	99.99999337
GOTERM_BP_FAT	GO:0048232~male gamete generation	5	2.283105023	0.627732236	"SPAG9, NDRG3, BAX, PEBP1, PAFAH1B1"	190	308	13528	1.155844156	1	0.994614132	99.99999337

GOTERM_BP_FAT GO:0048610~reproductive cellular process 3 1.369863014 0.664468878 "BAX, PEBP1, PAFAH1B1" 190 162 13528 1.318518519 1 0.996320953 99.99999883

Annotation Cluster 64 Enrichment Score: 0.2830702997527534
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0030246~carbohydrate binding 7 3.196347032 0.377270486 "APP, AIM1L, PFKL, PFKP, PAFAH1B1, CALR, THBS2" 183 354 12983 1.402874255 1 0.971460821 99.87334029
GOTERM_MF_FAT GO:0008201~heparin binding 3 1.369863014 0.424876616 "APP, PAFAH1B1, THBS2" 183 103 12983 2.066369569 1 0.978042843 99.95868068
GOTERM_MF_FAT GO:0005539~glycosaminoglycan binding 3 1.369863014 0.587068865 "APP, PAFAH1B1, THBS2" 183 140 12983 1.520257611 1 0.993997678 99.9996114
GOTERM_MF_FAT GO:0001871~pattern binding 3 1.369863014 0.639030955 "APP, PAFAH1B1, THBS2" 183 154 12983 1.382052374 1 0.99701717 99.99994155
GOTERM_MF_FAT GO:0030247~polysaccharide binding 3 1.369863014 0.639030955 "APP, PAFAH1B1, THBS2" 183 154 12983 1.382052374 1 0.99701717 99.99994155

Annotation Cluster 65 Enrichment Score: 0.2705763808969452
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0042802~identical protein binding 12 5.479452055 0.286607428 "APP, TP53I3, IMPA1, NRBP1, PFKL, BAX, STXBP1, FHL2, PAFAH1B1, QPRT, ACP1, TRADD" 183 640 12983 1.33022541 1 0.965317711 99.1408209
GOTERM_MF_FAT GO:0042803~protein homodimerization activity 5 2.283105023 0.692836845 "TP53I3, NRBP1, BAX, PAFAH1B1, QPRT" 183 334 12983 1.062056215 1 0.998702586 99.99999398
GOTERM_MF_FAT GO:0046983~protein dimerization activity 7 3.196347032 0.776877314 "PEF1, TP53I3, NRBP1, BAX, PPP2CA, PAFAH1B1, QPRT" 183 542 12983 0.916268425 1 0.999704477 99.99999993

Annotation Cluster 66 Enrichment Score: 0.2637249212828502
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0001503~ossification 3 1.369863014 0.479417014 "MINPP1, HSPG2, FHL2" 190 115 13528 1.857391304 1 0.979301962 99.99819026
GOTERM_BP_FAT GO:0060348~bone development 3 1.369863014 0.515015331 "MINPP1, HSPG2, FHL2" 190 123 13528 1.736585366 1 0.983891059 99.99944659
GOTERM_BP_FAT GO:0001501~skeletal system development 5 2.283105023 0.655075921 "MINPP1, HSPG2, FHL2, COL12A1, PRDX1" 190 319 13528 1.115987461 1 0.995909066 99.99999815

Annotation Cluster 67 Enrichment Score: 0.25774024212189034
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0043523~regulation of neuron apoptosis 3 1.369863014 0.358946661 "GPX1, BAX, RASA1" 190 90 13528 2.373333333 1 0.951520929 99.94113696
GOTERM_BP_FAT GO:0048514~blood vessel morphogenesis 4 1.826484018 0.566110391 "GPX1, BAX, ERAP1, RASA1" 190 211 13528 1.349763033 1 0.989767601 99.99991404
GOTERM_BP_FAT GO:0001568~blood vessel development 4 1.826484018 0.669043834 "GPX1, BAX, ERAP1, RASA1" 190 245 13528 1.16244898 1 0.996507923 99.99999907
GOTERM_BP_FAT GO:0001944~vasculature development 4 1.826484018 0.684941396 "GPX1, BAX, ERAP1, RASA1" 190 251 13528 1.134661355 1 0.997073173 99.99999959

Annotation Cluster 68 Enrichment Score: 0.2555276452556588
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_CC_FAT	GO:0005764~lysosome	4	1.826484018	0.515805422	"PLEKHF1, GM2A, AP3M1, VPS4B"	168	211	12782	1.442338073	1	0.877172184	99.99261768
GOTERM_CC_FAT	GO:0000323~lytic vacuole	4	1.826484018	0.515805422	"PLEKHF1, GM2A, AP3M1, VPS4B"	168	211	12782	1.442338073	1	0.877172184	99.99261768
GOTERM_CC_FAT	GO:0005773~vacuole	4	1.826484018	0.643346967	"PLEKHF1, GM2A, AP3M1, VPS4B"	168	252	12782	1.207671958	1	0.94593064	99.99986618

Annotation Cluster 69	Enrichment Score: 0.24683512356403006
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0035258~steroid hormone receptor binding	3	1.369863014	0.099011507	"YWHAH, FHL2, CALR"	183	38	12983	5.600949094	1	0.808479102	76.9746994
GOTERM_CC_FAT	GO:0030424~axon	5	2.283105023	0.154742327	"MAPK1, APP, MYO6, PEBP1, FKBP15"	168	159	12782	2.392557652	1	0.502780059	88.97783759
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	3	1.369863014	0.164182204	"APP, MYO6, PAFAH1B1"	190	52	13528	4.107692308	1	0.817906882	95.02113573
GOTERM_BP_FAT	GO:0030518~steroid hormone receptor signaling pathway	3	1.369863014	0.194272725	"YWHAH, FHL2, CALR"	190	58	13528	3.682758621	1	0.846197558	97.30368385
GOTERM_BP_FAT	GO:0030522~intracellular receptor-mediated signaling pathway	3	1.369863014	0.281981319	"YWHAH, FHL2, CALR"	190	75	13528	2.848	1	0.920980242	99.60778345
GOTERM_CC_FAT	GO:0043005~neuron projection	7	3.196347032	0.289783045	"MAPK1, APP, MYO6, NCDN, PEBP1, FKBP15, PAFAH1B1"	168	342	12782	1.557261209	1	0.661619797	98.87644211
GOTERM_MF_FAT	GO:0035257~nuclear hormone receptor binding	3	1.369863014	0.293697134	"YWHAH, FHL2, CALR"	183	77	12983	2.764104748	1	0.966030124	99.25357369
GOTERM_BP_FAT	GO:0006417~regulation of translation	4	1.826484018	0.299759022	"MAPK1, EIF4G3, APP, CALR"	190	137	13528	2.078832117	1	0.929577475	99.74213385
GOTERM_BP_FAT	GO:0010608~posttranscriptional regulation of gene expression	5	2.283105023	0.339802651	"MAPK1, EIF4G3, APP, SND1, CALR"	190	211	13528	1.687203791	1	0.944329455	99.90370312
GOTERM_MF_FAT	GO:0051427~hormone receptor binding	3	1.369863014	0.350345388	"YWHAH, FHL2, CALR"	183	88	12983	2.418591654	1	0.97320817	99.77008341
GOTERM_CC_FAT	GO:0044463~cell projection part	5	2.283105023	0.366009954	"MAPK1, APP, MYO6, PEBP1, MAPRE1"	168	234	12782	1.625712251	1	0.751759438	99.74661485
GOTERM_CC_FAT	GO:0043025~cell soma	4	1.826484018	0.377770328	"MAPK1, MYO6, PEBP1, PAFAH1B1"	168	168	12782	1.811507937	1	0.761675213	99.80179626
GOTERM_BP_FAT	GO:0007268~synaptic transmission	6	2.739726027	0.403161708	"MAPK1, APP, MYO6, PEBP1, PAFAH1B1, ALDH9A1"	190	298	13528	1.433557047	1	0.965559233	99.9821899
GOTERM_BP_FAT	GO:0007610~behavior	8	3.652968037	0.483820208	"MAPK1, APP, MYO6, GM2A, PEBP1, PAFAH1B1, ASL, RIC8A"	190	469	13528	1.214498934	1	0.980029818	99.99842997
GOTERM_BP_FAT	GO:0007626~locomotory behavior	5	2.283105023	0.536793009	"MAPK1, APP, MYO6, PAFAH1B1, ASL"	190	274	13528	1.299270073	1	0.986400632	99.99974338
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	6	2.739726027	0.541923077	"MAPK1, APP, MYO6, PEBP1, PAFAH1B1, ALDH9A1"	190	350	13528	1.220571429	1	0.987023666	99.999787
GOTERM_BP_FAT	GO:0031175~neuron projection development	4	1.826484018	0.69775233	"APP, MYO6, STXBP1, PAFAH1B1"	190	256	13528	1.1125	1	0.997487098	99.9999998
GOTERM_BP_FAT	GO:0048666~neuron development	5	2.283105023	0.701281611	"APP, MYO6, STXBP1, PRKCI, PAFAH1B1"	190	339	13528	1.050147493	1	0.997538985	99.99999983
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	8	3.652968037	0.738894249	"MAPK1, APP, MYO6, FAT1, TXN, PEBP1, PAFAH1B1, ALDH9A1"	190	600	13528	0.949333333	1	0.998630877	99.99999998
GOTERM_BP_FAT	GO:0045596~negative regulation of cell differentiation	3	1.369863014	0.807954959	"MAPK1, YWHAH, CALR"	190	216	13528	0.988888889	1	0.999545759	100
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	7	3.196347032	0.89166894	"MAPK1, APP, YWHAH, MYO6, FHL2, PEBP1, CALR"	190	644	13528	0.773913043	1	0.999947059	100

GOTERM_BP_FAT GO:0030030~cell projection organization 4 1.826484018 0.891758548 "APP, MYO6, STXBP1, PAFAH1B1" 190 368 13528 0.773913043 1 0.999945785 100

GOTERM_BP_FAT GO:0010604~positive regulation of macromolecule metabolic process 9 4.109589041 0.917837157 "MAPK1, APP, YWHAH, MYO6, TRIM32, FHL2, NRD1, CALR, CUL1" 190 857 13528 0.747724621 1 0.999981333 100

GOTERM_BP_FAT GO:0031328~positive regulation of cellular biosynthetic process 7 3.196347032 0.921690358 "MAPK1, APP, PLA2G4A, YWHAH, MYO6, FHL2, CALR" 190 685 13528 0.727591241 1 0.999983911 100

GOTERM_BP_FAT GO:0009891~positive regulation of biosynthetic process 7 3.196347032 0.927812997 "MAPK1, APP, PLA2G4A, YWHAH, MYO6, FHL2, CALR" 190 695 13528 0.717122302 1 0.999988337 100

GOTERM_BP_FAT GO:0008284~positive regulation of cell proliferation 4 1.826484018 0.931987868 "MAPK1, PLA2G4A, CALR, PNP" 190 414 13528 0.687922705 1 0.999990094 100

GOTERM_BP_FAT "GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process" 6 2.739726027 0.940289058 "MAPK1, APP, YWHAH, MYO6, FHL2, CALR" 190 624 13528 0.684615385 1 0.999993752 100

GOTERM_BP_FAT GO:0050890~cognition 9 4.109589041 0.94432949 "MAPK1, GPX1, APP, CASP3, MYO6, GM2A, PAFAH1B1, WDR1, RIC8A" 190 909 13528 0.704950495 1 0.999995047 100

GOTERM_BP_FAT GO:0010557~positive regulation of macromolecule biosynthetic process 6 2.739726027 0.954433319 "MAPK1, APP, YWHAH, MYO6, FHL2, CALR" 190 654 13528 0.653211009 1 0.999997645 100

GOTERM_BP_FAT GO:0045941~positive regulation of transcription 5 2.283105023 0.958180539 "MAPK1, APP, YWHAH, MYO6, FHL2" 190 564 13528 0.631205674 1 0.999998298 100

GOTERM_BP_FAT GO:0010628~positive regulation of gene expression 5 2.283105023 0.964667684 "MAPK1, APP, YWHAH, MYO6, FHL2" 190 581 13528 0.612736661 1 0.999999095 100

GOTERM_BP_FAT GO:0050877~neurological system process 11 5.02283105 0.978139276 "MAPK1, GPX1, APP, CASP3, MYO6, GM2A, PEBP1, PAFAH1B1, WDR1, ALDH9A1, RIC8A" 190 1210 13528 0.647272727 1 0.999999849 100

GOTERM_BP_FAT "GO:0045893~positive regulation of transcription, DNA-dependent" 3 1.369863014 0.991369333 "APP, MYO6, FHL2" 190 477 13528 0.447798742 1 0.999999996 100

GOTERM_BP_FAT GO:0051254~positive regulation of RNA metabolic process 3 1.369863014 0.991796596 "APP, MYO6, FHL2" 190 481 13528 0.444074844 1 0.999999997 100

GOTERM_BP_FAT GO:0006357~regulation of transcription from RNA polymerase II promoter 5 2.283105023 0.992353901 "APP, MYO6, FHL2, NEDD8, CALR" 190 727 13528 0.489683631 1 0.999999997 100

GOTERM_BP_FAT GO:0051252~regulation of RNA metabolic process 8 3.652968037 0.999998622 "APP, MYO6, YWHAQ, FHL2, NEDD8, NFKB2, CALR, RASA1" 190 1813 13528 0.3141754 1 1 100

GOTERM_BP_FAT "GO:0006355~regulation of transcription, DNA-dependent" 7 3.196347032 0.999999535 "APP, MYO6, YWHAQ, FHL2, NEDD8, NFKB2, CALR" 190 1773 13528 0.281105471 1 1 100

GOTERM_BP_FAT GO:0045449~regulation of transcription 13 5.936073059 0.999999903 "MAPK1, APP, YWHAH, MYO6, PTGES2, ASCC3, SND1, PPP2CA, YWHAQ, FHL2, NEDD8, NFKB2, CALR" 190 2601 13528 0.35586313 1 1 100

Annotation Cluster 70 Enrichment Score: 0.24148493234136614

Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR

GOTERM_BP_FAT GO:0042113~B cell activation 3 1.369863014 0.287164704 "SWAP70, IGBP1, BAX" 190 76 13528 2.810526316 1 0.923368725 99.65254996

GOTERM_BP_FAT GO:0001775~cell activation 5 2.283105023 0.571901831 "SWAP70, IGBP1, BAX, STXBP1, NFKB2" 190 287 13528 1.240418118 1 0.990185955 99.99993134

GOTERM_BP_FAT GO:0046649~lymphocyte activation 3 1.369863014 0.76995121 "SWAP70, IGBP1, BAX" 190 199 13528 1.073366834 1 0.999124746 100

GOTERM_BP_FAT	GO:0045321~leukocyte activation	3	1.369863014	0.855351299	"SWAP70, IGBP1, BAX"	190	242	13528	0.882644628	1	0.999843316	100

Annotation Cluster 71	Enrichment Score: 0.2149198811099221
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	3	1.369863014	0.164182204	"APP, MYO6, PAFAH1B1"	190	52	13528	4.107692308	1	0.817906882	95.02113573
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	7	3.196347032	0.379966613	"APP, CFL1, STXBP1, PRKCI, PAFAH1B1, CLASP1, CAP1"	190	356	13528	1.4	1	0.959732104	99.96629881
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	5	2.283105023	0.473153691	"APP, DNM1L, BAX, STXBP1, PAFAH1B1"	190	256	13528	1.390625	1	0.978718845	99.99778946
GOTERM_BP_FAT	GO:0030182~neuron differentiation	7	3.196347032	0.577415587	"APP, TUBB, MYO6, TUBB2A, STXBP1, PRKCI, PAFAH1B1"	190	438	13528	1.137899543	1	0.990707203	99.99994473
GOTERM_BP_FAT	GO:0031175~neuron projection development	4	1.826484018	0.69775233	"APP, MYO6, STXBP1, PAFAH1B1"	190	256	13528	1.1125	1	0.997487098	99.9999998
GOTERM_BP_FAT	GO:0048666~neuron development	5	2.283105023	0.701281611	"APP, MYO6, STXBP1, PRKCI, PAFAH1B1"	190	339	13528	1.050147493	1	0.997538985	99.99999983
GOTERM_BP_FAT	GO:0007409~axonogenesis	3	1.369863014	0.755057757	"APP, STXBP1, PAFAH1B1"	190	193	13528	1.106735751	1	0.998933954	99.99999999
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	3	1.369863014	0.793031548	"APP, STXBP1, PAFAH1B1"	190	209	13528	1.022009569	1	0.999409928	100
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	3	1.369863014	0.801679633	"APP, STXBP1, PAFAH1B1"	190	213	13528	1.002816901	1	0.999495302	100
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	3	1.369863014	0.858517692	"APP, STXBP1, PAFAH1B1"	190	244	13528	0.875409836	1	0.999854644	100
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	3	1.369863014	0.860077147	"APP, STXBP1, PAFAH1B1"	190	245	13528	0.871836735	1	0.999854606	100
GOTERM_BP_FAT	GO:0030030~cell projection organization	4	1.826484018	0.891758548	"APP, MYO6, STXBP1, PAFAH1B1"	190	368	13528	0.773913043	1	0.999945785	100

Annotation Cluster 72	Enrichment Score: 0.21065394118510178
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0050863~regulation of T cell activation	3	1.369863014	0.488465436	"CASP3, AP3D1, PNP"	190	117	13528	1.825641026	1	0.98050559	99.9986503
GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	3	1.369863014	0.615501505	"CASP3, AP3D1, PNP"	190	148	13528	1.443243243	1	0.993928312	99.99998861
GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	3	1.369863014	0.677510205	"CASP3, AP3D1, PNP"	190	166	13528	1.286746988	1	0.996825883	99.9999994
GOTERM_BP_FAT	GO:0050865~regulation of cell activation	3	1.369863014	0.705351244	"CASP3, AP3D1, PNP"	190	175	13528	1.220571429	1	0.997657169	99.99999987

Annotation Cluster 73	Enrichment Score: 0.17571165197619484
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	6	2.739726027	0.471992516	"DCTD, SRM, SPR, QPRT, ASL, PNP"	190	325	13528	1.314461538	1	0.979057925	99.99770654
GOTERM_BP_FAT	GO:0009165~nucleotide biosynthetic process	3	1.369863014	0.736644469	"DCTD, QPRT, PNP"	190	186	13528	1.148387097	1	0.99860073	99.99999998
GOTERM_BP_FAT	"GO:0034404~nucleobase, nucleoside and nucleotide biosynthetic process"	3	1.369863014	0.755057757	"DCTD, QPRT, PNP"	190	193	13528	1.106735751	1	0.998933954	99.99999999

GOTERM_BP_FAT "GO:0034654~nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process" 3 1.369863014 0.755057757 "DCTD, QPRT, PNP" 190 193 13528 1.106735751 1 0.998933954 99.99999999

Annotation Cluster 74 Enrichment Score: 0.13078196872173417
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0010627~regulation of protein kinase cascade 5 2.283105023 0.464883053 "GPX1, PPP2CA, PEBP1, PRDX1, TRADD" 190 249 13528 1.429718876 1 0.977943474 99.9971315
GOTERM_BP_FAT GO:0009967~positive regulation of signal transduction 3 1.369863014 0.920643831 "GPX1, PEBP1, TRADD" 190 295 13528 0.724067797 1 0.999983463 100
GOTERM_BP_FAT GO:0010647~positive regulation of cell communication 3 1.369863014 0.946713854 "GPX1, PEBP1, TRADD" 190 329 13528 0.649240122 1 0.999995746 100

Annotation Cluster 75 Enrichment Score: 0.0871323023389306
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0033554~cellular response to stress 10 4.566210046 0.394119892 "MAPK1, GPX1, CASP3, MYO6, VCP, BAX, ERO1L, HSPA5, MYOF, PRDX1" 190 566 13528 1.25795053 1 0.96352975 99.97709678
GOTERM_BP_FAT GO:0006974~response to DNA damage stimulus 5 2.283105023 0.769336127 "MAPK1, CASP3, MYO6, VCP, BAX" 190 373 13528 0.954423592 1 0.999150554 100
GOTERM_CC_FAT GO:0005730~nucleolus 4 1.826484018 0.99537559 "MAPK1, CASP3, VCP, ZNF259" 168 698 12782 0.436007641 1 0.999996812 100
GOTERM_BP_FAT GO:0007600~sensory perception 5 2.283105023 0.996971782 "MAPK1, GPX1, CASP3, MYO6, WDR1" 190 810 13528 0.439506173 1 1 100
GOTERM_CC_FAT GO:0005654~nucleoplasm 5 2.283105023 0.997508368 "MAPK1, CASP3, MYO6, NFKB2, CUL1" 168 882 12782 0.431311413 1 0.999999158 100
GOTERM_CC_FAT GO:0031981~nuclear lumen 8 3.652968037 0.999712916 "MAPK1, CASP3, MYO6, VCP, CFL1, ZNF259, NFKB2, CUL1" 168 1450 12782 0.419770115 1 0.99999999 100

Annotation Cluster 76 Enrichment Score: 0.04934369649233727
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_MF_FAT GO:0003713~transcription coactivator activity 3 1.369863014 0.805407821 "TRIM32, FHL2, NFKB2" 183 214 12983 0.994561054 1 0.999805203 99.99999999
GOTERM_MF_FAT GO:0016563~transcription activator activity 5 2.283105023 0.831169589 "YWHAH, PTGES2, TRIM32, FHL2, NFKB2" 183 410 12983 0.865187258 1 0.999884208 100
GOTERM_MF_FAT GO:0008134~transcription factor binding 6 2.739726027 0.850988275 "DIP2B, SKIV2L, SND1, TRIM32, FHL2, NFKB2" 183 513 12983 0.829770236 1 0.999923206 100
GOTERM_MF_FAT GO:0003712~transcription cofactor activity 4 1.826484018 0.887797262 "SND1, TRIM32, FHL2, NFKB2" 183 363 12983 0.781766999 1 0.999978794 100
GOTERM_MF_FAT GO:0030528~transcription regulator activity 7 3.196347032 0.999988386 "YWHAH, PTGES2, SND1, TRIM32, FHL2, NFKB2, CALR" 183 1512 12983 0.328450718 1 1 100
GOTERM_BP_FAT GO:0006350~transcription 4 1.826484018 1 "ASCC3, SND1, FHL2, NFKB2" 190 2101 13528 0.135554498 1 1 100

Annotation Cluster 77 Enrichment Score: 0.033287695325948094
Category Term Count % PValue Genes List Total Pop Hits Pop Total Fold Enrichment Bonferroni Benjamini FDR
GOTERM_BP_FAT GO:0006812~cation transport 6 2.739726027 0.890283989 "SRI, NUDT9, SLC12A4, TPT1, VPS4B, SLC4A7" 190 553 13528 0.772513562 1 0.999945509 100
GOTERM_BP_FAT GO:0030001~metal ion transport 5 2.283105023 0.893746 "SRI, SLC12A4, TPT1, VPS4B, SLC4A7" 190 465 13528 0.765591398 1 0.999948654 100

GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	3	1.369863014	0.939325651	"SLC12A4, VPS4B, SLC4A7"	190	318	13528	0.671698113	1	0.999993522	100
GOTERM_BP_FAT	GO:0006811~ion transport	6	2.739726027	0.984669221	"SRI, NUDT9, SLC12A4, TPT1, VPS4B, SLC4A7"	190	768	13528	0.55625	1	0.999999962	100

Annotation Cluster 78	Enrichment Score: 0.024030024077235285
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	3	1.369863014	0.924666059	"HSPG2, COL12A1, CALR"	168	320	12782	0.71328125	1	0.998479865	100
GOTERM_CC_FAT	GO:0031012~extracellular matrix	3	1.369863014	0.942741633	"HSPG2, COL12A1, CALR"	168	345	12782	0.661594203	1	0.999183397	100
GOTERM_CC_FAT	GO:0044421~extracellular region part	8	3.652968037	0.971700272	"COPA, TPT1, RNH1, HSPG2, PEBP1, COL12A1, CALR, RNPEP"	168	960	12782	0.634027778	1	0.99980508	100

Annotation Cluster 79	Enrichment Score: 0.011152891974420332
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_MF_FAT	GO:0046872~metal ion binding	49	22.37442922	0.956138149	"COPA, IMPA1, HMOX2, APP, TP53I3, NT5C2, TPT1, ERAP1, MICAL1, TBC1D9B, PFKL, PRKCI, PFKP, NRD1, VAT1, TRIM32, RNPEP, SRI, ARFGAP3, FHL3, FHL2, CALR, ADPRHL2, PEF1, ANXA7, NUDT9, FAT1, PPP2CA, SLC4A7, IDH1, GLO1, HSPA5, EHD1, THBS2, DCTD, NPLOC4, SLC12A4, S100A10, TRIM26, CAPN2, CSRP2, PLEKHF1, ITPA, HSP90B1, PLA2G4A, HEBP1, ZNF259, SUMF1, NLN"	183	4140	12983	0.839691402	1	0.999999751	100
GOTERM_MF_FAT	GO:0043167~ion binding	50	22.83105023	0.961149581	"COPA, IMPA1, PNP, HMOX2, TP53I3, APP, NT5C2, TPT1, ERAP1, MICAL1, TBC1D9B, PFKL, PRKCI, PFKP, NRD1, VAT1, TRIM32, RNPEP, SRI, ARFGAP3, FHL3, FHL2, CALR, ANXA7, PEF1, ADPRHL2, NUDT9, PPP2CA, FAT1, SLC4A7, IDH1, GLO1, HSPA5, EHD1, THBS2, DCTD, NPLOC4, SLC12A4, S100A10, TRIM26, CAPN2, CSRP2, PLEKHF1, ITPA, HSP90B1, PLA2G4A, HEBP1, SUMF1, ZNF259, NLN"	183	4241	12983	0.836422485	1	0.999999835	100
GOTERM_MF_FAT	GO:0043169~cation binding	49	22.37442922	0.963553381	"COPA, IMPA1, HMOX2, APP, TP53I3, NT5C2, TPT1, ERAP1, MICAL1, TBC1D9B, PFKL, PRKCI, PFKP, NRD1, VAT1, TRIM32, RNPEP, SRI, ARFGAP3, FHL3, FHL2, CALR, ADPRHL2, PEF1, ANXA7, NUDT9, FAT1, PPP2CA, SLC4A7, IDH1, GLO1, HSPA5, EHD1, THBS2, DCTD, NPLOC4, SLC12A4, S100A10, TRIM26, CAPN2, CSRP2, PLEKHF1, ITPA, HSP90B1, PLA2G4A, HEBP1, ZNF259, SUMF1, NLN"	183	4179	12983	0.831855086	1	0.999999855	100
GOTERM_MF_FAT	GO:0008270~zinc ion binding	21	9.589041096	0.996017268	"DCTD, NPLOC4, ARFGAP3, PRKCI, FHL3, FHL2, NRD1, TRIM26, CSRP2, CALR, VAT1, PLEKHF1, TP53I3, APP, TRIM32, ZNF259, ERAP1, MICAL1, NLN, GLO1, RNPEP"	183	2311	12983	0.644678693	1	1	100
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	26	11.87214612	0.997197694	"ARFGAP3, FHL3, FHL2, CALR, HMOX2, APP, TP53I3, NUDT9, PPP2CA, IDH1, ERAP1, MICAL1, GLO1, DCTD, NPLOC4, PRKCI, TRIM26, NRD1, CSRP2, VAT1, PLEKHF1, TRIM32, HEBP1, ZNF259, NLN, RNPEP"	183	2785	12983	0.662326476	1	1	100

Supplemental Table S1: Complete list of transcripts
(TPM values determined by RNAseq)

Gene_ID	Ctrl 1	Ctrl 2	RDEB 1	RDEB 2		Gene symbol
ENSG00000000003	20.2902	15.7178	11.3918	8.96712	ENSG00000000003	TSPAN6
ENSG00000000005	0	0	0	0.0480926	ENSG00000000005	TNMD
ENSG00000000419	40.722	28.8613	29.6138	16.5946	ENSG00000000419	DPM1
ENSG00000000457	4.8933	5.69116	5.45957	5.50523	ENSG00000000457	SCYL3
ENSG00000000460	4.12165	9.44353	4.52266	5.60594	ENSG00000000460	C1orf112
ENSG00000000938	0.270948	0.352427	0.58923	0.493015	ENSG00000000938	FGR
ENSG00000000971	1.27821	7.0824	10.5073	20.7521	ENSG00000000971	CFH
ENSG00000001036	26.4986	26.8745	22.08	27.2024	ENSG00000001036	FUCA2
ENSG00000001084	43.7965	81.5388	92.0273	42.6146	ENSG00000001084	GCLC
ENSG00000001167	5.58118	6.95661	7.40318	10.6932	ENSG00000001167	NFYA
ENSG00000001460	9.90991	18.3708	11.1664	11.7658	ENSG00000001460	STPG1
ENSG00000001461	39.9513	36.5145	26.2763	30.7439	ENSG00000001461	NIPAL3
ENSG00000001497	11.7884	14.1561	16.2133	12.7677	ENSG00000001497	LAS1L
ENSG00000001561	0.831428	0.290096	0.140971	0.203544	ENSG00000001561	ENPP4
ENSG00000001617	61.4966	136.955	94.4597	46.8156	ENSG00000001617	SEMA3F
ENSG00000001626	9.92211	28.0115	24.3632	44.6324	ENSG00000001626	CFTR
ENSG00000001629	28.6627	47.2531	39.5246	48.549	ENSG00000001629	ANKIB1
ENSG00000001630	219.375	171.292	67.0218	86.8908	ENSG00000001630	CYP51A1
ENSG00000001631	17.9403	29.5672	35.4802	30.8089	ENSG00000001631	KRIT1
ENSG00000002016	9.20713	17.1667	15.2593	13.9574	ENSG00000002016	RAD52
ENSG00000002079	6.25	8.50481	1.91211	3.50863	ENSG00000002079	MYH16
ENSG00000002330	33.9178	35.8357	24.2854	18.3647	ENSG00000002330	BAD
ENSG00000002549	21.0791	28.2794	23.5276	24.7398	ENSG00000002549	LAP3
ENSG00000002586	108.808	111.677	42.3487	76.6503	ENSG00000002586	CD99
ENSG00000002587	10.4722	8.03751	1.14604	3.67416	ENSG00000002587	HS3ST1
ENSG00000002726	3.23514	1.80306	1.73943	6.4617	ENSG00000002726	AOC1
ENSG00000002745	0.0520782	0.0801409	0.060538	0.0954722	ENSG00000002745	WNT16
ENSG00000002746	0.808743	2.87273	5.22832	4.19984	ENSG00000002746	HECW1
ENSG00000002822	25.5008	30.1969	30.6467	48.2362	ENSG00000002822	MAD1L1
ENSG00000002834	62.1713	50.4296	32.4188	60.8452	ENSG00000002834	LASP1
ENSG00000002919	8.84854	10.9491	13.4545	10.0877	ENSG00000002919	SNX11
ENSG00000002933	0.997422	27.0872	4.45502	15.0366	ENSG00000002933	TMEM176A
ENSG00000003056	88.4783	107.208	84.5323	50.8796	ENSG00000003056	M6PR
ENSG00000003096	0.954695	1.9197	4.21233	2.54301	ENSG00000003096	KLHL13
ENSG00000003137	0.442761	1.41264	1.43813	4.55657	ENSG00000003137	CYP26B1
ENSG00000003147	9.45251	6.25889	7.36729	6.0676	ENSG00000003147	ICA1
ENSG00000003249	6.18426	1.83093	1.90232	1.83966	ENSG00000003249	DBNDD1
ENSG00000003393	21.7429	26.8576	23.9447	25.6029	ENSG00000003393	ALS2
ENSG00000003400	9.45582	12.0054	12.3895	17.4737	ENSG00000003400	CASP10
ENSG00000003402	153.153	105.687	108.054	137.585	ENSG00000003402	CFLAR
ENSG00000003436	16.8075	32.1493	29.4809	67.7042	ENSG00000003436	TFPI
ENSG00000003509	9.99706	11.559	15.0883	10.3483	ENSG00000003509	NDUFAF7
ENSG00000003756	82.5946	124.455	116.838	117.009	ENSG00000003756	RBM5
ENSG00000003987	3.08395	4.77971	4.43415	7.24408	ENSG00000003987	MTMR7
ENSG00000003989	0.932257	0.5907	0.538758	1.56042	ENSG00000003989	SLC7A2
ENSG00000004059	73.9834	60.9557	49.9771	27.1474	ENSG00000004059	ARF5
ENSG00000004139	0.745595	0.803426	1.03564	2.26124	ENSG00000004139	SARM1
ENSG00000004142	28.74	18.9717	20.2268	12.5321	ENSG00000004142	POLDIP2
ENSG00000004399	3.54283	5.31761	6.74125	48.1254	ENSG00000004399	PLXND1
ENSG00000004455	74.1658	78.7901	109.326	67.2295	ENSG00000004455	AK2

ENSG00000004468	1.2464	2.93749	3.21698	5.02832	ENSG00000004468	CD38
ENSG00000004478	76.5425	67.8787	53.2309	44.6677	ENSG00000004478	FKBP4
ENSG00000004487	45.0588	48.4725	43.3566	42.4332	ENSG00000004487	KDM1A
ENSG00000004534	33.2521	64.655	61.2386	92.1967	ENSG00000004534	RBM6
ENSG00000004660	1.48656	3.68134	3.52823	2.79092	ENSG00000004660	CAMKK1
ENSG00000004700	23.6051	39.9054	21.786	28.4331	ENSG00000004700	RECQL
ENSG00000004766	32.7363	26.4115	26.6969	26.795	ENSG00000004766	VPS50
ENSG00000004776	0.508458	0.497598	0.965272	1.60552	ENSG00000004776	HSPB6
ENSG00000004777	1.48899	4.58798	1.28443	8.31762	ENSG00000004777	ARHGAP33
ENSG00000004779	49.361	36.2699	29.0602	18.5714	ENSG00000004779	NDUFAB1
ENSG00000004799	0.758961	0.334563	0.793412	0.926789	ENSG00000004799	PDK4
ENSG00000004809	2.96693	5.77804	4.80843	8.13981	ENSG00000004809	SLC22A16
ENSG00000004838	0.563232	1.1041	0.691542	1.8988	ENSG00000004838	ZMYND10
ENSG00000004846	1.50814	3.03445	2.78287	3.87664	ENSG00000004846	ABCB5
ENSG00000004848	0.148235	0.351233	0.375261	0.426835	ENSG00000004848	ARX
ENSG00000004864	12.9007	17.6753	16.8218	14.0564	ENSG00000004864	SLC25A13
ENSG00000004866	19.6499	22.7425	16.9646	23.0747	ENSG00000004866	ST7
ENSG00000004897	33.8893	47.8515	32.5425	54.0208	ENSG00000004897	CDC27
ENSG00000004939	0.419987	0.289248	0.650615	1.22317	ENSG00000004939	SLC4A1
ENSG00000004948	0.289155	0.257953	0.458532	0.630803	ENSG00000004948	CALCR
ENSG00000004961	9.45511	7.33272	7.95671	5.58615	ENSG00000004961	HCCS
ENSG00000004975	25.7746	25.7169	23.294	20.6977	ENSG00000004975	DVL2
ENSG00000005001	151.678	6.93701	9.36655	26.1349	ENSG00000005001	PRSS22
ENSG00000005007	46.7398	65.8605	56.8521	42.693	ENSG00000005007	UPF1
ENSG00000005020	23.4874	25.2295	20.2821	19.8259	ENSG00000005020	SKAP2
ENSG00000005022	49.1829	86.2521	63.925	33.1819	ENSG00000005022	SLC25A5
ENSG00000005059	6.37602	12.9235	4.92775	4.78787	ENSG00000005059	MCUB
ENSG00000005073	0.228994	0.338251	0.784658	0.874629	ENSG00000005073	HOXA11
ENSG00000005075	26.7152	13.2061	15.484	10.5145	ENSG00000005075	POLR2J
ENSG00000005100	5.19435	5.7346	8.53301	6.88931	ENSG00000005100	DHX33
ENSG00000005102	0.201029	0.159583	0.0537869	0.783716	ENSG00000005102	MEOX1
ENSG00000005108	0.280253	0.262267	0.237083	1.22525	ENSG00000005108	THSD7A
ENSG00000005156	15.9942	29.377	23.274	25.3317	ENSG00000005156	LIG3
ENSG00000005175	17.5209	16.4943	17.0301	17.6659	ENSG00000005175	RPAP3
ENSG00000005187	10.7681	31.4287	29.0738	40.8779	ENSG00000005187	ACSM3
ENSG00000005189	4.2076	8.0061	4.03923	7.5863	ENSG00000005189	REXO5
ENSG00000005194	24.4453	25.5393	29.496	21.1518	ENSG00000005194	CIAPIN1
ENSG00000005238	34.5577	20.3474	15.1752	15.888	ENSG00000005238	FAM214B
ENSG00000005243	13.7563	9.04312	15.7567	18.108	ENSG00000005243	COPZ2
ENSG00000005249	0.188034	0.320829	0.227135	0.372328	ENSG00000005249	PRKAR2B
ENSG00000005302	10.898	12.2096	18.4735	17.4885	ENSG00000005302	MSL3
ENSG00000005339	12.9002	20.1714	23.9823	29.4091	ENSG00000005339	CREBBP
ENSG00000005379	0.126463	2.22221	0.827608	2.68022	ENSG00000005379	TSPOAP1
ENSG00000005381	0.242193	0.415618	0.345134	0.788837	ENSG00000005381	MPO
ENSG00000005421	0.674019	0.959755	0.786993	0.947733	ENSG00000005421	PON1
ENSG00000005436	11.0961	12.7688	10.9754	9.71306	ENSG00000005436	GCFC2
ENSG00000005448	27.7281	45.5334	24.3813	22.6282	ENSG00000005448	WDR54
ENSG00000005469	11.81	13.098	11.3776	9.8988	ENSG00000005469	CROT
ENSG00000005471	1.56169	4.28941	3.24566	5.05309	ENSG00000005471	ABCB4
ENSG00000005483	31.5835	49.3637	43.8984	64.4928	ENSG00000005483	KMT2E
ENSG00000005486	15.3129	9.60571	16.0252	5.48187	ENSG00000005486	RHBDD2
ENSG00000005513	0.169445	0.137772	0.136001	0.257357	ENSG00000005513	SOX8
ENSG00000005700	19.9001	31.046	31.4559	34.7399	ENSG00000005700	IBTK
ENSG00000005801	28.2018	59.5522	60.4312	59.759	ENSG00000005801	ZNF195

ENSG00000005810	20.7434	42.027	48.1872	52.445	ENSG00000005810	MYCBP2
ENSG00000005812	17.0497	19.6743	20.5906	11.7735	ENSG00000005812	FBXL3
ENSG00000005844	1.13402	5.05524	2.81989	8.11751	ENSG00000005844	ITGAL
ENSG00000005882	9.02779	6.45419	7.8807	8.90499	ENSG00000005882	PDK2
ENSG00000005884	680.195	1240.42	814.21	568.769	ENSG00000005884	ITGA3
ENSG00000005889	13.6405	21.6314	21.1079	30.1124	ENSG00000005889	ZFX
ENSG00000005893	94.2741	92.4899	117.559	56.0519	ENSG00000005893	LAMP2
ENSG00000005955	20.8354	21.7184	41.7651	38.7559	ENSG00000005955	ZNF403
ENSG00000005961	0.19204	0.58594	0.475011	1.44017	ENSG00000005961	ITGA2B
ENSG00000005981	1.54855	3.28545	3.04543	5.64545	ENSG00000005981	ASB4
ENSG00000006007	31.728	31.9563	21.5405	13.2065	ENSG00000006007	GDE1
ENSG00000006015	31.0685	35.9274	27.0351	27.3364	ENSG00000006015	C19orf60
ENSG00000006016	3.88007	10.0194	10.2005	3.751	ENSG00000006016	CRLF1
ENSG00000006025	3.51829	11.6069	10.6237	6.43505	ENSG00000006025	OSBPL7
ENSG00000006042	19.0415	17.7291	16.9645	22.9275	ENSG00000006042	TMEM98
ENSG00000006047	1.16074	2.48547	2.129	2.90177	ENSG00000006047	YBX2
ENSG00000006059	0.211251	0.0590885	0.133061	0.0571692	ENSG00000006059	KRT33A
ENSG00000006071	0.133692	0.696164	1.0115	0.877158	ENSG00000006071	ABCC8
ENSG00000006074	0.178204	0.300311	0.232682	0.38965	ENSG00000006074	CCL18
ENSG00000006075	0	0.0374442	0	0.0851049	ENSG00000006075	CCL3
ENSG00000006114	11.3429	19.8217	20.2361	37.0168	ENSG00000006114	SYNRG
ENSG00000006116	0.321885	0.735146	0.794796	1.15106	ENSG00000006116	CACNG3
ENSG00000006118	88.5574	84.8587	85.774	74.46	ENSG00000006118	TMEM132A
ENSG00000006125	17.0859	36.1953	20.0672	29.0564	ENSG00000006125	AP2B1
ENSG00000006128	0.240306	0.416463	0.167297	0.840042	ENSG00000006128	TAC1
ENSG00000006194	17.431	18.2815	29.3454	10.6887	ENSG00000006194	ZNF263
ENSG00000006210	0.942411	2.78266	2.60482	2.92717	ENSG00000006210	CX3CL1
ENSG00000006282	32.4809	42.517	31.2093	27.0175	ENSG00000006282	SPATA20
ENSG00000006283	2.73695	5.10994	4.09231	7.00576	ENSG00000006283	CACNA1G
ENSG00000006327	282.693	316.656	165.397	87.2267	ENSG00000006327	TNFRSF12A
ENSG00000006377	0.381665	0.404025	0.48703	0.955646	ENSG00000006377	DLX6
ENSG00000006432	20.1583	11.4134	4.98496	7.93001	ENSG00000006432	MAP3K9
ENSG00000006451	28.1395	22.5299	21.5998	52.7229	ENSG00000006451	RALA
ENSG00000006453	43.0903	48.9858	34.1401	31.5268	ENSG00000006453	BAIAP2L1
ENSG00000006459	8.41675	11.1655	13.1696	11.6464	ENSG00000006459	KDM7A
ENSG00000006468	1.76745	6.83649	3.50693	31.1785	ENSG00000006468	ETV1
ENSG00000006530	8.06733	10.9772	10.652	9.3074	ENSG00000006530	AGK
ENSG00000006534	1.45084	2.32124	3.1526	6.13126	ENSG00000006534	ALDH3B1
ENSG00000006555	5.94407	6.25686	7.85795	3.88904	ENSG00000006555	TTC22
ENSG00000006576	11.5349	15.5865	9.09454	10.8364	ENSG00000006576	PHTF2
ENSG00000006606	0	0.0677545	0.06117	0.0756507	ENSG00000006606	CCL26
ENSG00000006607	19.5031	27.5286	33.6755	30.4022	ENSG00000006607	FARP2
ENSG00000006611	0.585439	0.390093	0.317355	0.595297	ENSG00000006611	USH1C
ENSG00000006625	30.8036	21.6126	19.3159	14.0133	ENSG00000006625	GGCT
ENSG00000006634	4.76658	21.5659	6.60257	8.19053	ENSG00000006634	DBF4
ENSG00000006638	1.60614	4.77191	4.43061	7.85297	ENSG00000006638	TBXA2R
ENSG00000006652	35.7407	39.5878	59.9623	30.6592	ENSG00000006652	IFRD1
ENSG00000006659	0.316148	0.89235	0.510911	1.68394	ENSG00000006659	LGALS14
ENSG00000006695	5.26542	7.22393	7.552	5.34886	ENSG00000006695	COX10
ENSG00000006704	6.98881	5.35987	7.35166	6.59465	ENSG00000006704	GTF2IRD1
ENSG00000006712	18.8207	17.5873	19.0112	16.6568	ENSG00000006712	PAF1
ENSG00000006715	32.4009	32.1644	35.137	36.7854	ENSG00000006715	VPS41
ENSG00000006740	0.82853	1.30761	1.18197	3.54207	ENSG00000006740	ARHGAP44
ENSG00000006744	49.9111	55.6863	68.3651	47.512	ENSG00000006744	ELAC2

ENSG00000006747	2.34141	6.94002	5.2191	10.7124	ENSG00000006747	SCIN
ENSG00000006756	17.0824	21.2437	19.29	22.0369	ENSG00000006756	ARSD
ENSG00000006757	5.57531	8.23409	9.37489	6.29279	ENSG00000006757	PNPLA4
ENSG00000006788	0.0338012	0.0321204	0.0189675	0.256085	ENSG00000006788	MYH13
ENSG00000006831	46.1025	73.1094	55.83	80.8031	ENSG00000006831	ADIPOR2
ENSG00000006837	6.18048	12.1323	12.6367	17.9891	ENSG00000006837	CDKL3
ENSG00000007001	0.518614	0.847393	0.930912	1.28896	ENSG00000007001	UPP2
ENSG00000007038	6.11019	7.80852	7.9309	6.49362	ENSG00000007038	PRSS21
ENSG00000007047	21.0274	24.5474	27.8705	31.9024	ENSG00000007047	MARK4
ENSG00000007062	0.419795	2.12777	2.71614	6.98431	ENSG00000007062	PROM1
ENSG00000007080	13.611	14.2215	15.415	22.8641	ENSG00000007080	CCDC124
ENSG00000007129	0.410807	0.393616	0.190741	0.625361	ENSG00000007129	CEACAM21
ENSG00000007168	365.463	258.839	240.121	191.756	ENSG00000007168	PAFAH1B1
ENSG00000007171	0	0.0249059	0.0112595	0.014216	ENSG00000007171	NOS2
ENSG00000007174	0.837814	2.14516	2.03921	3.50324	ENSG00000007174	DNAH9
ENSG00000007202	73.9326	76.7359	75.4405	64.7084	ENSG00000007202	KIAA0100
ENSG00000007216	0.0514112	0.10803	0.0719334	0.190137	ENSG00000007216	SLC13A2
ENSG00000007237	0.837422	0.641193	0.833155	5.12775	ENSG00000007237	GAS7
ENSG00000007255	3.15112	3.59252	5.59133	2.62498	ENSG00000007255	TRAPPC6A
ENSG00000007264	1.07028	4.24921	4.37802	9.23351	ENSG00000007264	MATK
ENSG00000007306	0.509504	0.316787	0.116813	0.510046	ENSG00000007306	CEACAM7
ENSG00000007312	1.15567	1.39672	1.30667	1.25842	ENSG00000007312	CD79B
ENSG00000007314	0.0067823	0.257702	0.506148	0.912743	ENSG00000007314	SCN4A
ENSG00000007341	21.8401	38.2494	32.9435	32.8993	ENSG00000007341	ST7L
ENSG00000007350	0.0638874	0	0.00939236	0.0355251	ENSG00000007350	TKTL1
ENSG00000007372	1.03666	0.768989	1.2746	2.44644	ENSG00000007372	PAX6
ENSG00000007376	13.9321	12.8525	16.8644	7.20828	ENSG00000007376	RPUSD1
ENSG00000007384	36.9313	42.1682	36.4759	33.1193	ENSG00000007384	RHBDF1
ENSG00000007392	22.1088	36.3635	41.1644	47.8752	ENSG00000007392	LUC7L
ENSG00000007402	0.482819	0.741927	0.717016	1.08767	ENSG00000007402	CACNA2D2
ENSG00000007516	2.06167	2.53338	2.08724	1.91828	ENSG00000007516	BAIAP3
ENSG00000007520	27.5493	19.3204	20.5418	13.482	ENSG00000007520	TSR3
ENSG00000007541	37.6106	41.8617	42.8947	32.844	ENSG00000007541	PIGQ
ENSG00000007545	9.18605	9.05863	12.4113	10.529	ENSG00000007545	CRAMP1
ENSG00000007866	16.8409	15.8251	17.9114	13.0754	ENSG00000007866	TEAD3
ENSG00000007908	0.564234	1.84684	1.12558	0.990902	ENSG00000007908	SELE
ENSG00000007923	23.0164	29.0847	33.0401	30.16	ENSG00000007923	DNAJC11
ENSG00000007933	1.4879	4.25724	5.49082	10.1312	ENSG00000007933	FMO3
ENSG00000007944	1.99435	2.03722	1.25535	3.45509	ENSG00000007944	MYLIP
ENSG00000007952	0.153218	0.35873	0.190778	0.4339	ENSG00000007952	NOX1
ENSG00000007968	0.778932	0.902842	0.657794	1.34668	ENSG00000007968	E2F2
ENSG00000008018	106.628	78.78	50.0271	45.8197	ENSG00000008018	PSMB1
ENSG00000008056	0.0518818	0.316956	0.240703	0.227977	ENSG00000008056	SYN1
ENSG00000008083	20.4964	27.5657	24.8434	25.2016	ENSG00000008083	JARID2
ENSG00000008086	3.59127	4.09873	3.51917	3.11861	ENSG00000008086	CDKL5
ENSG00000008118	3.17354	4.91722	1.76411	4.97214	ENSG00000008118	CAMK1G
ENSG00000008128	22.7919	27.8102	29.1686	26.4878	ENSG00000008128	CDK11A
ENSG00000008130	37.237	30.6781	46.946	28.9516	ENSG00000008130	NADK
ENSG00000008196	0.32935	0.384555	0.991271	0.742112	ENSG00000008196	TFAP2B
ENSG00000008197	0.0668671	0.125054	0.116482	0.287501	ENSG00000008197	TFAP2D
ENSG00000008226	1.54437	1.85542	2.52554	2.61998	ENSG00000008226	DLEC1
ENSG00000008256	19.484	15.2609	13.7116	26.6684	ENSG00000008256	CYTH3
ENSG00000008277	1.15915	2.68588	1.96901	2.85359	ENSG00000008277	ADAM22
ENSG00000008282	40.8071	96.4851	67.5995	38.0298	ENSG00000008282	SYPL1

ENSG00000008283	24.8398	26.4808	17.6657	10.8974	ENSG00000008283	CYB561
ENSG00000008294	67.892	71.2851	67.631	87.2318	ENSG00000008294	SPAG9
ENSG00000008300	0.521798	1.11423	1.85036	1.87467	ENSG00000008300	CELSR3
ENSG00000008311	11.3903	21.5351	5.99078	17.702	ENSG00000008311	AASS
ENSG00000008323	14.8405	10.9115	7.84095	9.13661	ENSG00000008323	PLEKHG6
ENSG00000008324	7.21138	8.03164	7.61917	6.38586	ENSG00000008324	SS18L2
ENSG00000008382	5.78097	10.5577	8.56371	7.89926	ENSG00000008382	MPND
ENSG00000008394	57.7172	72.8758	155.455	70.4006	ENSG00000008394	MGST1
ENSG00000008405	4.19341	5.62868	5.12212	4.60119	ENSG00000008405	CRY1
ENSG00000008438	0.27762	0.533507	1.52613	0.600561	ENSG00000008438	PGLYRP1
ENSG00000008441	2.88144	10.4602	6.29642	10.7614	ENSG00000008441	NFIX
ENSG00000008513	32.57	24.5752	23.1362	40.8775	ENSG00000008513	ST3GAL1
ENSG00000008516	1.69013	3.10331	4.39262	4.57612	ENSG00000008516	MMP25
ENSG00000008517	2.35807	4.55404	9.44722	10.1188	ENSG00000008517	IL32
ENSG00000008710	48.6623	172.569	231.377	114.012	ENSG00000008710	PKD1
ENSG00000008735	1.29767	0.386958	0.844791	0.652484	ENSG00000008735	MAPK8IP2
ENSG00000008838	29.9019	43.3789	37.6492	54.1262	ENSG00000008838	MED24
ENSG00000008853	10.5629	10.9611	11.9114	11.2317	ENSG00000008853	RHOBTB2
ENSG00000008869	18.2624	18.7684	20.3586	25.005	ENSG00000008869	HEATR5B
ENSG00000008952	40.9057	33.4343	33.7868	37.8379	ENSG00000008952	SEC62
ENSG00000008988	431.816	368.025	278.876	194.613	ENSG00000008988	RPS20
ENSG00000009307	147.231	144.106	134.366	128.582	ENSG00000009307	CSDE1
ENSG00000009335	56.0178	57.2183	57.8104	66.2327	ENSG00000009335	UBE3C
ENSG00000009413	11.6905	28.3649	28.3158	39.7097	ENSG00000009413	REV3L
ENSG00000009694	0.104703	0.195466	0.191768	0.640937	ENSG00000009694	TENM1
ENSG00000009709	0.135225	0.714218	0.464676	0.76835	ENSG00000009709	PAX7
ENSG00000009724	1.31882	3.50113	3.83336	2.79432	ENSG00000009724	MASP2
ENSG00000009765	1.38676	3.19599	3.2597	6.77753	ENSG00000009765	IYD
ENSG00000009780	13.454	12.6539	13.4178	13.2816	ENSG00000009780	FAM76A
ENSG00000009790	95.6706	23.6835	28.2028	29.2532	ENSG00000009790	TRAF3IP3
ENSG00000009830	30.856	39.859	36.6129	42.3899	ENSG00000009830	POMT2
ENSG00000009844	24.7823	14.4055	14.6011	11.4015	ENSG00000009844	VTA1
ENSG00000009950	1.25665	1.36967	2.06257	3.08772	ENSG00000009950	MLXIPL
ENSG00000009954	9.0146	14.2028	14.6036	15.1899	ENSG00000009954	BAZ1B
ENSG00000010017	22.9175	18.7995	19.0905	16.6891	ENSG00000010017	RANBP9
ENSG00000010030	0	0.263291	0.650626	0.258472	ENSG00000010030	ETV7
ENSG00000010072	11.7135	9.30227	10.3356	7.95248	ENSG00000010072	SPRTN
ENSG00000010165	7.0288	8.75726	8.18771	8.37879	ENSG00000010165	METTL13
ENSG00000010219	13.9309	23.2249	28.5569	16.9233	ENSG00000010219	DYRK4
ENSG00000010244	105.189	93.9276	108.033	87.8783	ENSG00000010244	ZNF207
ENSG00000010256	125.463	160.956	103.42	82.1474	ENSG00000010256	UQCRC1
ENSG00000010270	18.2093	22.9597	12.2357	15.6749	ENSG00000010270	STARD3NL
ENSG00000010278	815.039	695.718	190.08	152.374	ENSG00000010278	CD9
ENSG00000010282	0.0326134	0.179056	0.162613	0.189275	ENSG00000010282	HHATL
ENSG00000010292	9.03204	45.3755	11.9028	21.4904	ENSG00000010292	NCAPD2
ENSG00000010295	1.04184	1.80437	1.10564	8.48255	ENSG00000010295	IFFO1
ENSG00000010310	6.97208	10.9473	8.6529	14.3017	ENSG00000010310	GIPR
ENSG00000010318	5.45088	12.4979	9.72843	10.2668	ENSG00000010318	PHF7
ENSG00000010319	0.0437818	0.253458	0.229381	0.096449	ENSG00000010319	SEMA3G
ENSG00000010322	42.3151	72.336	79.0028	58.1445	ENSG00000010322	NISCH
ENSG00000010327	0.869651	0.473625	1.1733	2.1723	ENSG00000010327	STAB1
ENSG00000010361	5.65945	8.67467	7.82081	9.94797	ENSG00000010361	FUZ
ENSG00000010379	0.773061	0.748496	0.785953	1.73849	ENSG00000010379	SLC6A13
ENSG00000010404	28.7435	22.9149	17.6238	19.4741	ENSG00000010404	IDS

ENSG00000010438	44.9216	15.024	12.4585	20.1983	ENSG00000010438	PRSS3
ENSG00000010539	7.19855	9.14012	10.4834	10.3416	ENSG00000010539	ZNF200
ENSG00000010610	0.308375	0.821533	0.638384	1.10022	ENSG00000010610	CD4
ENSG00000010626	1.62672	0.60047	1.61305	1.82063	ENSG00000010626	LRRC23
ENSG00000010671	0.389096	2.10936	2.53574	2.40177	ENSG00000010671	BTK
ENSG00000010704	5.97398	8.65228	3.84844	5.85641	ENSG00000010704	HFE
ENSG00000010803	7.88783	17.9431	16.5197	16.6657	ENSG00000010803	SCMH1
ENSG00000010810	42.7847	63.0746	87.1849	127.969	ENSG00000010810	FYN
ENSG00000010818	16.676	19.105	22.08	21.8328	ENSG00000010818	HIVEP2
ENSG00000010932	0.217206	0.245232	0.442257	0.484741	ENSG00000010932	FMO1
ENSG00000011007	23.0488	17.9525	21.3621	17.2242	ENSG00000011007	ELOA
ENSG00000011009	47.501	29.7623	28.4446	16.7619	ENSG00000011009	LYPLA2
ENSG00000011021	10.6931	21.2365	13.5707	29.2633	ENSG00000011021	CLCN6
ENSG00000011028	20.605	70.9028	130.754	126.2	ENSG00000011028	MRC2
ENSG00000011052	4.53091	4.81432	2.08432	3.86123	ENSG00000011052	NME1-NME2
ENSG00000011083	0.0728442	0.0440228	0.315177	0.807924	ENSG00000011083	SLC6A7
ENSG00000011105	11.1328	19.1975	13.3889	32.7465	ENSG00000011105	TSPAN9
ENSG00000011114	20.9099	21.7782	21.407	27.6241	ENSG00000011114	BTBD7
ENSG00000011132	11.2424	11.121	11.5457	14.2067	ENSG00000011132	APBA3
ENSG00000011143	6.73865	12.6955	14.6066	6.31789	ENSG00000011143	MKS1
ENSG00000011198	17.4063	12.9527	15.6391	8.70066	ENSG00000011198	ABHD5
ENSG00000011201	1.01034	2.69441	2.37252	2.04343	ENSG00000011201	ANOS1
ENSG00000011243	55.8693	58.3612	87.0328	50.0353	ENSG00000011243	AKAP8L
ENSG00000011258	5.49973	8.91468	9.53977	11.4278	ENSG00000011258	MBTD1
ENSG00000011260	18.6315	17.9538	15.9019	17.3805	ENSG00000011260	UTP18
ENSG00000011275	15.1846	20.441	21.9735	24.8887	ENSG00000011275	RNF216
ENSG00000011295	29.782	34.1814	32.6758	29.8873	ENSG00000011295	TTC19
ENSG00000011304	101.718	119.089	102.122	77.5724	ENSG00000011304	PTBP1
ENSG00000011332	1.4007	2.86898	2.75083	4.7371	ENSG00000011332	DPF1
ENSG00000011347	3.12624	6.81951	9.08796	6.45745	ENSG00000011347	SYT7
ENSG00000011376	19.3048	17.3834	14.0639	16.0004	ENSG00000011376	LARS2
ENSG00000011405	42.8127	57.5243	33.8273	52.9123	ENSG00000011405	PIK3C2A
ENSG00000011422	95.2305	94.7131	33.6046	72.6985	ENSG00000011422	PLAUR
ENSG00000011426	35.6296	135.067	8.58746	43.0557	ENSG00000011426	ANLN
ENSG00000011451	12.9568	14.5343	16.8256	20.0819	ENSG00000011451	WIZ
ENSG00000011454	22.718	44.5905	39.3093	34.5152	ENSG00000011454	RABGAP1
ENSG00000011465	14.9758	23.3915	17.8009	345.508	ENSG00000011465	DCN
ENSG00000011478	10.02	16.5771	12.2562	12.668	ENSG00000011478	QPCTL
ENSG00000011485	22.9954	24.911	29.9967	30.479	ENSG00000011485	PPP5C
ENSG00000011523	3.4632	8.69793	8.10619	8.59977	ENSG00000011523	CEP68
ENSG00000011566	19.8622	22.9964	29.5888	44.8268	ENSG00000011566	MAP4K3
ENSG00000011590	2.06295	2.36794	4.17828	1.74481	ENSG00000011590	ZBTB32
ENSG00000011600	0.571316	0.136993	0.123665	0.464804	ENSG00000011600	TYROBP
ENSG00000011638	31.2633	25.0283	36.8135	16.3829	ENSG00000011638	TMEM159
ENSG00000011677	0.0769124	0.227052	0.300853	0.655785	ENSG00000011677	GABRA3
ENSG00000012048	6.44485	19.7929	6.54273	19.8134	ENSG00000012048	BRCA1
ENSG00000012061	98.6585	117.746	49.0483	98.9293	ENSG00000012061	ERCC1
ENSG00000012124	8.49774	18.0825	15.0844	33.2998	ENSG00000012124	CD22
ENSG00000012174	5.55917	7.71381	6.08813	6.57309	ENSG00000012174	MBTPS2
ENSG00000012211	7.29162	12.4695	16.2688	9.21606	ENSG00000012211	PRICKLE3
ENSG00000012223	0.0789657	0.0354724	0.032071	0.179696	ENSG00000012223	LTF
ENSG00000012232	37.7417	61.9696	39.2568	51.1944	ENSG00000012232	EXTL3
ENSG00000012504	0.492237	0.474361	0.57498	0.490056	ENSG00000012504	NR1H4
ENSG00000012660	35.9436	69.0278	25.334	45.7367	ENSG00000012660	ELOVL5

ENSG00000012779	0.436208	0.24474	0	0.0121534	ENSG00000012779	ALOX5
ENSG00000012817	16.4321	22.3333	19.5991	2.50431	ENSG00000012817	KDM5D
ENSG00000012822	62.2729	42.4599	58.9878	47.5405	ENSG00000012822	CALCOCO1
ENSG00000012963	4.50969	5.21188	4.35854	3.45765	ENSG00000012963	UBR7
ENSG00000012983	25.9047	30.9914	28.7419	41.269	ENSG00000012983	MAP4K5
ENSG00000013016	10.0946	2.53665	2.09399	7.91239	ENSG00000013016	EHD3
ENSG00000013275	47.8566	28.4773	26.021	23.4809	ENSG00000013275	PSMC4
ENSG00000013288	11.9723	13.5589	13.6578	12.3831	ENSG00000013288	MAN2B2
ENSG00000013293	6.48603	14.5802	11.1174	17.5482	ENSG00000013293	SLC7A14
ENSG00000013297	8.05669	22.8671	17.2542	147.137	ENSG00000013297	CLDN11
ENSG00000013306	75.8498	59.083	66.9831	40.6457	ENSG00000013306	SLC25A39
ENSG00000013364	130.683	117.473	77.8182	117.613	ENSG00000013364	MVP
ENSG00000013374	21.8458	27.7289	28.2966	31.7425	ENSG00000013374	NUB1
ENSG00000013375	31.1485	48.5616	42.9964	65.1637	ENSG00000013375	PGM3
ENSG00000013392	1.3764	2.15777	2.23837	2.49397	ENSG00000013392	RWDD2A
ENSG00000013441	54.5279	41.8247	54.8314	31.6682	ENSG00000013441	CLK1
ENSG00000013503	8.33725	16.0639	13.3166	13.9307	ENSG00000013503	POLR3B
ENSG00000013523	11.0947	15.0552	14.7905	14.7489	ENSG00000013523	ANGEL1
ENSG00000013561	26.0058	23.8102	18.9578	15.2664	ENSG00000013561	RNF14
ENSG00000013563	3.04144	1.99205	0.447087	2.05178	ENSG00000013563	DNASE1L1
ENSG00000013573	19.7427	51.8331	32.5137	51.3912	ENSG00000013573	DDX11
ENSG00000013583	10.9029	13.0963	10.2439	13.2001	ENSG00000013583	HEBP1
ENSG00000013588	176.419	13.8453	2.37153	13.6077	ENSG00000013588	GPRC5A
ENSG00000013619	2.60E-08	0.742706	0.693007	3.90465	ENSG00000013619	MAMLD1
ENSG00000013725	3.61608	7.65994	9.12821	14.3081	ENSG00000013725	CD6
ENSG00000013810	4.6635	24.1525	4.8504	17.0488	ENSG00000013810	TACC3
ENSG00000014123	15.6918	21.7175	16.328	12.6696	ENSG00000014123	UFL1
ENSG00000014138	7.04498	14.2634	7.00266	13.3009	ENSG00000014138	POLA2
ENSG00000014164	5.10439	6.17461	7.46471	6.75603	ENSG00000014164	ZC3H3
ENSG00000014216	288.711	175.643	130.597	115.29	ENSG00000014216	CAPN1
ENSG00000014257	5.74526	3.03632	2.88715	3.1588	ENSG00000014257	ACPP
ENSG00000014641	73.1277	85.9844	58.2066	56.4594	ENSG00000014641	MDH1
ENSG00000014824	26.3504	24.7616	22.8319	21.43	ENSG00000014824	SLC30A9
ENSG00000014914	2.89657	8.98324	4.89979	5.32756	ENSG00000014914	MTMR11
ENSG00000014919	17.5946	22.6241	26.0956	23.8004	ENSG00000014919	COX15
ENSG00000015133	4.47794	14.8311	17.0889	8.14305	ENSG00000015133	CCDC88C
ENSG00000015153	10.3877	17.7443	16.1707	22.9439	ENSG00000015153	YAF2
ENSG00000015171	10.1806	14.0881	15.1295	14.8534	ENSG00000015171	ZMYND11
ENSG00000015285	0.214931	0.519037	0.593166	0.333921	ENSG00000015285	WAS
ENSG00000015413	0.350808	0.5464	0.44895	0.495293	ENSG00000015413	DPEP1
ENSG00000015475	20.1927	13.1168	15.9378	12.1325	ENSG00000015475	BID
ENSG00000015479	146.204	187.769	166.802	150.906	ENSG00000015479	MATR3
ENSG00000015520	0.341501	0.114673	0.0468398	0.157084	ENSG00000015520	NPC1L1
ENSG00000015532	25.7291	51.3789	40.1368	32.2292	ENSG00000015532	XYLT2
ENSG00000015568	55.0048	55.7177	82.8319	81.0172	ENSG00000015568	RGPD5
ENSG00000015592	0.99496	1.99957	1.53384	2.58038	ENSG00000015592	STMN4
ENSG00000015676	47.3581	53.8964	68.1625	53.3416	ENSG00000015676	NUDCD3
ENSG00000016082	1.98961	7.58452	0.8644	0.980344	ENSG00000016082	ISL1
ENSG00000016391	0.277363	0.446411	0.60918	0.823671	ENSG00000016391	CHDH
ENSG00000016402	3.70323	3.0596	1.01216	0.528008	ENSG00000016402	IL20RA
ENSG00000016490	0	0.0845171	0.0916964	0.0385618	ENSG00000016490	CLCA1
ENSG00000016602	5.3008	0.307347	2.76011	0.619862	ENSG00000016602	CLCA4
ENSG00000016864	38.2856	64.8641	38.7649	44.1326	ENSG00000016864	GLT8D1
ENSG00000017260	56.9472	78.3275	67.2569	75.8097	ENSG00000017260	ATP2C1

ENSG00000017373	0.609831	1.0646	1.33026	1.02998	ENSG00000017373	SRCIN1
ENSG00000017427	0.914985	1.86343	1.90244	2.48416	ENSG00000017427	IGF1
ENSG00000017483	118.776	108.964	108.053	50.1427	ENSG00000017483	SLC38A5
ENSG00000017621	0.870206	1.2943	1.19934	1.24189	ENSG00000017621	MAGIX
ENSG00000017797	30.3762	31.1322	31.0345	31.6471	ENSG00000017797	RALBP1
ENSG00000018189	29.0465	39.3545	40.4185	55.1614	ENSG00000018189	RUFY3
ENSG00000018236	36.6364	150.175	41.0422	63.1396	ENSG00000018236	CNTN1
ENSG00000018280	6.63201	10.1968	12.4785	14.9366	ENSG00000018280	SLC11A1
ENSG00000018408	11.3946	20.9737	12.6896	29.9638	ENSG00000018408	WWTR1
ENSG00000018510	10.1323	11.1413	9.83842	11.3275	ENSG00000018510	AGPS
ENSG00000018607	0	0.155276	0	0	ENSG00000018607	ZNF806
ENSG00000018610	11.0854	10.4139	12.1615	12.0593	ENSG00000018610	CXorf56
ENSG00000018625	1.25182	3.27427	3.41526	2.46527	ENSG00000018625	ATP1A2
ENSG00000018699	12.8021	18.7145	16.7893	12.726	ENSG00000018699	TTC27
ENSG00000018869	7.37015	3.76489	3.36021	2.17577	ENSG00000018869	ZNF582
ENSG00000019102	1.82859	0.443531	0.0456652	0.392738	ENSG00000019102	VSIG2
ENSG00000019144	23.3877	54.0388	58.3813	99.702	ENSG00000019144	PHLDB1
ENSG00000019169	4.07086	0.732466	0.538404	0.576102	ENSG00000019169	MARCO
ENSG00000019186	9.67374	2.12134	0.200304	3.2082	ENSG00000019186	CYP24A1
ENSG00000019485	2.19591	4.99755	5.80222	2.77668	ENSG00000019485	PRDM11
ENSG00000019505	0.115398	0.386402	0.270502	0.69189	ENSG00000019505	SYT13
ENSG00000019549	34.5054	30.5696	34.8176	57.5859	ENSG00000019549	SNAI2
ENSG00000019582	3.4118	8.80469	3.27636	4.3208	ENSG00000019582	CD74
ENSG00000019991	0.204797	0.644576	0.475801	5.39419	ENSG00000019991	HGF
ENSG00000019995	10.2009	9.79395	13.549	12.713	ENSG00000019995	ZRANB1
ENSG00000020129	11.7292	8.89469	16.7727	12.3668	ENSG00000020129	NCDN
ENSG00000020181	0.300783	0.243962	0.750587	14.8698	ENSG00000020181	ADGRA2
ENSG00000020219	0.035738	0	0.0311561	0.156593	ENSG00000020219	CCT8L1P
ENSG00000020256	13.1639	24.6648	20.1463	21.7545	ENSG00000020256	ZFP64
ENSG00000020426	30.2877	40.871	27.8955	31.0287	ENSG00000020426	MNAT1
ENSG00000020577	19.2543	21.7264	21.5173	36.5011	ENSG00000020577	SAMD4A
ENSG00000020633	0.141246	0.848448	0.66834	4.7559	ENSG00000020633	RUNX3
ENSG00000020922	10.4248	16.8987	10.2338	20.7411	ENSG00000020922	MRE11
ENSG00000021300	1.18982	1.11269	2.1797	3.36066	ENSG00000021300	PLEKHB1
ENSG00000021355	139.24	61.5584	10.0782	36.2269	ENSG00000021355	SERPINB1
ENSG00000021461	1.06399	1.56754	1.85025	3.75225	ENSG00000021461	CYP3A43
ENSG00000021488	0.562267	1.11158	0.980241	1.77277	ENSG00000021488	SLC7A9
ENSG00000021574	7.61983	7.60927	6.82655	5.79622	ENSG00000021574	SPAST
ENSG00000021645	0.667508	1.59903	0.960932	1.75312	ENSG00000021645	NRXN3
ENSG00000021762	11.3073	20.9495	14.5027	29.1912	ENSG00000021762	OSBPL5
ENSG00000021776	18.0173	24.0492	18.9999	19.001	ENSG00000021776	AQR
ENSG00000021826	11.9941	21.7228	15.8791	14.109	ENSG00000021826	CPS1
ENSG00000021852	0	0.129583	0.371656	0.30592	ENSG00000021852	C8B
ENSG00000022267	39.7771	57.6017	33.974	40.0439	ENSG00000022267	FHL1
ENSG00000022277	29.2055	27.6489	23.2889	22.3366	ENSG00000022277	RTFDC1
ENSG00000022355	0.529018	1.27165	1.06778	2.81363	ENSG00000022355	GABRA1
ENSG00000022556	1.7071	3.4412	2.66344	2.44994	ENSG00000022556	NLRP2
ENSG00000022567	5.64653	7.54342	7.10206	5.79215	ENSG00000022567	SLC45A4
ENSG00000022840	57.2591	59.7653	68.0648	98.3945	ENSG00000022840	RNF10
ENSG00000022976	12.5281	10.4517	16.0503	14.4269	ENSG00000022976	ZNF839
ENSG00000023041	17.7313	29.2993	27.3072	18.6877	ENSG00000023041	ZDHHC6
ENSG00000023171	0.108124	0.255699	0.285622	0.859378	ENSG00000023171	GRAMD1B
ENSG00000023191	94.1579	92.4525	90.1587	64.0223	ENSG00000023191	RNH1
ENSG00000023228	38.3743	39.0358	30.8341	38.4798	ENSG00000023228	NDUFS1

ENSG00000023287	20.5051	19.465	21.4706	23.6717	ENSG00000023287	RB1CC1
ENSG00000023318	18.4657	28.2892	13.5026	11.8042	ENSG00000023318	ERP44
ENSG00000023330	26.5517	25.9564	23.0075	21.8798	ENSG00000023330	ALAS1
ENSG00000023445	6.81716	9.30173	5.78456	11.803	ENSG00000023445	BIRC3
ENSG00000023516	11.5232	13.0257	11.5158	14.2332	ENSG00000023516	AKAP11
ENSG00000023572	10.9922	8.58023	9.64769	10.0765	ENSG00000023572	GLRX2
ENSG00000023608	8.12336	9.24729	6.60146	9.04513	ENSG00000023608	SNAPC1
ENSG00000023697	31.9184	22.6579	21.29	17.7688	ENSG00000023697	DERA
ENSG00000023734	58.6973	40.6348	44.6662	40.4121	ENSG00000023734	STRAP
ENSG00000023839	2.937	5.09973	4.58237	8.92446	ENSG00000023839	ABCC2
ENSG00000023892	13.5327	31.1534	16.995	13.393	ENSG00000023892	DEF6
ENSG00000023902	2.22117	2.11572	2.06268	8.06039	ENSG00000023902	PLEKHO1
ENSG00000023909	9.85071	13.8733	11.8123	17.9103	ENSG00000023909	GCLM
ENSG00000024048	17.2454	27.7971	21.6362	24.3434	ENSG00000024048	UBR2
ENSG00000024422	46.3792	58.5922	52.1316	77.9201	ENSG00000024422	EHD2
ENSG00000024526	4.36926	18.8373	2.03323	6.20934	ENSG00000024526	DEPDC1
ENSG00000024862	2.68556	2.70982	1.72362	2.38122	ENSG00000024862	CCDC28A
ENSG00000025039	2.69201	0.890804	0.730354	1.33458	ENSG00000025039	RRAGD
ENSG00000025156	3.78822	5.98642	5.53267	4.39911	ENSG00000025156	HSF2
ENSG00000025293	17.2897	19.9113	20.871	35.6987	ENSG00000025293	PHF20
ENSG00000025423	0.154035	0.517253	0.309234	0.629861	ENSG00000025423	HSD17B6
ENSG00000025434	4.8091	4.94398	3.55976	4.85629	ENSG00000025434	NR1H3
ENSG00000025708	22.1373	40.2454	161.612	38.9757	ENSG00000025708	TYMP
ENSG00000025770	20.854	28.0918	21.2865	31.3112	ENSG00000025770	NCAPH2
ENSG00000025772	12.7505	14.5961	10.7711	8.25829	ENSG00000025772	TOMM34
ENSG00000025796	38.573	73.9943	80.9419	97.1626	ENSG00000025796	SEC63
ENSG00000025800	39.0657	28.5435	28.6849	22.1616	ENSG00000025800	KPNA6
ENSG00000026025	221.926	426.607	128.731	953.688	ENSG00000026025	VIM
ENSG00000026036	3.32352	8.06564	4.65001	6.65974	ENSG00000026036	RTEL1-TNFRSF6B
ENSG00000026103	17.8471	28.3283	14.1312	14.2185	ENSG00000026103	FAS
ENSG00000026297	13.3684	11.8222	6.25024	9.07027	ENSG00000026297	RNASET2
ENSG00000026508	663.488	1346.89	689.593	933.028	ENSG00000026508	CD44
ENSG00000026559	53.2172	36.6846	26.9503	23.929	ENSG00000026559	KCNG1
ENSG00000026652	11.9333	21.4996	13.457	17.5009	ENSG00000026652	AGPAT4
ENSG00000026751	8.7681	5.498	3.33398	5.76761	ENSG00000026751	SLAMF7
ENSG00000026950	4.9355	11.2856	8.50975	11.6325	ENSG00000026950	BTN3A1
ENSG00000027001	8.13757	14.5137	9.74093	8.36219	ENSG00000027001	MIPEP
ENSG00000027075	26.6854	48.3097	44.7188	60.4902	ENSG00000027075	PRKCH
ENSG00000027644	0.0314823	0.0202456	0.06407	0.0809256	ENSG00000027644	INSRR
ENSG00000027697	54.2214	53.2247	74.3166	25.2143	ENSG00000027697	IFNGR1
ENSG00000027847	25.4003	25.361	24.4341	15.3173	ENSG00000027847	B4GALT7
ENSG00000027869	0.890456	7.00916	3.11187	6.08049	ENSG00000027869	SH2D2A
ENSG00000028116	21.3636	28.804	20.7826	18.2025	ENSG00000028116	VRK2
ENSG00000028137	0.876035	1.08759	1.3882	3.66785	ENSG00000028137	TNFRSF1B
ENSG00000028203	75.552	97.1463	111.746	74.8907	ENSG00000028203	VEZT
ENSG00000028277	3.32971	23.9449	19.7679	40.1982	ENSG00000028277	POU2F2
ENSG00000028310	24.044	35.5529	34.2889	35.9496	ENSG00000028310	BRD9
ENSG00000028528	33.8513	44.7807	36.2893	68.794	ENSG00000028528	SNX1
ENSG00000028839	17.5359	18.8258	16.9174	16.3268	ENSG00000028839	TBPL1
ENSG00000029153	60.4532	49.4376	23.8758	29.8555	ENSG00000029153	ARNTL2
ENSG00000029363	56.1182	68.8472	66.8127	66.429	ENSG00000029363	BCLAF1
ENSG00000029364	58.7916	49.0071	43.5802	31.9459	ENSG00000029364	SLC39A9
ENSG00000029534	0.453605	0.993551	0.658779	1.12161	ENSG00000029534	ANK1
ENSG00000029559	0	0.114325	0.154982	0.194191	ENSG00000029559	IBSP

ENSG00000029639	15.5695	35.294	20.3249	20.9938	ENSG00000029639	TFB1M
ENSG00000029725	21.6325	23.6125	28.8977	32.9262	ENSG00000029725	RABEP1
ENSG00000029993	26.4062	16.5759	8.69718	15.572	ENSG00000029993	HMGB3
ENSG00000030066	17.3132	30.6013	29.7494	43.7039	ENSG00000030066	NUP160
ENSG00000030110	22.0844	27.1124	23.7151	12.9155	ENSG00000030110	BAK1
ENSG00000030304	0.0727587	0.901725	0.612939	1.13486	ENSG00000030304	MUSK
ENSG00000030419	31.2138	17.3299	8.11759	15.0769	ENSG00000030419	IKZF2
ENSG00000030582	275.76	328.182	286.694	161.201	ENSG00000030582	GRN
ENSG00000031003	12.4592	18.1846	15.6975	24.5008	ENSG00000031003	FAM13B
ENSG00000031081	1.98491	1.66006	1.93914	6.67246	ENSG00000031081	ARHGAP31
ENSG00000031691	2.7868	4.8689	2.07173	1.888	ENSG00000031691	CENPQ
ENSG00000031698	97.0072	140.18	156.413	65.1182	ENSG00000031698	SARS
ENSG00000031823	29.1946	37.4568	34.6216	43.4908	ENSG00000031823	RANBP3
ENSG00000032219	7.18575	12.6475	10.6075	13.9126	ENSG00000032219	ARID4A
ENSG00000032389	16.7922	19.7408	16.8695	15.5108	ENSG00000032389	EIPR1
ENSG00000032444	61.7869	66.377	67.1272	305.873	ENSG00000032444	PNPLA6
ENSG00000032742	4.57337	11.9714	13.1769	11.6133	ENSG00000032742	IFT88
ENSG00000033011	19.4665	20.8542	23.4933	22.8619	ENSG00000033011	ALG1
ENSG00000033030	13.3878	19.1925	19.1782	16.8643	ENSG00000033030	ZCCHC8
ENSG00000033050	35.6544	23.2537	44.4284	22.1183	ENSG00000033050	ABCF2
ENSG00000033100	56.0698	46.0295	40.0127	47.0208	ENSG00000033100	CHPF2
ENSG00000033122	2.66967	5.91107	2.50809	6.14209	ENSG00000033122	LRRC7
ENSG00000033170	53.1344	146.599	125.175	263.983	ENSG00000033170	FUT8
ENSG00000033178	142.071	134.313	50.2045	107.47	ENSG00000033178	UBA6
ENSG00000033327	2.77179	1.59702	2.44258	4.36972	ENSG00000033327	GAB2
ENSG00000033627	45.1267	32.9442	34.0588	49.5386	ENSG00000033627	ATP6V0A1
ENSG00000033800	32.256	26.9405	28.0813	33.2351	ENSG00000033800	PIAS1
ENSG00000033867	40.3131	120.137	51.8621	107.328	ENSG00000033867	SLC4A7
ENSG00000034053	6.43372	5.94343	7.97483	15.6359	ENSG00000034053	APBA2
ENSG00000034152	21.4843	15.001	14.317	27.9045	ENSG00000034152	MAP2K3
ENSG00000034239	1.58355	3.17581	2.49132	2.66932	ENSG00000034239	EFCAB1
ENSG00000034510	1924.84	1822.3	533.254	997.785	ENSG00000034510	TMSB10
ENSG00000034533	2.54567	4.39323	4.09086	2.75858	ENSG00000034533	ASTE1
ENSG00000034677	22.7957	44.7952	49.7966	39.5321	ENSG00000034677	RNF19A
ENSG00000034693	21.0865	16.3663	26.3951	11.6767	ENSG00000034693	PEX3
ENSG00000034713	41.9957	18.1456	17.9196	24.7254	ENSG00000034713	GABARAPL2
ENSG00000034971	0.0268085	0.0774864	0.0700506	0.0882423	ENSG00000034971	MYOC
ENSG00000035115	20.8817	29.9143	38.7892	29.4619	ENSG00000035115	SH3YL1
ENSG00000035141	17.5556	12.8054	11.3994	8.83832	ENSG00000035141	FAM136A
ENSG00000035403	146.275	121.775	63.0743	105.705	ENSG00000035403	VCL
ENSG00000035499	4.03377	14.4364	3.55065	6.79961	ENSG00000035499	DEPDC1B
ENSG00000035664	13.3481	12.5207	17.3698	28.8404	ENSG00000035664	DAPK2
ENSG00000035681	13.7262	21.6806	32.192	24.1874	ENSG00000035681	NSMAF
ENSG00000035687	12.9895	24.0252	22.5996	21.3895	ENSG00000035687	ADSS
ENSG00000035720	0.0767673	0.659851	0.367085	0.581139	ENSG00000035720	STAP1
ENSG00000035862	29.7931	6.16132	7.71953	116.55	ENSG00000035862	TIMP2
ENSG00000035928	39.8813	69.7353	56.0829	84.1151	ENSG00000035928	RFC1
ENSG00000036054	31.4099	22.5502	20.1569	23.7038	ENSG00000036054	TBC1D23
ENSG00000036257	47.7272	64.6424	61.3251	96.2051	ENSG00000036257	CUL3
ENSG00000036448	0.762268	0.277089	0.35636	0.94577	ENSG00000036448	MYOM2
ENSG00000036473	0	0.0350571	0.0318371	0	ENSG00000036473	OTC
ENSG00000036530	8.56805	18.5379	17.9573	38.4167	ENSG00000036530	CYP46A1
ENSG00000036549	30.5568	52.5128	52.1928	51.8013	ENSG00000036549	ZZZ3
ENSG00000036565	0.998537	3.14761	5.22299	5.49734	ENSG00000036565	SLC18A1

ENSG00000036672	0.690967	0.355603	0.814695	0.98826	ENSG00000036672	USP2
ENSG00000036828	0.0963968	0.299128	0.244405	0.283655	ENSG00000036828	CASR
ENSG00000037042	16.4332	20.2995	16.6325	18.94	ENSG00000037042	TUBG2
ENSG00000037241	25.88	21.1146	19.3679	12.2947	ENSG00000037241	RPL26L1
ENSG00000037280	0.607479	0.66906	0.892426	0.996102	ENSG00000037280	FLT4
ENSG00000037474	32.3525	40.2012	46.7616	46.4485	ENSG00000037474	NSUN2
ENSG00000037637	10.7024	11.7394	15.6018	10.4676	ENSG00000037637	FBXO42
ENSG00000037749	37.183	36.5307	36.6986	28.3526	ENSG00000037749	MFAP3
ENSG00000037757	24.9355	29.8514	30.3997	28.7404	ENSG00000037757	MRI1
ENSG00000037897	6.00914	7.57562	9.39041	6.49119	ENSG00000037897	METTL1
ENSG00000037965	1.15731	1.89969	3.11672	5.45272	ENSG00000037965	HOXC8
ENSG00000038002	21.6611	10.7319	25.3961	6.80641	ENSG00000038002	AGA
ENSG00000038210	20.8958	42.2218	35.7854	71.0074	ENSG00000038210	PI4K2B
ENSG00000038219	23.0391	30.06	35.8357	40.7049	ENSG00000038219	BOD1L1
ENSG00000038274	14.603	16.0527	15.4251	12.8211	ENSG00000038274	MAT2B
ENSG00000038295	2.40942	3.49687	9.45717	4.70356	ENSG00000038295	TLL1
ENSG00000038358	26.5722	27.6488	26.7578	25.9127	ENSG00000038358	EDC4
ENSG00000038382	109.034	109.371	111.577	257.442	ENSG00000038382	TRIO
ENSG00000038427	3.08751	13.116	22.2377	57.3167	ENSG00000038427	VCAN
ENSG00000038532	25.5384	17.7053	21.4368	27.6865	ENSG00000038532	CLEC16A
ENSG00000038945	4.83611	10.9833	9.38281	10.3489	ENSG00000038945	MSR1
ENSG00000039068	408.222	299.3	339.407	148.792	ENSG00000039068	CDH1
ENSG00000039123	38.4143	58.1774	52.1136	56.7537	ENSG00000039123	SKIV2L2
ENSG00000039139	1.15658	1.08937	1.93699	3.18187	ENSG00000039139	DNAH5
ENSG00000039319	22.7824	32.2944	28.6216	37.5548	ENSG00000039319	ZFYVE16
ENSG00000039523	26.5779	28.8032	26.9415	46.7725	ENSG00000039523	RIPOR1
ENSG00000039537	0.0614025	0.0591233	0.0527445	0.233916	ENSG00000039537	C6
ENSG00000039560	29.2324	37.4703	39.9569	102.594	ENSG00000039560	RAI14
ENSG00000039600	0.0667987	0.178865	0.0874871	0.168257	ENSG00000039600	SOX30
ENSG00000039650	24.4825	37.1674	32.16	37.5155	ENSG00000039650	PNKP
ENSG00000039987	2.26372	1.64745	3.33424	2.81965	ENSG00000039987	BEST2
ENSG00000040199	4.36288	6.52827	7.14321	9.90126	ENSG00000040199	PHLPP2
ENSG00000040275	9.28493	18.4271	11.3474	20.5912	ENSG00000040275	SPDL1
ENSG00000040341	19.8493	32.3034	23.3581	34.9623	ENSG00000040341	STAU2
ENSG00000040487	16.6826	18.2238	15.071	13.0039	ENSG00000040487	PQLC2
ENSG00000040531	20.8013	21.0039	18.5033	16.8032	ENSG00000040531	CTNS
ENSG00000040608	8.88308	11.8484	3.8589	3.41388	ENSG00000040608	RTN4R
ENSG00000040633	26.5652	14.46	18.4889	14.8779	ENSG00000040633	PHF23
ENSG00000040731	0.23297	0.803128	0.740351	1.20078	ENSG00000040731	CDH10
ENSG00000040933	12.2532	15.3315	19.2927	18.4761	ENSG00000040933	INPP4A
ENSG00000041353	15.8717	4.90652	5.03109	1.8383	ENSG00000041353	RAB27B
ENSG00000041357	58.4363	47.2363	34.8197	29.4925	ENSG00000041357	PSMA4
ENSG00000041515	0.872104	1.7163	3.50295	2.49705	ENSG00000041515	MYO16
ENSG00000041802	26.8355	20.8968	32.7746	20.1168	ENSG00000041802	LSG1
ENSG00000041880	4.43732	9.98134	7.65047	7.31087	ENSG00000041880	PARP3
ENSG00000041982	8.62601	250.264	381.094	108.162	ENSG00000041982	TNC
ENSG00000041988	7.15484	9.29091	8.71557	5.74419	ENSG00000041988	THAP3
ENSG00000042062	5.9171	10.058	4.89906	19.4542	ENSG00000042062	RIPOR3
ENSG00000042088	12.1383	26.6004	15.9251	17.5543	ENSG00000042088	TDP1
ENSG00000042286	1.42843	3.56952	3.36466	4.2467	ENSG00000042286	AIFM2
ENSG00000042304	1.02104	2.47433	2.37252	3.8701	ENSG00000042304	C2orf83
ENSG00000042317	11.6117	22.3051	17.1567	23.7609	ENSG00000042317	SPATA7
ENSG00000042429	29.8354	31.9789	33.3025	36.4779	ENSG00000042429	MED17
ENSG00000042445	40.8399	55.6789	43.5566	25.2389	ENSG00000042445	RETSAT

ENSG00000042493	169.972	163.163	87.3841	60.2351	ENSG00000042493	CAPG
ENSG00000042753	77.2893	70.0982	55.4394	45.2944	ENSG00000042753	AP2S1
ENSG00000042781	0.586282	0.878765	0.85055	1.30061	ENSG00000042781	USH2A
ENSG00000042813	0.252188	1.56007	1.09832	2.24464	ENSG00000042813	ZPBP
ENSG00000042832	2.45513	2.17585	2.68222	5.26501	ENSG00000042832	TG
ENSG00000042980	0.853793	1.8659	1.85223	2.25764	ENSG00000042980	ADAM28
ENSG00000043039	4.13366	7.97156	4.44264	5.01163	ENSG00000043039	BARX2
ENSG00000043093	14.7883	12.1884	13.3303	14.6924	ENSG00000043093	DCUN1D1
ENSG00000043143	7.36276	19.0603	15.6563	13.1788	ENSG00000043143	JADE2
ENSG00000043355	1.30608	3.9338	2.10562	11.4419	ENSG00000043355	ZIC2
ENSG00000043462	0.917071	2.24537	1.83178	3.12509	ENSG00000043462	LCP2
ENSG00000043514	20.9431	29.5149	28.5385	18.1519	ENSG00000043514	TRIT1
ENSG00000043591	0.46238	0.84233	1.09673	1.66938	ENSG00000043591	ADRB1
ENSG00000044012	0.11847	0	0.20535	0.127456	ENSG00000044012	GUCA2B
ENSG00000044090	9.2424	14.2712	13.1539	20.46	ENSG00000044090	CUL7
ENSG00000044115	251.85	234.96	181.498	211.286	ENSG00000044115	CTNNA1
ENSG00000044446	26.0803	42.671	35.1882	45.2137	ENSG00000044446	PHKA2
ENSG00000044459	2.18078	6.16682	4.63304	10.5807	ENSG00000044459	CNTLN
ENSG00000044524	0.310337	0.253673	0.440551	0.574841	ENSG00000044524	EPHA3
ENSG00000044574	116.838	314.29	161.893	199.447	ENSG00000044574	HSPA5
ENSG00000046604	83.523	120.31	77.5195	46.1762	ENSG00000046604	DSG2
ENSG00000046647	7.56794	12.9167	9.18988	9.07682	ENSG00000046647	GEMIN8
ENSG00000046651	14.89	16.8621	18.2071	19.5476	ENSG00000046651	OFD1
ENSG00000046653	2.33116	1.76602	4.25995	5.40858	ENSG00000046653	GPM6B
ENSG00000046774	0.0283203	0.0552121	0.0504782	0.168069	ENSG00000046774	MAGEC2
ENSG00000046889	0.611301	0.904665	0.860478	1.58744	ENSG00000046889	PREX2
ENSG00000047056	11.9198	12.0504	12.4805	17.5572	ENSG00000047056	WDR37
ENSG00000047188	18.7318	20.4738	20.3589	21.5982	ENSG00000047188	YTHDC2
ENSG00000047230	8.51837	12.7469	7.90811	14.9485	ENSG00000047230	CTPS2
ENSG00000047249	46.4787	40.484	40.7155	33.0659	ENSG00000047249	ATP6V1H
ENSG00000047315	62.8334	54.8709	58.3126	55.1234	ENSG00000047315	POLR2B
ENSG00000047346	13.8911	12.4329	12.7608	12.7515	ENSG00000047346	FAM214A
ENSG00000047365	25.1674	26.85	24.3305	11.0332	ENSG00000047365	ARAP2
ENSG00000047410	47.5892	61.0715	55.4	61.9807	ENSG00000047410	TPR
ENSG00000047457	2.63722	2.60454	4.49254	4.53626	ENSG00000047457	CP
ENSG00000047578	13.6409	16.7763	21.0963	15.0863	ENSG00000047578	KIAA0556
ENSG00000047579	2.67399	4.3508	3.32669	4.88047	ENSG00000047579	DTNBP1
ENSG00000047597	0.150852	0.179428	0.16178	0.186865	ENSG00000047597	XK
ENSG00000047617	0.740182	1.22779	0.295485	0.194833	ENSG00000047617	ANO2
ENSG00000047621	21.7668	43.9693	40.7117	66.9614	ENSG00000047621	C12orf4
ENSG00000047634	3.25011	5.72073	3.398	5.43294	ENSG00000047634	SCML1
ENSG00000047644	8.7958	14.2473	14.8784	12.3167	ENSG00000047644	WWC3
ENSG00000047648	0.496254	0.482866	0.740684	1.66287	ENSG00000047648	ARHGAP6
ENSG00000047662	0.227164	0.537038	0.5741	1.0586	ENSG00000047662	FAM184B
ENSG00000047849	91.9731	107.982	119.66	172.745	ENSG00000047849	MAP4
ENSG00000047932	14.8844	12.3321	21.4656	17.2519	ENSG00000047932	GOPC
ENSG00000047936	0.952371	0.171158	2.69108	0.607418	ENSG00000047936	ROS1
ENSG00000048028	6.92357	20.828	16.3713	13.787	ENSG00000048028	USP28
ENSG00000048052	27.0363	22.9337	19.2943	20.7774	ENSG00000048052	HDAC9
ENSG00000048140	35.3859	23.868	20.0192	14.7976	ENSG00000048140	TSPAN17
ENSG00000048162	22.8492	27.9391	31.3029	23.6958	ENSG00000048162	NOP16
ENSG00000048342	11.663	29.1631	25.4811	37.033	ENSG00000048342	CC2D2A
ENSG00000048392	15.647	15.2507	19.1894	18.7821	ENSG00000048392	RRM2B
ENSG00000048405	14.5812	18.6058	20.3508	18.2264	ENSG00000048405	ZNF800

ENSG00000048462	0.773014	1.81748	0.96298	1.72078	ENSG00000048462	TNFRSF17
ENSG00000048471	16.5583	41.5171	21.032	37.4787	ENSG00000048471	SNX29
ENSG00000048540	2.78106	6.59304	7.89035	10.0743	ENSG00000048540	LMO3
ENSG00000048544	19.3634	26.6584	18.5472	14.0768	ENSG00000048544	MRPS10
ENSG00000048545	0.0366518	0.137772	0.095759	0.0995441	ENSG00000048545	GUCA1A
ENSG00000048649	17.6405	25.2417	28.2306	38.2519	ENSG00000048649	RSF1
ENSG00000048707	34.4941	40.6842	42.3202	41.0572	ENSG00000048707	VPS13D
ENSG00000048740	1.77109	2.26004	1.38298	1.46754	ENSG00000048740	CELF2
ENSG00000048828	39.9009	46.0589	44.5601	38.397	ENSG00000048828	FAM120A
ENSG00000048991	14.8874	30.162	32.4294	57.5569	ENSG00000048991	R3HDM1
ENSG00000049089	3.28928	6.55835	2.52066	3.85593	ENSG00000049089	COL9A2
ENSG00000049130	11.6272	17.1748	19.4283	19.6283	ENSG00000049130	KITLG
ENSG00000049167	6.14148	9.91169	12.776	9.31357	ENSG00000049167	ERCC8
ENSG00000049192	16.7595	26.2739	12.2645	59.2473	ENSG00000049192	ADAMTS6
ENSG00000049239	8.94456	21.9265	18.6802	15.3915	ENSG00000049239	H6PD
ENSG00000049245	56.5322	34.7269	34.848	29.4186	ENSG00000049245	VAMP3
ENSG00000049246	3.74469	6.07441	4.5811	3.81619	ENSG00000049246	PER3
ENSG00000049247	0.302368	0.0573045	0.170866	0.178414	ENSG00000049247	UTS2
ENSG00000049249	0.471504	0.999621	2.43816	1.6813	ENSG00000049249	TNFRSF9
ENSG00000049283	27.17	36.2609	17.7201	59.892	ENSG00000049283	EPN3
ENSG00000049323	5.29477	8.126	50.6178	101.776	ENSG00000049323	LTBP1
ENSG00000049449	45.4175	62.0208	58.3135	57.6939	ENSG00000049449	RCN1
ENSG00000049540	4.24356	25.1053	11.0417	19.7796	ENSG00000049540	ELN
ENSG00000049541	3.92664	7.13318	4.01465	4.82383	ENSG00000049541	RFC2
ENSG00000049618	9.83905	14.6428	19.2554	18.3373	ENSG00000049618	ARID1B
ENSG00000049656	102.021	100.248	61.6392	48.288	ENSG00000049656	CLPTM1L
ENSG00000049759	53.3764	58.4513	42.7885	62.8564	ENSG00000049759	NEDD4L
ENSG00000049768	0.758167	0.749504	0.936844	0.618571	ENSG00000049768	FOXP3
ENSG00000049769	0.518269	1.00531	1.26986	1.23054	ENSG00000049769	PPP1R3F
ENSG00000049860	79.5108	100.361	53.5014	41.6292	ENSG00000049860	HEXB
ENSG00000049883	5.56609	9.33198	9.38997	6.55492	ENSG00000049883	PTCD2
ENSG00000050030	0.268717	0.353039	0.335098	0.770882	ENSG00000050030	NEXMIF
ENSG00000050130	48.5982	64.7658	42.3948	43.4886	ENSG00000050130	JKAMP
ENSG00000050165	74.8249	172.483	130.354	112.763	ENSG00000050165	DKK3
ENSG00000050327	21.7556	15.7199	18.0788	7.5935	ENSG00000050327	ARHGEF5
ENSG00000050344	21.0664	39.0326	42.3462	17.7251	ENSG00000050344	NFE2L3
ENSG00000050393	9.08183	9.74071	6.6461	9.77892	ENSG00000050393	MCUR1
ENSG00000050405	256.478	269.389	180.382	170.109	ENSG00000050405	LIMA1
ENSG00000050426	19.6898	35.6544	37.825	26.7454	ENSG00000050426	LETMD1
ENSG00000050438	3.62056	6.64879	5.89102	13.5085	ENSG00000050438	SLC4A8
ENSG00000050555	0.0956098	0.283732	0.300994	0.63835	ENSG00000050555	LAMC3
ENSG00000050628	0.813622	0.98319	1.28035	1.95467	ENSG00000050628	PTGER3
ENSG00000050730	0.699864	1.87645	1.29265	6.24636	ENSG00000050730	TNIP3
ENSG00000050748	13.7122	18.3635	13.3936	16.9803	ENSG00000050748	MAPK9
ENSG00000050767	0.736145	1.11512	1.76053	0.617962	ENSG00000050767	COL23A1
ENSG00000050820	50.6743	58.0408	50.7038	64.3779	ENSG00000050820	BCAR1
ENSG00000051009	14.6482	12.6626	16.1901	12.3735	ENSG00000051009	FAM160A2
ENSG00000051108	67.1955	186.15	102.477	103.077	ENSG00000051108	HERPUD1
ENSG00000051128	88.2409	78.1536	49.2642	48.8262	ENSG00000051128	HOMER3
ENSG00000051180	2.98279	9.4471	5.30723	7.81444	ENSG00000051180	RAD51
ENSG00000051341	4.64526	14.1001	6.87171	13.0673	ENSG00000051341	POLQ
ENSG00000051382	7.61391	14.8357	9.12031	13.252	ENSG00000051382	PIK3CB
ENSG00000051523	36.1154	85.1288	50.5203	44.2984	ENSG00000051523	CYBA
ENSG00000051596	17.3108	32.7291	23.6756	19.5614	ENSG00000051596	THOC3

ENSG00000051620	102.705	45.912	33.3707	26.0971	ENSG00000051620	HEBP2
ENSG00000051825	9.91999	29.924	17.8299	27.4707	ENSG00000051825	MPHOSPH9
ENSG00000052126	27.313	50.4967	31.6895	55.3619	ENSG00000052126	PLEKHA5
ENSG00000052344	128.247	76.8745	66.9016	25.207	ENSG00000052344	PRSS8
ENSG00000052723	19.2284	20.5111	25.1419	11.5352	ENSG00000052723	SIKE1
ENSG00000052749	16.9199	15.5668	23.9015	14.6549	ENSG00000052749	RRP12
ENSG00000052795	11.3039	13.2072	13.4889	19.5609	ENSG00000052795	FNIP2
ENSG00000052802	596.484	407.137	65.8824	144.612	ENSG00000052802	MSMO1
ENSG00000052841	36.2551	82.5553	94.0805	74.3741	ENSG00000052841	TTC17
ENSG00000052850	0.176238	0.492142	0.473005	0.583067	ENSG00000052850	ALX4
ENSG00000053108	2.37754	4.38223	7.18054	13.9461	ENSG00000053108	FSTL4
ENSG00000053254	23.4316	42.3418	55.9466	85.9744	ENSG00000053254	FOXN3
ENSG00000053328	2.05497	2.45632	1.7467	4.49074	ENSG00000053328	METTL24
ENSG00000053371	19.3964	15.4751	11.8564	11.4943	ENSG00000053371	AKR7A2
ENSG00000053372	21.6128	19.9791	23.3527	15.6281	ENSG00000053372	MRTO4
ENSG00000053438	5.70984	7.13689	8.45531	6.24296	ENSG00000053438	NNAT
ENSG00000053501	6.10274	11.0917	8.18743	14.3735	ENSG00000053501	USE1
ENSG00000053524	2.9156	4.48892	4.97415	6.94825	ENSG00000053524	MCF2L2
ENSG00000053702	1.34004	2.10677	3.03796	3.23812	ENSG00000053702	NRIP2
ENSG00000053747	2597.41	3257.39	1099.73	2351.47	ENSG00000053747	LAMA3
ENSG00000053770	11.3773	17.0521	20.1345	13.7642	ENSG00000053770	AP5M1
ENSG00000053900	15.6954	25.8665	20.6277	18.764	ENSG00000053900	ANAPC4
ENSG00000053918	0.278289	0.313223	0.248641	0.798608	ENSG00000053918	KCNQ1
ENSG00000054116	45.381	35.9941	33.011	28.7215	ENSG00000054116	TRAPPC3
ENSG00000054118	51.0214	48.5147	57.4306	55.4109	ENSG00000054118	THRAP3
ENSG00000054148	46.3991	46.7706	52.8104	30.628	ENSG00000054148	PHPT1
ENSG00000054179	1.65492	4.3683	3.9645	0.99855	ENSG00000054179	ENTPD2
ENSG00000054219	1.57559	6.89305	3.84916	2.95417	ENSG00000054219	LY75
ENSG00000054267	19.4888	20.7991	25.2415	30.4194	ENSG00000054267	ARID4B
ENSG00000054277	19.5265	19.401	9.34875	14.811	ENSG00000054277	OPN3
ENSG00000054282	20.3944	37.5731	41.8595	66.7741	ENSG00000054282	SDCCAG8
ENSG00000054356	2.5088	7.75218	5.72172	14.1153	ENSG00000054356	PTPRN
ENSG00000054392	2.60473	3.70243	2.29732	2.64866	ENSG00000054392	HHAT
ENSG00000054523	28.7923	26.664	28.67	32.6306	ENSG00000054523	KIF1B
ENSG00000054598	11.198	3.914	4.14343	2.65337	ENSG00000054598	FOXC1
ENSG00000054611	13.366	14.1305	17.1696	16.5365	ENSG00000054611	TBC1D22A
ENSG00000054654	29.8322	72.0799	46.334	56.2608	ENSG00000054654	SYNE2
ENSG00000054690	4.22351	8.08008	6.16708	5.89495	ENSG00000054690	PLEKHH1
ENSG00000054793	10.0143	7.69339	7.65859	5.98123	ENSG00000054793	ATP9A
ENSG00000054796	0.106596	0.0766655	0.094264	0.235372	ENSG00000054796	SPO11
ENSG00000054803	0.0364104	0.0707194	0.0160893	0.168761	ENSG00000054803	CBLN4
ENSG00000054938	0.141751	0.1969	1.19415	0.416845	ENSG00000054938	CHRDL2
ENSG00000054965	11.2873	14.4118	13.5867	14.971	ENSG00000054965	FAM168A
ENSG00000054967	9.37812	15.5624	8.89946	10.5125	ENSG00000054967	RELT
ENSG00000054983	29.335	48.8825	52.8172	87.5154	ENSG00000054983	GALC
ENSG00000055044	51.2488	74.7643	66.4672	59.0874	ENSG00000055044	NOP58
ENSG00000055070	29.3199	28.0541	26.8004	24.4995	ENSG00000055070	SZRD1
ENSG00000055118	0.0632515	0.161559	0.322193	0.498365	ENSG00000055118	KCNH2
ENSG00000055130	20.1124	22.0837	21.0177	19.5257	ENSG00000055130	CUL1
ENSG00000055147	12.9608	16.5032	14.211	16.6017	ENSG00000055147	FAM114A2
ENSG00000055163	4.20349	7.79918	5.20799	9.82171	ENSG00000055163	CYFIP2
ENSG00000055208	15.2807	19.9515	19.6122	25.8619	ENSG00000055208	TAB2
ENSG00000055211	30.4531	33.7683	24.6351	21.0241	ENSG00000055211	GINM1
ENSG00000055332	17.4742	27.7204	18.8597	33.9022	ENSG00000055332	EIF2AK2

ENSG00000055483	17.5437	25.0877	37.1761	28.7987	ENSG00000055483	USP36
ENSG00000055609	32.9447	43.3687	38.1949	50.6363	ENSG00000055609	KMT2C
ENSG00000055732	8.60036	8.28884	6.839	10.7325	ENSG00000055732	MCOLN3
ENSG00000055813	0.0949861	0.183436	0.0947804	0.239334	ENSG00000055813	CCDC85A
ENSG00000055917	17.8537	29.6606	28.0133	34.546	ENSG00000055917	PUM2
ENSG00000055950	27.2066	24.9187	22.9496	16.6038	ENSG00000055950	MRPL43
ENSG00000055955	1.59025	3.79135	6.03468	7.47521	ENSG00000055955	ITIH4
ENSG00000055957	2.3852	4.7121	5.443	5.50697	ENSG00000055957	ITIH1
ENSG00000056050	5.47502	8.50119	8.56771	7.80694	ENSG00000056050	HPF1
ENSG00000056097	38.259	35.6458	47.7203	35.691	ENSG00000056097	ZFR
ENSG00000056277	2.01383	3.62124	3.04574	3.48618	ENSG00000056277	ZNF280C
ENSG00000056291	0.428495	1.11359	0.481063	1.31558	ENSG00000056291	NPFFR2
ENSG00000056487	1.02313	1.76141	3.67631	2.47148	ENSG00000056487	PHF21B
ENSG00000056558	1.3209	2.28913	2.15093	1.81974	ENSG00000056558	TRAF1
ENSG00000056586	30.8356	23.0496	31.6318	30.5706	ENSG00000056586	RC3H2
ENSG00000056661	3.51257	5.23901	5.01702	7.1717	ENSG00000056661	PCGF2
ENSG00000056736	1.01448	1.35789	1.37105	1.53184	ENSG00000056736	IL17RB
ENSG00000056972	27.7354	38.7382	32.3202	22.2342	ENSG00000056972	TRAF3IP2
ENSG00000056998	0.0951174	0.289114	0.430994	0.633554	ENSG00000056998	GYG2
ENSG00000057019	575.4	492.242	100.243	388.081	ENSG00000057019	DCBLD2
ENSG00000057149	61.6855	12.7446	16.5607	14.9905	ENSG00000057149	SERPINB3
ENSG00000057252	35.0669	33.3339	17.423	15.996	ENSG00000057252	SOAT1
ENSG00000057294	55.0058	39.6816	16.0928	20.4794	ENSG00000057294	PKP2
ENSG00000057468	0.0667771	0.0965916	0.39299	0.149409	ENSG00000057468	MSH4
ENSG00000057593	0.175504	0.426514	0.539214	0.660513	ENSG00000057593	F7
ENSG00000057608	100.952	82.4159	58.247	58.9588	ENSG00000057608	GDI2
ENSG00000057657	25.3234	17.6491	14.0995	39.2621	ENSG00000057657	PRDM1
ENSG00000057663	17.3191	18.5972	12.3897	12.8978	ENSG00000057663	ATG5
ENSG00000057704	26.6684	15.3344	7.02754	13.1493	ENSG00000057704	TMCC3
ENSG00000057757	17.1734	15.0764	18.6597	12.5909	ENSG00000057757	PITHD1
ENSG00000057935	19.7261	25.9221	24.4055	32.5655	ENSG00000057935	MTA3
ENSG00000058056	1.12149	2.20856	1.87104	5.17478	ENSG00000058056	USP13
ENSG00000058063	84.6071	76.8601	50.3854	47.6533	ENSG00000058063	ATP11B
ENSG00000058085	3810.78	5261.78	1710.87	3132.33	ENSG00000058085	LAMC2
ENSG00000058091	10.6126	8.3834	7.13332	19.5516	ENSG00000058091	CDK14
ENSG00000058262	132.555	171.427	165.987	92.5484	ENSG00000058262	SEC61A1
ENSG00000058272	50.23	62.6375	51.2682	72.0287	ENSG00000058272	PPP1R12A
ENSG00000058335	0.130959	1.55955	0.771157	1.0747	ENSG00000058335	RASGRF1
ENSG00000058404	9.21493	10.6963	11.0031	12.3112	ENSG00000058404	CAMK2B
ENSG00000058453	24.8272	54.7253	41.4081	55.2333	ENSG00000058453	CROCC
ENSG00000058600	30.4482	39.5176	45.6831	31.9637	ENSG00000058600	POLR3E
ENSG00000058668	119.006	124.171	62.4545	70.5201	ENSG00000058668	ATP2B4
ENSG00000058673	79.6063	89.7108	84.0081	79.0996	ENSG00000058673	ZC3H11A
ENSG00000058729	19.3158	18.4608	21.7686	16.7502	ENSG00000058729	RIOK2
ENSG00000058799	22.4317	16.1794	10.6508	7.82342	ENSG00000058799	YIPF1
ENSG00000058804	18.1686	35.6745	12.3641	8.19996	ENSG00000058804	NDC1
ENSG00000058866	1.16878	2.09739	1.65267	3.11164	ENSG00000058866	DGKG
ENSG00000059122	38.0867	65.701	64.4945	63.4971	ENSG00000059122	FLYWCH1
ENSG00000059145	7.33957	8.98838	11.1762	12.4308	ENSG00000059145	UNKL
ENSG00000059377	6.37358	17.1562	10.553	18.2179	ENSG00000059377	TBXAS1
ENSG00000059378	17.6402	44.9709	37.5002	45.6175	ENSG00000059378	PARP12
ENSG00000059573	26.0312	32.255	22.235	28.6246	ENSG00000059573	ALDH18A1
ENSG00000059588	10.6131	17.8808	17.5425	23.1245	ENSG00000059588	TARBP1
ENSG00000059691	9.06489	9.70232	11.0605	7.59591	ENSG00000059691	GATB

ENSG00000059728	15.4807	9.2422	11.0664	4.76024	ENSG00000059728	MXD1
ENSG00000059758	36.0779	56.7516	41.768	81.9213	ENSG00000059758	CDK17
ENSG00000059769	13.225	5.66739	4.26297	10.9484	ENSG00000059769	DNAJC25
ENSG00000059804	22.5229	63.9528	52.7738	48.2195	ENSG00000059804	SLC2A3
ENSG00000059915	1.44059	2.45874	2.47883	2.85102	ENSG00000059915	PSD
ENSG00000060069	13.233	11.3641	13.2986	15.9296	ENSG00000060069	CTDP1
ENSG00000060138	111.598	121.104	150.85	99.0748	ENSG00000060138	YBX3
ENSG00000060140	4.96963	8.31524	4.4387	6.54006	ENSG00000060140	STYK1
ENSG00000060237	75.6675	79.903	110.119	112.891	ENSG00000060237	WNK1
ENSG00000060303	0	0.198001	0	0.439373	ENSG00000060303	RPS17P5
ENSG00000060339	38.8389	47.294	61.8091	55.9077	ENSG00000060339	CCAR1
ENSG00000060491	23.1932	15.7322	15.2211	18.2081	ENSG00000060491	OGFR
ENSG00000060558	52.6443	48.0602	29.641	15.8713	ENSG00000060558	GNA15
ENSG00000060566	0.0245794	0.144255	0.110825	0.189164	ENSG00000060566	CREB3L3
ENSG00000060642	14.2376	21.7737	12.5684	5.69727	ENSG00000060642	PIGV
ENSG00000060656	20.4691	20.7919	14.9385	17.2078	ENSG00000060656	PTPRU
ENSG00000060688	21.3731	26.7546	27.5772	17.951	ENSG00000060688	SNRNP40
ENSG00000060709	1.06149	1.25042	2.27711	1.65759	ENSG00000060709	RIMBP2
ENSG00000060718	1.51138	1.1893	1.58663	53.6521	ENSG00000060718	COL11A1
ENSG00000060749	10.1144	16.662	12.6459	19.0358	ENSG00000060749	QSER1
ENSG00000060762	15.3889	12.5894	10.7863	9.73284	ENSG00000060762	MPC1
ENSG00000060971	23.6773	35.113	38.94	43.6515	ENSG00000060971	ACAA1
ENSG00000060982	7.45029	12.7211	33.3559	28.3559	ENSG00000060982	BCAT1
ENSG00000061273	29.2645	38.2276	33.1747	53.9795	ENSG00000061273	HDAC7
ENSG00000061337	0.833318	1.68402	0.929862	1.11775	ENSG00000061337	LZTS1
ENSG00000061455	0.948338	2.22947	0.860491	0.964574	ENSG00000061455	PRDM6
ENSG00000061492	0	0.0483294	0	0.0548148	ENSG00000061492	WNT8A
ENSG00000061656	7.08979	8.42092	6.39855	10.3942	ENSG00000061656	SPAG4
ENSG00000061676	100.401	113.894	96.1158	87.6963	ENSG00000061676	NCKAP1
ENSG00000061794	29.7452	18.9247	14.9165	12.2178	ENSG00000061794	MRPS35
ENSG00000061918	3.2277	0.683838	0.466464	3.03517	ENSG00000061918	GUCY1B3
ENSG00000061936	18.7625	24.6586	27.6078	32.3976	ENSG00000061936	SFSWAP
ENSG00000061938	21.9325	39.1462	35.5758	38.6965	ENSG00000061938	TNK2
ENSG00000061987	16.4877	31.936	25.2255	37.1266	ENSG00000061987	MON2
ENSG00000062038	627.863	1010.59	830.513	308.476	ENSG00000062038	CDH3
ENSG00000062096	0.0562749	0.273411	0.167241	0.629053	ENSG00000062096	ARSF
ENSG00000062194	30.0045	41.7399	34.0756	37.8586	ENSG00000062194	GPBP1
ENSG00000062282	4.49462	3.96415	12.8892	4.50545	ENSG00000062282	DGAT2
ENSG00000062370	2.75733	5.48613	4.54892	5.04933	ENSG00000062370	ZNF112
ENSG00000062485	66.0734	66.6659	68.1702	74.682	ENSG00000062485	CS
ENSG00000062524	0.143736	0.0356781	0	0.0592801	ENSG00000062524	LTK
ENSG00000062582	35.4436	36.7557	20.587	25.0945	ENSG00000062582	MRPS24
ENSG00000062598	11.0575	14.0008	13.6952	15.2041	ENSG00000062598	ELMO2
ENSG00000062650	21.8496	19.4353	24.3803	23.0341	ENSG00000062650	WAPL
ENSG00000062716	249.043	243.038	162.189	280.738	ENSG00000062716	VMP1
ENSG00000062725	18.1143	15.4997	18.4408	14.9113	ENSG00000062725	APPBP2
ENSG00000062822	15.3821	34.1115	14.837	19.326	ENSG00000062822	POLD1
ENSG00000063015	3.96817	1.6904	2.6771	3.56195	ENSG00000063015	SEZ6
ENSG00000063046	159.812	135.418	130.427	136.197	ENSG00000063046	EIF4B
ENSG00000063127	2.50262	3.53754	5.18114	10.6914	ENSG00000063127	SLC6A16
ENSG00000063169	4.21276	6.51871	7.64928	12.7188	ENSG00000063169	BICRA
ENSG00000063176	9.24432	11.7431	11.3559	16.4141	ENSG00000063176	SPHK2
ENSG00000063177	608.729	442.248	362.995	236.017	ENSG00000063177	RPL18
ENSG00000063180	1.61869	2.58694	5.18382	1.46469	ENSG00000063180	CA11

ENSG00000063241	13.5306	21.1563	12.208	10.1258	ENSG00000063241	ISOC2
ENSG00000063244	55.5504	56.8681	59.2703	56.3822	ENSG00000063244	U2AF2
ENSG00000063245	35.9256	31.4445	27.0671	29.29	ENSG00000063245	EPN1
ENSG00000063322	12.3768	10.9634	11.7579	12.6843	ENSG00000063322	MED29
ENSG00000063438	1.08288	1.39119	2.06679	26.3182	ENSG00000063438	AHRR
ENSG00000063515	0	0	0	0	ENSG00000063515	GSC2
ENSG00000063587	0.914306	1.35958	1.51305	1.99595	ENSG00000063587	ZNF275
ENSG00000063601	16.2165	13.7313	9.93321	13.3898	ENSG00000063601	MTMR1
ENSG00000063660	89.4666	170.847	158.503	62.0074	ENSG00000063660	GPC1
ENSG00000063761	6.88789	5.81233	8.0246	7.4776	ENSG00000063761	ADCK1
ENSG00000063854	24.7491	21.0383	21.2038	21.1751	ENSG00000063854	HAGH
ENSG00000063978	100.925	89.2481	86.3009	69.7119	ENSG00000063978	RNF4
ENSG00000064012	15.2168	22.8424	21.2099	28.9398	ENSG00000064012	CASP8
ENSG00000064042	9.51291	8.08772	4.85212	9.93655	ENSG00000064042	LIMCH1
ENSG00000064102	17.611	23.8076	21.0619	19.8734	ENSG00000064102	INTS13
ENSG00000064115	112.788	157.271	120.972	53.6146	ENSG00000064115	TM7SF3
ENSG00000064195	0.637018	0.588237	1.52406	1.29071	ENSG00000064195	DLX3
ENSG00000064199	7.58773	13.7743	7.18923	12.5779	ENSG00000064199	SPA17
ENSG00000064201	0.64682	0.975616	1.15157	1.10916	ENSG00000064201	TSPAN32
ENSG00000064205	2.51708	3.17806	3.52962	4.93637	ENSG00000064205	WISP2
ENSG00000064218	0.178929	0.495646	0	0.711585	ENSG00000064218	DMRT3
ENSG00000064225	18.7008	29.9692	12.5542	36.3729	ENSG00000064225	ST3GAL6
ENSG00000064270	12.5014	48.3819	28.9353	20.9773	ENSG00000064270	ATP2C2
ENSG00000064300	0.652731	32.679	3.13858	4.76423	ENSG00000064300	NGFR
ENSG00000064309	1.45502	2.59261	1.90178	2.95287	ENSG00000064309	CDON
ENSG00000064313	23.8781	30.4499	28.2718	31.1648	ENSG00000064313	TAF2
ENSG00000064393	19.1967	23.4185	19.1131	37.2897	ENSG00000064393	HIPK2
ENSG00000064419	18.2219	22.2803	17.9962	16.4754	ENSG00000064419	TNPO3
ENSG00000064489	3.92692	3.33669	2.43089	4.02264	ENSG00000064489	BORCS8-MEF2B
ENSG00000064490	43.1369	46.9604	53.4997	26.5498	ENSG00000064490	RFXANK
ENSG00000064545	20.1431	32.2595	24.968	20.9233	ENSG00000064545	TMEM161A
ENSG00000064547	17.8644	19.0892	19.2953	6.94062	ENSG00000064547	LPAR2
ENSG00000064601	67.721	46.3455	47.1147	47.9983	ENSG00000064601	CTSA
ENSG00000064607	46.7798	66.13	60.7852	68.1129	ENSG00000064607	SUGP2
ENSG00000064651	19.1464	32.8375	20.2087	24.0377	ENSG00000064651	SLC12A2
ENSG00000064652	22.196	17.1674	22.9908	17.5433	ENSG00000064652	SNX24
ENSG00000064655	0.575444	3.70425	3.36945	12.9664	ENSG00000064655	EYA2
ENSG00000064666	107.434	125.616	89.1269	98.9499	ENSG00000064666	CNN2
ENSG00000064687	21.7265	37.272	22.0761	26.4485	ENSG00000064687	ABCA7
ENSG00000064692	1.00122	1.15343	1.38958	3.8158	ENSG00000064692	SNCAIP
ENSG00000064703	6.31364	7.89985	7.30413	5.24619	ENSG00000064703	DDX20
ENSG00000064726	47.2073	63.5832	60.9932	95.4036	ENSG00000064726	BTBD1
ENSG00000064763	9.14331	15.5389	12.5834	14.8023	ENSG00000064763	FAR2
ENSG00000064787	0.660068	0.967073	0.938421	1.99962	ENSG00000064787	BCAS1
ENSG00000064835	0.116881	0.114216	0.411086	0.114451	ENSG00000064835	POU1F1
ENSG00000064886	6.9982	1.66214	1.40655	1.96566	ENSG00000064886	CHI3L2
ENSG00000064932	37.9048	49.2445	55.2745	51.8131	ENSG00000064932	SBNO2
ENSG00000064933	11.5679	24.511	18.1743	26.402	ENSG00000064933	PMS1
ENSG00000064961	27.5801	38.8108	31.8711	40.0851	ENSG00000064961	HMG20B
ENSG00000064989	4.83854	9.43827	9.02175	12.4607	ENSG00000064989	CALCRL
ENSG00000064995	11.7466	11.622	14.4198	12.3895	ENSG00000064995	TAF11
ENSG00000064999	10.3889	9.6312	9.64322	7.82405	ENSG00000064999	ANKS1A
ENSG00000065000	58.0514	61.4882	66.7233	51.7838	ENSG00000065000	AP3D1
ENSG00000065029	9.65178	14.3126	13.1847	14.0438	ENSG00000065029	ZNF76

ENSG00000065054	4.88222	5.50817	5.71794	12.0347	ENSG00000065054	SLC9A3R2
ENSG00000065057	4.94057	8.45283	3.49092	7.82794	ENSG00000065057	NTHL1
ENSG00000065060	3.87978	6.92274	6.81381	4.18619	ENSG00000065060	UHRF1BP1
ENSG00000065135	40.7634	33.0661	26.8529	20.9326	ENSG00000065135	GNAI3
ENSG00000065150	45.7574	69.8093	60.9248	76.8639	ENSG00000065150	IPO5
ENSG00000065154	112.537	80.8311	43.4157	60.0824	ENSG00000065154	OAT
ENSG00000065183	15.5426	17.3113	19.0303	13.2165	ENSG00000065183	WDR3
ENSG00000065243	46.7342	38.6226	32.0825	35.1517	ENSG00000065243	PKN2
ENSG00000065268	17.1209	34.4693	19.4437	12.8618	ENSG00000065268	WDR18
ENSG00000065308	3.75814	11.8167	9.43498	39.3673	ENSG00000065308	TRAM2
ENSG00000065320	0.387695	1.23711	2.86184	2.27942	ENSG00000065320	NTN1
ENSG00000065325	0.572065	1.1018	1.16915	1.95172	ENSG00000065325	GLP2R
ENSG00000065328	2.17372	8.11424	1.10703	5.24278	ENSG00000065328	MCM10
ENSG00000065357	145.78	281.677	249.746	187.106	ENSG00000065357	DGKA
ENSG00000065361	47.9521	32.5184	21.6285	20.9089	ENSG00000065361	ERBB3
ENSG00000065371	0.482862	0.426342	0.264466	0.467896	ENSG00000065371	ROPN1
ENSG00000065413	1.94556	2.48263	1.53226	6.56322	ENSG00000065413	ANKRD44
ENSG00000065427	66.6498	57.168	38.3395	37.1449	ENSG00000065427	KARS
ENSG00000065457	37.359	51.0205	60.749	47.9844	ENSG00000065457	ADAT1
ENSG00000065485	16.237	33.8508	25.2723	38.0322	ENSG00000065485	PDIA5
ENSG00000065491	5.76087	4.27634	4.65421	3.57855	ENSG00000065491	TBC1D22B
ENSG00000065518	62.9333	45.8405	30.3927	22.9665	ENSG00000065518	NDUFB4
ENSG00000065526	23.4125	33.6582	33.0975	38.6982	ENSG00000065526	SPEN
ENSG00000065534	10.047	14.2698	17.7368	38.9425	ENSG00000065534	MYLK
ENSG00000065548	40.5499	37.9661	45.4644	34.6283	ENSG00000065548	ZC3H15
ENSG00000065559	20.3591	25.0496	19.2426	18.283	ENSG00000065559	MAP2K4
ENSG00000065600	19.2062	21.4748	11.164	10.0953	ENSG00000065600	TMEM206
ENSG00000065609	0.158276	0.754233	1.22273	1.80853	ENSG00000065609	SNAP91
ENSG00000065613	69.5606	45.5684	42.323	36.6694	ENSG00000065613	SLK
ENSG00000065615	11.3561	13.7481	12.7341	20.2292	ENSG00000065615	CYB5R4
ENSG00000065618	1244.03	2030.98	1093.88	890.269	ENSG00000065618	COL17A1
ENSG00000065621	19.6897	35.5826	33.3527	23.0825	ENSG00000065621	GSTO2
ENSG00000065665	9.20008	14.3104	13.1924	12.3739	ENSG00000065665	SEC61A2
ENSG00000065675	2.38936	4.14182	2.81157	1.74894	ENSG00000065675	PRKCQ
ENSG00000065717	2.43811	5.58037	9.25529	9.81496	ENSG00000065717	TLE2
ENSG00000065802	12.9063	25.5041	30.5988	24.2254	ENSG00000065802	ASB1
ENSG00000065809	4.29086	11.6344	4.14145	9.87534	ENSG00000065809	FAM107B
ENSG00000065833	24.2966	14.6697	14.6184	15.6507	ENSG00000065833	ME1
ENSG00000065882	27.6305	44.7588	23.4597	44.3876	ENSG00000065882	TBC1D1
ENSG00000065883	16.8566	20.6382	23.4818	22.2428	ENSG00000065883	CDK13
ENSG00000065911	17.0919	83.9122	90.2734	27.6047	ENSG00000065911	MTHFD2
ENSG00000065923	16.5862	16.4265	5.48013	8.0662	ENSG00000065923	SLC9A7
ENSG00000065970	5.80276	7.39312	9.64525	11.0053	ENSG00000065970	FOXJ2
ENSG00000065978	149.669	164.211	113.359	102.922	ENSG00000065978	YBX1
ENSG00000065989	0.382044	0.86528	0.545026	2.44661	ENSG00000065989	PDE4A
ENSG00000066027	14.3084	21.8978	14.4625	14.3616	ENSG00000066027	PPP2R5A
ENSG00000066032	0.16342	0.29134	0.391294	0.996151	ENSG00000066032	CTNNA2
ENSG00000066044	28.2452	42.488	39.655	62.3861	ENSG00000066044	ELAVL1
ENSG00000066056	0.901644	1.79997	2.07475	3.86955	ENSG00000066056	TIE1
ENSG00000066084	36.1186	22.0982	22.1386	22.0614	ENSG00000066084	DIP2B
ENSG00000066117	27.2121	58.8307	47.8093	34.5983	ENSG00000066117	SMARCD1
ENSG00000066135	22.5572	30.1148	46.1098	28.3948	ENSG00000066135	KDM4A
ENSG00000066136	16.1273	21.9143	22.2519	22.7497	ENSG00000066136	NFYC
ENSG00000066185	0.1	0.382601	0.299637	0.271086	ENSG00000066185	ZMYND12

ENSG00000066230	19.9258	10.4346	35.5762	8.02821	ENSG00000066230	SLC9A3
ENSG00000066248	2.03734	2.56103	2.43032	3.35063	ENSG00000066248	NGEF
ENSG00000066279	5.39843	32.6245	2.56178	12.9188	ENSG00000066279	ASPM
ENSG00000066294	0.537797	1.05698	0.788657	1.63124	ENSG00000066294	CD84
ENSG00000066322	129.964	169.669	71.9595	38.7035	ENSG00000066322	ELOVL1
ENSG00000066336	0.342982	0.246652	0.339128	0.116551	ENSG00000066336	SPI1
ENSG00000066379	1.76344	1.90335	1.53231	0.855655	ENSG00000066379	ZNRD1
ENSG00000066382	1.00077	2.95387	2.32722	4.67503	ENSG00000066382	MPPED2
ENSG00000066405	0.649029	2.14684	1.88532	4.30394	ENSG00000066405	CLDN18
ENSG00000066422	17.4108	18.6851	19.1247	20.2171	ENSG00000066422	ZBTB11
ENSG00000066427	20.1818	28.3977	26.6258	35.9981	ENSG00000066427	ATXN3
ENSG00000066455	20.6101	15.7978	17.7161	13.5739	ENSG00000066455	GOLGA5
ENSG00000066468	10.4947	23.6789	26.7633	13.4862	ENSG00000066468	FGFR2
ENSG00000066557	9.94214	11.407	7.90668	8.7713	ENSG00000066557	LRRC40
ENSG00000066583	4.28238	4.76011	3.65884	4.47618	ENSG00000066583	ISOC1
ENSG00000066629	13.5853	9.23539	11.958	27.7587	ENSG00000066629	EML1
ENSG00000066651	13.7984	26.4816	23.5554	14.9929	ENSG00000066651	TRMT11
ENSG00000066654	19.2596	19.2076	25.2104	15.9702	ENSG00000066654	THUMPD1
ENSG00000066697	17.3267	23.7115	11.3281	24.993	ENSG00000066697	MSANTD3
ENSG00000066735	0.340077	0.284343	0.193235	0.357543	ENSG00000066735	KIF26A
ENSG00000066739	9.32528	17.7102	17.7763	19.806	ENSG00000066739	ATG2B
ENSG00000066777	34.2762	47.4084	42.4012	42.4284	ENSG00000066777	ARFGEF1
ENSG00000066813	9.66763	31.2617	33.0831	38.5643	ENSG00000066813	ACSM2B
ENSG00000066827	3.85798	4.46814	4.181	7.24033	ENSG00000066827	ZFAT
ENSG00000066855	30.2314	49.8403	34.0542	43.7008	ENSG00000066855	MTFR1
ENSG00000066923	6.17527	7.85914	9.4561	11.805	ENSG00000066923	STAG3
ENSG00000066926	10.6623	7.52828	12.6381	9.00804	ENSG00000066926	FECH
ENSG00000066933	19.3053	35.2931	29.9524	38.1157	ENSG00000066933	MYO9A
ENSG00000067048	22.8024	31.8113	25.1854	0.451518	ENSG00000067048	DDX3Y
ENSG00000067057	106.833	94.1427	55.4361	83.472	ENSG00000067057	PFKP
ENSG00000067064	94.0933	38.8541	16.4304	46.1843	ENSG00000067064	IDI1
ENSG00000067066	42.6598	85.7709	80.0424	110.699	ENSG00000067066	SP100
ENSG00000067082	70.2429	64.5773	55.1519	151.868	ENSG00000067082	KLF6
ENSG00000067113	7.72467	11.0187	11.3957	7.59003	ENSG00000067113	PLPP1
ENSG00000067141	11.1137	31.1716	30.0328	30.4052	ENSG00000067141	NEO1
ENSG00000067167	133.939	122.634	92.2431	56.7461	ENSG00000067167	TRAM1
ENSG00000067177	2.92766	3.5494	3.07844	1.69032	ENSG00000067177	PHKA1
ENSG00000067182	147.544	146.083	101.357	58.8762	ENSG00000067182	TNFRSF1A
ENSG00000067191	7.12787	9.5505	14.4228	13.0404	ENSG00000067191	CACNB1
ENSG00000067208	43.0101	33.0412	32.3072	75.2034	ENSG00000067208	EVI5
ENSG00000067221	12.8055	9.73893	13.2077	6.77335	ENSG00000067221	STOML1
ENSG00000067225	810.762	814.339	614.086	613.27	ENSG00000067225	PKM
ENSG00000067248	17.3208	17.4468	13.6938	15.932	ENSG00000067248	DHX29
ENSG00000067334	24.9638	28.695	29.1273	33.1353	ENSG00000067334	DNTTIP2
ENSG00000067365	24.4085	24.5003	46.1502	35.3622	ENSG00000067365	METTL22
ENSG00000067369	16.2956	23.9996	34.8991	29.338	ENSG00000067369	TP53BP1
ENSG00000067445	1.7734	4.79323	2.30561	7.0599	ENSG00000067445	TRO
ENSG00000067533	13.3175	11.6236	11.7502	10.7128	ENSG00000067533	RRP15
ENSG00000067560	148.626	113.886	78.7794	110.028	ENSG00000067560	RHOA
ENSG00000067596	27.579	33.1462	28.0464	27.5306	ENSG00000067596	DHX8
ENSG00000067601	5.37156	4.71419	5.8275	4.15763	ENSG00000067601	PMS2P4
ENSG00000067606	28.6249	32.9397	32.4965	26.7241	ENSG00000067606	PRKCZ
ENSG00000067646	6.00848	5.66845	6.87843	0.316864	ENSG00000067646	ZFY
ENSG00000067704	63.2597	64.3045	44.2412	33.9182	ENSG00000067704	IARS2

ENSG00000067715	5.37543	4.92717	9.11173	9.87192	ENSG00000067715	SYT1
ENSG00000067798	46.8715	87.4299	46.331	143.982	ENSG00000067798	NAV3
ENSG00000067829	13.2432	10.9375	11.4417	9.30879	ENSG00000067829	IDH3G
ENSG00000067836	17.4227	15.0541	11.0862	6.58422	ENSG00000067836	ROGDI
ENSG00000067840	0.262064	0.243797	0.268805	0.279114	ENSG00000067840	PDZD4
ENSG00000067842	0.254553	0.470077	0.436185	0.673166	ENSG00000067842	ATP2B3
ENSG00000067900	26.4145	45.3328	48.1943	65.8625	ENSG00000067900	ROCK1
ENSG00000067955	30.3732	38.5176	28.3652	34.0638	ENSG00000067955	CBFB
ENSG00000067992	3.04963	4.89	3.11299	5.90073	ENSG00000067992	PDK3
ENSG00000068001	24.5025	22.147	12.4125	8.03161	ENSG00000068001	HYAL2
ENSG00000068024	15.4486	18.5821	23.6225	84.5993	ENSG00000068024	HDAC4
ENSG00000068028	6.14637	7.01161	5.912	6.24327	ENSG00000068028	RASSF1
ENSG00000068078	22.1129	83.224	65.3182	23.5763	ENSG00000068078	FGFR3
ENSG00000068079	11.8417	29.6187	23.0777	31.352	ENSG00000068079	IFI35
ENSG00000068097	12.3235	22.618	18.3465	18.9949	ENSG00000068097	HEATR6
ENSG00000068120	25.5028	29.8541	34.4509	25.1055	ENSG00000068120	COASY
ENSG00000068137	22.2739	29.9159	32.0298	14.1291	ENSG00000068137	PLEKHH3
ENSG00000068305	14.963	27.9988	30.4477	25.9283	ENSG00000068305	MEF2A
ENSG00000068308	11.1845	9.14964	10.0762	8.41283	ENSG00000068308	OTUD5
ENSG00000068323	8.66349	8.20364	17.4769	12.9973	ENSG00000068323	TFE3
ENSG00000068354	2.00044	1.95348	3.02316	3.37218	ENSG00000068354	TBC1D25
ENSG00000068366	38.9926	62.6172	35.6465	63.9197	ENSG00000068366	ACSL4
ENSG00000068383	6.66766	7.62587	5.47718	7.80336	ENSG00000068383	INPP5A
ENSG00000068394	4.99587	3.68374	4.05098	3.36238	ENSG00000068394	GPKOW
ENSG00000068400	10.7219	17.8427	20.3373	22.298	ENSG00000068400	GRIPAP1
ENSG00000068438	28.2933	21.6229	22.2273	16.2441	ENSG00000068438	FTSJ1
ENSG00000068489	13.3681	34.8754	11.4735	29.7216	ENSG00000068489	PRR11
ENSG00000068615	0.714742	2.07732	1.1262	1.89615	ENSG00000068615	REEP1
ENSG00000068650	22.9111	32.9474	28.9667	39.9546	ENSG00000068650	ATP11A
ENSG00000068654	19.3982	22.8009	34.7304	21.4315	ENSG00000068654	POLR1A
ENSG00000068697	57.2137	72.2324	62.7203	56.5241	ENSG00000068697	LAPTM4A
ENSG00000068724	15.71	20.4015	12.8467	30.649	ENSG00000068724	TTC7A
ENSG00000068745	59.5835	80.0483	86.8029	59.5445	ENSG00000068745	IP6K2
ENSG00000068781	1.6055	3.04633	3.02908	2.69897	ENSG00000068781	STON1-GTF2A1L
ENSG00000068784	7.56161	13.8906	11.8245	13.5277	ENSG00000068784	SRBD1
ENSG00000068793	54.8329	62.3235	43.4025	49.8296	ENSG00000068793	CYFIP1
ENSG00000068796	19.3148	27.2527	21.2935	27.344	ENSG00000068796	KIF2A
ENSG00000068831	1.25037	1.85523	1.49586	3.28455	ENSG00000068831	RASGRP2
ENSG00000068878	38.9479	50.3344	36.5996	57.5415	ENSG00000068878	PSME4
ENSG00000068885	26.8538	47.9249	43.6291	54.2567	ENSG00000068885	IFT80
ENSG00000068903	29.9736	45.9925	42.2673	50.9552	ENSG00000068903	SIRT2
ENSG00000068912	37.0289	36.015	21.4241	31.4598	ENSG00000068912	ERLEC1
ENSG00000068971	27.9857	21.3052	29.4279	20.0797	ENSG00000068971	PPP2R5B
ENSG00000068976	0.902632	2.36769	2.39945	4.30938	ENSG00000068976	PYGM
ENSG00000068985	0	0	0.0889759	0	ENSG00000068985	PAGE1
ENSG00000069011	30.3649	4.0276	2.01132	5.48585	ENSG00000069011	PITX1
ENSG00000069018	0.822155	2.27421	2.26251	2.13175	ENSG00000069018	TRPC7
ENSG00000069020	65.5461	70.552	60.0645	44.0027	ENSG00000069020	MAST4
ENSG00000069122	0.061613	0.0970606	0.115495	0.267973	ENSG00000069122	ADGRF5
ENSG00000069188	13.6219	34.9373	61.457	49.0872	ENSG00000069188	SDK2
ENSG00000069206	0.24171	0.865677	0.796992	1.54411	ENSG00000069206	ADAM7
ENSG00000069248	22.6481	36.5799	26.367	32.6369	ENSG00000069248	NUP133
ENSG00000069275	25.1722	64.5376	53.4448	45.3123	ENSG00000069275	NUCKS1
ENSG00000069329	69.0957	54.3517	44.49	45.0024	ENSG00000069329	VPS35

ENSG00000069345	46.7319	35.0379	34.4333	27.1913	ENSG00000069345	DNAJA2
ENSG00000069399	10.1401	8.33655	8.42931	13.3911	ENSG00000069399	BCL3
ENSG00000069424	1.38474	5.41558	5.95263	8.11921	ENSG00000069424	KCNAB2
ENSG00000069431	3.19579	6.25093	6.24846	14.9589	ENSG00000069431	ABCC9
ENSG00000069482	7.95726	1.28753	1.24388	0.940155	ENSG00000069482	GAL
ENSG00000069493	4.36619	25.5321	20.7472	21.5909	ENSG00000069493	CLEC2D
ENSG00000069509	4.94626	5.54183	4.57332	3.85044	ENSG00000069509	FUNDC1
ENSG00000069535	2.69964	3.75772	4.27126	7.2372	ENSG00000069535	MAOB
ENSG00000069667	10.3088	8.37942	7.96664	26.7881	ENSG00000069667	RORA
ENSG00000069696	1.59087	4.63177	3.26612	9.44876	ENSG00000069696	DRD4
ENSG00000069702	2.76128	1.13916	1.36497	3.27312	ENSG00000069702	TGFBR3
ENSG00000069712	2.24566	3.15854	1.31925	2.59835	ENSG00000069712	KIAA1107
ENSG00000069764	2.76164	5.18701	3.267	3.63726	ENSG00000069764	PLA2G10
ENSG00000069812	99.383	36.6588	77.3428	33.6958	ENSG00000069812	HES2
ENSG00000069849	78.9257	120.307	88.7098	70.2954	ENSG00000069849	ATP1B3
ENSG00000069869	148.856	344.91	371.343	974.435	ENSG00000069869	NEDD4
ENSG00000069943	20.3872	36.8426	30.89	39.5943	ENSG00000069943	PIGB
ENSG00000069956	65.1259	75.4424	82.6282	51.8017	ENSG00000069956	MAPK6
ENSG00000069966	16.6979	19.3746	17.1294	26.776	ENSG00000069966	GNB5
ENSG00000069974	4.15189	12.0461	12.8266	14.7319	ENSG00000069974	RAB27A
ENSG00000069998	9.29516	13.6887	14.8745	9.15839	ENSG00000069998	HDHD5
ENSG00000070010	31.6739	21.421	27.2426	16.7765	ENSG00000070010	UFD1
ENSG00000070018	11.1848	15.119	13.1803	15.3248	ENSG00000070018	LRP6
ENSG00000070019	0.141132	0.0684708	0.0450267	0.108746	ENSG00000070019	GUCY2C
ENSG00000070031	0.508923	1.41444	0.852682	2.11941	ENSG00000070031	SCT
ENSG00000070047	18.9634	19.4688	19.2752	22.5942	ENSG00000070047	PHRF1
ENSG00000070061	22.7367	27.9881	21.1031	18.5269	ENSG00000070061	ELP1
ENSG00000070081	31.8386	79.4295	30.4365	56.3462	ENSG00000070081	NUCB2
ENSG00000070087	45.3506	54.7842	60.5683	52.1031	ENSG00000070087	PFN2
ENSG00000070159	29.898	38.0635	30.2808	34.8287	ENSG00000070159	PTPN3
ENSG00000070182	11.6547	22.418	12.5406	10.9357	ENSG00000070182	SPTB
ENSG00000070190	81.103	39.3251	30.5232	18.0976	ENSG00000070190	DAPP1
ENSG00000070193	0.229555	0.253277	0.404959	0.969445	ENSG00000070193	FGF10
ENSG00000070214	27.4876	40.8507	22.7731	20.5202	ENSG00000070214	SLC44A1
ENSG00000070269	14.0758	25.3091	23.5389	20.5647	ENSG00000070269	TMEM260
ENSG00000070366	18.4883	23.7393	27.4416	35.4085	ENSG00000070366	SMG6
ENSG00000070367	28.8804	22.0874	27.4564	29.0895	ENSG00000070367	EXOC5
ENSG00000070371	6.64859	13.1392	22.8144	16.1143	ENSG00000070371	CLTCL1
ENSG00000070388	0.632908	1.32026	1.51101	1.943	ENSG00000070388	FGF22
ENSG00000070404	156.928	87.9328	73.3784	66.3626	ENSG00000070404	FSTL3
ENSG00000070413	60.3114	53.2293	56.6913	22.5687	ENSG00000070413	DGCR2
ENSG00000070423	52.287	50.2915	56.6455	28.5304	ENSG00000070423	RNF126
ENSG00000070444	15.7104	17.9685	20.0226	17.7022	ENSG00000070444	MNT
ENSG00000070476	9.77645	17.0911	17.464	11.4803	ENSG00000070476	ZXDC
ENSG00000070495	15.026	12.6295	14.6334	14.5044	ENSG00000070495	JMJD6
ENSG00000070501	21.1797	30.8251	21.737	29.431	ENSG00000070501	POLB
ENSG00000070526	4.25943	4.8102	6.27126	10.7829	ENSG00000070526	ST6GALNAC1
ENSG00000070540	21.6831	26.7265	29.4513	50.1731	ENSG00000070540	WIPI1
ENSG00000070601	9.61442	19.0964	16.0918	39.7116	ENSG00000070601	FRMPD1
ENSG00000070610	32.8139	44.6082	45.444	38.9939	ENSG00000070610	GBA2
ENSG00000070614	83.7505	57.137	76.334	72.3439	ENSG00000070614	NDST1
ENSG00000070669	16.268	174.049	133.614	61.7451	ENSG00000070669	ASNS
ENSG00000070718	14.7735	22.8879	19.1301	20.1096	ENSG00000070718	AP3M2
ENSG00000070729	2.60224	1.7924	1.42722	2.3749	ENSG00000070729	CNGB1

ENSG00000070731	86.0417	83.0291	93.6817	54.169	ENSG00000070731	ST6GALNAC2
ENSG00000070748	0	0.0217531	0.0590472	0.517007	ENSG00000070748	CHAT
ENSG00000070756	264.706	276.266	336.001	368.889	ENSG00000070756	PABPC1
ENSG00000070759	1.83055	2.04593	1.94863	1.04489	ENSG00000070759	TESK2
ENSG00000070761	15.6768	18.1532	12.7664	9.47931	ENSG00000070761	CFAP20
ENSG00000070770	19.5456	22.6894	28.309	20.1548	ENSG00000070770	CSNK2A2
ENSG00000070778	8.21395	10.3338	11.7564	14.2645	ENSG00000070778	PTPN21
ENSG00000070785	17.2018	23.2424	21.6926	25.5743	ENSG00000070785	EIF2B3
ENSG00000070808	0.865927	1.58112	1.23898	2.29165	ENSG00000070808	CAMK2A
ENSG00000070814	14.04	31.5832	19.9941	26.8755	ENSG00000070814	TCOF1
ENSG00000070831	169.475	98.1512	83.5551	61.7762	ENSG00000070831	CDC42
ENSG00000070882	36.9727	49.945	28.7166	36.0805	ENSG00000070882	OSBPL3
ENSG00000070886	0.467182	0.832508	0.6412	0.913117	ENSG00000070886	EPHA8
ENSG00000070915	0.381689	0.709857	0.569231	0.916136	ENSG00000070915	SLC12A3
ENSG00000070950	10.3179	18.41	10.9081	19.4942	ENSG00000070950	RAD18
ENSG00000070961	24.4531	42.6093	46.9564	42.6853	ENSG00000070961	ATP2B1
ENSG00000070985	0.224049	0.192266	0.238308	0.185318	ENSG00000070985	TRPM5
ENSG00000071051	26.0329	23.196	35.9046	19.6928	ENSG00000071051	NCK2
ENSG00000071054	88.883	74.1849	50.3376	105.859	ENSG00000071054	MAP4K4
ENSG00000071073	2.25902	1.45418	0.847596	1.12196	ENSG00000071073	MGAT4A
ENSG00000071082	725.634	574.677	430.073	275.512	ENSG00000071082	RPL31
ENSG00000071127	125.767	122.258	103.564	110.265	ENSG00000071127	WDR1
ENSG00000071189	32.3022	36.2163	29.1953	36.0328	ENSG00000071189	SNX13
ENSG00000071203	0.371462	0.353124	0.119526	0.22433	ENSG00000071203	MS4A12
ENSG00000071205	12.1738	18.6001	14.1085	22.9791	ENSG00000071205	ARHGAP10
ENSG00000071242	6.5505	12.962	18.4786	18.3072	ENSG00000071242	RPS6KA2
ENSG00000071243	3.5395	5.49471	5.17585	3.44878	ENSG00000071243	ING3
ENSG00000071246	1.13492	1.59839	1.86829	3.91935	ENSG00000071246	VASH1
ENSG00000071282	3.24991	2.82257	2.31471	27.861	ENSG00000071282	LMCD1
ENSG00000071462	17.9022	14.6602	13.3499	18.0763	ENSG00000071462	BUD23
ENSG00000071537	39.0554	53.6557	50.1958	34.5714	ENSG00000071537	SEL1L
ENSG00000071539	4.17819	13.39	3.30891	7.722	ENSG00000071539	TRIP13
ENSG00000071553	2.06025	1.38779	1.48162	0.794598	ENSG00000071553	ATP6AP1
ENSG00000071564	32.2769	34.3925	36.6792	29.8316	ENSG00000071564	TCF3
ENSG00000071575	2.02374	7.35752	4.50221	16.0953	ENSG00000071575	TRIB2
ENSG00000071626	73.6212	89.742	99.7099	80.025	ENSG00000071626	DAZAP1
ENSG00000071655	33.642	38.5508	49.1473	36.8719	ENSG00000071655	MBD3
ENSG00000071677	0	0	0	0	ENSG00000071677	PRLH
ENSG00000071794	12.0051	28.2535	20.7669	27.4357	ENSG00000071794	HLTF
ENSG00000071859	18.2638	11.8046	14.8055	18.9645	ENSG00000071859	FAM50A
ENSG00000071889	24.2719	26.5902	26.427	24.1077	ENSG00000071889	FAM3A
ENSG00000071894	51.2439	64.3012	82.2049	187.393	ENSG00000071894	CPSF1
ENSG00000071909	3.54371	2.68267	3.32946	2.73981	ENSG00000071909	MYO3B
ENSG00000071967	23.8831	38.1853	41.8092	52.954	ENSG00000071967	CYBRD1
ENSG00000071991	6.57692	20.8132	15.4755	36.424	ENSG00000071991	CDH19
ENSG00000071994	39.4248	36.2547	33.5037	20.4593	ENSG00000071994	PDCD2
ENSG00000072041	101.756	93.4575	57.3806	35.5515	ENSG00000072041	SLC6A15
ENSG00000072042	135.708	128.237	63.7832	48.3892	ENSG00000072042	RDH11
ENSG00000072062	19.2357	16.0606	12.3982	16.0088	ENSG00000072062	PRKACA
ENSG00000072071	14.6123	13.0439	19.7514	12.6371	ENSG00000072071	ADGRL1
ENSG00000072080	19.0977	48.3459	55.0097	126.407	ENSG00000072080	SPP2
ENSG00000072110	283.087	319.39	228.038	433.885	ENSG00000072110	ACTN1
ENSG00000072121	12.9039	13.8956	17.2981	17.9526	ENSG00000072121	ZFYVE26
ENSG00000072133	1.69543	1.46406	2.94933	1.59095	ENSG00000072133	RPS6KA6

ENSG00000072134	27.2338	42.8792	34.1841	41.8121	ENSG00000072134	EPN2
ENSG00000072135	8.08225	17.8017	15.8531	19.2784	ENSG00000072135	PTPN18
ENSG00000072163	0.5081	0.592583	0.669204	3.39009	ENSG00000072163	LIMS2
ENSG00000072182	0.692777	0.75037	1.00325	1.19401	ENSG00000072182	ASIC4
ENSG00000072195	30.4995	55.0139	42.8325	36.0582	ENSG00000072195	SPEG
ENSG00000072201	10.57	1.44269	1.21871	3.90534	ENSG00000072201	LNX1
ENSG00000072210	51.9336	70.6738	45.623	37.2815	ENSG00000072210	ALDH3A2
ENSG00000072274	75.4466	53.2411	68.4895	73.8298	ENSG00000072274	TFRC
ENSG00000072310	210.766	258.249	170.706	122.868	ENSG00000072310	SREBF1
ENSG00000072315	0.100534	0.58386	0.350679	0.536531	ENSG00000072315	TRPC5
ENSG00000072364	51.3885	39.767	61.2598	66.0438	ENSG00000072364	AFF4
ENSG00000072401	10.2358	7.39429	8.23466	8.28219	ENSG00000072401	UBE2D1
ENSG00000072415	12.789	12.8954	8.53477	13.9684	ENSG00000072415	MPP5
ENSG00000072422	5.52381	3.81252	5.85838	7.30872	ENSG00000072422	RHOBTB1
ENSG00000072444	0	0	0	0	ENSG00000072444	ASAH2C
ENSG00000072501	14.4034	24.3782	14.0787	28.1585	ENSG00000072501	SMC1A
ENSG00000072506	15.2836	9.89143	11.5168	7.04157	ENSG00000072506	HSD17B10
ENSG00000072518	22.032	25.4927	26.4804	27.1684	ENSG00000072518	MARK2
ENSG00000072571	5.71216	42.7536	2.22948	8.2372	ENSG00000072571	HMMR
ENSG00000072609	42.81	35.8652	51.1676	60.5787	ENSG00000072609	CHFR
ENSG00000072657	0.935577	5.66327	2.18116	4.70271	ENSG00000072657	TRHDE
ENSG00000072682	64.5664	102.467	96.2097	117.18	ENSG00000072682	P4HA2
ENSG00000072694	0.850137	1.98097	1.91499	2.5227	ENSG00000072694	FCGR2B
ENSG00000072736	6.87017	11.5134	11.3306	10.0544	ENSG00000072736	NFATC3
ENSG00000072756	18.5009	30.1809	33.209	51.8625	ENSG00000072756	TRNT1
ENSG00000072778	352.073	383.789	408.759	205.61	ENSG00000072778	ACADVL
ENSG00000072786	28.6526	51.9894	33.0348	71.7399	ENSG00000072786	STK10
ENSG00000072803	39.4734	29.1127	33.8058	43.0444	ENSG00000072803	FBXW11
ENSG00000072818	14.4113	27.0213	22.5529	28.9388	ENSG00000072818	ACAP1
ENSG00000072832	4.32884	8.5273	10.8512	15.4147	ENSG00000072832	CRMP1
ENSG00000072840	23.7246	35.8391	45.8637	71.1931	ENSG00000072840	EVC
ENSG00000072849	62.2147	49.7387	24.8815	21.6817	ENSG00000072849	DERL2
ENSG00000072858	9.6802	18.911	19.3658	40.6793	ENSG00000072858	SIDT1
ENSG00000072864	46.116	55.4167	41.3464	41.6256	ENSG00000072864	NDE1
ENSG00000072952	1.19483	1.51015	1.28492	2.2197	ENSG00000072952	MRVI1
ENSG00000072954	2.55029	4.90106	3.01822	3.3241	ENSG00000072954	TMEM38A
ENSG00000072958	27.2754	30.6255	25.3486	26.508	ENSG00000072958	AP1M1
ENSG00000073008	57.8104	54.3404	67.9585	24.5773	ENSG00000073008	PVR
ENSG00000073009	21.2978	21.3171	28.9449	20.901	ENSG00000073009	IKBKG
ENSG00000073050	10.847	12.7854	9.52658	11.7572	ENSG00000073050	XRCC1
ENSG00000073060	21.5984	41.6758	33.8378	27.9014	ENSG00000073060	SCARB1
ENSG00000073067	0.673881	0.528161	1.93677	1.34216	ENSG00000073067	CYP2W1
ENSG00000073111	8.35511	18.3181	6.53881	11.5527	ENSG00000073111	MCM2
ENSG00000073146	0.438734	1.34305	1.45953	2.3508	ENSG00000073146	MOV10L1
ENSG00000073150	0.41335	0.954026	0.404654	1.26014	ENSG00000073150	PANX2
ENSG00000073169	17.6826	20.5691	16.7087	14.921	ENSG00000073169	SELENOO
ENSG00000073282	64.9553	156.792	167.73	67.0612	ENSG00000073282	TP63
ENSG00000073331	17.6763	50.6341	48.7448	51.4775	ENSG00000073331	ALPK1
ENSG00000073350	65.5406	22.7891	19.0644	13.4934	ENSG00000073350	LLGL2
ENSG00000073417	11.6516	23.7639	21.9238	36.3216	ENSG00000073417	PDE8A
ENSG00000073464	0.315839	0.228084	2.2444	0.505953	ENSG00000073464	CLCN4
ENSG00000073536	10.123	13.851	13.0739	10.102	ENSG00000073536	NLE1
ENSG00000073578	64.9278	84.3693	65.6028	92.6134	ENSG00000073578	SDHA
ENSG00000073584	48.4601	39.2729	46.92	33.0524	ENSG00000073584	SMARCE1

ENSG00000073598	0.149995	0.247429	0.249165	0.147036	ENSG00000073598	FNDC8
ENSG00000073605	5.72163	15.3981	23.1269	22.3183	ENSG00000073605	GSDMB
ENSG00000073614	31.2411	44.4718	51.915	52.8645	ENSG00000073614	KDM5A
ENSG00000073670	0.152816	0.194644	0.164282	0.525153	ENSG00000073670	ADAM11
ENSG00000073711	11.8561	17.8917	15.226	22.1214	ENSG00000073711	PPP2R3A
ENSG00000073712	10.3307	13.3246	12.8946	31.3269	ENSG00000073712	FERMT2
ENSG00000073734	0.0975044	0.0433499	0.039196	0.0642469	ENSG00000073734	ABCB11
ENSG00000073737	43.7782	3.89004	0.792573	3.71625	ENSG00000073737	DHRS9
ENSG00000073754	0.248018	0.42406	0.870346	0.742271	ENSG00000073754	CD5L
ENSG00000073756	69.409	50.9738	34.9234	44.7479	ENSG00000073756	PTGS2
ENSG00000073792	102.942	155.031	106.223	175.314	ENSG00000073792	IGF2BP2
ENSG00000073803	15.1572	13.6532	18.4604	19.751	ENSG00000073803	MAP3K13
ENSG00000073849	10.3796	27.1157	21.5675	18.6717	ENSG00000073849	ST6GAL1
ENSG00000073861	0.0859922	0.103695	0.0562465	0.449096	ENSG00000073861	TBX21
ENSG00000073905	0	0.0796681	0.144192	0	ENSG00000073905	VDAC1P1
ENSG00000073910	0.671914	1.24368	1.09301	2.08141	ENSG00000073910	FRY
ENSG00000073921	123.996	114.947	109.408	125.105	ENSG00000073921	PICALM
ENSG00000073969	11.5412	11.9455	10.9261	11.9364	ENSG00000073969	NSF
ENSG00000074047	0.453459	0.254228	0.581978	13.6668	ENSG00000074047	GLI2
ENSG00000074054	65.145	57.393	64.5492	62.6086	ENSG00000074054	CLASP1
ENSG00000074071	35.0208	31.6406	28.2279	20.6557	ENSG00000074071	MRPS34
ENSG00000074181	35.8398	22.8621	87.2179	62.258	ENSG00000074181	NOTCH3
ENSG00000074201	53.697	72.3949	72.3854	57.068	ENSG00000074201	CLNS1A
ENSG00000074211	4.14599	4.82646	2.00646	8.59468	ENSG00000074211	PPP2R2C
ENSG00000074219	5.75988	9.01216	12.7275	15.0762	ENSG00000074219	TEAD2
ENSG00000074266	10.3763	14.5576	12.6298	17.1674	ENSG00000074266	EED
ENSG00000074276	1.59722	2.44042	2.19451	4.40324	ENSG00000074276	CDHR2
ENSG00000074317	0.808196	0.358791	0.0369116	0.73237	ENSG00000074317	SNCB
ENSG00000074319	50.6287	24.6704	27.7321	23.3511	ENSG00000074319	TSG101
ENSG00000074356	18.7333	28.3066	30.1817	31.8234	ENSG00000074356	NCBP3
ENSG00000074370	0.333429	0.490972	0.415014	2.07311	ENSG00000074370	ATP2A3
ENSG00000074410	41.7138	81.6895	145.118	29.3444	ENSG00000074410	CA12
ENSG00000074416	20.1305	18.454	21.5253	45.8827	ENSG00000074416	MGLL
ENSG00000074527	9.85271	17.9583	29.8637	14.0889	ENSG00000074527	NTN4
ENSG00000074582	24.333	38.4173	33.2275	22.174	ENSG00000074582	BCS1L
ENSG00000074590	8.26834	5.94859	14.6582	9.33378	ENSG00000074590	NUAK1
ENSG00000074603	17.6212	18.3988	20.1412	23.4539	ENSG00000074603	DPP8
ENSG00000074621	7.61114	16.3846	15.6202	13.814	ENSG00000074621	SLC24A1
ENSG00000074657	34.3839	44.3996	65.5388	62.0139	ENSG00000074657	ZNF532
ENSG00000074660	0.541269	1.14908	0.838063	1.67959	ENSG00000074660	SCARF1
ENSG00000074695	61.7444	95.884	60.0766	69.5993	ENSG00000074695	LMAN1
ENSG00000074696	68.4659	84.8761	32.1509	34.3009	ENSG00000074696	HACD3
ENSG00000074706	0.356673	1.02798	1.04157	1.82011	ENSG00000074706	IPCEF1
ENSG00000074755	19.6591	25.9614	28.6808	29.93	ENSG00000074755	ZZEF1
ENSG00000074771	0	0.0265552	0	0.0302374	ENSG00000074771	NOX3
ENSG00000074800	588.102	617.005	276.738	344.224	ENSG00000074800	ENO1
ENSG00000074803	0.154763	0.485948	0.671187	0.4975	ENSG00000074803	SLC12A1
ENSG00000074842	68.885	78.3517	32.3279	41.5261	ENSG00000074842	MYDGF
ENSG00000074855	6.51649	4.63664	4.03968	5.71279	ENSG00000074855	ANO8
ENSG00000074935	5.18	24.9352	20.0874	12.2883	ENSG00000074935	TUBE1
ENSG00000074964	25.3422	10.1403	9.52543	13.0337	ENSG00000074964	ARHGEF10L
ENSG00000074966	2.63016	2.39739	4.01382	5.93619	ENSG00000074966	TXK
ENSG00000075035	6.63794	7.89206	9.82793	11.9318	ENSG00000075035	WSCD2
ENSG00000075043	0.178766	0.0965145	0.0714906	0.634009	ENSG00000075043	KCNQ2

ENSG00000075073	2.79462	6.74236	7.02669	10.5229	ENSG00000075073	TACR2
ENSG00000075089	16.2314	22.3258	26.6844	23.1623	ENSG00000075089	ACTR6
ENSG00000075131	6.24065	7.91548	5.41391	8.92907	ENSG00000075131	TIPIN
ENSG00000075142	49.6079	48.066	36.5809	33.1023	ENSG00000075142	SRI
ENSG00000075151	48.9357	49.9235	59.3186	66.8106	ENSG00000075151	EIF4G3
ENSG00000075188	18.951	26.9053	18.1753	15.5926	ENSG00000075188	NUP37
ENSG00000075213	8.46426	22.6199	3.56385	7.46778	ENSG00000075213	SEMA3A
ENSG00000075218	3.33735	15.6714	4.39545	13.891	ENSG00000075218	GTSE1
ENSG00000075223	319.096	221.242	205.418	186.093	ENSG00000075223	SEMA3C
ENSG00000075234	15.3706	15.9982	14.5416	19.828	ENSG00000075234	TTC38
ENSG00000075239	32.9604	70.177	44.1327	83.0003	ENSG00000075239	ACAT1
ENSG00000075240	21.7935	30.1257	24.4279	13.0273	ENSG00000075240	GRAMD4
ENSG00000075275	24.352	55.1834	65.3379	29.706	ENSG00000075275	CELSR1
ENSG00000075290	0.106647	0.153952	0.209386	0.0875005	ENSG00000075290	WNT8B
ENSG00000075292	64.5694	105.23	94.9096	128.134	ENSG00000075292	ZNF638
ENSG00000075303	4.64638	11.0099	5.98345	9.69793	ENSG00000075303	SLC25A40
ENSG00000075336	12.5107	14.2582	13.9951	14.4568	ENSG00000075336	TIMM21
ENSG00000075340	0.992572	1.70669	1.46649	2.25281	ENSG00000075340	ADD2
ENSG00000075388	0.0489228	0.125049	0.170288	0	ENSG00000075388	FGF4
ENSG00000075391	46.3487	35.5202	28.9362	52.6044	ENSG00000075391	RASAL2
ENSG00000075399	9.28626	13.5437	21.548	20.1323	ENSG00000075399	VPS9D1
ENSG00000075407	11.7152	18.9571	22.3209	27.0596	ENSG00000075407	ZNF37A
ENSG00000075413	100.144	155.533	111.923	164.229	ENSG00000075413	MARK3
ENSG00000075415	224.137	186.171	147.811	123.418	ENSG00000075415	SLC25A3
ENSG00000075420	44.7751	59.4519	67.1808	100.864	ENSG00000075420	FNDC3B
ENSG00000075426	52.0489	42.9058	83.0148	44.4804	ENSG00000075426	FOSL2
ENSG00000075429	0.155211	0.149216	0.202222	0.33688	ENSG00000075429	CACNG5
ENSG00000075461	0.139961	0.12853	0.168484	0.13662	ENSG00000075461	CACNG4
ENSG00000075539	65.8751	114.001	76.4507	118.58	ENSG00000075539	FRYL
ENSG00000075568	33.7503	46.3358	42.153	39.1389	ENSG00000075568	TMEM131
ENSG00000075618	130.094	188.701	81.193	122.025	ENSG00000075618	FSCN1
ENSG00000075624	2436.93	2083.6	706.115	1384.96	ENSG00000075624	ACTB
ENSG00000075643	2.04524	6.54453	11.7507	4.12293	ENSG00000075643	MOCOS
ENSG00000075651	24.4686	18.7738	21.8537	21.7923	ENSG00000075651	PLD1
ENSG00000075673	180.617	8.367	8.5008	22.282	ENSG00000075673	ATP12A
ENSG00000075702	6.61151	17.3119	12.7009	25.0805	ENSG00000075702	WDR62
ENSG00000075711	147.676	91.9697	100.323	105.388	ENSG00000075711	DLG1
ENSG00000075785	38.8456	38.9328	41.4185	52.6141	ENSG00000075785	RAB7A
ENSG00000075790	78.9625	96.8111	37.63	46.7789	ENSG00000075790	BCAP29
ENSG00000075826	3.32212	7.42725	7.44943	9.03413	ENSG00000075826	SEC31B
ENSG00000075856	28.5114	43.3319	48.2113	44.6404	ENSG00000075856	SART3
ENSG00000075884	2.30713	5.43227	5.94948	10.2156	ENSG00000075884	ARHGAP15
ENSG00000075886	1.16192	1.45448	1.59344	2.00777	ENSG00000075886	TUBA3D
ENSG00000075891	0.635229	0.601581	0.757282	0.957578	ENSG00000075891	PAX2
ENSG00000075914	27.3529	31.4392	29.7298	27.0981	ENSG00000075914	EXOSC7
ENSG00000075945	17.9216	22.1182	13.6144	20.1242	ENSG00000075945	KIFAP3
ENSG00000075975	10.9889	10.1803	12.1496	7.7444	ENSG00000075975	MKRN2
ENSG00000076003	3.62706	9.47402	3.07762	11.8544	ENSG00000076003	MCM6
ENSG00000076043	59.8428	66.32	66.7455	66.3737	ENSG00000076043	REXO2
ENSG00000076053	8.86629	10.0351	12.6219	12.1169	ENSG00000076053	RBM7
ENSG00000076067	14.1987	20.2348	13.5361	37.0414	ENSG00000076067	RBMS2
ENSG00000076108	48.4845	59.1864	59.5601	66.1111	ENSG00000076108	BAZ2A
ENSG00000076201	16.4976	24.8017	22.0542	18.5627	ENSG00000076201	PTPN23
ENSG00000076242	15.0579	25.6748	21.003	18.8287	ENSG00000076242	MLH1

ENSG00000076248	8.96634	9.62879	9.10965	7.42003	ENSG00000076248	UNG
ENSG00000076258	3.95826	2.42251	3.92501	1.65114	ENSG00000076258	FMO4
ENSG00000076321	14.0919	12.262	16.9625	9.48318	ENSG00000076321	KLHL20
ENSG00000076344	0.40456	0.549763	0.795616	1.49926	ENSG00000076344	RGS11
ENSG00000076351	2.75909	4.8179	3.76511	6.07628	ENSG00000076351	SLC46A1
ENSG00000076356	11.2684	26.7555	21.1194	23.7012	ENSG00000076356	PLXNA2
ENSG00000076382	4.52505	21.8505	5.30325	9.70936	ENSG00000076382	SPAG5
ENSG00000076513	62.2657	32.6931	27.6863	40.3606	ENSG00000076513	ANKRD13A
ENSG00000076554	14.4852	27.868	21.8706	21.3576	ENSG00000076554	TPD52
ENSG00000076555	10.199	18.3891	17.3724	27.7732	ENSG00000076555	ACACB
ENSG00000076604	83.9744	96.0821	67.2762	43.8591	ENSG00000076604	TRAF4
ENSG00000076641	4.46294	9.06251	4.87442	35.9482	ENSG00000076641	PAG1
ENSG00000076650	4.80068	4.89304	6.2203	8.33562	ENSG00000076650	GPATCH1
ENSG00000076662	2.6703	2.4864	1.61534	3.50541	ENSG00000076662	ICAM3
ENSG00000076685	63.9449	50.4896	57.8817	53.195	ENSG00000076685	NT5C2
ENSG00000076706	3.9004	42.9532	22.3281	20.1696	ENSG00000076706	MCAM
ENSG00000076716	1.17641	2.65508	6.25667	2.88564	ENSG00000076716	GPC4
ENSG00000076770	3.86235	6.12232	6.50291	3.9358	ENSG00000076770	MBNL3
ENSG00000076826	15.5403	6.13274	8.11175	4.01513	ENSG00000076826	CAMSAP3
ENSG00000076864	4.45342	7.83266	5.366	4.81858	ENSG00000076864	RAP1GAP
ENSG00000076924	16.6706	18.6467	16.2356	12.518	ENSG00000076924	XAB2
ENSG00000076928	30.5878	39.8569	33.8053	68.0656	ENSG00000076928	ARHGEF1
ENSG00000076944	33.1813	34.1128	41.6817	32.9885	ENSG00000076944	STXBP2
ENSG00000076984	8.18976	15.4484	13.3274	21.0402	ENSG00000076984	MAP2K7
ENSG00000077009	0.107734	0	0	0	ENSG00000077009	NMRK2
ENSG00000077044	6.59496	16.2247	12.7157	15.9582	ENSG00000077044	DGKD
ENSG00000077063	0.659691	0.63198	1.40553	2.86567	ENSG00000077063	CTTNBP2
ENSG00000077080	0.246857	0.036277	0.406016	0.131621	ENSG00000077080	ACTL6B
ENSG00000077092	0.363047	1.61273	0.821122	6.91737	ENSG00000077092	RARB
ENSG00000077097	40.9245	49.2658	42.9465	60.6094	ENSG00000077097	TOP2B
ENSG00000077147	108.047	106.24	95.9779	72.9259	ENSG00000077147	TM9SF3
ENSG00000077150	27.0842	29.5183	34.8433	34.1903	ENSG00000077150	NFKB2
ENSG00000077152	6.76804	14.1897	3.06073	4.4621	ENSG00000077152	UBE2T
ENSG00000077157	11.2301	16.1117	14.9143	18.9819	ENSG00000077157	PPP1R12B
ENSG00000077232	63.9248	114.733	77.3947	54.4069	ENSG00000077232	DNAJC10
ENSG00000077235	45.8636	60.2246	43.7943	46.8564	ENSG00000077235	GTF3C1
ENSG00000077238	96.8889	161.746	106.284	97.2224	ENSG00000077238	IL4R
ENSG00000077254	68.0027	116.441	90.5376	178.003	ENSG00000077254	USP33
ENSG00000077264	0.437499	1.08352	1.00146	1.5262	ENSG00000077264	PAK3
ENSG00000077274	0.0951451	0.377755	0.101217	0.297596	ENSG00000077274	CAPN6
ENSG00000077279	0.350163	0.596507	0.662219	1.02661	ENSG00000077279	DCX
ENSG00000077312	23.2381	30.5843	23.6601	16.7887	ENSG00000077312	SNRPA
ENSG00000077327	0.373196	0.855128	0.328385	1.21823	ENSG00000077327	SPAG6
ENSG00000077348	5.49861	6.56768	8.11825	4.45553	ENSG00000077348	EXOSC5
ENSG00000077380	73.7851	67.4703	53.5878	58.3703	ENSG00000077380	DYNC1I2
ENSG00000077420	3.44008	4.04473	2.1277	10.2907	ENSG00000077420	APBB1IP
ENSG00000077454	13.1792	18.8178	14.0876	17.9938	ENSG00000077454	LRCH4
ENSG00000077458	17.8305	25.7005	22.3845	15.1014	ENSG00000077458	FAM76B
ENSG00000077463	12.5339	9.22555	13.1634	9.90787	ENSG00000077463	SIRT6
ENSG00000077498	3.11374	1.32287	0.372396	0.990681	ENSG00000077498	TYR
ENSG00000077514	13.4103	21.8522	16.1758	20.812	ENSG00000077514	POLD3
ENSG00000077522	0.0110515	0.0731968	0.0306939	0.0773248	ENSG00000077522	ACTN2
ENSG00000077549	32.1504	37.674	33.1712	43.8283	ENSG00000077549	CAPZB
ENSG00000077585	16.9063	16.5015	14.6727	22.2272	ENSG00000077585	GPR137B

ENSG00000077616	0.956817	1.79891	1.54043	2.31726	ENSG00000077616	NAALAD2
ENSG00000077684	2.17418	8.36983	4.98428	10.963	ENSG00000077684	JADE1
ENSG00000077713	8.3962	7.12003	8.2872	8.27121	ENSG00000077713	SLC25A43
ENSG00000077721	32.4772	21.6816	25.6191	21.2492	ENSG00000077721	UBE2A
ENSG00000077782	5.7944	14.139	10.427	55.8824	ENSG00000077782	FGFR1
ENSG00000077800	0.268074	0.259554	0.289958	1.25766	ENSG00000077800	FKBP6
ENSG00000077809	106.767	151.67	149.856	182.197	ENSG00000077809	GTF2I
ENSG00000077935	0.115569	0.259895	0.385881	0.437976	ENSG00000077935	SMC1B
ENSG00000077942	24.9883	75.3288	44.7782	114.318	ENSG00000077942	FBLN1
ENSG00000077943	0.13909	0.443909	0.322414	1.70402	ENSG00000077943	ITGA8
ENSG00000077984	0.135056	0.265307	0.99495	0.293736	ENSG00000077984	CST7
ENSG00000078018	15.2947	10.4987	10.2643	7.1207	ENSG00000078018	MAP2
ENSG00000078043	16.9767	37.3252	34.703	55.106	ENSG00000078043	PIAS2
ENSG00000078053	0.314434	0.742167	0.403555	2.67235	ENSG00000078053	AMPH
ENSG00000078061	21.8766	22.2162	19.2877	16.3598	ENSG00000078061	ARAF
ENSG00000078070	9.96882	12.0543	15.4402	14.2929	ENSG00000078070	MCCC1
ENSG00000078081	1.15437	4.80215	6.36806	1.39458	ENSG00000078081	LAMP3
ENSG00000078098	9.69809	3.2472	23.4893	83.2102	ENSG00000078098	FAP
ENSG00000078114	17.0711	3.80717	7.28264	8.95815	ENSG00000078114	NEBL
ENSG00000078124	12.4941	27.1995	7.78444	9.44354	ENSG00000078124	ACER3
ENSG00000078140	19.1055	15.5204	15.9542	20.047	ENSG00000078140	UBE2K
ENSG00000078142	39.2114	44.9695	48.0966	51.1026	ENSG00000078142	PIK3C3
ENSG00000078177	3.63115	5.4211	5.84417	6.90213	ENSG00000078177	N4BP2
ENSG00000078237	15.0057	9.83325	24.9801	14.471	ENSG00000078237	TIGAR
ENSG00000078246	8.24533	8.56524	8.04643	9.96643	ENSG00000078246	TULP3
ENSG00000078269	9.82974	27.2962	13.7455	31.289	ENSG00000078269	SYNJ2
ENSG00000078295	3.2017	7.25637	7.6821	12.0799	ENSG00000078295	ADCY2
ENSG00000078304	46.5573	64.6494	52.6287	69.3398	ENSG00000078304	PPP2R5C
ENSG00000078319	6.4746	16.4982	12.1414	12.3083	ENSG00000078319	PMS2P1
ENSG00000078328	0.595456	2.20091	1.20545	1.48454	ENSG00000078328	RBFOX1
ENSG00000078369	78.4694	75.7032	81.4248	80.5259	ENSG00000078369	GNB1
ENSG00000078399	13.2369	25.5632	24.7304	10.24	ENSG00000078399	HOXA9
ENSG00000078401	42.4934	8.06107	6.62105	7.90228	ENSG00000078401	EDN1
ENSG00000078403	21.866	33.5456	34.4659	41.3966	ENSG00000078403	MLLT10
ENSG00000078487	0.982795	3.05215	3.43063	3.2586	ENSG00000078487	ZCWPW1
ENSG00000078549	0.0864617	0.165785	0.133315	0.245829	ENSG00000078549	ADCYAP1R1
ENSG00000078579	0.0339368	0.196789	0.178143	0.260332	ENSG00000078579	FGF20
ENSG00000078589	0	0	0	0	ENSG00000078589	P2RY10
ENSG00000078596	7.31864	4.09161	3.57159	2.06025	ENSG00000078596	ITM2A
ENSG00000078618	55.2567	84.9334	78.3275	103.254	ENSG00000078618	NRDC
ENSG00000078668	41.1018	36.9834	23.8147	26.4304	ENSG00000078668	VDAC3
ENSG00000078674	46.7642	79.5785	72.3554	74.5351	ENSG00000078674	PCM1
ENSG00000078687	1.50713	2.54984	2.78907	4.2084	ENSG00000078687	TNRC6C
ENSG00000078699	4.19899	10.5878	10.6191	15.0751	ENSG00000078699	CBFA2T2
ENSG00000078725	0.353744	0.401418	0.31248	0.528983	ENSG00000078725	BRINP1
ENSG00000078747	81.5201	84.0679	43.8583	50.6472	ENSG00000078747	ITCH
ENSG00000078795	2.74764	6.55716	5.46867	9.04324	ENSG00000078795	PKD2L2
ENSG00000078804	2.52791	0.795405	2.0251	3.25512	ENSG00000078804	TP53INP2
ENSG00000078808	87.5439	71.4923	61.5569	45.0705	ENSG00000078808	SDF4
ENSG00000078814	4.8218	7.5027	8.46028	13.1758	ENSG00000078814	MYH7B
ENSG00000078898	0.202101	0	0.10397	0.0327262	ENSG00000078898	BPIFB2
ENSG00000078900	1.4351	1.46659	2.78759	1.83081	ENSG00000078900	TP73
ENSG00000078902	38.6008	24.322	42.6605	20.9858	ENSG00000078902	TOLLIP
ENSG00000078967	22.5042	42.1244	36.7403	49.2344	ENSG00000078967	UBE2D4

ENSG00000079101	1.87566	3.29476	1.93695	4.2382	ENSG00000079101	CLUL1
ENSG00000079102	2.77306	5.79944	4.77018	21.5137	ENSG00000079102	RUNX1T1
ENSG00000079112	1.00174	2.24144	2.27373	3.29218	ENSG00000079112	CDH17
ENSG00000079134	20.4059	44.4383	35.2319	40.5162	ENSG00000079134	THOC1
ENSG00000079150	0.942876	1.87113	2.5703	7.70263	ENSG00000079150	FKBP7
ENSG00000079156	5.86043	17.7427	23.942	24.3414	ENSG00000079156	OSBPL6
ENSG00000079215	11.125	20.9601	20.94	115.966	ENSG00000079215	SLC1A3
ENSG00000079246	120.322	129.926	92.4225	102.685	ENSG00000079246	XRCC5
ENSG00000079257	7.50244	8.74846	6.00545	7.12652	ENSG00000079257	LXN
ENSG00000079263	1.89917	1.81321	2.98445	3.61356	ENSG00000079263	SP140
ENSG00000079277	33.5187	61.0224	39.4208	54.6978	ENSG00000079277	MKNK1
ENSG00000079308	5.88204	8.31786	11.2202	45.0272	ENSG00000079308	TNS1
ENSG00000079313	14.1585	17.1475	15.9007	14.6914	ENSG00000079313	REXO1
ENSG00000079332	53.2689	34.4334	37.1669	42.3028	ENSG00000079332	SAR1A
ENSG00000079335	1.40929	2.97779	1.95279	2.33085	ENSG00000079335	CDC14A
ENSG00000079337	13.6099	34.3874	7.15623	19.2278	ENSG00000079337	RAPGEF3
ENSG00000079385	22.0141	10.3858	8.002	10.5848	ENSG00000079385	CEACAM1
ENSG00000079387	9.65826	18.0194	16.9561	16.3134	ENSG00000079387	SENP1
ENSG00000079393	0.205236	0.40115	0.309864	0.197516	ENSG00000079393	DUSP13
ENSG00000079432	22.211	29.285	38.8343	30.9906	ENSG00000079432	CIC
ENSG00000079435	10.6837	16.6623	7.78075	13.6678	ENSG00000079435	LIPE
ENSG00000079459	133.63	167.761	52.4478	115.149	ENSG00000079459	FDFT1
ENSG00000079462	15.3238	14.8893	11.5772	8.75725	ENSG00000079462	PAFAH1B3
ENSG00000079482	10.9705	11.8947	8.95997	11.785	ENSG00000079482	OPHN1
ENSG00000079557	0.200762	0.192049	0.151723	0.869078	ENSG00000079557	AFM
ENSG00000079616	13.7079	45.8069	18.8693	16.5394	ENSG00000079616	KIF22
ENSG00000079689	0.201463	0.155236	0.140321	0.220463	ENSG00000079689	SCGN
ENSG00000079691	12.7588	17.0475	16.9935	10.4416	ENSG00000079691	CARMIL1
ENSG00000079739	14.39	21.9892	16.728	15.6349	ENSG00000079739	PGM1
ENSG00000079785	30.731	33.7677	34.8119	32.5646	ENSG00000079785	DDX1
ENSG00000079805	95.947	110.647	110.178	120.45	ENSG00000079805	DNM2
ENSG00000079819	9.16555	28.38	13.9056	41.1593	ENSG00000079819	EPB41L2
ENSG00000079841	0.546762	1.2261	1.19413	2.1531	ENSG00000079841	RIMS1
ENSG00000079931	0.987429	2.96881	1.72267	8.09291	ENSG00000079931	MOXD1
ENSG00000079950	26.3264	18.6104	15.2235	20.381	ENSG00000079950	STX7
ENSG00000079974	7.97182	13.7807	14.0347	14.4073	ENSG00000079974	RABL2B
ENSG00000079999	17.674	18.4476	16.5456	14.3365	ENSG00000079999	KEAP1
ENSG00000080007	1.33519	2.24489	1.44453	4.16658	ENSG00000080007	DDX43
ENSG00000080031	0.823722	0.802325	0.418073	1.08269	ENSG00000080031	PTPRH
ENSG00000080166	2.05806	1.41815	0.905297	0.707374	ENSG00000080166	DCT
ENSG00000080189	25.3742	35.8481	28.5246	19.6826	ENSG00000080189	SLC35C2
ENSG00000080200	10.1099	13.8744	8.38356	12.5413	ENSG00000080200	CRYBG3
ENSG00000080224	1.57459	1.97512	2.61244	3.42674	ENSG00000080224	EPHA6
ENSG00000080293	0.650705	0.990931	1.24762	2.21907	ENSG00000080293	SCTR
ENSG00000080298	1.85043	4.95768	2.4975	7.72583	ENSG00000080298	RFX3
ENSG00000080345	21.6287	36.5016	30.6279	39.9878	ENSG00000080345	RIF1
ENSG00000080371	27.1312	24.215	32.455	30.453	ENSG00000080371	RAB21
ENSG00000080493	0.686615	0.180033	0.265286	0.466505	ENSG00000080493	SLC4A4
ENSG00000080503	14.3545	25.2466	22.9406	20.8173	ENSG00000080503	SMARCA2
ENSG00000080511	2.38988	6.25009	6.02119	5.48928	ENSG00000080511	RDH8
ENSG00000080546	12.0994	17.6219	21.0164	14.0153	ENSG00000080546	SESN1
ENSG00000080561	6.78655	9.23487	7.13489	4.17935	ENSG00000080561	MID2
ENSG00000080572	0.869849	1.41905	1.72802	2.65761	ENSG00000080572	PIH1D3
ENSG00000080573	1.04917	2.16069	7.04528	97.6718	ENSG00000080573	COL5A3

ENSG00000080603	19.4351	19.1953	27.8439	28.5945	ENSG00000080603	SRCAP
ENSG00000080608	33.2229	49.0042	45.097	42.5147	ENSG00000080608	PUM3
ENSG00000080618	0.0718723	0.449255	0.377109	0.474534	ENSG00000080618	CPB2
ENSG00000080644	1.09279	3.45578	2.8026	4.70019	ENSG00000080644	CHRNA3
ENSG00000080709	0.855461	1.47103	1.15946	1.88492	ENSG00000080709	KCNN2
ENSG00000080802	13.5017	15.6373	12.5466	18.7875	ENSG00000080802	CNOT4
ENSG00000080815	47.0969	39.1445	40.1307	30.8599	ENSG00000080815	PSEN1
ENSG00000080819	15.8406	14.1246	10.6736	13.6004	ENSG00000080819	CPOX
ENSG00000080822	73.9024	65.4969	57.0096	37.2332	ENSG00000080822	CLDND1
ENSG00000080823	30.4107	37.0424	27.8513	68.0407	ENSG00000080823	MOK
ENSG00000080824	172.259	152.467	77.9212	197.732	ENSG00000080824	HSP90AA1
ENSG00000080839	3.16017	7.1301	2.0966	5.12054	ENSG00000080839	RBL1
ENSG00000080845	12.3398	13.2991	12.142	18.7175	ENSG00000080845	DLGAP4
ENSG00000080854	4.2316	0.622214	0.915811	2.30248	ENSG00000080854	IGSF9B
ENSG00000080910	0.0855153	0.502621	0.202081	0	ENSG00000080910	CFHR2
ENSG00000080947	10.5847	14.5109	10.0549	19.0489	ENSG00000080947	CROCCP3
ENSG00000080986	11.0077	40.9672	17.5654	26.5325	ENSG00000080986	NDC80
ENSG00000081014	9.77616	11.536	14.1496	11.4805	ENSG00000081014	AP4E1
ENSG00000081019	5.46067	6.25753	5.65051	5.37756	ENSG00000081019	RSBN1
ENSG00000081026	3.88257	7.62499	6.04315	6.67655	ENSG00000081026	MAGI3
ENSG00000081041	5.93276	5.71996	5.69551	8.40558	ENSG00000081041	CXCL2
ENSG00000081051	0.632468	0.186779	0.422956	0.582357	ENSG00000081051	AFP
ENSG00000081052	0.532619	0.822382	0.42354	0.975503	ENSG00000081052	COL4A4
ENSG00000081059	4.82019	9.63753	8.49257	11.3582	ENSG00000081059	TCF7
ENSG00000081087	55.06	51.5991	36.3749	38.1547	ENSG00000081087	OSTM1
ENSG00000081138	0.29824	0.933325	0.750856	1.40855	ENSG00000081138	CDH7
ENSG00000081148	0.369729	0.538599	0.61947	0.906878	ENSG00000081148	IMPG2
ENSG00000081154	31.1448	35.3853	40.1896	38.4647	ENSG00000081154	PCNP
ENSG00000081177	22.5846	25.6428	25.8745	24.5132	ENSG00000081177	EXD2
ENSG00000081181	3.49756	7.96133	6.5232	2.35445	ENSG00000081181	ARG2
ENSG00000081189	7.50076	4.84606	4.58215	21.0246	ENSG00000081189	MEF2C
ENSG00000081237	3.8083	6.3762	5.56907	9.8551	ENSG00000081237	PTPRC
ENSG00000081248	0.0355706	0.0342958	0.0631717	0.0294212	ENSG00000081248	CACNA1S
ENSG00000081277	266.494	145.53	211.934	80.3481	ENSG00000081277	PKP1
ENSG00000081307	17.1082	23.1755	23.5754	20.3738	ENSG00000081307	UBA5
ENSG00000081320	13.7519	18.0557	9.00146	21.8822	ENSG00000081320	STK17B
ENSG00000081377	9.41192	11.0244	7.71721	12.7575	ENSG00000081377	CDC14B
ENSG00000081386	5.25257	6.86687	5.72919	5.34576	ENSG00000081386	ZNF510
ENSG00000081479	0.0606518	0.183522	0.233731	0.301052	ENSG00000081479	LRP2
ENSG00000081665	28.1172	44.9289	45.4506	55.4929	ENSG00000081665	ZNF506
ENSG00000081692	17.5265	12.8463	12.8574	9.81739	ENSG00000081692	JMJD4
ENSG00000081721	17.3679	16.1465	17.7969	13.5151	ENSG00000081721	DUSP12
ENSG00000081760	38.0841	53.5159	52.4139	76.2943	ENSG00000081760	AACS
ENSG00000081791	33.4788	65.231	35.8039	28.809	ENSG00000081791	KIAA0141
ENSG00000081800	0.0686952	0.116488	0.132746	0.4445	ENSG00000081800	SLC13A1
ENSG00000081803	0.176189	1.12575	0.437879	1.4912	ENSG00000081803	CADPS2
ENSG00000081818	0.0648944	0.0371863	0.0471534	0.124347	ENSG00000081818	PCDHB4
ENSG00000081842	0.0823114	0.097346	0.0523417	0.107388	ENSG00000081842	PCDHA6
ENSG00000081853	1.2369	0.402636	0.864188	0.584828	ENSG00000081853	PCDHGA2
ENSG00000081870	14.7666	25.8324	18.7382	24.8717	ENSG00000081870	HSPB11
ENSG00000081913	10.6779	13.605	10.609	15.4629	ENSG00000081913	PHLPP1
ENSG00000081923	23.38	45.5238	22.1557	39.5076	ENSG00000081923	ATP8B1
ENSG00000081985	0.987542	1.38794	2.67372	1.37425	ENSG00000081985	IL12RB2

ENSG00000082014	11.7241	15.6441	20.1042	20.6286	ENSG00000082014	SMARCD3
ENSG00000082068	19.6794	20.7429	20.8258	28.6791	ENSG00000082068	WDR70
ENSG00000082074	0.47719	1.22855	2.47623	0.513811	ENSG00000082074	FYB1
ENSG00000082126	2.80591	4.9348	4.05222	13.3766	ENSG00000082126	MPP4
ENSG00000082146	9.71105	10.9052	10.0511	8.39215	ENSG00000082146	STRADB
ENSG00000082153	229.675	187.447	108.369	104.378	ENSG00000082153	BZW1
ENSG00000082175	0.0344496	0.389388	0.416587	0.922286	ENSG00000082175	PGR
ENSG00000082196	0.702963	1.97236	2.23794	2.56399	ENSG00000082196	C1QTNF3
ENSG00000082212	9.4721	19.7553	13.8668	12.2977	ENSG00000082212	ME2
ENSG00000082213	16.5343	15.5328	18.6175	15.5307	ENSG00000082213	C5orf22
ENSG00000082258	19.3647	23.3895	30.6427	23.0035	ENSG00000082258	CCNT2
ENSG00000082269	31.9129	24.0084	27.5603	20.7685	ENSG00000082269	FAM135A
ENSG00000082293	3.78905	20.4975	12.134	21.0947	ENSG00000082293	COL19A1
ENSG00000082397	1.31036	1.19595	1.16026	23.2677	ENSG00000082397	EPB41L3
ENSG00000082438	16.2941	32.006	44.7791	18.3565	ENSG00000082438	COBLL1
ENSG00000082458	9.6765	14.4117	9.57955	6.3704	ENSG00000082458	DLG3
ENSG00000082482	0.169424	0.529516	0.278368	17.2145	ENSG00000082482	KCNK2
ENSG00000082497	1.98717	3.73234	0.478376	1.82874	ENSG00000082497	SERTAD4
ENSG00000082512	1.42538	4.07537	4.06647	7.64582	ENSG00000082512	TRAF5
ENSG00000082515	8.96042	8.79832	9.73978	11.5696	ENSG00000082515	MRPL22
ENSG00000082516	6.51025	9.04626	8.67686	7.1522	ENSG00000082516	GEMIN5
ENSG00000082556	0.193122	0.426172	0.342118	0.628415	ENSG00000082556	OPRK1
ENSG00000082641	147.787	204.037	308.786	100.612	ENSG00000082641	NFE2L1
ENSG00000082684	0.609552	0.236391	3.59633	1.48096	ENSG00000082684	SEMA5B
ENSG00000082701	67.2049	68.6776	57.7451	59.1965	ENSG00000082701	GSK3B
ENSG00000082781	66.857	147.609	44.3351	104.613	ENSG00000082781	ITGB5
ENSG00000082805	26.9407	55.1014	47.3395	71.5168	ENSG00000082805	ERC1
ENSG00000082898	83.6483	166.01	125.197	129.243	ENSG00000082898	XPO1
ENSG00000082929	2.7552	2.16142	3.88954	4.03294	ENSG00000082929	LINC01587
ENSG00000082996	41.3972	47.8514	32.4566	24.4792	ENSG00000082996	RNF13
ENSG00000083067	0.996753	2.63206	2.80365	3.98264	ENSG00000083067	TRPM3
ENSG00000083093	10.4398	13.1078	14.6639	8.96105	ENSG00000083093	PALB2
ENSG00000083097	14.2457	24.5993	37.022	15.7561	ENSG00000083097	DOPEY1
ENSG00000083099	16.963	16.6091	18.1141	18.8523	ENSG00000083099	LYRM2
ENSG00000083123	5.5938	13.7872	13.9408	19.1711	ENSG00000083123	BCKDHB
ENSG00000083168	13.6995	18.9595	21.8987	21.5684	ENSG00000083168	KAT6A
ENSG00000083223	23.1033	30.8486	25.7478	32.2247	ENSG00000083223	ZCCHC6
ENSG00000083290	18.9403	26.0302	22.9213	31.2585	ENSG00000083290	ULK2
ENSG00000083307	23.3244	36.451	32.7465	20.1282	ENSG00000083307	GRHL2
ENSG00000083312	99.4605	104.822	88.1411	86.5064	ENSG00000083312	TNPO1
ENSG00000083444	36.6882	83.9463	61.7016	103.1	ENSG00000083444	PLOD1
ENSG00000083454	1.5196	2.54962	1.66366	3.11862	ENSG00000083454	P2RX5
ENSG00000083457	9.10482	12.1106	11.9496	11.8345	ENSG00000083457	ITGAE
ENSG00000083520	28.3796	21.1921	21.1556	20.1457	ENSG00000083520	DIS3
ENSG00000083535	8.64822	17.5876	15.6861	22.472	ENSG00000083535	PIBF1
ENSG00000083544	7.26215	11.9547	9.77866	15.7514	ENSG00000083544	TDRD3
ENSG00000083635	3.05555	3.3167	3.44396	2.82808	ENSG00000083635	NUFIP1
ENSG00000083642	6.68191	14.8518	9.55293	19.9197	ENSG00000083642	PDS5B
ENSG00000083720	10.778	21.7209	16.0102	20.9315	ENSG00000083720	OXCT1
ENSG00000083750	6.85066	11.0741	14.5112	10.5418	ENSG00000083750	RRAGB
ENSG00000083782	0.11528	0.110912	0.132618	0.167687	ENSG00000083782	EPYC
ENSG00000083799	22.7122	26.4896	27.7126	29.6865	ENSG00000083799	CYLD
ENSG00000083807	6.4773	12.8381	15.9558	16.295	ENSG00000083807	SLC27A5
ENSG00000083812	7.82371	5.78637	8.81674	4.01696	ENSG00000083812	ZNF324

ENSG00000083814	2.62646	5.8531	5.43208	3.48524	ENSG00000083814	ZNF671
ENSG00000083817	5.48774	2.97563	4.87963	2.30495	ENSG00000083817	ZNF416
ENSG00000083828	9.70199	16.0574	16.5462	21.3641	ENSG00000083828	ZNF586
ENSG00000083838	6.57894	7.90145	10.4354	5.00982	ENSG00000083838	ZNF446
ENSG00000083842	0.398342	0.507422	3.56749	2.96869	ENSG00000083842	ZNF8
ENSG00000083844	21.6393	23.4395	25.0608	14.9842	ENSG00000083844	ZNF264
ENSG00000083845	380.344	330.939	273.082	149.967	ENSG00000083845	RPS5
ENSG00000083857	320.099	273.893	467.513	402.016	ENSG00000083857	FAT1
ENSG00000083896	43.8041	50.6541	55.3213	42.4653	ENSG00000083896	YTHDC1
ENSG00000083937	46.2639	23.3835	25.8615	18.5272	ENSG00000083937	CHMP2B
ENSG00000084070	7.73838	10.2605	8.9569	10.6595	ENSG00000084070	SMAP2
ENSG00000084072	20.1429	21.4455	24.5302	20.3995	ENSG00000084072	PPIE
ENSG00000084073	69.1268	61.4332	48.6747	37.9612	ENSG00000084073	ZMPSTE24
ENSG00000084090	34.294	42.395	45.1282	29.9772	ENSG00000084090	STARD7
ENSG00000084092	7.9021	10.3367	8.01684	6.59459	ENSG00000084092	NOA1
ENSG00000084093	22.5123	22.8492	26.9505	23.2807	ENSG00000084093	REST
ENSG00000084110	1.14368	1.28783	2.4586	0.795145	ENSG00000084110	HAL
ENSG00000084112	15.4519	30.1589	16.2047	53.0029	ENSG00000084112	SSH1
ENSG00000084207	1001.59	616.068	384.899	248.838	ENSG00000084207	GSTP1
ENSG00000084234	262.452	379.25	271.993	300.79	ENSG00000084234	APLP2
ENSG00000084444	3.84485	5.01964	3.81286	4.52502	ENSG00000084444	FAM234B
ENSG00000084453	3.78538	10.0275	8.52276	17.2183	ENSG00000084453	SLCO1A2
ENSG00000084463	19.4324	20.514	16.4954	18.4541	ENSG00000084463	WBP11
ENSG00000084623	98.2115	69.1375	55.7536	40.9025	ENSG00000084623	EIF3I
ENSG00000084628	0.414665	0.419493	0.457341	0.399706	ENSG00000084628	NKAIN1
ENSG00000084636	80.1623	231.477	353.97	251.876	ENSG00000084636	COL16A1
ENSG00000084652	17.7703	22.6771	20.1298	18.5074	ENSG00000084652	TXLNA
ENSG00000084674	0.284323	0.538622	0.486671	0.878229	ENSG00000084674	APOB
ENSG00000084676	5.50089	5.79697	6.1083	11.5395	ENSG00000084676	NCOA1
ENSG00000084693	15.9423	15.3961	16.9309	15.0149	ENSG00000084693	AGBL5
ENSG00000084710	0.962797	0.881856	0.906074	2.23319	ENSG00000084710	EFR3B
ENSG00000084731	10.7315	8.66454	8.48442	11.8885	ENSG00000084731	KIF3C
ENSG00000084733	134.328	82.9907	102.184	71.9995	ENSG00000084733	RAB10
ENSG00000084734	1.64317	1.70776	0.83832	2.74771	ENSG00000084734	GCKR
ENSG00000084754	68.2897	78.2155	73.2476	64.0927	ENSG00000084754	HADHA
ENSG00000084764	10.5942	20.3632	21.0012	17.4541	ENSG00000084764	MAPRE3
ENSG00000084774	22.6267	51.6779	47.1901	61.6537	ENSG00000084774	CAD
ENSG00000085063	1041.72	588.492	155.986	295.43	ENSG00000085063	CD59
ENSG00000085117	190.519	250.444	80.1017	160.875	ENSG00000085117	CD82
ENSG00000085185	2.19877	3.15211	3.78939	4.90552	ENSG00000085185	BCORL1
ENSG00000085224	10.9737	16.458	7.27591	16.4958	ENSG00000085224	ATRX
ENSG00000085231	24.5255	22.4732	29.4552	20.1856	ENSG00000085231	AK6
ENSG00000085265	0	0.0443463	0	0.100667	ENSG00000085265	FCN1
ENSG00000085274	8.31255	10.4934	12.971	6.91953	ENSG00000085274	MYNN
ENSG00000085276	9.64928	13.4922	7.49254	15.3718	ENSG00000085276	MECOM
ENSG00000085365	45.0186	50.7065	44.4483	38.3668	ENSG00000085365	SCAMP1
ENSG00000085377	16.3657	24.0483	22.5123	19.7229	ENSG00000085377	PREP
ENSG00000085382	11.7633	22.8737	19.5489	34.8801	ENSG00000085382	HACE1
ENSG00000085415	21.8912	25.5541	26.3259	26.8885	ENSG00000085415	SEH1L
ENSG00000085433	23.2607	15.6517	15.2346	12.9107	ENSG00000085433	WDR47
ENSG00000085449	41.5358	45.5573	35.0064	44.8204	ENSG00000085449	WDFY1
ENSG00000085465	2.70325	3.37957	5.63363	2.46848	ENSG00000085465	OVGP1
ENSG00000085491	25.1309	23.6728	23.5867	18.7303	ENSG00000085491	SLC25A24
ENSG00000085511	23.0263	33.8451	20.7769	29.8124	ENSG00000085511	MAP3K4

ENSG00000085514	1.58406	1.19029	0.853894	1.29069	ENSG00000085514	PILRA
ENSG00000085552	6.87776	16.7588	17.66	4.76717	ENSG00000085552	IGSF9
ENSG00000085563	0.0924888	0.151582	0.17469	0.0892517	ENSG00000085563	ABCB1
ENSG00000085644	4.44874	3.54738	6.4018	4.5747	ENSG00000085644	ZNF213
ENSG00000085662	21.7568	31.165	28.4909	43.9186	ENSG00000085662	AKR1B1
ENSG00000085719	88.8506	79.1198	58.0277	55.996	ENSG00000085719	CPNE3
ENSG00000085721	17.656	22.7311	28.0133	16.0045	ENSG00000085721	RRN3
ENSG00000085733	207.521	236.461	248.259	206.846	ENSG00000085733	CTTN
ENSG00000085741	0.489267	0.534696	0.684182	1.29234	ENSG00000085741	WNT11
ENSG00000085760	18.1124	26.4113	26.3233	14.6112	ENSG00000085760	MTIF2
ENSG00000085788	38.2103	42.6149	36.6437	42.6459	ENSG00000085788	DDHD2
ENSG00000085831	9.61559	4.21408	4.48818	6.05025	ENSG00000085831	TTC39A
ENSG00000085832	37.2674	43.4753	32.0576	42.4019	ENSG00000085832	EPS15
ENSG00000085840	1.44753	3.87255	0.739462	2.71125	ENSG00000085840	ORC1
ENSG00000085871	36.4557	39.6105	20.0615	8.67424	ENSG00000085871	MGST2
ENSG00000085872	9.43249	10.98	12.2587	14.2705	ENSG00000085872	CHERP
ENSG00000085978	26.9028	24.6773	19.2324	23.2897	ENSG00000085978	ATG16L1
ENSG00000085982	27.3094	43.797	48.2558	58.6294	ENSG00000085982	USP40
ENSG00000085998	51.7031	76.9254	47.428	66.457	ENSG00000085998	POMGNT1
ENSG00000085999	2.14195	7.92943	3.48384	11.6409	ENSG00000085999	RAD54L
ENSG00000086015	9.47969	14.1718	14.0746	23.0191	ENSG00000086015	MAST2
ENSG00000086061	58.2241	26.3951	28.9866	37.1267	ENSG00000086061	DNAJA1
ENSG00000086062	33.0172	49.2597	57.444	48.2804	ENSG00000086062	B4GALT1
ENSG00000086065	56.0468	28.4786	19.8867	23.8456	ENSG00000086065	CHMP5
ENSG00000086102	19.7457	33.112	38.888	46.2083	ENSG00000086102	NFX1
ENSG00000086159	0.271652	0.514021	0.433594	0.471186	ENSG00000086159	AQP6
ENSG00000086189	14.06	19.2012	15.3476	14.6399	ENSG00000086189	DIMT1
ENSG00000086200	11.2489	20.4782	11.7194	26.375	ENSG00000086200	IPO11
ENSG00000086205	1.71	5.0247	3.07051	9.15922	ENSG00000086205	FOLH1
ENSG00000086232	27.3853	33.6272	27.4911	35.2286	ENSG00000086232	EIF2AK1
ENSG00000086288	0.164919	0.147788	0.208823	0.165428	ENSG00000086288	NME8
ENSG00000086289	0.0658974	0.802492	0.131207	3.65949	ENSG00000086289	EPDR1
ENSG00000086300	2.91957	5.13755	5.55841	7.69484	ENSG00000086300	SNX10
ENSG00000086475	17.3921	24.8316	18.8581	15.9054	ENSG00000086475	SEPHS1
ENSG00000086504	32.0111	27.508	24.3951	17.4929	ENSG00000086504	MRPL28
ENSG00000086506	0.825316	0.395925	0.595597	0.147406	ENSG00000086506	HBQ1
ENSG00000086544	49.0573	19.1351	18.6944	19.4282	ENSG00000086544	ITPKC
ENSG00000086548	170.707	3.50749	1.50171	7.16563	ENSG00000086548	CEACAM6
ENSG00000086570	67.5528	126.703	149.335	45.0622	ENSG00000086570	FAT2
ENSG00000086589	17.2549	23.3187	20.8928	12.3613	ENSG00000086589	RBM22
ENSG00000086598	265.91	128.203	130.654	342.329	ENSG00000086598	TMED2
ENSG00000086619	4.21481	10.4855	4.6335	10.5254	ENSG00000086619	ERO1B
ENSG00000086666	46.6664	51.2033	35.329	52.3242	ENSG00000086666	ZFAND6
ENSG00000086696	4.87566	6.57866	3.85121	4.11694	ENSG00000086696	HSD17B2
ENSG00000086712	4.70537	6.86751	9.28127	7.2633	ENSG00000086712	TXLNG
ENSG00000086717	1.80895	1.94305	1.45487	2.83449	ENSG00000086717	PPEF1
ENSG00000086730	1.83486	1.91684	2.3194	5.19722	ENSG00000086730	LAT2
ENSG00000086758	81.9717	93.1574	112.542	106.736	ENSG00000086758	HUWE1
ENSG00000086827	9.33324	10.1154	8.95132	7.28499	ENSG00000086827	ZW10
ENSG00000086848	10.4173	13.152	13.3361	15.0321	ENSG00000086848	ALG9
ENSG00000086967	0	0	0.166515	0.0333294	ENSG00000086967	MYBPC2
ENSG00000086991	0.232846	0.600676	0.554968	2.36665	ENSG00000086991	NOX4
ENSG00000087008	16.9939	14.0379	13.9654	9.69277	ENSG00000087008	ACOX3
ENSG00000087053	12.0511	13.0377	12.3936	11.823	ENSG00000087053	MTMR2

ENSG00000087074	66.9771	60.1626	65.719	24.6168	ENSG00000087074	PPP1R15A
ENSG00000087076	3.35613	0.608636	0.907739	3.59047	ENSG00000087076	HSD17B14
ENSG00000087077	64.5291	84.9756	85.9822	55.0525	ENSG00000087077	TRIP6
ENSG00000087085	1.50723	0.197454	0.641378	0.783826	ENSG00000087085	ACHE
ENSG00000087086	790.072	541.358	236.931	403.138	ENSG00000087086	FTL
ENSG00000087087	49.462	44.7793	54.3852	61.0735	ENSG00000087087	SRRT
ENSG00000087088	39.6326	35.0192	38.9616	42.4964	ENSG00000087088	BAX
ENSG00000087095	10.3259	15.9959	11.1925	16.6497	ENSG00000087095	NLK
ENSG00000087111	31.3456	33.3562	29.7271	23.6465	ENSG00000087111	PIGS
ENSG00000087116	0.558953	0.677075	2.80768	90.7428	ENSG00000087116	ADAMTS2
ENSG00000087128	24.3897	2.94974	0.423861	4.3696	ENSG00000087128	TMPRSS11E
ENSG00000087152	37.2591	43.6701	42.5557	35.441	ENSG00000087152	ATXN7L3
ENSG00000087157	18.291	25.7009	28.4181	26.9112	ENSG00000087157	PGS1
ENSG00000087191	16.9543	18.2561	24.1592	21.0721	ENSG00000087191	PSMC5
ENSG00000087206	28.287	44.5551	51.9232	59.9027	ENSG00000087206	UIMC1
ENSG00000087237	0.0753176	0.145108	0.196754	0.407066	ENSG00000087237	CETP
ENSG00000087245	9.3556	33.1226	12.3063	226.779	ENSG00000087245	MMP2
ENSG00000087250	0.197028	0	1.53201	0.451797	ENSG00000087250	MT3
ENSG00000087253	32.7288	30.3533	12.9672	19.3203	ENSG00000087253	LPCAT2
ENSG00000087258	0.884994	3.56089	1.01978	2.01697	ENSG00000087258	GNAO1
ENSG00000087263	32.9622	31.079	37.2228	21.3948	ENSG00000087263	OGFOD1
ENSG00000087266	25.8438	32.8952	56.489	27.9501	ENSG00000087266	SH3BP2
ENSG00000087269	18.4935	17.6532	23.5403	16.312	ENSG00000087269	NOP14
ENSG00000087274	72.2147	82.2325	69.5062	80.9008	ENSG00000087274	ADD1
ENSG00000087299	3.52875	6.79816	5.69791	7.41871	ENSG00000087299	L2HGDH
ENSG00000087301	1.74749	5.5877	2.43197	3.8484	ENSG00000087301	TXNDC16
ENSG00000087302	56.6894	50.7269	50.6188	48.1054	ENSG00000087302	C14orf166
ENSG00000087303	2.38208	3.64374	3.93508	22.8678	ENSG00000087303	NID2
ENSG00000087338	5.11282	7.49806	7.32064	8.0339	ENSG00000087338	GMCL1
ENSG00000087365	69.6329	72.1364	68.062	82.2558	ENSG00000087365	SF3B2
ENSG00000087448	14.488	27.713	14.4007	19.3081	ENSG00000087448	KLHL42
ENSG00000087460	268.823	203.697	140.339	184.069	ENSG00000087460	GNAS
ENSG00000087470	84.047	106.117	78.9747	91.591	ENSG00000087470	DNM1L
ENSG00000087494	410.862	317.905	89.2099	254.698	ENSG00000087494	PTHLH
ENSG00000087495	41.824	18.5076	18.1023	32.7592	ENSG00000087495	PHACTR3
ENSG00000087502	93.5176	83.6426	52.4304	45.9052	ENSG00000087502	ERGIC2
ENSG00000087510	8.48106	9.25347	6.41542	7.54695	ENSG00000087510	TFAP2C
ENSG00000087586	6.70624	22.2756	4.76874	9.44763	ENSG00000087586	AURKA
ENSG00000087589	0.925311	1.47561	1.53651	2.51161	ENSG00000087589	CASS4
ENSG00000087842	8.23516	9.35786	4.95514	7.98584	ENSG00000087842	PIR
ENSG00000087884	17.9138	35.4909	35.007	52.8823	ENSG00000087884	AAMDC
ENSG00000087903	19.9521	26.8499	27.435	33.5301	ENSG00000087903	RFX2
ENSG00000087916	35.3457	1.99784	1.42712	5.92437	ENSG00000087916	SLC6A14
ENSG00000087995	14.4678	14.2038	16.2625	14.6677	ENSG00000087995	METTL2A
ENSG00000088002	55.8734	10.3764	12.826	9.60997	ENSG00000088002	SULT2B1
ENSG00000088035	15.7297	33.1457	18.4813	25.7834	ENSG00000088035	ALG6
ENSG00000088038	0.451388	0.355499	0.725781	0.459573	ENSG00000088038	CNOT3
ENSG00000088053	0.133284	0.247489	0.256662	0.413123	ENSG00000088053	GP6
ENSG00000088179	17.0754	29.2111	18.7401	20.1395	ENSG00000088179	PTPN4
ENSG00000088205	30.5198	35.0791	37.7611	32.9654	ENSG00000088205	DDX18
ENSG00000088247	56.3741	49.2361	60.1914	67.8943	ENSG00000088247	KHSRP
ENSG00000088256	44.2639	52.042	50.5934	59.5907	ENSG00000088256	GNA11
ENSG00000088280	13.5989	23.4695	20.1985	40.5437	ENSG00000088280	ASAP3
ENSG00000088298	16.2103	21.7391	15.7316	10.5638	ENSG00000088298	EDEM2

ENSG00000088305	0.836918	2.3063	1.84637	1.70487	ENSG00000088305	DNMT3B
ENSG00000088320	0.0344555	0.0331966	0.0300473	0.0377543	ENSG00000088320	REM1
ENSG00000088325	9.46707	43.7937	5.96539	16.0687	ENSG00000088325	TPX2
ENSG00000088340	4.57741	7.89635	5.89514	11.0025	ENSG00000088340	FER1L4
ENSG00000088356	5.4604	3.09848	5.72815	2.6425	ENSG00000088356	PDRG1
ENSG00000088367	8.17893	1.93753	1.70328	4.7613	ENSG00000088367	EPB41L1
ENSG00000088386	4.96013	2.43378	2.38507	5.58915	ENSG00000088386	SLC15A1
ENSG00000088387	84.6209	61.6142	50.3858	75.5835	ENSG00000088387	DOCK9
ENSG00000088448	147.713	221.72	113.634	227.71	ENSG00000088448	ANKRD10
ENSG00000088451	7.17835	8.91361	7.72901	5.50457	ENSG00000088451	TGDS
ENSG00000088538	1.26631	0.466425	0.680424	0.472565	ENSG00000088538	DOCK3
ENSG00000088543	1.29949	3.54995	1.71309	4.13612	ENSG00000088543	C3orf18
ENSG00000088682	15.5714	19.2729	22.0928	12.7807	ENSG00000088682	COQ9
ENSG00000088726	255.159	103.18	116.904	117.913	ENSG00000088726	TMEM40
ENSG00000088727	4.20622	3.65943	4.24999	3.22223	ENSG00000088727	KIF9
ENSG00000088756	3.66218	6.66111	7.98955	12.7376	ENSG00000088756	ARHGAP28
ENSG00000088766	30.6568	37.3161	32.5313	33.6179	ENSG00000088766	CRLS1
ENSG00000088782	0	0	0	0	ENSG00000088782	DEFB127
ENSG00000088808	17.357	30.3066	23.7819	24.5497	ENSG00000088808	PPP1R13B
ENSG00000088812	34.5431	39.7614	32.2226	25.8945	ENSG00000088812	ATRN
ENSG00000088826	6.6288	9.14272	9.27592	7.28433	ENSG00000088826	SMOX
ENSG00000088827	0.0995712	0.168068	0.141107	0.315251	ENSG00000088827	SIGLEC1
ENSG00000088832	59.3165	72.0448	48.0627	81.9307	ENSG00000088832	FKBP1A
ENSG00000088833	30.634	19.7608	25.3965	22.7682	ENSG00000088833	NSFL1C
ENSG00000088836	12.6359	12.6561	11.7124	7.30048	ENSG00000088836	SLC4A11
ENSG00000088854	8.69651	15.2585	14.7239	13.4218	ENSG00000088854	C20orf194
ENSG00000088876	6.9695	8.50056	12.1277	11.9882	ENSG00000088876	ZNF343
ENSG00000088881	0.0982112	0.165714	0.281095	5.30251	ENSG00000088881	EBF4
ENSG00000088882	0.069727	0.0896226	0.0607688	0.306379	ENSG00000088882	CPXM1
ENSG00000088888	19.5914	15.9362	18.9605	16.5701	ENSG00000088888	MAVS
ENSG00000088899	4.1846	1.8323	4.62162	2.16528	ENSG00000088899	LZTS3
ENSG00000088926	0.453975	0.558118	0.837958	0.901484	ENSG00000088926	F11
ENSG00000088930	27.9041	33.4231	31.2281	28.5036	ENSG00000088930	XRN2
ENSG00000088986	174.08	106.936	93.5328	69.3988	ENSG00000088986	DYNLL1
ENSG00000088992	0.555558	0.951305	1.33508	2.56248	ENSG00000088992	TESC
ENSG00000089006	59.8299	102.081	81.6369	86.8096	ENSG00000089006	SNX5
ENSG00000089009	626.318	438.412	391.33	243.548	ENSG00000089009	RPL6
ENSG00000089012	0.0938709	0	0.0722533	0	ENSG00000089012	SIRPG
ENSG00000089022	28.5609	36.3754	38.0458	30.3573	ENSG00000089022	MAPKAPK5
ENSG00000089041	0.861398	1.78413	4.31714	1.88172	ENSG00000089041	P2RX7
ENSG00000089048	7.62546	7.0807	8.37854	9.48466	ENSG00000089048	ESF1
ENSG00000089050	6.75509	7.71936	6.28084	7.01939	ENSG00000089050	RBBP9
ENSG00000089053	34.6337	43.4402	41.685	53.8922	ENSG00000089053	ANAPC5
ENSG00000089057	13.0658	18.3062	11.5621	10.1573	ENSG00000089057	SLC23A2
ENSG00000089060	16.3754	22.4927	23.5559	20.579	ENSG00000089060	SLC8B1
ENSG00000089063	34.501	31.8823	24.2121	20.6353	ENSG00000089063	TMEM230
ENSG00000089091	2.65979	4.75596	4.60786	6.32852	ENSG00000089091	DZANK1
ENSG00000089094	3.87698	6.46592	6.01116	8.14294	ENSG00000089094	KDM2B
ENSG00000089101	2.13241	6.21148	5.81028	7.18033	ENSG00000089101	CFAP61
ENSG00000089116	0.71454	0.868229	1.53527	0.52724	ENSG00000089116	LHX5
ENSG00000089123	8.4059	15.4654	15.3848	13.5318	ENSG00000089123	TASP1
ENSG00000089127	18.1383	24.7192	19.4761	20.6478	ENSG00000089127	OAS1
ENSG00000089154	77.0732	66.6433	72.7204	79.4622	ENSG00000089154	GCN1
ENSG00000089157	709.172	631.955	461.554	259.619	ENSG00000089157	RPLP0

ENSG00000089159	130.155	136.912	90.5802	141.117	ENSG00000089159	PXN
ENSG00000089163	0.836241	0.401175	0.51231	0.823791	ENSG00000089163	SIRT4
ENSG00000089169	5.36928	7.46645	7.43867	9.16269	ENSG00000089169	RPH3A
ENSG00000089177	5.29386	10.3755	13.0875	9.27605	ENSG00000089177	KIF16B
ENSG00000089195	11.0747	6.05666	8.69882	4.72922	ENSG00000089195	TRMT6
ENSG00000089199	0.701576	2.38525	1.50137	2.93414	ENSG00000089199	CHGB
ENSG00000089220	82.2677	48.799	47.0648	40.3087	ENSG00000089220	PEBP1
ENSG00000089225	0.381505	0.714651	0.505671	0.870592	ENSG00000089225	TBX5
ENSG00000089234	11.8834	9.15842	11.9124	7.83529	ENSG00000089234	BRAP
ENSG00000089248	42.3181	82.3774	40.4596	37.6044	ENSG00000089248	ERP29
ENSG00000089250	5.74107	9.35965	1.59372	5.70838	ENSG00000089250	NOS1
ENSG00000089280	21.29	38.8741	38.8579	61.008	ENSG00000089280	FUS
ENSG00000089289	14.9345	10.9459	9.0876	6.92405	ENSG00000089289	IGBP1
ENSG00000089327	200.947	127.542	53.6433	60.5689	ENSG00000089327	FXYD5
ENSG00000089335	11.7372	17.3743	20.8749	15.9509	ENSG00000089335	ZNF302
ENSG00000089351	18.0092	29.2649	28.5038	37.1056	ENSG00000089351	GRAMD1A
ENSG00000089356	1010.04	364.386	280.265	139.656	ENSG00000089356	FXYD3
ENSG00000089472	1.63871	1.08299	3.60346	4.32235	ENSG00000089472	HEPH
ENSG00000089486	20.5893	17.5688	27.0665	18.1246	ENSG00000089486	CDIP1
ENSG00000089505	1.70845	5.78565	0.694652	3.30986	ENSG00000089505	CMTM1
ENSG00000089558	0	0.0281211	0.0120456	0.0320351	ENSG00000089558	KCNH4
ENSG00000089597	67.4171	133.428	106.722	132.286	ENSG00000089597	GANAB
ENSG00000089639	8.3508	8.10764	6.5804	6.91538	ENSG00000089639	GMIP
ENSG00000089682	10.9892	15.318	14.5128	14.2877	ENSG00000089682	RBM41
ENSG00000089685	4.69628	18.2455	5.35053	11.8409	ENSG00000089685	BIRC5
ENSG00000089692	0.0985452	0.516016	0.647494	0.481565	ENSG00000089692	LAG3
ENSG00000089693	68.7046	60.8414	75.1566	48.521	ENSG00000089693	MLF2
ENSG00000089723	5.19543	2.41891	2.22033	2.62245	ENSG00000089723	OTUB2
ENSG00000089737	46.945	49.6985	46.7876	49.1456	ENSG00000089737	DDX24
ENSG00000089775	5.33348	10.9901	10.7983	11.0285	ENSG00000089775	ZBTB25
ENSG00000089818	15.7177	13.3277	15.7821	13.832	ENSG00000089818	NECAP1
ENSG00000089820	0.885998	1.6818	0.986356	1.8138	ENSG00000089820	ARHGAP4
ENSG00000089847	0.0966889	0.47249	0.415587	0.534915	ENSG00000089847	ANKRD24
ENSG00000089876	31.6471	23.0577	25.7684	18.1302	ENSG00000089876	DHX32
ENSG00000089902	28.1567	32.974	31.2998	29.3379	ENSG00000089902	RCOR1
ENSG00000089916	36.2756	47.794	45.51	46.1535	ENSG00000089916	GPATCH2L
ENSG00000090006	27.7784	93.3035	77.8418	89.9368	ENSG00000090006	LTBP4
ENSG00000090013	45.8901	33.3096	21.3228	16.5106	ENSG00000090013	BLVRB
ENSG00000090020	19.2398	32.0851	37.1394	24.6414	ENSG00000090020	SLC9A1
ENSG00000090054	89.055	94.5123	67.7754	66.2592	ENSG00000090054	SPTLC1
ENSG00000090060	44.2897	62.6025	68.7887	88.3347	ENSG00000090060	PAPOLA
ENSG00000090061	13.8287	17.1574	19.4624	16.6943	ENSG00000090061	CCNK
ENSG00000090097	19.6683	18.124	23.3432	12.3364	ENSG00000090097	PCBP4
ENSG00000090104	1.00033	1.8537	1.8705	1.61798	ENSG00000090104	RGS1
ENSG00000090238	26.3914	15.691	15.6347	16.0671	ENSG00000090238	YPEL3
ENSG00000090263	21.2594	24.7121	21.1639	18.8441	ENSG00000090263	MRPS33
ENSG00000090266	85.6251	77.9053	52.7582	62.4702	ENSG00000090266	NDUFB2
ENSG00000090273	25.1199	19.5657	25.183	31.6273	ENSG00000090273	NUDC
ENSG00000090316	32.133	24.2102	36.3698	31.8689	ENSG00000090316	MAEA
ENSG00000090339	3.55875	4.28165	5.34673	24.5962	ENSG00000090339	ICAM1
ENSG00000090372	53.4175	47.1113	58.7574	52.1047	ENSG00000090372	STRN4
ENSG00000090376	0.296709	0.803873	1.05064	7.96288	ENSG00000090376	IRAK3
ENSG00000090382	0.754596	1.1648	1.42842	3.14479	ENSG00000090382	LYZ
ENSG00000090402	0.00886192	0	0.00773382	0.137218	ENSG00000090402	SI

ENSG00000090432	24.0723	18.0317	15.0354	9.48612	ENSG00000090432	MUL1
ENSG00000090447	5.06817	8.3259	6.95832	8.88503	ENSG00000090447	TFAP4
ENSG00000090470	8.30772	9.19563	18.6418	17.2699	ENSG00000090470	PDCD7
ENSG00000090487	29.2285	46.7219	50.6166	64.6222	ENSG00000090487	SPG21
ENSG00000090512	0.0589317	0.0389905	0.766583	0.177189	ENSG00000090512	FETUB
ENSG00000090520	56.228	72.114	41.2563	36.003	ENSG00000090520	DNAJB11
ENSG00000090530	99.3602	28.2398	56.2839	54.8789	ENSG00000090530	P3H2
ENSG00000090534	0.502873	0.525559	0.046545	0.174644	ENSG00000090534	THPO
ENSG00000090539	3.6099	7.23877	7.05507	13.6315	ENSG00000090539	CHRD
ENSG00000090554	2.63855	8.24958	5.99426	11.3065	ENSG00000090554	FLT3LG
ENSG00000090565	11.7868	19.6273	21.3035	31.3134	ENSG00000090565	RAB11FIP3
ENSG00000090581	35.2666	31.6704	36.0873	37.1753	ENSG00000090581	GNPTG
ENSG00000090612	18.9455	18.7331	19.8186	18.03	ENSG00000090612	ZNF268
ENSG00000090615	50.619	53.5043	60.7027	84.5129	ENSG00000090615	GOLGA3
ENSG00000090621	53.1913	88.6782	100.415	94.384	ENSG00000090621	PABPC4
ENSG00000090659	0.625486	1.14583	1.30795	2.02343	ENSG00000090659	CD209
ENSG00000090661	25.5394	11.8012	17.5837	14.2149	ENSG00000090661	CERS4
ENSG00000090674	11.3079	16.6633	15.3223	15.8595	ENSG00000090674	MCOLN1
ENSG00000090686	25.3295	47.3405	39.4605	62.4142	ENSG00000090686	USP48
ENSG00000090776	111.957	171.483	113.972	74.1422	ENSG00000090776	EFNB1
ENSG00000090857	7.955	14.4335	14.206	14.5378	ENSG00000090857	PDPR
ENSG00000090861	29.2122	97.3754	107.588	71.3754	ENSG00000090861	AARS
ENSG00000090863	62.0556	118.827	87.7415	104.993	ENSG00000090863	GLG1
ENSG00000090889	2.27106	14.0725	1.76527	5.40984	ENSG00000090889	KIF4A
ENSG00000090905	20.6709	31.1894	32.8927	46.8732	ENSG00000090905	TNRC6A
ENSG00000090920	0.492803	0.686261	1.71639	1.13692	ENSG00000090920	FCGBP
ENSG00000090924	21.5684	32.6037	29.8481	45.1573	ENSG00000090924	PLEKHG2
ENSG00000090932	0.540906	0.32219	0.478533	0.288436	ENSG00000090932	DLL3
ENSG00000090971	11.081	16.8012	10.7589	13.6406	ENSG00000090971	NAT14
ENSG00000090975	11.0544	11.3725	8.91284	11.9567	ENSG00000090975	PITPNM2
ENSG00000090989	30.7469	25.9748	28.3745	25.905	ENSG00000090989	EXOC1
ENSG00000091009	19.7549	17.4801	15.892	17.9539	ENSG00000091009	RBM27
ENSG00000091010	0.102293	0.0978917	0.222989	0.111007	ENSG00000091010	POU4F3
ENSG00000091039	32.3119	32.5731	32.6704	39.8431	ENSG00000091039	OSBPL8
ENSG00000091073	30.7108	60.4227	95.4277	50.2733	ENSG00000091073	DTX2
ENSG00000091106	0.488458	1.00225	1.41395	0.951589	ENSG00000091106	NLRC4
ENSG00000091127	10.9431	10.894	16.798	14.5269	ENSG00000091127	PUS7
ENSG00000091128	0.568394	1.4913	1.20557	2.28245	ENSG00000091128	LAMB4
ENSG00000091129	6.93145	36.5583	6.603	31.5833	ENSG00000091129	NRCAM
ENSG00000091136	78.1616	166.594	115.799	214.385	ENSG00000091136	LAMB1
ENSG00000091137	0.607128	1.47863	0.845645	1.25449	ENSG00000091137	SLC26A4
ENSG00000091138	0.367872	0.125363	0.4624	0.280485	ENSG00000091138	SLC26A3
ENSG00000091140	29.5926	30.434	33.0131	24.6339	ENSG00000091140	DLD
ENSG00000091157	8.262	18.5544	13.0359	18.4035	ENSG00000091157	WDR7
ENSG00000091164	22.5613	18.5416	16.2704	19.8053	ENSG00000091164	TXNL1
ENSG00000091181	0.951539	1.64757	1.22516	1.93517	ENSG00000091181	IL5RA
ENSG00000091262	1.75196	4.47873	4.48919	7.54277	ENSG00000091262	ABCC6
ENSG00000091317	63.5069	53.2336	28.9083	19.6063	ENSG00000091317	CMTM6
ENSG00000091409	893.172	1185.02	401.749	572.417	ENSG00000091409	ITGA6
ENSG00000091428	2.08099	3.30425	2.72698	5.46451	ENSG00000091428	RAPGEF4
ENSG00000091436	26.4392	41.2072	37.8611	38.9812	ENSG00000091436	MAP3K20
ENSG00000091482	0	0.133028	0	0	ENSG00000091482	SMPX
ENSG00000091483	39.4923	43.1743	25.9199	28.556	ENSG00000091483	FH
ENSG00000091490	33.6783	41.4321	40.0895	17.1985	ENSG00000091490	SEL1L3

ENSG00000091513	0.908782	2.04195	1.56532	2.96247	ENSG00000091513	TF
ENSG00000091527	66.8236	53.9417	64.5234	60.4715	ENSG00000091527	CDV3
ENSG00000091536	3.28866	7.95837	5.77442	9.46473	ENSG00000091536	MYO15A
ENSG00000091542	20.7818	20.864	23.0361	17.7719	ENSG00000091542	ALKBH5
ENSG00000091583	0.703961	0.66639	0.528166	1.63905	ENSG00000091583	APOH
ENSG00000091592	28.4831	40.368	62.5948	40.0124	ENSG00000091592	NLRP1
ENSG00000091622	8.64322	18.3096	23.9633	11.821	ENSG00000091622	PITPNM3
ENSG00000091640	28.9322	42.4554	50.2695	66.5975	ENSG00000091640	SPAG7
ENSG00000091651	12.5258	30.4686	19.7536	30.5442	ENSG00000091651	ORC6
ENSG00000091656	8.27455	17.3434	15.8738	26.5784	ENSG00000091656	ZFHX4
ENSG00000091664	0.0137778	0.131985	0.096695	0.165716	ENSG00000091664	SLC17A6
ENSG00000091704	0.199681	0.167395	0.09764	0.192722	ENSG00000091704	CPA1
ENSG00000091732	7.41171	10.2479	8.24265	7.46705	ENSG00000091732	ZC3HC1
ENSG00000091831	1.57466	4.10834	1.76946	1.19615	ENSG00000091831	ESR1
ENSG00000091844	1.49173	2.26197	1.98994	4.57129	ENSG00000091844	RGS17
ENSG00000091879	1.46109	4.12026	4.01648	5.36885	ENSG00000091879	ANGPT2
ENSG00000091947	23.0733	30.5432	21.2341	13.3324	ENSG00000091947	TMEM101
ENSG00000091972	3.02045	7.45182	7.57264	16.7833	ENSG00000091972	CD200
ENSG00000091986	30.0394	12.2827	15.1461	158.654	ENSG00000091986	CCDC80
ENSG00000092009	0.200237	0.256759	0.776623	0.0825282	ENSG00000092009	CMA1
ENSG00000092010	40.5306	56.4514	35.765	33.222	ENSG00000092010	PSME1
ENSG00000092020	10.5327	12.2884	9.44608	12.233	ENSG00000092020	PPP2R3C
ENSG00000092036	12.3091	24.1091	12.8407	12.1259	ENSG00000092036	HAUS4
ENSG00000092051	0.180709	0.328596	0.336724	0.754094	ENSG00000092051	JPH4
ENSG00000092054	0	0	0.0152745	0.0578478	ENSG00000092054	MYH7
ENSG00000092067	0	0.0716707	0.129573	0.162944	ENSG00000092067	CEBPE
ENSG00000092068	9.40903	37.4967	31.3749	36.11	ENSG00000092068	SLC7A8
ENSG00000092094	11.9957	15.9185	24.662	21.0745	ENSG00000092094	OSGEP
ENSG00000092096	3.70159	3.66805	2.41381	11.6471	ENSG00000092096	SLC22A17
ENSG00000092098	31.9102	39.0293	38.3458	29.9326	ENSG00000092098	RNF31
ENSG00000092108	44.9582	56.0628	55.4315	74.9462	ENSG00000092108	SCFD1
ENSG00000092140	33.3367	77.34	42.6204	72.0656	ENSG00000092140	G2E3
ENSG00000092148	89.0644	87.7042	70.9208	83.3605	ENSG00000092148	HECTD1
ENSG00000092199	232.815	243.371	224.487	200.922	ENSG00000092199	HNRNPC
ENSG00000092200	0.610725	2.86833	3.62996	3.06771	ENSG00000092200	RPGRIP1
ENSG00000092201	30.8287	46.7431	40.6334	49.1166	ENSG00000092201	SUPT16H
ENSG00000092203	23.3059	15.3948	17.9156	15.1594	ENSG00000092203	TOX4
ENSG00000092208	13.002	20.7906	20.6136	22.4396	ENSG00000092208	GEMIN2
ENSG00000092295	42.6405	29.8497	26.99	14.2233	ENSG00000092295	TGM1
ENSG00000092330	40.6353	45.4381	35.4238	41.9831	ENSG00000092330	TINF2
ENSG00000092345	0.0359093	0.190309	0.0782098	0.13813	ENSG00000092345	DAZL
ENSG00000092377	0.659819	1.42663	1.25108	0.103783	ENSG00000092377	TBL1Y
ENSG00000092421	2.32246	4.58481	6.0321	7.01495	ENSG00000092421	SEMA6A
ENSG00000092439	22.4979	41.9467	44.2815	36.3025	ENSG00000092439	TRPM7
ENSG00000092445	11.1443	11.8785	8.84305	10.8158	ENSG00000092445	TYRO3
ENSG00000092470	3.11328	8.82991	2.94555	9.07648	ENSG00000092470	WDR76
ENSG00000092529	16.8291	17.302	23.3202	11.6916	ENSG00000092529	CAPN3
ENSG00000092531	47.5313	38.2989	25.8383	45.7508	ENSG00000092531	SNAP23
ENSG00000092607	0.168263	0.31132	0.313719	3.53924	ENSG00000092607	TBX15
ENSG00000092621	5.90092	86.4366	57.9644	31.949	ENSG00000092621	PHGDH
ENSG00000092758	5.5599	6.00297	5.86088	26.8646	ENSG00000092758	COL9A3
ENSG00000092820	205.761	101.454	90.1933	65.7577	ENSG00000092820	EZR
ENSG00000092841	1124.3	511.448	227.728	372.382	ENSG00000092841	MYL6
ENSG00000092847	5.02254	4.81063	5.00996	5.43645	ENSG00000092847	AGO1

ENSG00000092850	0.18046	0.625281	0.690366	0.379811	ENSG00000092850	TEKT2
ENSG00000092853	3.47501	7.45678	1.13918	7.9568	ENSG00000092853	CLSPN
ENSG00000092871	23.2857	21.2176	11.4967	16.3191	ENSG00000092871	RFFL
ENSG00000092929	3.24787	7.33825	10.3483	6.7154	ENSG00000092929	UNC13D
ENSG00000092931	20.3025	26.0218	24.6393	28.8207	ENSG00000092931	MFSD11
ENSG00000092964	25.1443	34.7339	20.2683	48.6435	ENSG00000092964	DPYSL2
ENSG00000092969	6.71222	4.18752	8.7445	13.3473	ENSG00000092969	TGFB2
ENSG00000092978	13.2933	20.0264	23.6487	20.1014	ENSG00000092978	GPATCH2
ENSG00000093000	35.4229	43.6514	36.0485	37.5637	ENSG00000093000	NUP50
ENSG00000093009	2.74807	14.2363	2.63217	6.90602	ENSG00000093009	CDC45
ENSG00000093010	91.4105	77.8674	74.452	55.7011	ENSG00000093010	COMT
ENSG00000093072	1.27268	5.58746	3.50212	10.5216	ENSG00000093072	ADA2
ENSG00000093134	4.25225	8.35818	8.58736	13.9149	ENSG00000093134	VNN3
ENSG00000093144	24.92	36.3958	36.1152	53.004	ENSG00000093144	ECHDC1
ENSG00000093167	123.94	71.8775	57.33	91.3782	ENSG00000093167	LRRFIP2
ENSG00000093183	35.9211	44.9459	33.4542	36.2556	ENSG00000093183	SEC22C
ENSG00000093217	5.95194	15.0125	10.6912	21.6555	ENSG00000093217	XYLB
ENSG00000094631	14.4364	26.5106	25.9218	39.5232	ENSG00000094631	HDAC6
ENSG00000094661	0	0	0	0	ENSG00000094661	OR1I1
ENSG00000094755	28.3587	16.8287	23.3598	60.7372	ENSG00000094755	GABRP
ENSG00000094796	4.42504	0	1.32465	0	ENSG00000094796	KRT31
ENSG00000094804	6.16139	16.2115	4.09397	10.4984	ENSG00000094804	CDC6
ENSG00000094841	6.43911	6.4426	6.59487	7.09058	ENSG00000094841	UPRT
ENSG00000094880	17.0245	21.5302	19.243	17.6408	ENSG00000094880	CDC23
ENSG00000094914	19.4605	32.3115	33.2587	24.152	ENSG00000094914	AAAS
ENSG00000094916	9.34969	20.0082	19.3644	25.1754	ENSG00000094916	CBX5
ENSG00000094963	0.842841	0.796825	0.983113	1.8398	ENSG00000094963	FMO2
ENSG00000094975	17.997	20.404	14.5901	19.049	ENSG00000094975	SUCO
ENSG00000095002	6.00725	11.9851	5.04414	9.53044	ENSG00000095002	MSH2
ENSG00000095015	8.66241	9.6882	8.26228	5.61429	ENSG00000095015	MAP3K1
ENSG00000095059	26.8797	31.9058	23.2008	26.8095	ENSG00000095059	DHPS
ENSG00000095066	82.9148	122.585	113.586	170.037	ENSG00000095066	HOOK2
ENSG00000095110	0.554958	0.249157	0.325351	1.37656	ENSG00000095110	NXPE1
ENSG00000095139	26.9447	17.2236	16.8587	21.5735	ENSG00000095139	ARCN1
ENSG00000095203	14.8065	4.57922	8.80957	4.23118	ENSG00000095203	EPB41L4B
ENSG00000095209	16.5315	18.377	14.8016	24.6901	ENSG00000095209	TMEM38B
ENSG00000095261	11.752	15.3646	14.3308	18.086	ENSG00000095261	PSMD5
ENSG00000095303	0.350976	15.4382	6.0621	5.09416	ENSG00000095303	PTGS1
ENSG00000095319	30.4077	39.67	36.1773	35.6013	ENSG00000095319	NUP188
ENSG00000095321	3.77132	6.02195	7.17788	8.49245	ENSG00000095321	CRAT
ENSG00000095370	0.264261	0.519438	0.498717	0.484957	ENSG00000095370	SH2D3C
ENSG00000095380	31.021	25.401	17.7721	19.5256	ENSG00000095380	NANS
ENSG00000095383	36.3631	29.7291	28.6405	21.1528	ENSG00000095383	TBC1D2
ENSG00000095397	2.99212	4.2029	3.87284	4.60491	ENSG00000095397	WHRN
ENSG00000095464	0.679555	1.23873	2.32846	1.55227	ENSG00000095464	PDE6C
ENSG00000095485	13.9501	16.3367	15.0255	15.9118	ENSG00000095485	CWF19L1
ENSG00000095539	2.99455	4.08436	5.61886	4.34508	ENSG00000095539	SEMA4G
ENSG00000095564	24.3121	34.5429	36.3379	31.6864	ENSG00000095564	BTAF1
ENSG00000095574	2.82563	2.24003	3.53199	5.27884	ENSG00000095574	IKZF5
ENSG00000095585	2.86203	3.69246	6.97858	6.71333	ENSG00000095585	BLNK
ENSG00000095587	1.52869	3.34082	2.73732	5.87434	ENSG00000095587	TLL2
ENSG00000095596	0.0263888	0	0	0	ENSG00000095596	CYP26A1
ENSG00000095627	0.0604607	0.189255	0.180284	0.492299	ENSG00000095627	TDRD1
ENSG00000095637	0.65096	0.885525	0.597215	1.57007	ENSG00000095637	SORBS1

ENSG00000095713	0.102732	0.357204	0.645611	0.751715	ENSG00000095713	CRTAC1
ENSG00000095739	5.79858	18.2307	8.747	2.47287	ENSG00000095739	BAMBI
ENSG00000095752	5.60055	8.81389	8.78098	12.6092	ENSG00000095752	IL11
ENSG00000095777	0.952086	1.53621	1.76776	3.44031	ENSG00000095777	MYO3A
ENSG00000095787	52.5164	59.3282	64.5637	64.939	ENSG00000095787	WAC
ENSG00000095794	6.7979	7.76766	6.89323	9.01333	ENSG00000095794	CREM
ENSG00000095906	24.5134	27.4281	27.1174	20.0909	ENSG00000095906	NUBP2
ENSG00000095917	0	0	0	0	ENSG00000095917	TPSD1
ENSG00000095932	0.157092	0.752705	0.589499	0.559001	ENSG00000095932	SMIM24
ENSG00000095951	15.1366	24.4795	26.1608	25.5953	ENSG00000095951	HIVEP1
ENSG00000095970	0.261866	0.508079	2.89748	0.491868	ENSG00000095970	TREM2
ENSG00000095981	0.0824164	0	0.0811729	0.101921	ENSG00000095981	KCNK16
ENSG00000096006	1.99871	0.496384	0.448748	0.952011	ENSG00000096006	CRISP3
ENSG00000096060	11.5543	17.8617	19.042	20.4894	ENSG00000096060	FKBP5
ENSG00000096063	35.8984	47.7798	41.6473	49.0916	ENSG00000096063	SRPK1
ENSG00000096070	6.15103	7.02578	7.44827	8.41743	ENSG00000096070	BRPF3
ENSG00000096080	22.6629	18.8746	20.5786	8.39811	ENSG00000096080	MRPS18A
ENSG00000096088	0.275841	0.727585	0.163474	0.798761	ENSG00000096088	PGC
ENSG00000096092	11.5694	13.9033	5.25715	4.47985	ENSG00000096092	TMEM14A
ENSG00000096093	20.5937	39.883	40.5076	78.6144	ENSG00000096093	EFHC1
ENSG00000096150	247.777	184.299	163.52	84.5791	ENSG00000096150	RPS18
ENSG00000096155	2.72683	3.94211	4.18653	25.7392	ENSG00000096155	BAG6
ENSG00000096171	2.80712	7.18785	5.91591	8.61059	ENSG00000096171	VARS
ENSG00000096264	0.729506	1.26394	1.0483	2.09737	ENSG00000096264	NCR2
ENSG00000096384	441.87	329.233	284.415	253.598	ENSG00000096384	HSP90AB1
ENSG00000096395	0	0	0	0.150903	ENSG00000096395	MLN
ENSG00000096401	10.9404	12.977	8.99901	10.3239	ENSG00000096401	CDC5L
ENSG00000096433	57.2309	65.3738	61.3707	45.1096	ENSG00000096433	ITPR3
ENSG00000096654	2.59788	4.33897	2.85032	2.15951	ENSG00000096654	ZNF184
ENSG00000096696	946.513	424.72	616.199	352.273	ENSG00000096696	DSP
ENSG00000096717	3.94783	5.69271	6.80054	5.13235	ENSG00000096717	SIRT1
ENSG00000096746	9.98221	11.0912	13.1177	24.9955	ENSG00000096746	HNRNPH3
ENSG00000096872	7.84608	13.9057	15.9869	15.3571	ENSG00000096872	IFT74
ENSG00000096968	5.65133	10.4783	7.62223	11.4291	ENSG00000096968	JAK2
ENSG00000096996	2.11392	4.16355	4.43497	7.13047	ENSG00000096996	IL12RB1
ENSG00000097007	17.5572	20.8323	25.7999	28.2788	ENSG00000097007	ABL1
ENSG00000097021	79.6937	30.8306	24.0377	26.5802	ENSG00000097021	ACOT7
ENSG00000097033	36.1691	26.0106	25.0131	26.2718	ENSG00000097033	SH3GLB1
ENSG00000097046	2.47757	5.13793	2.39982	6.38079	ENSG00000097046	CDC7
ENSG00000097096	3.1667	3.59735	3.55646	4.49279	ENSG00000097096	SYDE2
ENSG00000099139	6.40672	3.96216	2.85493	4.79315	ENSG00000099139	PCSK5
ENSG00000099194	761.277	777.868	183.717	378.457	ENSG00000099194	SCD
ENSG00000099203	18.4777	19.7775	10.5759	8.02524	ENSG00000099203	TMED1
ENSG00000099204	21.013	14.1519	33.1441	7.43688	ENSG00000099204	ABLIM1
ENSG00000099219	16.3032	43.657	18.2176	13.3295	ENSG00000099219	ERMP1
ENSG00000099246	84.2101	50.5649	70.4215	51.8724	ENSG00000099246	RAB18
ENSG00000099250	30.5098	93.2276	45.8944	131.397	ENSG00000099250	NRP1
ENSG00000099251	5.94154	11.9658	7.77793	7.9714	ENSG00000099251	HSD17B7P2
ENSG00000099256	1.68558	2.88364	1.77409	2.59193	ENSG00000099256	PRTFDC1
ENSG00000099260	1.7785	2.42323	4.95309	2.57914	ENSG00000099260	PALMD
ENSG00000099282	5.17411	3.79471	1.62883	3.84607	ENSG00000099282	TSPAN15
ENSG00000099284	10.9414	8.21284	9.28856	5.71809	ENSG00000099284	H2AFY2
ENSG00000099290	8.24995	5.79653	5.87196	6.77653	ENSG00000099290	WASHC2A
ENSG00000099308	2.71457	4.17626	4.06623	4.24877	ENSG00000099308	MAST3

ENSG00000099326	10.6941	13.8342	22.677	12.4223	ENSG00000099326	MZF1
ENSG00000099330	5.77062	8.36741	6.50638	15.7902	ENSG00000099330	OCEL1
ENSG00000099331	27.2245	35.733	27.4785	59.5297	ENSG00000099331	MYO9B
ENSG00000099337	40.8273	40.9165	34.927	38.8081	ENSG00000099337	KCNK6
ENSG00000099338	4.31132	8.03427	7.82032	10.0824	ENSG00000099338	CATSPERG
ENSG00000099341	111.518	69.9618	64.237	43.8805	ENSG00000099341	PSMD8
ENSG00000099364	29.739	22.6582	27.1957	17.1224	ENSG00000099364	FBXL19
ENSG00000099365	3.12914	7.89894	6.30557	9.9621	ENSG00000099365	STX1B
ENSG00000099377	3.04166	3.99104	3.10215	4.13191	ENSG00000099377	HSD3B7
ENSG00000099381	3.65603	2.94003	4.20519	3.90999	ENSG00000099381	SETD1A
ENSG00000099385	24.0576	20.6734	20.3777	21.0205	ENSG00000099385	BCL7C
ENSG00000099399	0.0357628	0.1727	0.0622894	0.196585	ENSG00000099399	MAGEB2
ENSG00000099617	0.644178	0.405264	0.519148	0.953502	ENSG00000099617	EFNA2
ENSG00000099622	65.3522	74.8266	125.778	79.1666	ENSG00000099622	CIRBP
ENSG00000099624	33.5278	38.4215	31.6726	38.1553	ENSG00000099624	ATP5D
ENSG00000099625	7.8112	5.59294	6.26959	5.32581	ENSG00000099625	CBARP
ENSG00000099715	0.251725	0.694881	0.698509	1.08433	ENSG00000099715	PCDH11Y
ENSG00000099721	0	0	0	0	ENSG00000099721	AMELY
ENSG00000099725	26.7536	47.3393	48.411	18.0079	ENSG00000099725	PRKY
ENSG00000099769	0.363669	0.60612	1.56367	0.603254	ENSG00000099769	IGFALS
ENSG00000099783	33.2654	40.4812	46.854	57.9724	ENSG00000099783	HNRNPM
ENSG00000099785	15.4599	12.0606	9.2169	11.2882	ENSG00000099785	MARCH2
ENSG00000099795	74.2521	62.3742	39.2825	32.0767	ENSG00000099795	NDUFB7
ENSG00000099797	114.024	91.3393	42.4113	54.5811	ENSG00000099797	TECR
ENSG00000099800	36.0568	28.8775	33.4696	18.1303	ENSG00000099800	TIMM13
ENSG00000099804	68.9358	46.5603	53.5922	32.5138	ENSG00000099804	CDC34
ENSG00000099810	41.7038	62.385	52.7281	69.9604	ENSG00000099810	MTAP
ENSG00000099812	19.667	20.1705	17.4611	8.24082	ENSG00000099812	MISP
ENSG00000099814	29.3478	26.9975	40.4135	22.9795	ENSG00000099814	CEP170B
ENSG00000099817	43.6632	32.7543	41.2549	22.9569	ENSG00000099817	POLR2E
ENSG00000099821	24.1164	33.7152	28.4552	24.0806	ENSG00000099821	POLRMT
ENSG00000099822	0.697981	0.661149	0.447921	1.37174	ENSG00000099822	HCN2
ENSG00000099834	2.07033	4.42901	2.97472	5.21372	ENSG00000099834	CDHR5
ENSG00000099840	3.17073	8.15344	6.47801	3.38163	ENSG00000099840	IZUMO4
ENSG00000099849	40.6872	23.7745	27.4157	12.9959	ENSG00000099849	RASSF7
ENSG00000099860	55.419	16.9615	14.5155	33.4062	ENSG00000099860	GADD45B
ENSG00000099864	1.58316	2.88225	3.68932	8.04844	ENSG00000099864	PALM
ENSG00000099866	0.494208	1.22929	1.01306	1.76726	ENSG00000099866	MADCAM1
ENSG00000099875	117.738	146.243	149.072	52.2618	ENSG00000099875	MKNK2
ENSG00000099889	10.2564	29.4193	23.2712	9.34304	ENSG00000099889	ARVCF
ENSG00000099899	33.1242	32.5709	34.9445	25.6093	ENSG00000099899	TRMT2A
ENSG00000099901	59.5998	71.5864	45.2247	41.6636	ENSG00000099901	RANBP1
ENSG00000099904	28.5248	23.2942	31.6018	23.8217	ENSG00000099904	ZDHHC8
ENSG00000099910	17.0841	18.9605	19.264	31.7481	ENSG00000099910	KLHL22
ENSG00000099917	66.4211	63.1235	60.0375	76.3043	ENSG00000099917	MED15
ENSG00000099937	0.182182	0.562828	0.73808	0.964091	ENSG00000099937	SERPIND1
ENSG00000099940	9.29907	5.56888	10.739	8.38863	ENSG00000099940	SNAP29
ENSG00000099942	25.3736	30.3324	37.249	16.1485	ENSG00000099942	CRKL
ENSG00000099949	53.6574	61.6092	62.9728	57.439	ENSG00000099949	LZTR1
ENSG00000099953	1.26195	3.0593	3.3055	7.51266	ENSG00000099953	MMP11
ENSG00000099954	0.324857	0.376907	0.84565	0.838934	ENSG00000099954	CECR2
ENSG00000099956	20.5516	25.9631	22.3476	17.496	ENSG00000099956	SMARCB1
ENSG00000099957	1.14237	3.9402	5.1673	3.25596	ENSG00000099957	P2RX6
ENSG00000099958	2.19794	3.27015	1.11943	2.07686	ENSG00000099958	DERL3

ENSG00000099960	0.891124	0.605313	0.962534	0.291777	ENSG00000099960	SLC7A4
ENSG00000099968	26.0022	28.4801	35.4546	23.0323	ENSG00000099968	BCL2L13
ENSG00000099974	4.2318	6.36404	6.00993	6.45511	ENSG00000099974	DDTL
ENSG00000099977	24.3713	38.3671	12.8075	15.0911	ENSG00000099977	DDT
ENSG00000099984	2.06501	3.10731	1.04053	2.22429	ENSG00000099984	GSTT2
ENSG00000099985	0.0612219	0.118804	0.369174	0.466477	ENSG00000099985	OSM
ENSG00000099991	21.9132	34.6998	29.4192	34.819	ENSG00000099991	CABIN1
ENSG00000099992	20.5817	17.1347	14.2303	17.0536	ENSG00000099992	TBC1D10A
ENSG00000099994	0.187775	0.170705	0.195112	2.15121	ENSG00000099994	SUSD2
ENSG00000099995	32.9997	31.6373	27.4999	30.3295	ENSG00000099995	SF3A1
ENSG00000099998	0.36686	0.898594	1.67627	13.5371	ENSG00000099998	GGT5
ENSG00000099999	19.3428	26.4503	23.4098	17.9824	ENSG00000099999	RNF215
ENSG00000100003	151.136	75.6658	48.3164	50.4689	ENSG00000100003	SEC14L2
ENSG00000100012	0.492768	0.612359	1.10191	2.07215	ENSG00000100012	SEC14L3
ENSG00000100014	16.3729	22.1142	20.9565	17.6127	ENSG00000100014	SPECC1L
ENSG00000100023	23.6308	29.0723	24.1158	31.0225	ENSG00000100023	PPIL2
ENSG00000100024	1.86776	3.71579	4.06532	7.327	ENSG00000100024	UPB1
ENSG00000100027	1.01164	1.33658	1.9717	1.86614	ENSG00000100027	YPEL1
ENSG00000100028	42.0557	36.2734	31.9732	25.7243	ENSG00000100028	SNRPD3
ENSG00000100029	33.6101	30.8009	44.4031	22.3457	ENSG00000100029	PES1
ENSG00000100030	61.1055	39.6861	34.611	32.852	ENSG00000100030	MAPK1
ENSG00000100031	6.68023	16.6651	15.391	6.19274	ENSG00000100031	GGT1
ENSG00000100033	2.62618	2.65836	13.8305	14.6274	ENSG00000100033	PRODH
ENSG00000100034	31.1315	43.0525	28.8006	35.2765	ENSG00000100034	PPM1F
ENSG00000100036	7.33897	8.04582	5.11666	5.36974	ENSG00000100036	SLC35E4
ENSG00000100038	36.7967	37.2094	34.7316	28.0606	ENSG00000100038	TOP3B
ENSG00000100053	0.513277	0.845881	1.21065	0.631654	ENSG00000100053	CRYBB3
ENSG00000100055	4.05884	7.62749	8.35573	11.5521	ENSG00000100055	CYTH4
ENSG00000100056	6.41081	5.4824	9.25006	5.26852	ENSG00000100056	ESS2
ENSG00000100058	15.6667	26.5001	40.0478	53.5272	ENSG00000100058	CRYBB2P1
ENSG00000100060	13.5896	24.767	12.6295	16.4751	ENSG00000100060	MFNG
ENSG00000100065	43.4294	71.2423	39.3396	38.4194	ENSG00000100065	CARD10
ENSG00000100068	4.0187	6.78678	8.01583	12.1863	ENSG00000100068	LRP5L
ENSG00000100075	25.7868	22.6344	11.6134	15.2142	ENSG00000100075	SLC25A1
ENSG00000100077	3.95985	6.66017	8.03014	4.06243	ENSG00000100077	GRK3
ENSG00000100078	0.491271	0.920108	0.249422	0.224881	ENSG00000100078	PLA2G3
ENSG00000100079	3.25823	4.05303	3.45092	3.89066	ENSG00000100079	LGALS2
ENSG00000100083	51.1879	67.7158	70.1519	57.3002	ENSG00000100083	GGA1
ENSG00000100084	4.50253	5.18039	6.79874	6.15029	ENSG00000100084	HIRA
ENSG00000100092	37.2311	47.2715	36.5155	18.8964	ENSG00000100092	SH3BP1
ENSG00000100095	0.192322	0.397442	0.878499	0.870698	ENSG00000100095	SEZ6L
ENSG00000100097	209.505	737.41	274.909	451.27	ENSG00000100097	LGALS1
ENSG00000100099	17.8791	30.217	33.6887	25.868	ENSG00000100099	HPS4
ENSG00000100100	29.2093	23.7211	45.6463	13.9733	ENSG00000100100	PIK3IP1
ENSG00000100101	9.99417	9.44112	10.3929	9.0381	ENSG00000100101	NOL12
ENSG00000100104	16.9582	14.2497	18.7151	17.994	ENSG00000100104	SRRD
ENSG00000100105	3.93959	7.31625	5.69264	8.15489	ENSG00000100105	PATZ1
ENSG00000100106	32.9746	40.219	25.3201	28.5117	ENSG00000100106	TRIOBP
ENSG00000100109	28.7305	30.614	32.9222	31.9571	ENSG00000100109	TFIP11
ENSG00000100116	3.47628	8.68514	4.82293	5.77838	ENSG00000100116	GCAT
ENSG00000100121	0	0.105672	0.166217	0	ENSG00000100121	GGTLC2
ENSG00000100122	0.110105	0.267039	0.335218	0.241404	ENSG00000100122	CRYBB1
ENSG00000100124	10.3633	12.6331	15.5577	16.6172	ENSG00000100124	ANKRD54
ENSG00000100129	148.243	119.179	120.355	78.6869	ENSG00000100129	EIF3L

ENSG00000100138	46.2495	38.5009	34.3799	25.9703	ENSG00000100138	SNU13
ENSG00000100139	97.868	76.8837	137.346	42.1828	ENSG00000100139	MICALL1
ENSG00000100142	26.0223	18.6984	17.625	25.5396	ENSG00000100142	POLR2F
ENSG00000100146	0.74061	0.664698	0.708692	1.56736	ENSG00000100146	SOX10
ENSG00000100147	5.97999	11.7859	4.35055	4.69673	ENSG00000100147	CCDC134
ENSG00000100150	8.59371	19.9454	14.6713	25.1084	ENSG00000100150	DEPDC5
ENSG00000100151	30.3532	35.0805	38.9353	22.9739	ENSG00000100151	PICK1
ENSG00000100154	3.25066	9.46204	8.57913	16.1403	ENSG00000100154	TTC28
ENSG00000100156	1.44683	1.22638	3.04929	1.00592	ENSG00000100156	SLC16A8
ENSG00000100162	6.5545	18.3415	7.66859	23.4005	ENSG00000100162	CENPM
ENSG00000100167	2.89601	0.269453	0.423877	0.844195	ENSG00000100167	SEPT3
ENSG00000100170	8.68593	2.4643	2.35518	3.92023	ENSG00000100170	SLC5A1
ENSG00000100191	0.0277593	0.026754	0.145118	0.0304626	ENSG00000100191	SLC5A4
ENSG00000100196	13.2613	15.8465	3.70925	14.2004	ENSG00000100196	KDELR3
ENSG00000100197	2.04938	2.4239	4.61119	1.55287	ENSG00000100197	CYP2D6
ENSG00000100201	135.693	148.23	169.784	169.943	ENSG00000100201	DDX17
ENSG00000100206	1.22097	2.45176	2.1261	5.42158	ENSG00000100206	DMC1
ENSG00000100207	9.89564	12.164	13.5351	9.07179	ENSG00000100207	TCF20
ENSG00000100209	9.21895	20.5818	17.9348	22.9972	ENSG00000100209	HSCB
ENSG00000100211	19.1017	21.6943	30.8571	23.4125	ENSG00000100211	CBY1
ENSG00000100216	22.9421	15.9207	13.5684	12.0803	ENSG00000100216	TOMM22
ENSG00000100218	0.445275	0.710453	0.421142	0.797911	ENSG00000100218	RSPH14
ENSG00000100219	66.3296	135.726	125.724	34.3701	ENSG00000100219	XBP1
ENSG00000100220	61.806	42.2222	35.6782	34.2906	ENSG00000100220	RTCB
ENSG00000100221	25.9763	30.4286	25.8407	16.8162	ENSG00000100221	JOSD1
ENSG00000100225	34.0495	39.3347	33.7555	28.4645	ENSG00000100225	FBXO7
ENSG00000100226	25.4288	38.9212	31.4924	32.0068	ENSG00000100226	GTPBP1
ENSG00000100227	12.5693	15.0402	12.8476	11.5146	ENSG00000100227	POLDIP3
ENSG00000100228	1.2689	4.39173	4.15828	2.32916	ENSG00000100228	RAB36
ENSG00000100234	39.0236	26.2373	42.0522	48.3059	ENSG00000100234	TIMP3
ENSG00000100239	31.148	33.7088	33.1629	28.0549	ENSG00000100239	PPP6R2
ENSG00000100241	63.5389	54.8922	62.4832	37.9004	ENSG00000100241	SBF1
ENSG00000100242	56.1888	114.079	57.3505	43.3535	ENSG00000100242	SUN2
ENSG00000100243	42.6963	43.3262	29.3107	43.2857	ENSG00000100243	CYB5R3
ENSG00000100246	8.59054	6.45718	6.33761	3.81557	ENSG00000100246	DNAL4
ENSG00000100249	0	0.121652	0.0540033	0.204663	ENSG00000100249	C22orf31
ENSG00000100253	0.793938	2.03203	2.01392	4.45505	ENSG00000100253	MIOX
ENSG00000100258	39.3361	52.7506	43.1268	37.4744	ENSG00000100258	LMF2
ENSG00000100263	27.8248	22.9293	30.5525	20.6213	ENSG00000100263	RHBDD3
ENSG00000100266	26.5511	35.952	28.5058	39.9299	ENSG00000100266	PACSIN2
ENSG00000100271	1.31062	1.69696	3.68321	1.83899	ENSG00000100271	TTLL1
ENSG00000100276	1.98284	3.99627	2.85042	3.35874	ENSG00000100276	RASL10A
ENSG00000100280	26.8664	29.5434	29.8184	21.8754	ENSG00000100280	AP1B1
ENSG00000100281	7.28152	12.9691	11.275	14.6994	ENSG00000100281	HMGXB4
ENSG00000100284	23.5218	10.7942	20.9179	21.1873	ENSG00000100284	TOM1
ENSG00000100285	0.515229	0.317466	1.45002	1.30751	ENSG00000100285	NEFH
ENSG00000100288	36.1867	61.0323	53.832	36.5136	ENSG00000100288	CHKB
ENSG00000100290	3.46612	4.68693	4.46426	2.44294	ENSG00000100290	BIK
ENSG00000100292	24.8996	3.35448	2.4212	9.21845	ENSG00000100292	HMOX1
ENSG00000100294	7.31866	7.21657	10.1122	4.47003	ENSG00000100294	MCAT
ENSG00000100296	17.5554	22.7722	33.5036	29.0957	ENSG00000100296	THOC5
ENSG00000100297	15.2011	46.3746	11.7484	27.7502	ENSG00000100297	MCM5
ENSG00000100298	0.540481	1.40565	1.95694	1.47666	ENSG00000100298	APOBEC3H
ENSG00000100299	34.5481	44.9461	39.0277	37.2453	ENSG00000100299	ARSA

ENSG00000100300	173.134	167.643	116.828	75.0571	ENSG00000100300	TSPO
ENSG00000100302	0.209861	0.2185	2.66357	0.409867	ENSG00000100302	RASD2
ENSG00000100304	19.2782	26.4941	20.7294	11.2191	ENSG00000100304	TTLL12
ENSG00000100307	2.14175	2.25752	2.97611	5.20293	ENSG00000100307	CBX7
ENSG00000100311	11.4803	11.5678	6.12339	6.82645	ENSG00000100311	PDGFB
ENSG00000100312	0.315202	0.436366	0.387271	0.164771	ENSG00000100312	ACR
ENSG00000100314	0.144715	0.337861	0.171458	0.162646	ENSG00000100314	CABP7
ENSG00000100316	319.342	461.432	401.143	293.62	ENSG00000100316	RPL3
ENSG00000100319	8.53722	7.30997	7.45118	7.02032	ENSG00000100319	ZMAT5
ENSG00000100320	38.7571	53.3826	62.6542	63.8273	ENSG00000100320	RBFOX2
ENSG00000100321	2.93019	1.50157	1.46905	2.85499	ENSG00000100321	SYNGR1
ENSG00000100324	5.61681	10.5263	11.6062	10.9613	ENSG00000100324	TAB1
ENSG00000100325	36.116	42.4864	54.2753	42.3787	ENSG00000100325	ASCC2
ENSG00000100330	23.8275	23.3942	30.9463	29.2065	ENSG00000100330	MTMR3
ENSG00000100335	17.0375	15.3873	21.6854	14.66	ENSG00000100335	MIEF1
ENSG00000100336	7.44118	21.9403	15.9632	24.9178	ENSG00000100336	APOL4
ENSG00000100341	0.531658	0.893879	0.996854	1.55714	ENSG00000100341	PNPLA5
ENSG00000100342	1.29981	6.44576	3.98305	4.74033	ENSG00000100342	APOL1
ENSG00000100344	16.3347	15.4873	14.4929	30.9155	ENSG00000100344	PNPLA3
ENSG00000100345	388.159	527.121	483.031	852.721	ENSG00000100345	MYH9
ENSG00000100346	0.0670142	1.23034	0.109567	0.220009	ENSG00000100346	CACNA1I
ENSG00000100347	18.9	16.678	15.2567	22.4329	ENSG00000100347	SAMM50
ENSG00000100348	7.90826	8.29653	9.50544	11.8865	ENSG00000100348	TXN2
ENSG00000100350	2.4764	5.65947	4.58756	5.40966	ENSG00000100350	FOXRED2
ENSG00000100351	1.65956	1.94777	0.98375	3.76948	ENSG00000100351	GRAP2
ENSG00000100353	154.547	125.953	138.083	91.3399	ENSG00000100353	EIF3D
ENSG00000100354	12.8057	22.805	16.7215	30.5971	ENSG00000100354	TNRC6B
ENSG00000100359	49.9154	51.8339	34.3338	36.0059	ENSG00000100359	SGSM3
ENSG00000100360	12.1384	15.2185	18.0709	13.832	ENSG00000100360	IFT27
ENSG00000100362	0	0	0	0	ENSG00000100362	PVALB
ENSG00000100364	69.2744	62.7477	67.7329	38.5726	ENSG00000100364	KIAA0930
ENSG00000100365	0.182015	0.35828	0.802633	0.319727	ENSG00000100365	NCF4
ENSG00000100368	0.425517	0.546708	0.332895	0.592132	ENSG00000100368	CSF2RB
ENSG00000100372	19.7319	20.1482	20.7036	13.7419	ENSG00000100372	SLC25A17
ENSG00000100373	0	0	0.0961406	0	ENSG00000100373	UPK3A
ENSG00000100376	12.099	57.755	62.5574	36.6867	ENSG00000100376	FAM118A
ENSG00000100379	9.62474	9.10687	8.71728	8.8802	ENSG00000100379	KCTD17
ENSG00000100380	104.094	64.673	61.3997	61.2965	ENSG00000100380	ST13
ENSG00000100385	1.43221	4.89426	2.73699	9.15607	ENSG00000100385	IL2RB
ENSG00000100387	31.6902	21.7619	17.4187	20.3317	ENSG00000100387	RBX1
ENSG00000100393	16.9418	20.4381	21.4999	18.7146	ENSG00000100393	EP300
ENSG00000100395	12.508	19.1427	20.3615	16.8834	ENSG00000100395	L3MBTL2
ENSG00000100399	0.576973	0.916321	1.05356	0.120722	ENSG00000100399	CHADL
ENSG00000100401	54.0516	75.6442	51.8195	39.4745	ENSG00000100401	RANGAP1
ENSG00000100403	21.5424	26.5686	24.3182	27.3268	ENSG00000100403	ZC3H7B
ENSG00000100410	18.5742	21.2004	20.3454	15.09	ENSG00000100410	PHF5A
ENSG00000100412	37.3514	50.8198	35.8542	32.1306	ENSG00000100412	ACO2
ENSG00000100413	11.1675	13.5392	16.2589	10.8074	ENSG00000100413	POLR3H
ENSG00000100416	26.4376	37.6659	46.4222	36.0748	ENSG00000100416	TRMU
ENSG00000100417	8.97769	16.7447	15.0708	14.6663	ENSG00000100417	PMM1
ENSG00000100418	24.376	25.2142	41.9851	22.9683	ENSG00000100418	DESI1
ENSG00000100422	8.23442	7.76768	5.87768	9.63671	ENSG00000100422	CERK
ENSG00000100425	16.403	17.9885	28.0058	21.2808	ENSG00000100425	BRD1
ENSG00000100426	6.93487	6.0341	8.97201	7.33514	ENSG00000100426	ZBED4

ENSG00000100427	0.0150689	0.0874813	0.0994619	0.195804	ENSG00000100427	MLC1
ENSG00000100429	18.99	20.5347	20.3251	21.1957	ENSG00000100429	HDAC10
ENSG00000100433	0.453277	1.20033	1.92015	0.479368	ENSG00000100433	KCNK10
ENSG00000100439	15.6479	7.16972	11.0122	8.33277	ENSG00000100439	ABHD4
ENSG00000100441	42.5494	50.4432	46.0164	29.6011	ENSG00000100441	KHNYN
ENSG00000100442	17.6394	16.3637	19.8074	18.7332	ENSG00000100442	FKBP3
ENSG00000100445	4.2521	8.3184	10.3403	6.39333	ENSG00000100445	SDR39U1
ENSG00000100448	0	0	0.0749854	0.0775995	ENSG00000100448	CTSG
ENSG00000100450	0	0.332906	0.365339	0.225805	ENSG00000100450	GZMH
ENSG00000100453	0	0	0.778976	0.480657	ENSG00000100453	GZMB
ENSG00000100461	32.4245	51.3949	44.9711	63.5777	ENSG00000100461	RBM23
ENSG00000100462	55.38	40.0236	47.2759	31.0989	ENSG00000100462	PRMT5
ENSG00000100473	1.22699	1.9356	1.0186	1.62815	ENSG00000100473	COCH
ENSG00000100478	9.60263	19.7164	13.4449	14.4574	ENSG00000100478	AP4S1
ENSG00000100479	11.5025	23.7251	11.215	27.6761	ENSG00000100479	POLE2
ENSG00000100483	5.04305	5.95053	7.24803	5.16522	ENSG00000100483	VCPKMT
ENSG00000100485	14.6773	15.7954	12.8157	16.9582	ENSG00000100485	SOS2
ENSG00000100490	13.7707	28.2712	39.4936	56.3421	ENSG00000100490	CDKL1
ENSG00000100503	24.7467	30.6022	22.6273	32.0844	ENSG00000100503	NIN
ENSG00000100504	67.3943	119.772	79.8769	73.4123	ENSG00000100504	PYGL
ENSG00000100505	0.195146	0.216736	0.459925	0.77975	ENSG00000100505	TRIM9
ENSG00000100519	63.8078	69.2494	63.0024	62.2691	ENSG00000100519	PSMC6
ENSG00000100522	12.5245	13.5371	18.7653	27.0913	ENSG00000100522	GNPNAT1
ENSG00000100523	4.02494	12.7062	14.2746	16.8467	ENSG00000100523	DDHD1
ENSG00000100526	3.86859	21.7478	2.646	6.56674	ENSG00000100526	CDKN3
ENSG00000100528	51.8136	54.5253	39.7625	21.7589	ENSG00000100528	CNIH1
ENSG00000100532	6.7105	9.93991	9.28499	7.76694	ENSG00000100532	CGRRF1
ENSG00000100554	75.6927	51.9801	42.8908	51.7	ENSG00000100554	ATP6V1D
ENSG00000100557	1.41782	4.31839	3.58382	6.74165	ENSG00000100557	C14orf105
ENSG00000100558	66.4898	104.552	28.1941	57.938	ENSG00000100558	PLEK2
ENSG00000100564	16.9367	18.3673	18.1651	16.8325	ENSG00000100564	PIGH
ENSG00000100565	0.375951	1.08228	0.76012	1.48115	ENSG00000100565	LRRC74A
ENSG00000100567	45.8834	48.2617	53.219	56.532	ENSG00000100567	PSMA3
ENSG00000100568	28.4331	17.3395	15.8868	11.4856	ENSG00000100568	VTI1B
ENSG00000100575	8.80957	13.4796	22.0102	11.9007	ENSG00000100575	TIMM9
ENSG00000100577	12.1474	15.1711	13.6588	6.46508	ENSG00000100577	GSTZ1
ENSG00000100578	19.4188	33.9917	22.7483	31.7962	ENSG00000100578	KIAA0586
ENSG00000100580	4.98054	6.95636	5.93961	6.81324	ENSG00000100580	TMED8
ENSG00000100583	0.763995	1.1851	1.76093	1.95032	ENSG00000100583	SAMD15
ENSG00000100591	64.6062	54.6749	66.2128	61.8914	ENSG00000100591	AHSA1
ENSG00000100592	44.8418	33.7772	33.8922	39.7389	ENSG00000100592	DAAM1
ENSG00000100593	0.194348	0.377652	0.207776	0.360369	ENSG00000100593	ISM2
ENSG00000100596	56.8392	50.1408	21.2746	38.3074	ENSG00000100596	SPTLC2
ENSG00000100599	4.60473	6.19938	7.13382	9.97588	ENSG00000100599	RIN3
ENSG00000100600	49.8441	78.7655	57.3553	71.6513	ENSG00000100600	LGMN
ENSG00000100601	6.05112	4.79482	6.64431	4.06801	ENSG00000100601	ALKBH1
ENSG00000100603	33.0681	37.068	29.9902	31.1825	ENSG00000100603	SNW1
ENSG00000100604	0.768913	1.66087	1.05243	1.77634	ENSG00000100604	CHGA
ENSG00000100605	23.0084	33.2819	23.6804	19.1569	ENSG00000100605	ITPK1
ENSG00000100612	62.7436	56.3636	52.9669	29.7134	ENSG00000100612	DHRS7
ENSG00000100614	26.9422	24.0556	25.9534	27.5093	ENSG00000100614	PPM1A
ENSG00000100625	2.66685	4.84386	3.94862	4.37413	ENSG00000100625	SIX4
ENSG00000100626	0.437803	1.32527	1.42611	1.56018	ENSG00000100626	GALNT16
ENSG00000100628	0.869982	0.968389	1.53229	1.37536	ENSG00000100628	ASB2

ENSG00000100629	3.17623	16.8205	4.02041	9.55697	ENSG00000100629	CEP128
ENSG00000100632	40.9588	33.131	34.9749	35.6289	ENSG00000100632	ERH
ENSG00000100644	117.677	104.748	110.652	262.851	ENSG00000100644	HIF1A
ENSG00000100647	31.5361	24.5696	31.3556	20.3904	ENSG00000100647	SUSD6
ENSG00000100650	152.471	132.635	154.216	123.889	ENSG00000100650	SRSF5
ENSG00000100652	0.713718	0.899537	1.15047	0.903781	ENSG00000100652	SLC10A1
ENSG00000100664	121.936	132.822	146.749	73.2051	ENSG00000100664	EIF5
ENSG00000100665	0.225865	0.780862	0.500648	0.840175	ENSG00000100665	SERPINA4
ENSG00000100678	0.73079	0.634711	0.645143	1.25963	ENSG00000100678	SLC8A3
ENSG00000100697	29.621	33.8703	28.049	25.4363	ENSG00000100697	DICER1
ENSG00000100711	29.9294	28.9072	24.1976	20.8017	ENSG00000100711	ZFYVE21
ENSG00000100714	33.3008	65.8972	47.5976	80.1556	ENSG00000100714	MTHFD1
ENSG00000100721	0.739087	2.03308	1.71627	2.32471	ENSG00000100721	TCL1A
ENSG00000100722	30.0882	33.6634	30.502	36.7215	ENSG00000100722	ZC3H14
ENSG00000100726	13.1387	25.9123	25.2216	19.7443	ENSG00000100726	TELO2
ENSG00000100731	45.7624	85.4917	78.5985	103.062	ENSG00000100731	PCNX1
ENSG00000100739	5.28394	12.167	11.2366	13.0703	ENSG00000100739	BDKRB1
ENSG00000100744	18.5733	9.71715	9.86369	6.41888	ENSG00000100744	GSKIP
ENSG00000100749	11.8764	27.8416	11.4624	23.7142	ENSG00000100749	VRK1
ENSG00000100764	59.0962	45.2067	31.442	29.1889	ENSG00000100764	PSMC1
ENSG00000100767	6.3027	12.177	14.6498	19.0675	ENSG00000100767	PAPLN
ENSG00000100784	4.49982	9.50021	3.41406	5.55563	ENSG00000100784	RPS6KA5
ENSG00000100796	36.4341	38.4187	50.9397	35.3154	ENSG00000100796	PPP4R3A
ENSG00000100802	4.99053	11.0439	7.8943	9.06295	ENSG00000100802	C14orf93
ENSG00000100804	62.2366	35.2124	27.8148	33.0356	ENSG00000100804	PSMB5
ENSG00000100811	36.8301	35.2919	40.6125	26.8546	ENSG00000100811	YY1
ENSG00000100813	60.2557	77.9622	103.428	92.919	ENSG00000100813	ACIN1
ENSG00000100814	29.7141	46.7678	52.1554	47.8965	ENSG00000100814	CCNB1IP1
ENSG00000100815	31.8388	31.5017	33.2463	29.8788	ENSG00000100815	TRIP11
ENSG00000100823	14.5091	10.6951	27.3355	23.764	ENSG00000100823	APEX1
ENSG00000100836	36.9012	55.1912	60.904	48.4234	ENSG00000100836	PABPN1
ENSG00000100842	2.45609	5.03652	8.01061	8.93599	ENSG00000100842	EFS
ENSG00000100852	62.2902	46.7571	69.7169	40.5369	ENSG00000100852	ARHGAP5
ENSG00000100865	18.8041	18.9569	20.2085	20.6183	ENSG00000100865	CINP
ENSG00000100867	1.45552	1.78437	1.95905	2.72564	ENSG00000100867	DHRS2
ENSG00000100883	31.3901	37.1411	30.8715	40.5572	ENSG00000100883	SRP54
ENSG00000100884	0.311546	0.229903	0.564145	0.389965	ENSG00000100884	CPNE6
ENSG00000100888	41.2373	44.7373	45.7745	51.3426	ENSG00000100888	CHD8
ENSG00000100889	4.89852	79.2396	84.9987	24.1267	ENSG00000100889	PCK2
ENSG00000100890	15.0645	17.3448	17.5768	15.1088	ENSG00000100890	KIAA0391
ENSG00000100897	12.6444	17.8031	18.4699	14.8576	ENSG00000100897	DCAF11
ENSG00000100902	82.8085	64.7001	51.1375	49.1959	ENSG00000100902	PSMA6
ENSG00000100906	90.0695	57.369	78.7435	63.7412	ENSG00000100906	NFKBIA
ENSG00000100908	10.3235	12.3961	17.7811	8.13193	ENSG00000100908	EMC9
ENSG00000100911	39.6664	61.9384	50.2195	36.6274	ENSG00000100911	PSME2
ENSG00000100916	2.75369	3.74663	4.79981	6.20383	ENSG00000100916	BRMS1L
ENSG00000100918	7.37083	11.0286	17.341	17.3675	ENSG00000100918	REC8
ENSG00000100926	45.1448	49.4691	32.7941	25.4613	ENSG00000100926	TM9SF1
ENSG00000100934	82.628	79.384	61.8734	110.533	ENSG00000100934	SEC23A
ENSG00000100938	37.1542	34.5255	31.4552	25.5785	ENSG00000100938	GMPR2
ENSG00000100941	23.9643	31.6438	36.795	39.639	ENSG00000100941	PNN
ENSG00000100949	33.4546	30.8008	27.4568	17.2173	ENSG00000100949	RABGGTA
ENSG00000100968	8.21138	20.3855	21.7579	49.5484	ENSG00000100968	NFATC4
ENSG00000100979	30.2036	90.143	107.696	28.2925	ENSG00000100979	PLTP

ENSG00000100982	3.82557	5.42881	4.2572	4.44388	ENSG00000100982	PCIF1
ENSG00000100983	28.7741	49.4315	38.8907	18.9768	ENSG00000100983	GSS
ENSG00000100985	5.45168	53.4702	132.727	85.5297	ENSG00000100985	MMP9
ENSG00000100987	0.272576	0.626344	0.597588	1.00973	ENSG00000100987	VSX1
ENSG00000100991	32.1165	28.64	29.8503	27.5285	ENSG00000100991	TRPC4AP
ENSG00000100994	794.306	424.573	174.173	245.457	ENSG00000100994	PYGB
ENSG00000100997	31.5253	38.345	22.508	22.2723	ENSG00000100997	ABHD12
ENSG00000101000	28.8741	86.9586	21.2997	18.4846	ENSG00000101000	PROCR
ENSG00000101003	8.17702	16.0888	11.6937	21.2517	ENSG00000101003	GINS1
ENSG00000101004	2.5598	6.78972	11.8544	11.3315	ENSG00000101004	NINL
ENSG00000101017	12.828	24.5001	9.59045	19.6394	ENSG00000101017	CD40
ENSG00000101019	44.6177	73.0001	80.5551	101.951	ENSG00000101019	UQCC1
ENSG00000101040	26.4264	76.4953	37.1639	49.1563	ENSG00000101040	ZMYND8
ENSG00000101049	0.525348	0.580777	1.07189	2.16869	ENSG00000101049	SGK2
ENSG00000101052	6.18412	10.086	8.63588	11.548	ENSG00000101052	IFT52
ENSG00000101057	2.16912	4.26068	1.38643	4.48903	ENSG00000101057	MYBL2
ENSG00000101074	0.177733	0.524975	0.278672	0.406879	ENSG00000101074	R3HDML
ENSG00000101076	0.252569	0.581253	0.846908	1.05476	ENSG00000101076	HNF4A
ENSG00000101079	10.1105	7.93448	6.2763	8.45079	ENSG00000101079	NDRG3
ENSG00000101082	0.526867	1.15633	0.961966	1.57522	ENSG00000101082	SLA2
ENSG00000101084	81.0346	33.9604	35.811	17.2719	ENSG00000101084	C20orf24
ENSG00000101096	1.26116	0.399795	0.228444	1.02512	ENSG00000101096	NFATC2
ENSG00000101098	0.132144	0.182923	0.199446	0.288865	ENSG00000101098	RIMS4
ENSG00000101104	12.1773	20.6089	38.9156	25.6995	ENSG00000101104	PABPC1L
ENSG00000101109	12.9058	23.9147	21.272	23.8779	ENSG00000101109	STK4
ENSG00000101115	0.769454	1.11088	2.66946	1.02525	ENSG00000101115	SALL4
ENSG00000101126	15.7398	28.7759	28.2442	30.7458	ENSG00000101126	ADNP
ENSG00000101132	21.4049	21.491	13.2116	15.9522	ENSG00000101132	PFDN4
ENSG00000101134	0.605971	0.701046	0.735833	1.0322	ENSG00000101134	DOK5
ENSG00000101138	12.5044	14.8711	13.0361	8.54648	ENSG00000101138	CSTF1
ENSG00000101144	0.240198	0.482915	0.430528	0.724402	ENSG00000101144	BMP7
ENSG00000101146	19.9887	20.7645	27.1585	19.4848	ENSG00000101146	RAE1
ENSG00000101150	47.9368	42.1037	56.6322	36.745	ENSG00000101150	TPD52L2
ENSG00000101152	66.9869	40.0538	42.2048	28.6195	ENSG00000101152	DNAJC5
ENSG00000101158	23.4455	29.7071	28.8224	29.4413	ENSG00000101158	NELFCD
ENSG00000101160	50.3196	69.3392	37.0056	41.3898	ENSG00000101160	CTSZ
ENSG00000101161	25.0877	22.0583	18.702	20.0561	ENSG00000101161	PRPF6
ENSG00000101162	0.450746	0.531619	0.558461	0.272762	ENSG00000101162	TUBB1
ENSG00000101166	46.4629	35.8758	42.4504	15.1489	ENSG00000101166	PRELID3B
ENSG00000101180	0.0348173	0.101062	0.211584	0	ENSG00000101180	HRH3
ENSG00000101181	20.1657	26.55	35.1364	23.4998	ENSG00000101181	MTG2
ENSG00000101182	108.042	119.603	93.5238	66.8115	ENSG00000101182	PSMA7
ENSG00000101187	12.9655	4.28965	1.23365	3.33007	ENSG00000101187	SLCO4A1
ENSG00000101188	0.131026	4.05623	0.091073	2.34598	ENSG00000101188	NTSR1
ENSG00000101189	15.3355	13.881	12.3942	10.6055	ENSG00000101189	MRGBP
ENSG00000101190	6.79919	8.86449	7.97776	7.16327	ENSG00000101190	TCFL5
ENSG00000101191	22.9416	21.8113	24.3721	25.7398	ENSG00000101191	DIDO1
ENSG00000101193	37.7592	22.5623	28.9787	18.6053	ENSG00000101193	GID8
ENSG00000101194	1.05201	1.28694	0.892068	15.7035	ENSG00000101194	SLC17A9
ENSG00000101197	0.358687	0.114739	0.207231	0	ENSG00000101197	BIRC7
ENSG00000101198	1.0442	1.78538	0.852997	1.86559	ENSG00000101198	NKAIN4
ENSG00000101199	60.293	59.9691	73.5647	70.3056	ENSG00000101199	ARFGAP1
ENSG00000101200	0	0	0	0.121517	ENSG00000101200	AVP
ENSG00000101203	0.256138	0.34665	0.404887	0.271274	ENSG00000101203	COL20A1

ENSG00000101204	0.435261	0.450669	0.350937	0.572429	ENSG00000101204	CHRNA4
ENSG00000101210	7.85757	0.944629	1.6105	2.29682	ENSG00000101210	EEF1A2
ENSG00000101213	28.2966	28.6435	20.4076	17.8416	ENSG00000101213	PTK6
ENSG00000101216	6.85388	6.1988	6.62141	4.22417	ENSG00000101216	GMEB2
ENSG00000101220	11.376	13.8138	15.7829	8.91267	ENSG00000101220	C20orf27
ENSG00000101222	0.182591	0.0351803	0.127205	0.19998	ENSG00000101222	SPEF1
ENSG00000101224	11.5377	39.4593	27.3308	26.9507	ENSG00000101224	CDC25B
ENSG00000101230	0.344751	0.694895	0.520507	0.538702	ENSG00000101230	ISM1
ENSG00000101236	9.65545	7.47553	7.72224	14.5911	ENSG00000101236	RNF24
ENSG00000101246	35.7539	39.5519	46.9133	33.544	ENSG00000101246	ARFRP1
ENSG00000101247	13.7825	20.355	23.1059	21.7175	ENSG00000101247	NDUFAF5
ENSG00000101251	0.887678	0.959974	0.747282	0.862104	ENSG00000101251	SEL1L2
ENSG00000101255	13.0554	107.553	137.689	18.5404	ENSG00000101255	TRIB3
ENSG00000101265	0.333746	0.599875	0.465961	0.680023	ENSG00000101265	RASSF2
ENSG00000101266	71.3306	86.3018	69.8395	60.8995	ENSG00000101266	CSNK2A1
ENSG00000101276	7.63643	7.606	5.55764	8.24042	ENSG00000101276	SLC52A3
ENSG00000101278	0.847356	2.76495	0.859726	1.11646	ENSG00000101278	RPS10P5
ENSG00000101280	0.0676201	0.324013	0.146616	0.368551	ENSG00000101280	ANGPT4
ENSG00000101282	0.29555	1.00209	0.509798	1.37865	ENSG00000101282	RSPO4
ENSG00000101290	23.2068	31.3758	22.0325	19.4776	ENSG00000101290	CDS2
ENSG00000101292	0	0.0501707	0.0841134	0.0705756	ENSG00000101292	PROKR2
ENSG00000101294	104.7	110.947	82.3411	89.6682	ENSG00000101294	HM13
ENSG00000101298	2.88094	3.44521	3.22644	3.24325	ENSG00000101298	SNPH
ENSG00000101306	0.055636	0.178819	0.242669	0.111541	ENSG00000101306	MYLK2
ENSG00000101307	2.28156	6.07164	5.79551	9.81787	ENSG00000101307	SIRPB1
ENSG00000101310	30.7426	27.0251	20.5714	15.1504	ENSG00000101310	SEC23B
ENSG00000101311	135.783	120.827	40.174	127.818	ENSG00000101311	FERMT1
ENSG00000101323	0.160344	0.0309007	0.111736	0.105473	ENSG00000101323	HAO1
ENSG00000101327	0	0.0432609	0.0195532	0.0492831	ENSG00000101327	PDYN
ENSG00000101331	0.0939	0.0915178	0.136981	0.150944	ENSG00000101331	CCM2L
ENSG00000101333	1.40635	2.32279	2.58735	11.6394	ENSG00000101333	PLCB4
ENSG00000101335	4.9365	5.53677	9.32323	40.2307	ENSG00000101335	MYL9
ENSG00000101336	0.462725	0.735636	0.459965	1.05339	ENSG00000101336	HCK
ENSG00000101337	34.5093	49.933	34.4216	29.1173	ENSG00000101337	TM9SF4
ENSG00000101342	0.316153	0.953622	0.252699	0.64177	ENSG00000101342	TLDC2
ENSG00000101343	9.639	10.8936	8.91188	9.58499	ENSG00000101343	CRNKL1
ENSG00000101346	29.5681	26.4492	30.0279	17.7219	ENSG00000101346	POFUT1
ENSG00000101347	3.74981	10.4446	5.17671	11.2113	ENSG00000101347	SAMHD1
ENSG00000101349	0.0364093	0.200274	0.095151	0.151166	ENSG00000101349	PAK5
ENSG00000101350	8.19757	6.9467	7.86452	8.93259	ENSG00000101350	KIF3B
ENSG00000101353	2.12187	5.38099	4.92069	6.30349	ENSG00000101353	MROH8
ENSG00000101361	129.814	157.806	204.941	118.482	ENSG00000101361	NOP56
ENSG00000101363	9.47388	14.0525	9.33615	7.84517	ENSG00000101363	MANBAL
ENSG00000101365	34.2585	35.6348	30.5583	20.4022	ENSG00000101365	IDH3B
ENSG00000101367	30.4426	18.7928	20.6739	22.0487	ENSG00000101367	MAPRE1
ENSG00000101384	88.1808	221.916	181.277	111.231	ENSG00000101384	JAG1
ENSG00000101391	13.7493	17.2222	19.3757	16.0632	ENSG00000101391	CDK5RAP1
ENSG00000101400	3.13723	2.38246	2.65643	2.14257	ENSG00000101400	SNTA1
ENSG00000101405	0.146415	0	0	0.313368	ENSG00000101405	OXT
ENSG00000101407	7.4003	11.5483	7.75107	8.94367	ENSG00000101407	TTI1
ENSG00000101412	1.60109	4.7229	0.873638	5.91689	ENSG00000101412	E2F1
ENSG00000101413	11.5899	12.1915	14.5454	13.4717	ENSG00000101413	RPRD1B
ENSG00000101417	4.82352	4.04268	3.84884	4.08747	ENSG00000101417	PXMP4
ENSG00000101421	12.9769	8.63721	9.8559	10.8465	ENSG00000101421	CHMP4B

ENSG00000101425	1.9578	3.57682	2.71296	8.81237	ENSG00000101425	BPI
ENSG00000101435	0.259629	0.0624281	0.169249	0	ENSG00000101435	CST9L
ENSG00000101438	0.021483	0.0207122	0.0564754	0.16594	ENSG00000101438	SLC32A1
ENSG00000101439	129.538	133.284	66.082	63.1152	ENSG00000101439	CST3
ENSG00000101440	0.486985	1.50761	2.00077	1.43721	ENSG00000101440	ASIP
ENSG00000101441	0	0	0	0	ENSG00000101441	CST4
ENSG00000101442	4.81136	5.289	4.33636	2.74368	ENSG00000101442	ACTR5
ENSG00000101443	0.593277	0.35191	0.353945	0.387231	ENSG00000101443	WFDC2
ENSG00000101444	68.5479	56.1522	59.47	30.6397	ENSG00000101444	AHCY
ENSG00000101445	0.08372	0.119815	0.110855	0.19157	ENSG00000101445	PPP1R16B
ENSG00000101446	0	0.183874	0.811365	0.922846	ENSG00000101446	SPINT3
ENSG00000101447	8.04694	16.8939	2.95297	6.09729	ENSG00000101447	FAM83D
ENSG00000101448	6.39882	16.562	15.0797	28.5337	ENSG00000101448	EPPIN
ENSG00000101452	4.49152	6.81706	6.39915	5.63292	ENSG00000101452	DHX35
ENSG00000101457	8.99422	8.66852	10.8803	12.025	ENSG00000101457	DNTTIP1
ENSG00000101460	9.10459	3.00226	2.75742	6.36359	ENSG00000101460	MAP1LC3A
ENSG00000101463	0.0219532	0.275135	0.172789	0.641355	ENSG00000101463	SYNDIG1
ENSG00000101464	20.2296	28.3988	11.8646	9.11836	ENSG00000101464	PIGU
ENSG00000101470	0.188425	0.401795	0.435589	0.453042	ENSG00000101470	TNNC2
ENSG00000101473	9.55806	9.6957	9.22405	7.9866	ENSG00000101473	ACOT8
ENSG00000101474	37.0873	58.6294	44.0797	27.5501	ENSG00000101474	APMAP
ENSG00000101489	0.817445	1.67694	2.45911	2.54606	ENSG00000101489	CELF4
ENSG00000101493	15.3968	18.8586	21.8417	17.0382	ENSG00000101493	ZNF516
ENSG00000101542	0.970398	1.96413	0.40254	2.4262	ENSG00000101542	CDH20
ENSG00000101544	28.2613	37.7905	33.8818	17.4452	ENSG00000101544	ADNP2
ENSG00000101546	13.0471	17.4839	24.1452	19.1463	ENSG00000101546	RBFA
ENSG00000101557	18.0046	25.9786	22.804	27.8435	ENSG00000101557	USP14
ENSG00000101558	108.08	87.9305	77.1376	66.9412	ENSG00000101558	VAPA
ENSG00000101574	3.98251	12.7896	9.19344	5.69775	ENSG00000101574	METTL4
ENSG00000101577	2.47175	6.29025	4.07574	11.0714	ENSG00000101577	LPIN2
ENSG00000101596	30.4712	63.2644	50.8985	70.7728	ENSG00000101596	SMCHD1
ENSG00000101605	2.49554	3.6315	3.73858	4.99176	ENSG00000101605	MYOM1
ENSG00000101608	218.842	239.595	135.219	168.884	ENSG00000101608	MYL12A
ENSG00000101624	11.0353	12.4861	8.18149	10.2988	ENSG00000101624	CEP76
ENSG00000101638	1.5123	1.67392	0.681303	2.36813	ENSG00000101638	ST8SIA5
ENSG00000101639	7.96467	21.4598	11.0985	18.1083	ENSG00000101639	CEP192
ENSG00000101654	19.3137	17.5646	21.9735	18.3484	ENSG00000101654	RNMT
ENSG00000101665	10.2242	9.64077	12.7138	12.3132	ENSG00000101665	SMAD7
ENSG00000101670	82.4476	92.363	32.8489	35.3302	ENSG00000101670	LIPG
ENSG00000101680	2.6273	8.82965	15.6429	20.2949	ENSG00000101680	LAMA1
ENSG00000101695	3.87302	7.12304	8.35887	10.7953	ENSG00000101695	RNF125
ENSG00000101745	8.63624	18.3102	15.6196	18.9198	ENSG00000101745	ANKRD12
ENSG00000101746	0.286714	0.963241	0.956271	1.10293	ENSG00000101746	NOL4
ENSG00000101751	12.5997	30.1459	14.4609	19.9957	ENSG00000101751	POLI
ENSG00000101752	27.5896	38.9447	30.5026	27.835	ENSG00000101752	MIB1
ENSG00000101773	34.511	93.6465	107.814	35.6707	ENSG00000101773	RBBP8
ENSG00000101782	67.2366	45.5672	55.25	37.7706	ENSG00000101782	RIOK3
ENSG00000101811	7.69334	8.13055	6.97033	6.68727	ENSG00000101811	CSTF2
ENSG00000101812	0.284093	0.855498	0.668813	0.609563	ENSG00000101812	H2BFM
ENSG00000101825	0.968664	5.58273	2.54629	4.57425	ENSG00000101825	MXRA5
ENSG00000101842	1.84486	3.50292	4.12112	4.54624	ENSG00000101842	VSIG1
ENSG00000101843	25.9359	15.3751	16.2166	13.1853	ENSG00000101843	PSMD10
ENSG00000101844	13.0147	6.59444	9.02872	7.04836	ENSG00000101844	ATG4A
ENSG00000101846	2.0782	0.797174	0.927476	1.10387	ENSG00000101846	STS

ENSG00000101849	3.33531	9.41542	13.0224	12.0985	ENSG00000101849	TBL1X
ENSG00000101850	1.14836	1.97218	1.95571	1.35195	ENSG00000101850	GPR143
ENSG00000101856	43.8579	42.6092	19.1068	23.2917	ENSG00000101856	PGRMC1
ENSG00000101868	3.35855	10.791	5.1704	8.84737	ENSG00000101868	POLA1
ENSG00000101871	5.83615	9.61266	5.86994	5.86969	ENSG00000101871	MID1
ENSG00000101882	8.11147	9.35015	10.243	12.9069	ENSG00000101882	NKAP
ENSG00000101883	0	0.040902	0	0.0461068	ENSG00000101883	RHOXF1
ENSG00000101888	3.17344	1.49848	1.65272	1.92447	ENSG00000101888	NXT2
ENSG00000101890	0.0291796	0.042212	0.0636098	0.016058	ENSG00000101890	GUCY2F
ENSG00000101892	0.340825	0.796391	0.894575	1.4786	ENSG00000101892	ATP1B4
ENSG00000101898	5.42492	9.16829	9.50382	9.375	ENSG00000101898	MCTS2P
ENSG00000101901	18.6986	41.7679	41.6449	47.1973	ENSG00000101901	ALG13
ENSG00000101911	10.7716	16.2684	8.13494	7.91894	ENSG00000101911	PRPS2
ENSG00000101916	0.191763	0.526398	0.334456	0.676515	ENSG00000101916	TLR8
ENSG00000101928	11.9494	8.60118	14.8618	12.7618	ENSG00000101928	MOSPD1
ENSG00000101935	10.0626	17.4389	14.1166	9.10037	ENSG00000101935	AMMECR1
ENSG00000101938	0.158634	0.54322	0.335744	0.915826	ENSG00000101938	CHRDL1
ENSG00000101940	17.5144	19.6427	12.5292	14.6763	ENSG00000101940	WDR13
ENSG00000101945	0	0.316099	2.13889	2.30485	ENSG00000101945	SUV39H1
ENSG00000101951	0	0.0187221	0	0.463658	ENSG00000101951	PAGE4
ENSG00000101955	66.9396	74.5526	28.6811	50.6827	ENSG00000101955	SRPX
ENSG00000101958	0.253713	0.656013	0.633874	1.3316	ENSG00000101958	GLRA2
ENSG00000101966	30.2819	26.8004	31.1187	36.7385	ENSG00000101966	XIAP
ENSG00000101972	37.1526	47.5858	46.0979	49.1369	ENSG00000101972	STAG2
ENSG00000101974	11.4393	14.1242	7.46408	10.7802	ENSG00000101974	ATP11C
ENSG00000101977	0.781143	1.79932	1.87219	2.23179	ENSG00000101977	MCF2
ENSG00000101981	0.111414	0.197203	0.0909975	0.294877	ENSG00000101981	F9
ENSG00000101986	1.80534	1.53359	1.31966	2.47447	ENSG00000101986	ABCD1
ENSG00000101997	0.987234	7.23328	5.55318	5.11743	ENSG00000101997	CCDC22
ENSG00000102001	1.32459	3.1351	2.79181	3.05745	ENSG00000102001	CACNA1F
ENSG00000102003	0.233857	2.06676	1.1219	1.96459	ENSG00000102003	SYP
ENSG00000102007	68.6859	88.462	40.5775	23.2975	ENSG00000102007	PLP2
ENSG00000102010	0	0.225557	0.227505	0.140244	ENSG00000102010	BMX
ENSG00000102021	0	0	0.0156153	0	ENSG00000102021	LUZP4
ENSG00000102024	161.209	101.928	45.1492	51.9082	ENSG00000102024	PLS3
ENSG00000102030	20.7449	18.4157	21.8755	18.0883	ENSG00000102030	NAA10
ENSG00000102032	3.09509	5.39385	3.92005	8.76365	ENSG00000102032	RENBP
ENSG00000102034	7.61566	7.66689	6.20626	6.22422	ENSG00000102034	ELF4
ENSG00000102038	12.3117	20.9237	11.6836	25.5611	ENSG00000102038	SMARCA1
ENSG00000102043	0.843478	0.703204	0.867136	0.658867	ENSG00000102043	MTMR8
ENSG00000102048	1.19145	1.30639	1.03691	2.38857	ENSG00000102048	ASB9
ENSG00000102053	0.363907	0.604	0.778942	0.995845	ENSG00000102053	ZC3H12B
ENSG00000102054	35.3192	52.768	29.9831	38.8007	ENSG00000102054	RBBP7
ENSG00000102055	0	0	0	0	ENSG00000102055	PPP1R2P9
ENSG00000102057	0.239584	1.11976	0.713732	1.28846	ENSG00000102057	KCND1
ENSG00000102069	0	0.250935	0.133672	0.338932	ENSG00000102069	UBE2NL
ENSG00000102076	0	0	0	0	ENSG00000102076	OPN1LW
ENSG00000102078	5.07548	6.40053	6.34553	6.49908	ENSG00000102078	SLC25A14
ENSG00000102080	0.0395549	0.2667	0.137758	0.155192	ENSG00000102080	TEX28P2
ENSG00000102081	7.09604	8.59752	8.924	9.85995	ENSG00000102081	FMR1
ENSG00000102096	2.75668	3.01003	2.75719	2.912	ENSG00000102096	PIM2
ENSG00000102098	0.800415	1.85578	1.62725	2.85578	ENSG00000102098	SCML2
ENSG00000102100	15.0084	9.21045	11.177	4.48751	ENSG00000102100	SLC35A2
ENSG00000102103	11.883	8.24741	17.7821	10.8463	ENSG00000102103	PQBP1

ENSG00000102104	0.281069	0.394486	0.785415	1.08634	ENSG00000102104	RS1
ENSG00000102109	0	0.337967	1.37293	0.521945	ENSG00000102109	PCSK1N
ENSG00000102119	9.13834	9.64404	9.55353	6.01932	ENSG00000102119	EMD
ENSG00000102125	10.2523	26.0426	14.8981	18.3945	ENSG00000102125	TAZ
ENSG00000102128	0.150599	0.580987	0.510803	0.633744	ENSG00000102128	RAB40AL
ENSG00000102144	193.113	129.978	80.9352	86.7691	ENSG00000102144	PGK1
ENSG00000102145	0.0265127	0.123725	0.084428	0.212289	ENSG00000102145	GATA1
ENSG00000102158	29.6359	32.8409	18.8215	18.2701	ENSG00000102158	MAGT1
ENSG00000102172	50.0828	36.2049	18.7162	28.0145	ENSG00000102172	SMS
ENSG00000102174	1.52566	2.36279	3.38837	2.75805	ENSG00000102174	PHEX
ENSG00000102178	13.1075	0.285038	10.7451	6.71145	ENSG00000102178	UBL4A
ENSG00000102181	9.10348	9.5241	9.65398	15.641	ENSG00000102181	CD99L2
ENSG00000102189	26.6456	24.2193	23.8036	25.5174	ENSG00000102189	EEA1
ENSG00000102195	0.0289529	0	0	0	ENSG00000102195	GPR50
ENSG00000102218	5.04355	3.24984	2.43234	2.91572	ENSG00000102218	RP2
ENSG00000102221	0.241822	0.502569	0.749708	0.256196	ENSG00000102221	JADE3
ENSG00000102225	24.3252	16.722	21.0775	15.8767	ENSG00000102225	CDK16
ENSG00000102226	6.06529	7.21987	7.51781	9.35227	ENSG00000102226	USP11
ENSG00000102230	0.612484	1.09161	2.05823	1.30957	ENSG00000102230	PCYT1B
ENSG00000102239	0.0395576	0.262587	0.188106	0.236908	ENSG00000102239	BRS3
ENSG00000102241	18.1378	14.175	12.9982	14.5979	ENSG00000102241	HTATSF1
ENSG00000102243	13.186	1.85606	2.25943	0.248113	ENSG00000102243	VGLL1
ENSG00000102245	0.51942	1.67001	1.7352	3.47568	ENSG00000102245	CD40LG
ENSG00000102265	46.952	110.296	20.6917	99.8954	ENSG00000102265	TIMP1
ENSG00000102271	0.281489	0.708491	0.667362	0.95605	ENSG00000102271	KLHL4
ENSG00000102287	41.0296	33.3552	64.8539	23.2951	ENSG00000102287	GABRE
ENSG00000102290	0.367289	0.793556	0.605483	1.47979	ENSG00000102290	PCDH11X
ENSG00000102302	5.07301	6.17076	6.76143	6.34737	ENSG00000102302	FGD1
ENSG00000102309	9.80609	8.18268	7.42431	9.11583	ENSG00000102309	PIN4
ENSG00000102312	25.9162	21.6114	13.2204	11.7089	ENSG00000102312	PORCN
ENSG00000102313	0.15792	0.198472	0.321286	0.729298	ENSG00000102313	ITIH6
ENSG00000102316	66.0858	80.7245	45.9685	71.5277	ENSG00000102316	MAGED2
ENSG00000102317	101.362	40.7798	46.8926	28.8715	ENSG00000102317	RBM3
ENSG00000102349	4.18771	9.05767	9.73899	11.0199	ENSG00000102349	KLF8
ENSG00000102359	11.6854	14.6891	2.50888	24.0385	ENSG00000102359	SRPX2
ENSG00000102362	3.17246	5.19204	1.45918	10.0564	ENSG00000102362	SYTL4
ENSG00000102383	12.1662	26.564	25.299	53.9732	ENSG00000102383	ZDHHC15
ENSG00000102384	6.0198	19.231	2.93415	15.5932	ENSG00000102384	CENPI
ENSG00000102385	0.20479	0.700198	0.361188	1.24438	ENSG00000102385	DRP2
ENSG00000102387	0.860765	0.606149	0.822818	1.24077	ENSG00000102387	TAF7L
ENSG00000102390	3.6572	3.722	3.59119	2.47347	ENSG00000102390	PBDC1
ENSG00000102393	10.6154	13.8046	6.23248	5.17589	ENSG00000102393	GLA
ENSG00000102401	8.95329	5.7352	8.30177	10.4198	ENSG00000102401	ARMCX3
ENSG00000102409	9.67565	10.5504	11.8703	8.61564	ENSG00000102409	BEX4
ENSG00000102445	0.216516	0.234661	0.885556	0.153697	ENSG00000102445	RUBCNL
ENSG00000102452	1.58424	2.35377	2.94924	5.39621	ENSG00000102452	NALCN
ENSG00000102466	0.516617	1.18357	0.862923	2.32802	ENSG00000102466	FGF14
ENSG00000102468	0.363789	0.791656	0.496011	1.10601	ENSG00000102468	HTR2A
ENSG00000102471	152.484	88.5564	63.6799	35.1186	ENSG00000102471	NDFIP2
ENSG00000102524	0.661337	3.18392	3.15407	4.20465	ENSG00000102524	TNFSF13B
ENSG00000102531	15.7532	20.334	16.1372	23.3833	ENSG00000102531	FNDC3A
ENSG00000102539	0.0480612	0.121812	0.125473	0.138351	ENSG00000102539	MLNR
ENSG00000102543	5.60327	6.68611	4.34482	4.39529	ENSG00000102543	CDADC1
ENSG00000102547	7.59746	4.82474	4.47175	6.4168	ENSG00000102547	CAB39L

ENSG00000102554	153.299	183.316	224.432	59.6814	ENSG00000102554	KLF5
ENSG00000102572	121.871	83.2332	84.3032	46.1828	ENSG00000102572	STK24
ENSG00000102575	6.28421	12.7131	6.16164	2.89281	ENSG00000102575	ACP5
ENSG00000102580	41.222	47.5708	26.6448	21.8089	ENSG00000102580	DNAJC3
ENSG00000102595	30.6246	74.3683	65.636	80.1604	ENSG00000102595	UGGT2
ENSG00000102606	17.415	28.6924	24.2694	27.629	ENSG00000102606	ARHGEF7
ENSG00000102678	0.337904	0.806903	0.381414	1.64232	ENSG00000102678	FGF9
ENSG00000102683	0.0354206	0.155642	0.57676	0.543297	ENSG00000102683	SGCG
ENSG00000102699	24.8935	36.428	14.8585	24.8451	ENSG00000102699	PARP4
ENSG00000102710	34.8045	53.9443	58.7585	57.9022	ENSG00000102710	SUPT20H
ENSG00000102738	14.8571	20.8862	17.0706	13.965	ENSG00000102738	MRPS31
ENSG00000102743	5.23316	6.18269	5.6095	4.09598	ENSG00000102743	SLC25A15
ENSG00000102753	11.2746	8.04771	8.61882	9.19755	ENSG00000102753	KPNA3
ENSG00000102755	0.69509	1.72824	1.52737	5.1156	ENSG00000102755	FLT1
ENSG00000102760	0.913471	0.986006	2.5059	7.35193	ENSG00000102760	RGCC
ENSG00000102763	8.77005	19.0839	17.1113	12.8516	ENSG00000102763	VWA8
ENSG00000102780	12.6829	21.3055	18.5703	17.5617	ENSG00000102780	DGKH
ENSG00000102781	7.78968	13.8871	7.81197	18.3557	ENSG00000102781	KATNAL1
ENSG00000102786	59.4637	62.1061	64.37	67.4093	ENSG00000102786	INTS6
ENSG00000102794	0.0517248	0.0249513	0.180289	0.0855878	ENSG00000102794	ACOD1
ENSG00000102796	6.05134	13.1097	14.2168	10.892	ENSG00000102796	DHRS12
ENSG00000102802	0.163946	0.294702	0.0820153	0.784387	ENSG00000102802	MEDAG
ENSG00000102804	38.2563	69.0519	61.9974	52.1984	ENSG00000102804	TSC22D1
ENSG00000102805	37.8899	25.5488	13.1517	8.79223	ENSG00000102805	CLN5
ENSG00000102837	0.0189451	0.0548012	0	0	ENSG00000102837	OLFM4
ENSG00000102854	3.95321	30.6536	35.0146	6.1025	ENSG00000102854	MSLN
ENSG00000102858	20.3951	19.9627	30.1759	32.8512	ENSG00000102858	MGRN1
ENSG00000102870	7.63051	6.70031	11.4135	6.89612	ENSG00000102870	ZNF629
ENSG00000102871	19.5432	15.5557	14.7588	9.10066	ENSG00000102871	TRADD
ENSG00000102878	6.11923	13.4106	9.05599	10.4614	ENSG00000102878	HSF4
ENSG00000102879	5.72096	9.45931	3.43865	4.5942	ENSG00000102879	CORO1A
ENSG00000102882	32.4331	34.258	28.2924	46.8421	ENSG00000102882	MAPK3
ENSG00000102886	10.279	2.79238	2.64975	1.60789	ENSG00000102886	GDPD3
ENSG00000102890	23.3463	36.8596	19.8245	15.2342	ENSG00000102890	ELMO3
ENSG00000102891	0	0	0	0	ENSG00000102891	MT4
ENSG00000102893	29.0354	53.6321	42.2404	45.7156	ENSG00000102893	PHKB
ENSG00000102897	12.1475	9.07907	7.49877	10.1489	ENSG00000102897	LYRM1
ENSG00000102898	63.8573	52.239	63.0224	55.4432	ENSG00000102898	NUTF2
ENSG00000102900	37.3844	69.2934	55.6696	54.8873	ENSG00000102900	NUP93
ENSG00000102901	39.4984	21.0584	30.8563	23.2115	ENSG00000102901	CENPT
ENSG00000102904	1.4989	2.4066	1.09207	1.81218	ENSG00000102904	TSNAXIP1
ENSG00000102908	21.4959	25.5119	28.4928	44.1952	ENSG00000102908	NFAT5
ENSG00000102910	36.9241	32.3423	31.0846	31.5153	ENSG00000102910	LONP2
ENSG00000102921	44.4745	39.1769	52.317	40.1119	ENSG00000102921	N4BP1
ENSG00000102924	0.139701	0.270782	0.285831	0.343127	ENSG00000102924	CBLN1
ENSG00000102931	25.9805	20.9659	14.7541	13.3251	ENSG00000102931	ARL2BP
ENSG00000102934	10.6705	17.7053	2.04174	1.88268	ENSG00000102934	PLLP
ENSG00000102935	0.096699	0.144575	0.363477	0.863292	ENSG00000102935	ZNF423
ENSG00000102962	1.64232	2.248	1.91752	4.92103	ENSG00000102962	CCL22
ENSG00000102967	4.32874	6.08711	7.61963	7.52749	ENSG00000102967	DHODH
ENSG00000102970	0.341369	0	0	0	ENSG00000102970	CCL17
ENSG00000102974	7.02557	10.4949	9.67778	8.90469	ENSG00000102974	CTCF
ENSG00000102977	10.2973	14.5629	7.84643	6.82125	ENSG00000102977	ACD
ENSG00000102978	25.7635	27.3907	25.1772	27.1574	ENSG00000102978	POLR2C

ENSG00000102981	0.343663	0.428196	0.406502	0.255974	ENSG00000102981	PARD6A
ENSG00000102984	5.57467	4.04987	5.77277	3.37565	ENSG00000102984	ZNF821
ENSG00000102996	12.9572	10.0408	5.7693	8.84079	ENSG00000102996	MMP15
ENSG00000103005	9.93029	12.5589	14.71	13.565	ENSG00000103005	USB1
ENSG00000103018	47.2139	34.5115	28.0997	26.4024	ENSG00000103018	CYB5B
ENSG00000103021	5.27399	11.1003	12.9636	13.1003	ENSG00000103021	CCDC113
ENSG00000103023	0.62918	2.21818	1.57123	1.86814	ENSG00000103023	PRSS54
ENSG00000103024	18.3546	27.9877	22.2149	17.209	ENSG00000103024	NME3
ENSG00000103034	28.5387	9.86656	13.8493	29.8355	ENSG00000103034	NDRG4
ENSG00000103035	54.3694	44.1232	45.4949	36.5211	ENSG00000103035	PSMD7
ENSG00000103037	15.9982	17.9534	17.9742	16.2853	ENSG00000103037	SETD6
ENSG00000103042	19.8221	18.3958	25.1965	21.5979	ENSG00000103042	SLC38A7
ENSG00000103043	19.0368	16.1831	23.3559	19.0856	ENSG00000103043	VAC14
ENSG00000103044	43.7821	48.4096	32.2489	28.698	ENSG00000103044	HAS3
ENSG00000103047	13.4318	20.0895	23.6304	30.7995	ENSG00000103047	TANGO6
ENSG00000103051	29.4025	29.262	28.9104	22.7942	ENSG00000103051	COG4
ENSG00000103056	6.74645	5.86565	6.35668	14.5632	ENSG00000103056	SMPD3
ENSG00000103061	13.0988	11.585	14.9187	10.928	ENSG00000103061	SLC7A6OS
ENSG00000103064	19.2209	21.1411	31.9058	28.9583	ENSG00000103064	SLC7A6
ENSG00000103066	15.8498	19.2958	19.3805	25.1236	ENSG00000103066	PLA2G15
ENSG00000103067	39.347	33.5992	50.0425	10.2091	ENSG00000103067	ESRP2
ENSG00000103089	3.46698	0.37535	0.165209	0.275393	ENSG00000103089	FA2H
ENSG00000103091	32.4981	62.3031	67.9425	101.564	ENSG00000103091	WDR59
ENSG00000103111	8.30082	8.34903	10.7038	10.0035	ENSG00000103111	MON1B
ENSG00000103121	15.7301	23.297	18.1623	27.7557	ENSG00000103121	CMC2
ENSG00000103126	14.5509	18.3997	21.0024	13.1315	ENSG00000103126	AXIN1
ENSG00000103145	13.8786	33.7809	13.5735	21.0588	ENSG00000103145	HCFC1R1
ENSG00000103148	8.85118	16.0321	16.3416	20.1089	ENSG00000103148	NPRL3
ENSG00000103150	3.94131	3.49003	3.56844	3.57007	ENSG00000103150	MLYCD
ENSG00000103152	29.666	31.9212	22.7927	18.7401	ENSG00000103152	MPG
ENSG00000103154	0.133006	0.233193	0.224681	0	ENSG00000103154	NECAB2
ENSG00000103160	8.09747	8.04492	6.5366	6.16576	ENSG00000103160	HSDL1
ENSG00000103168	19.3761	23.1937	28.0447	24.1054	ENSG00000103168	TAF1C
ENSG00000103174	11.4603	11.258	12.0804	13.2559	ENSG00000103174	NAGPA
ENSG00000103175	1.3717	2.43429	2.12608	3.97385	ENSG00000103175	WFDC1
ENSG00000103184	0.842747	1.72711	2.13311	3.44434	ENSG00000103184	SEC14L5
ENSG00000103187	24.3505	46.4119	35.0259	45.6217	ENSG00000103187	COTL1
ENSG00000103194	37.1216	47.328	47.8064	56.3056	ENSG00000103194	USP10
ENSG00000103196	11.3228	10.9498	12.6319	22.2708	ENSG00000103196	CRISPLD2
ENSG00000103197	41.5642	61.3363	73.8852	81.8936	ENSG00000103197	TSC2
ENSG00000103199	6.02102	10.1983	13.7387	11.4701	ENSG00000103199	ZNF500
ENSG00000103200	0	0	0	0	ENSG00000103200	AC069335.1
ENSG00000103202	46.1255	27.8703	23.1538	32.9597	ENSG00000103202	NME4
ENSG00000103222	21.1627	31.3253	40.3513	38.9758	ENSG00000103222	ABCC1
ENSG00000103226	47.6963	61.0582	81.3901	59.8357	ENSG00000103226	NOMO3
ENSG00000103227	9.82052	9.58827	6.36685	8.14149	ENSG00000103227	LMF1
ENSG00000103241	0.0871439	0.426779	0.293841	0.34474	ENSG00000103241	FOXF1
ENSG00000103245	20.7187	21.6552	25.4078	22.2401	ENSG00000103245	NARFL
ENSG00000103248	15.8121	28.0769	36.5467	23.4882	ENSG00000103248	MTHFSD
ENSG00000103249	58.207	51.7417	56.6105	35.1156	ENSG00000103249	CLCN7
ENSG00000103253	9.90667	28.0628	36.1164	10.6074	ENSG00000103253	HAGHL
ENSG00000103254	17.4729	24.0281	15.2392	15.4677	ENSG00000103254	FAM173A
ENSG00000103257	197.284	643.435	922.552	101.682	ENSG00000103257	SLC7A5
ENSG00000103260	32.7036	31.0428	19.0129	15.8344	ENSG00000103260	METRN

ENSG00000103264	19.2767	17.4543	35.3238	20.5666	ENSG00000103264	FBXO31
ENSG00000103266	41.17	35.091	37.2599	17.8825	ENSG00000103266	STUB1
ENSG00000103269	1.78109	9.74482	9.39116	2.13319	ENSG00000103269	RHBDL1
ENSG00000103274	7.65223	4.76644	3.96034	3.72513	ENSG00000103274	NUBP1
ENSG00000103275	41.2208	44.4495	40.7736	39.7166	ENSG00000103275	UBE2I
ENSG00000103310	0.273815	0.312101	0.414737	0.659797	ENSG00000103310	ZP2
ENSG00000103313	4.20274	7.04462	7.85869	12.4034	ENSG00000103313	MEFV
ENSG00000103316	4.05168	3.0565	2.3725	2.52276	ENSG00000103316	CRYM
ENSG00000103319	13.2613	21.3831	15.2526	20.0769	ENSG00000103319	EEF2K
ENSG00000103326	23.3963	24.0058	30.0013	24.3857	ENSG00000103326	CAPN15
ENSG00000103335	181.483	140.337	154.058	109.321	ENSG00000103335	PIEZO1
ENSG00000103342	63.9965	60.5272	58.7981	66.0934	ENSG00000103342	GSPT1
ENSG00000103343	4.43043	4.38941	5.44108	3.60008	ENSG00000103343	ZNF174
ENSG00000103351	7.38686	9.00161	12.0519	9.35068	ENSG00000103351	CLUAP1
ENSG00000103353	23.8979	28.2753	28.9086	31.3375	ENSG00000103353	UBFD1
ENSG00000103355	0.0650238	0.0659122	0.149176	0.249546	ENSG00000103355	PRSS33
ENSG00000103356	18.4116	24.2134	22.802	19.8575	ENSG00000103356	EARS2
ENSG00000103363	229.487	97.3989	75.4059	54.0083	ENSG00000103363	ELOB
ENSG00000103365	18.9249	28.2831	24.5955	23.3776	ENSG00000103365	GGA2
ENSG00000103375	0.139402	0.0447428	0	0	ENSG00000103375	AQP8
ENSG00000103381	3.13287	3.2209	2.57485	6.83228	ENSG00000103381	CPPED1
ENSG00000103404	12.6604	16.8059	22.4682	16.6163	ENSG00000103404	USP31
ENSG00000103415	69.7007	39.4595	30.7878	38.839	ENSG00000103415	HMOX2
ENSG00000103423	29.2547	37.2292	45.9522	36.8841	ENSG00000103423	DNAJA3
ENSG00000103426	0.304463	0	0	0	ENSG00000103426	CORO7-PAM16
ENSG00000103429	48.9554	54.7265	31.1942	26.8059	ENSG00000103429	BFAR
ENSG00000103449	0.244832	0.634194	0.324776	2.01447	ENSG00000103449	SALL1
ENSG00000103460	0.170571	0.305735	0.32465	0.423232	ENSG00000103460	TOX3
ENSG00000103472	0.0695072	0.472799	0.677913	0.810139	ENSG00000103472	RRN3P2
ENSG00000103479	27.6887	40.1994	29.404	44.1416	ENSG00000103479	RBL2
ENSG00000103485	31.4972	20.5859	14.3599	34.0398	ENSG00000103485	QPRT
ENSG00000103489	15.5453	16.8677	9.1139	23.5568	ENSG00000103489	XYLT1
ENSG00000103490	23.6124	32.9597	17.6845	11.7014	ENSG00000103490	PYCARD
ENSG00000103494	8.30812	14.5673	14.0798	22.8135	ENSG00000103494	RPGRIP1L
ENSG00000103495	31.1754	40.8008	38.7996	30.9198	ENSG00000103495	MAZ
ENSG00000103496	21.2436	17.9344	23.3405	20.3159	ENSG00000103496	STX4
ENSG00000103502	37.3134	31.2373	24.2703	18.6963	ENSG00000103502	CDIPT
ENSG00000103507	19.8517	11.2857	11.1164	11.2316	ENSG00000103507	BCKDK
ENSG00000103510	16.9965	17.6835	18.0681	15.5494	ENSG00000103510	KAT8
ENSG00000103512	53.6528	82.3611	72.4825	47.8858	ENSG00000103512	NOMO1
ENSG00000103522	0.639389	0.714825	1.01672	1.43078	ENSG00000103522	IL21R
ENSG00000103528	2.24206	1.85965	1.86454	3.78343	ENSG00000103528	SYT17
ENSG00000103534	0.909045	1.61198	1.02337	1.43052	ENSG00000103534	TMC5
ENSG00000103540	4.43792	8.61634	8.75882	12.1297	ENSG00000103540	CCP110
ENSG00000103544	25.2639	38.2974	41.3425	56.6227	ENSG00000103544	C16orf62
ENSG00000103546	0.437536	1.39197	1.29746	2.08404	ENSG00000103546	SLC6A2
ENSG00000103549	36.5572	32.1114	35.6108	26.9952	ENSG00000103549	RNF40
ENSG00000103550	13.0276	12.4973	12.577	8.93859	ENSG00000103550	KNOP1
ENSG00000103569	34.0485	2.26304	0.719941	1.56718	ENSG00000103569	AQP9
ENSG00000103591	22.1588	24.0022	29.461	15.99	ENSG00000103591	AAGAB
ENSG00000103599	4.628	12.2603	11.8183	8.08946	ENSG00000103599	IQCH
ENSG00000103642	19.0447	8.98177	10.0506	11.9381	ENSG00000103642	LACTB
ENSG00000103647	0.214683	1.16568	1.00953	0.886296	ENSG00000103647	CORO2B
ENSG00000103653	28.5491	28.2684	31.1477	20.3821	ENSG00000103653	CSK

ENSG00000103657	30.5412	51.978	44.3488	66.1658	ENSG00000103657	HERC1
ENSG00000103671	11.2939	12.3659	12.2061	16.223	ENSG00000103671	TRIP4
ENSG00000103707	8.89213	11.8944	10.8061	11.7515	ENSG00000103707	MTFMT
ENSG00000103710	0.0426964	0.195089	0.124263	0.151102	ENSG00000103710	RASL12
ENSG00000103723	6.83809	16.1683	17.071	28.3948	ENSG00000103723	AP3B2
ENSG00000103740	4.47132	7.88137	9.27323	14.2113	ENSG00000103740	ACSBG1
ENSG00000103742	0.715559	1.09519	0.974496	3.3655	ENSG00000103742	IGDCC4
ENSG00000103769	197.1	90.1445	69.7622	50.5763	ENSG00000103769	RAB11A
ENSG00000103811	55.1508	45.0049	10.6438	4.83595	ENSG00000103811	CTSH
ENSG00000103832	0	0.304682	0.0291708	0.190576	ENSG00000103832	GOLGA8UP
ENSG00000103852	7.10682	8.47023	10.2682	8.82433	ENSG00000103852	TTC23
ENSG00000103855	81.8941	110.766	52.2181	78.2768	ENSG00000103855	CD276
ENSG00000103876	5.59512	14.4949	16.8285	11.0143	ENSG00000103876	FAH
ENSG00000103888	1.69431	6.33356	4.59154	8.67132	ENSG00000103888	CEMIP
ENSG00000103932	17.4599	23.4691	22.576	33.2788	ENSG00000103932	RPAP1
ENSG00000103942	14.17	13.8932	24.0398	8.91966	ENSG00000103942	HOMER2
ENSG00000103966	24.0053	25.6277	14.2882	23.4561	ENSG00000103966	EHD4
ENSG00000103978	82.4482	89.2676	76.713	48.3928	ENSG00000103978	TMEM87A
ENSG00000103994	30.9877	39.9493	27.7657	42.9864	ENSG00000103994	ZNF106
ENSG00000103995	11.5268	25.7111	12.4076	33.7569	ENSG00000103995	CEP152
ENSG00000104043	0.32712	0.679796	0.804434	1.0248	ENSG00000104043	ATP8B4
ENSG00000104044	0.66242	0.127694	0.0777262	0.0588334	ENSG00000104044	OCA2
ENSG00000104047	19.2354	35.6757	35.0108	46.9583	ENSG00000104047	DTWD1
ENSG00000104055	4.20658	1.55843	1.0254	3.01614	ENSG00000104055	TGM5
ENSG00000104059	0.0114085	0.0440172	0.0795986	0.0376966	ENSG00000104059	FAM189A1
ENSG00000104064	20.5407	16.2259	19.2775	14.6349	ENSG00000104064	GABPB1
ENSG00000104067	83.8916	80.434	91.7067	94.5767	ENSG00000104067	TJP1
ENSG00000104081	0.830648	1.70002	0.914933	4.61278	ENSG00000104081	BMF
ENSG00000104093	27.7125	45.0965	42.6663	32.8413	ENSG00000104093	DMXL2
ENSG00000104112	0.530403	1.55312	1.2658	2.29941	ENSG00000104112	SCG3
ENSG00000104129	12.0965	17.2234	20.4276	17.9769	ENSG00000104129	DNAJC17
ENSG00000104131	14.6305	16.9981	25.497	24.0507	ENSG00000104131	EIF3J
ENSG00000104133	44.3908	82.3661	72.7148	84.0539	ENSG00000104133	SPG11
ENSG00000104140	7.61889	0.808462	2.92435	1.2141	ENSG00000104140	RHOV
ENSG00000104142	18.9473	9.23388	11.3003	10.6717	ENSG00000104142	VPS18
ENSG00000104147	1.27105	6.17625	1.27933	2.67281	ENSG00000104147	OIP5
ENSG00000104154	5.15816	5.02131	5.59364	6.97538	ENSG00000104154	SLC30A4
ENSG00000104164	142.153	325.25	304.448	702.409	ENSG00000104164	BLOC1S6
ENSG00000104177	8.0643	20.9165	16.7594	24.2881	ENSG00000104177	MYEF2
ENSG00000104205	11.3629	27.7975	21.6205	37.2398	ENSG00000104205	SGK3
ENSG00000104213	0.0297843	0.211741	1.01903	0.852172	ENSG00000104213	PDGFRL
ENSG00000104218	7.38183	11.4181	11.1398	15.1121	ENSG00000104218	CSPP1
ENSG00000104219	9.86445	17.414	5.54797	8.55876	ENSG00000104219	ZDHHC2
ENSG00000104221	7.7219	6.72465	5.73568	4.59269	ENSG00000104221	BRF2
ENSG00000104228	16.198	19.7747	18.6425	12.0847	ENSG00000104228	TRIM35
ENSG00000104231	21.8483	44.5668	48.372	18.2085	ENSG00000104231	ZFAND1
ENSG00000104237	0.0673662	1.07687	0.242547	0.979039	ENSG00000104237	RP1
ENSG00000104267	40.6466	13.2024	47.2906	6.24481	ENSG00000104267	CA2
ENSG00000104290	5.07818	5.91105	4.66476	2.88972	ENSG00000104290	FZD3
ENSG00000104299	10.0353	12.8173	13.8387	10.4302	ENSG00000104299	INTS9
ENSG00000104312	10.554	10.6379	12.8214	12.3357	ENSG00000104312	RIPK2
ENSG00000104313	0.288221	1.13432	0.810881	1.74363	ENSG00000104313	EYA1
ENSG00000104320	13.9604	23.3101	17.6627	18.5811	ENSG00000104320	NBN
ENSG00000104321	0.252049	0.545476	3.80504	10.2804	ENSG00000104321	TRPA1

ENSG00000104324	15.7615	30.9867	33.328	64.0965	ENSG00000104324	CPQ
ENSG00000104325	43.7232	48.7742	40.2229	56.5631	ENSG00000104325	DECR1
ENSG00000104327	118.554	27.9307	29.3066	75.3674	ENSG00000104327	CALB1
ENSG00000104331	47.0349	49.7064	36.9596	40.7493	ENSG00000104331	IMPAD1
ENSG00000104332	24.9312	16.5153	4.4086	8.00997	ENSG00000104332	SFRP1
ENSG00000104341	50.8246	61.7335	30.275	22.2545	ENSG00000104341	LAPTM4B
ENSG00000104343	19.067	18.2217	19.3114	17.3319	ENSG00000104343	UBE2W
ENSG00000104356	12.2841	15.4253	12.0229	14.2367	ENSG00000104356	POP1
ENSG00000104361	32.5729	28.1623	33.1254	17.8975	ENSG00000104361	NIPAL2
ENSG00000104365	40.9529	73.423	55.5563	72.4935	ENSG00000104365	IKBKB
ENSG00000104368	32.5402	53.3948	7.63948	60.218	ENSG00000104368	PLAT
ENSG00000104369	1.16465	2.30464	3.37609	2.02876	ENSG00000104369	JPH1
ENSG00000104371	0.847792	0.407622	0.429693	0.383874	ENSG00000104371	DKK4
ENSG00000104375	71.5128	123.011	104.318	218.633	ENSG00000104375	STK3
ENSG00000104381	6.22431	3.573	8.39195	4.74824	ENSG00000104381	GDAP1
ENSG00000104388	60.2045	54.3044	47.1573	57.1961	ENSG00000104388	RAB2A
ENSG00000104408	126.176	145.086	123.278	111.756	ENSG00000104408	EIF3E
ENSG00000104412	14.1413	19.2259	22.2016	27.3366	ENSG00000104412	EMC2
ENSG00000104413	77.5631	92.3055	96.5543	33.5164	ENSG00000104413	ESRP1
ENSG00000104415	0.127423	2.11123	0.245668	7.45206	ENSG00000104415	WISP1
ENSG00000104419	142.104	314.63	340.342	197.963	ENSG00000104419	NDRG1
ENSG00000104427	5.56168	14.4503	11.1845	13.2638	ENSG00000104427	ZC2HC1A
ENSG00000104432	1.79521	5.50671	2.2867	5.79232	ENSG00000104432	IL7
ENSG00000104435	0.209741	0.516848	0.60869	0.450729	ENSG00000104435	STMN2
ENSG00000104442	14.7901	9.73243	12.8413	9.13558	ENSG00000104442	ARMC1
ENSG00000104447	7.67057	18.2062	19.894	27.2829	ENSG00000104447	TRPS1
ENSG00000104450	7.00179	5.23934	5.66538	4.95511	ENSG00000104450	SPAG1
ENSG00000104472	7.03746	6.95531	7.25914	5.3231	ENSG00000104472	CHRAC1
ENSG00000104490	18.8708	27.7836	24.8245	35.0696	ENSG00000104490	NCALD
ENSG00000104497	5.41639	4.48559	2.56063	4.83887	ENSG00000104497	SNX16
ENSG00000104499	0	0.466974	0	1.04897	ENSG00000104499	GML
ENSG00000104517	39.1964	66.1152	61.2669	74.0341	ENSG00000104517	UBR5
ENSG00000104518	10.1325	38.7155	20.2868	27.7047	ENSG00000104518	GSDMD
ENSG00000104522	51.322	51.9951	50.3063	21.9886	ENSG00000104522	TSTA3
ENSG00000104524	7.82871	7.28134	9.6009	6.4075	ENSG00000104524	PYCR3
ENSG00000104529	261.601	286.433	229.41	204.488	ENSG00000104529	EEF1D
ENSG00000104537	2.21403	6.48899	5.39759	9.83833	ENSG00000104537	ANXA13
ENSG00000104549	178.639	177.259	50.9228	86.2229	ENSG00000104549	SQLE
ENSG00000104611	9.03654	6.54056	7.16627	5.59346	ENSG00000104611	SH2D4A
ENSG00000104613	30.3621	44.4274	47.4075	46.7626	ENSG00000104613	INTS10
ENSG00000104626	10.5005	9.90108	8.42504	12.5213	ENSG00000104626	ERI1
ENSG00000104635	44.1858	66.0499	58.1731	47.6676	ENSG00000104635	SLC39A14
ENSG00000104643	9.58881	10.5909	11.3489	11.5712	ENSG00000104643	MTMR9
ENSG00000104660	31.7539	33.7287	34.1932	26.3155	ENSG00000104660	LEPROTL1
ENSG00000104671	31.0921	25.431	23.2579	28.8297	ENSG00000104671	DCTN6
ENSG00000104679	14.023	16.0778	14.7533	15.7239	ENSG00000104679	R3HCC1
ENSG00000104687	8.78393	16.0806	7.10702	8.39363	ENSG00000104687	GSR
ENSG00000104689	30.661	45.8596	33.3595	23.9148	ENSG00000104689	TNFRSF10A
ENSG00000104695	52.3683	58.0749	55.306	64.1321	ENSG00000104695	PPP2CB
ENSG00000104714	11.6402	19.4062	30.1033	37.078	ENSG00000104714	ERICH1
ENSG00000104722	0.764709	0.412392	0.850344	1.08265	ENSG00000104722	NEFM
ENSG00000104723	106.65	156.908	70.3723	72.2131	ENSG00000104723	TUSC3
ENSG00000104728	14.3112	26.4259	29.8045	36.3035	ENSG00000104728	ARHGEF10
ENSG00000104731	15.5355	25.5774	33.3133	25.2751	ENSG00000104731	KLHDC4

ENSG00000104738	25.8952	47.7338	20.2459	39.5205	ENSG00000104738	MCM4
ENSG00000104755	0.0791667	0.254761	0.183954	0.243551	ENSG00000104755	ADAM2
ENSG00000104756	38.1439	34.0363	39.1195	39.6281	ENSG00000104756	KCTD9
ENSG00000104760	1.62494	4.73704	3.3049	6.43967	ENSG00000104760	FGL1
ENSG00000104763	77.5013	65.54	50.9167	36.5151	ENSG00000104763	ASAH1
ENSG00000104765	55.0287	20.863	22.6481	35.5242	ENSG00000104765	BNIP3L
ENSG00000104774	38.1695	31.9944	42.4608	37.1079	ENSG00000104774	MAN2B1
ENSG00000104783	10.1165	31.6642	0.737268	10.4203	ENSG00000104783	KCNN4
ENSG00000104804	1.17901	0.0626918	0	0.888422	ENSG00000104804	TULP2
ENSG00000104805	110.413	137.667	64.9223	92.0675	ENSG00000104805	NUCB1
ENSG00000104808	3.73113	3.14717	2.17883	0.798179	ENSG00000104808	DHDH
ENSG00000104812	31.9419	33.7647	35.9258	34.3393	ENSG00000104812	GYS1
ENSG00000104814	4.32168	6.52517	7.34484	11.7071	ENSG00000104814	MAP4K1
ENSG00000104818	0	0.127614	0.11321	0	ENSG00000104818	CGB2
ENSG00000104823	11.2631	22.0194	24.4347	23.9125	ENSG00000104823	ECH1
ENSG00000104824	112.779	149.53	119.024	99.2498	ENSG00000104824	HNRNPL
ENSG00000104825	9.24826	8.80239	7.96558	8.59152	ENSG00000104825	NFKBIB
ENSG00000104826	0.907138	1.16044	3.41409	2.15996	ENSG00000104826	LHB
ENSG00000104827	0.472024	0.297193	0.523687	0	ENSG00000104827	CGB3
ENSG00000104833	1.6383	2.79228	2.64777	4.02206	ENSG00000104833	TUBB4A
ENSG00000104835	16.4645	19.5007	17.0341	14.5064	ENSG00000104835	SARS2
ENSG00000104848	0.626831	1.31857	1.74328	2.51443	ENSG00000104848	KCNA7
ENSG00000104852	131.301	124.096	166.486	117.929	ENSG00000104852	SNRNP70
ENSG00000104853	45.5916	38.6385	33.3209	28.8289	ENSG00000104853	CLPTM1
ENSG00000104856	6.37849	8.94396	10.687	17.5011	ENSG00000104856	RELB
ENSG00000104859	31.2417	38.8213	45.2008	40.9265	ENSG00000104859	CLASRP
ENSG00000104863	5.04449	4.72094	4.21388	6.57608	ENSG00000104863	LIN7B
ENSG00000104866	21.0221	18.9087	24.828	20.3708	ENSG00000104866	PPP1R37
ENSG00000104870	18.1454	23.3943	14.2447	18.4779	ENSG00000104870	FCGRT
ENSG00000104872	29.897	33.7097	33.2079	23.9019	ENSG00000104872	PIH1D1
ENSG00000104879	0.346633	0.133495	0.120675	0.113864	ENSG00000104879	CKM
ENSG00000104880	37.273	20.2084	17.2005	16.5192	ENSG00000104880	ARHGEF18
ENSG00000104881	75.0926	77.4306	74.4804	64.3213	ENSG00000104881	PPP1R13L
ENSG00000104883	3.73634	3.53133	4.24485	2.08648	ENSG00000104883	PEX11G
ENSG00000104884	12.0269	11.6624	10.6515	18.0047	ENSG00000104884	ERCC2
ENSG00000104885	12.9232	25.9584	26.0555	39.8163	ENSG00000104885	DOT1L
ENSG00000104886	31.3314	25.9214	28.9889	17.7703	ENSG00000104886	PLEKHJ1
ENSG00000104888	1.3026	1.32806	1.41297	2.36111	ENSG00000104888	SLC17A7
ENSG00000104889	9.28299	24.3061	11.1026	19.6382	ENSG00000104889	RNASEH2A
ENSG00000104892	39.6184	25.1953	23.5892	18.5721	ENSG00000104892	KLC3
ENSG00000104894	0.432708	3.07836	4.86902	5.09225	ENSG00000104894	CD37
ENSG00000104897	24.1091	29.4559	30.6074	23.8528	ENSG00000104897	SF3A2
ENSG00000104899	2.05299	1.27566	3.08996	1.02467	ENSG00000104899	AMH
ENSG00000104901	0	0.430843	0.212156	0.830311	ENSG00000104901	DKKL1
ENSG00000104903	1.41012	3.41544	2.59138	3.34045	ENSG00000104903	LYL1
ENSG00000104904	288.745	190.082	138.9	125.49	ENSG00000104904	OAZ1
ENSG00000104907	27.4133	26.6671	37.0674	21.5271	ENSG00000104907	TRMT1
ENSG00000104915	29.0401	25.4985	15.613	14.9579	ENSG00000104915	STX10
ENSG00000104918	0.498966	0	0	0	ENSG00000104918	RETN
ENSG00000104921	0.0908672	0.0583769	0.0541675	0	ENSG00000104921	FCER2
ENSG00000104936	12.8956	23.4643	31.3502	38.9322	ENSG00000104936	DMPK
ENSG00000104938	0.350363	1.09755	1.08372	1.94256	ENSG00000104938	CLEC4M
ENSG00000104941	0.169803	0.12828	0.296644	0.163109	ENSG00000104941	RSPH6A
ENSG00000104946	8.2912	10.0652	14.5616	17.2284	ENSG00000104946	TBC1D17

ENSG00000104951	0.180944	0.334304	0.41971	0.501923	ENSG00000104951	IL4I1
ENSG00000104953	0.733521	1.12271	1.11396	1.97345	ENSG00000104953	TLE6
ENSG00000104957	24.6672	32.7817	33.8262	24.8893	ENSG00000104957	CCDC130
ENSG00000104960	63.249	62.6912	43.3285	58.7629	ENSG00000104960	PTOV1
ENSG00000104964	102.967	114.906	99.8934	64.6889	ENSG00000104964	AES
ENSG00000104967	3.20225	3.29422	5.1675	7.17899	ENSG00000104967	NOVA2
ENSG00000104969	27.9369	25.3338	28.8254	27.9623	ENSG00000104969	SGTA
ENSG00000104970	2.0718	4.22564	4.21425	7.67349	ENSG00000104970	KIR3DX1
ENSG00000104972	0.284177	0.431107	0.0259567	0.338158	ENSG00000104972	LILRB1
ENSG00000104973	25.4876	18.4679	19.0194	18.657	ENSG00000104973	MED25
ENSG00000104974	0.059703	0.108637	0.0554507	0.139663	ENSG00000104974	LILRA1
ENSG00000104976	7.43227	8.5467	8.61779	4.48097	ENSG00000104976	SNAPC2
ENSG00000104979	55.8096	32.9186	27.0807	21.7087	ENSG00000104979	C19orf53
ENSG00000104980	28.1767	47.9469	51.9285	27.2016	ENSG00000104980	TIMM44
ENSG00000104983	4.91419	8.93629	9.95221	9.05104	ENSG00000104983	CCDC61
ENSG00000104998	2.16237	6.7421	6.78982	5.08962	ENSG00000104998	IL27RA
ENSG00000105011	1.5672	4.44006	0.596709	1.77793	ENSG00000105011	ASF1B
ENSG00000105048	54.7254	54.2666	25.8139	37.2106	ENSG00000105048	TNNT1
ENSG00000105053	25.387	26.9061	27.3214	32.3308	ENSG00000105053	VRK3
ENSG00000105058	37.5356	27.6419	26.9746	28.331	ENSG00000105058	FAM32A
ENSG00000105063	26.5989	28.4178	31.1669	34.6731	ENSG00000105063	PPP6R1
ENSG00000105072	3.06902	4.50326	4.51621	6.27125	ENSG00000105072	C19orf44
ENSG00000105085	7.10532	8.22063	9.56298	7.87288	ENSG00000105085	MED26
ENSG00000105088	1.34826	1.15854	9.06138	15.4019	ENSG00000105088	OLFM2
ENSG00000105122	0.392493	0.128433	0.106333	0.293655	ENSG00000105122	RASAL3
ENSG00000105127	15.7655	19.1535	18.4715	20.3928	ENSG00000105127	AKAP8
ENSG00000105131	4.79944	0.697065	1.38613	1.47746	ENSG00000105131	EPHX3
ENSG00000105135	24.2021	38.8491	26.3261	16.4904	ENSG00000105135	ILVBL
ENSG00000105136	9.67652	16.4388	22.8283	6.08532	ENSG00000105136	ZNF419
ENSG00000105137	3.07251	4.32035	3.85796	9.68286	ENSG00000105137	SYDE1
ENSG00000105141	2.09457	4.64066	8.80186	8.76251	ENSG00000105141	CASP14
ENSG00000105143	2.95064	6.01476	6.07516	9.14424	ENSG00000105143	SLC1A6
ENSG00000105146	2.22721	2.06264	3.1899	2.12464	ENSG00000105146	AURKC
ENSG00000105171	29.7474	19.2546	17.634	9.9225	ENSG00000105171	POP4
ENSG00000105173	6.33531	4.19516	5.97317	4.28798	ENSG00000105173	CCNE1
ENSG00000105176	35.9552	61.5671	61.0534	61.2828	ENSG00000105176	URI1
ENSG00000105185	46.9551	57.6138	65.3491	43.7825	ENSG00000105185	PDCD5
ENSG00000105186	19.0641	19.6068	21.6448	20.7051	ENSG00000105186	ANKRD27
ENSG00000105193	41.8695	16.0819	58.2645	55.5165	ENSG00000105193	RPS16
ENSG00000105197	50.2845	54.2641	54.2583	62.6021	ENSG00000105197	TIMM50
ENSG00000105198	0.392197	0.224838	0.913711	0.412379	ENSG00000105198	LGALS13
ENSG00000105202	19.3068	53.6848	26.378	36.0598	ENSG00000105202	FBL
ENSG00000105204	9.09267	4.83429	9.8329	6.4951	ENSG00000105204	DYRK1B
ENSG00000105205	0	0	0	0	ENSG00000105205	CLC
ENSG00000105219	1.10931	0.899714	0.469992	1.06799	ENSG00000105219	CNTD2
ENSG00000105220	70.5024	83.1336	58.1085	109.772	ENSG00000105220	GPI
ENSG00000105221	65.6283	91.9834	78.2771	81.2749	ENSG00000105221	AKT2
ENSG00000105223	133.239	144.33	164.581	111.595	ENSG00000105223	PLD3
ENSG00000105227	1.67575	4.43595	5.20758	4.9075	ENSG00000105227	PRX
ENSG00000105229	18.6213	13.8505	16.025	16.5774	ENSG00000105229	PIAS4
ENSG00000105245	6.91694	7.34736	12.6708	15.4387	ENSG00000105245	NUMBL
ENSG00000105246	0.167383	0.150058	0.344371	0.72582	ENSG00000105246	EBI3
ENSG00000105248	6.88243	6.87214	5.59569	5.2308	ENSG00000105248	CCDC94
ENSG00000105251	0	0.0417303	0.0749811	0.0235996	ENSG00000105251	SHD

ENSG00000105254	67.2757	53.386	45.4622	47.8113	ENSG00000105254	TBCB
ENSG00000105255	0.402499	3.42062	3.552	7.3034	ENSG00000105255	FSD1
ENSG00000105258	31.5804	17.9979	18.1249	10.4393	ENSG00000105258	POLR2I
ENSG00000105261	0.885551	0.875737	1.21967	0.227995	ENSG00000105261	OVOL3
ENSG00000105270	1.01476	2.47279	1.62983	6.81732	ENSG00000105270	CLIP3
ENSG00000105278	1.57498	1.94014	1.76981	1.7462	ENSG00000105278	ZFR2
ENSG00000105281	78.7743	274.364	154.786	74.4282	ENSG00000105281	SLC1A5
ENSG00000105287	17.7194	22.0186	25.8784	23.5382	ENSG00000105287	PRKD2
ENSG00000105289	10.6261	1.125	1.7765	1.60165	ENSG00000105289	TJP3
ENSG00000105290	2.92028	4.23306	3.74223	11.0183	ENSG00000105290	APLP1
ENSG00000105298	13.4859	13.6104	15.6328	13.2338	ENSG00000105298	CACTIN
ENSG00000105321	13.7441	13.0408	15.7545	21.7393	ENSG00000105321	CCDC9
ENSG00000105323	58.3683	60.5919	56.9104	81.5243	ENSG00000105323	HNRNPUL1
ENSG00000105325	37.9518	34.8806	26.6754	22.0222	ENSG00000105325	FZR1
ENSG00000105327	4.38808	5.34334	6.62374	6.16585	ENSG00000105327	BBC3
ENSG00000105329	12.6945	30.3045	12.4553	31.3685	ENSG00000105329	TGFB1
ENSG00000105339	9.48683	21.4652	11.6347	17.8779	ENSG00000105339	DENND3
ENSG00000105341	7.87635	9.30261	7.95609	7.57048	ENSG00000105341	DMAC2
ENSG00000105352	0	0.067479	0.0613045	0.148222	ENSG00000105352	CEACAM4
ENSG00000105355	40.1356	30.6347	18.3822	36.0977	ENSG00000105355	PLIN3
ENSG00000105357	9.90374	1.94374	2.57832	4.5312	ENSG00000105357	MYH14
ENSG00000105364	26.2987	25.6647	26.9087	21.651	ENSG00000105364	MRPL4
ENSG00000105366	1.73738	3.25523	2.84462	5.51194	ENSG00000105366	SIGLEC8
ENSG00000105369	0.165303	0.183125	0.330569	0.273126	ENSG00000105369	CD79A
ENSG00000105370	0.074656	0	0	0	ENSG00000105370	LIM2
ENSG00000105371	1.30918	2.32543	1.19751	3.63656	ENSG00000105371	ICAM4
ENSG00000105372	599.243	453.51	407.359	238.937	ENSG00000105372	RPS19
ENSG00000105373	35.657	39.2566	36.6219	51.0649	ENSG00000105373	NOP53
ENSG00000105374	0.15805	0.257851	2.05213	0.770009	ENSG00000105374	NKG7
ENSG00000105376	0.680322	7.41533	7.17833	24.1903	ENSG00000105376	ICAM5
ENSG00000105379	32.0233	35.3983	20.7246	34.6224	ENSG00000105379	ETFB
ENSG00000105383	0.542487	1.36322	1.1774	1.93703	ENSG00000105383	CD33
ENSG00000105388	1.88893	0.0208347	0.450973	0.33727	ENSG00000105388	CEACAM5
ENSG00000105392	2.38563	4.5335	4.60844	8.17845	ENSG00000105392	CRX
ENSG00000105393	41.5119	51.5648	34.7246	34.3674	ENSG00000105393	BABAM1
ENSG00000105397	55.9256	72.9898	77.6247	97.6277	ENSG00000105397	TYK2
ENSG00000105398	0.808519	1.39279	1.34086	2.94471	ENSG00000105398	SULT2A1
ENSG00000105401	138.94	102.919	118.572	82.6044	ENSG00000105401	CDC37
ENSG00000105402	34.993	22.8963	28.4288	24.2558	ENSG00000105402	NAPA
ENSG00000105404	71.8721	51.0539	19.744	28.2056	ENSG00000105404	RABAC1
ENSG00000105409	1.23656	2.89502	1.74787	4.92945	ENSG00000105409	ATP1A3
ENSG00000105419	4.89238	7.32052	12.4817	18.6789	ENSG00000105419	MEIS3
ENSG00000105426	16.0227	26.4777	22.6201	33.9365	ENSG00000105426	PTPRS
ENSG00000105427	28.7581	10.0463	4.22562	25.263	ENSG00000105427	CNFN
ENSG00000105428	0	0	0	0	ENSG00000105428	ZNRF4
ENSG00000105429	8.27678	15.5216	14.7221	20.586	ENSG00000105429	MEGF8
ENSG00000105438	110.04	99.8713	56.926	59.4978	ENSG00000105438	KDELR1
ENSG00000105443	22.8519	25.0195	24.5701	16.2723	ENSG00000105443	CYTH2
ENSG00000105447	18.232	16.9721	17.4426	9.7643	ENSG00000105447	GRWD1
ENSG00000105464	0.336358	0.558034	0.409467	1.66745	ENSG00000105464	GRIN2D
ENSG00000105467	0.138628	0.0602189	0.360203	0.594214	ENSG00000105467	SYNGR4
ENSG00000105472	1.77112	1.07111	0.824748	24.5768	ENSG00000105472	CLEC11A
ENSG00000105479	1.2962	1.72531	3.26071	3.6936	ENSG00000105479	CCDC114
ENSG00000105483	9.95096	18.1089	18.1823	27.1863	ENSG00000105483	CARD8

ENSG00000105486	10.4706	26.5408	11.9109	25.1884	ENSG00000105486	LIG1
ENSG00000105492	0.305474	1.17487	1.39927	2.18434	ENSG00000105492	SIGLEC6
ENSG00000105497	4.63759	9.54319	12.2707	16.9897	ENSG00000105497	ZNF175
ENSG00000105499	10.928	27.0299	27.9596	46.0816	ENSG00000105499	PLA2G4C
ENSG00000105501	0.142476	0.323936	0.209985	0.0806473	ENSG00000105501	SIGLEC5
ENSG00000105507	1.52823	1.88166	4.46432	2.82827	ENSG00000105507	CABP5
ENSG00000105509	0.22133	0.156077	0.602443	0.180769	ENSG00000105509	HAS1
ENSG00000105514	13.4004	17.1744	21.3719	10.2235	ENSG00000105514	RAB3D
ENSG00000105516	13.1184	6.53742	3.68247	3.24637	ENSG00000105516	DBP
ENSG00000105518	39.149	46.771	34.5934	14.9203	ENSG00000105518	TMEM205
ENSG00000105519	6.115	11.1389	10.8207	12.307	ENSG00000105519	CAPS
ENSG00000105520	16.9845	10.0967	9.8492	14.3846	ENSG00000105520	PLPPR2
ENSG00000105523	4.78357	6.96743	2.98315	2.67917	ENSG00000105523	FAM83E
ENSG00000105538	2.22071	2.92176	3.98438	0.952649	ENSG00000105538	RASIP1
ENSG00000105549	1.17085	0.157581	0.477446	0.566591	ENSG00000105549	THEG
ENSG00000105550	0	0	0.376686	0	ENSG00000105550	FGF21
ENSG00000105552	10.7723	19.346	12.0498	12.4056	ENSG00000105552	BCAT2
ENSG00000105556	19.2814	23.155	20.7905	27.817	ENSG00000105556	MIER2
ENSG00000105559	4.3865	11.7496	14.1707	15.8685	ENSG00000105559	PLEKHA4
ENSG00000105568	169.422	105.938	84.1991	81.3597	ENSG00000105568	PPP2R1A
ENSG00000105576	479.993	723.677	1111.26	5474.54	ENSG00000105576	TNPO2
ENSG00000105583	64.5218	47.753	30.4381	24.0121	ENSG00000105583	WDR83OS
ENSG00000105605	1.09106	0.345977	0.618838	2.48116	ENSG00000105605	CACNG7
ENSG00000105607	6.73293	13.1872	11.6928	13.996	ENSG00000105607	GCDH
ENSG00000105609	0.107233	0.270673	0.190263	0.319057	ENSG00000105609	LILRB5
ENSG00000105610	0.0379363	0.107828	0.133195	0	ENSG00000105610	KLF1
ENSG00000105612	21.6063	34.2061	28.0414	16.3076	ENSG00000105612	DNASE2
ENSG00000105613	2.56503	6.39652	5.87403	8.6918	ENSG00000105613	MAST1
ENSG00000105617	0.418188	0.39575	0.408938	0.372155	ENSG00000105617	LENG1
ENSG00000105618	2.36758	1.90677	2.11706	1.49956	ENSG00000105618	PRPF31
ENSG00000105619	0.586232	0.553337	0.745755	0.452985	ENSG00000105619	TFPT
ENSG00000105639	1.28328	2.51536	2.68137	3.98204	ENSG00000105639	JAK3
ENSG00000105640	581.695	458.511	380.268	231.216	ENSG00000105640	RPL18A
ENSG00000105641	0.865534	1.72087	1.64968	2.47335	ENSG00000105641	SLC5A5
ENSG00000105642	2.02148	2.04881	1.16279	4.12456	ENSG00000105642	KCNN1
ENSG00000105643	4.44211	4.71754	7.60016	4.81586	ENSG00000105643	ARRDC2
ENSG00000105647	14.4679	21.263	23.1892	22.9973	ENSG00000105647	PIK3R2
ENSG00000105649	1.11796	0.817683	0.827182	0.779383	ENSG00000105649	RAB3A
ENSG00000105650	3.72985	4.52062	4.02885	7.52103	ENSG00000105650	PDE4C
ENSG00000105655	4.15661	12.0908	9.06866	5.42399	ENSG00000105655	ISYNA1
ENSG00000105656	11.1499	13.1867	11.7932	12.6095	ENSG00000105656	ELL
ENSG00000105662	2.35633	5.03085	3.68565	3.24964	ENSG00000105662	CRTC1
ENSG00000105664	3.2273	6.63542	8.02099	11.8082	ENSG00000105664	COMP
ENSG00000105668	0.652452	0.951545	1.05069	1.38662	ENSG00000105668	UPK1A
ENSG00000105669	94.188	59.8072	52.9315	40.2763	ENSG00000105669	COPE
ENSG00000105671	21.492	19.0295	21.2168	18.982	ENSG00000105671	DDX49
ENSG00000105672	0.560045	0.283905	0.434468	0.402491	ENSG00000105672	ETV2
ENSG00000105675	0.11839	0.099414	0.463615	0.113388	ENSG00000105675	ATP4A
ENSG00000105676	12.8107	14.6097	19.0072	11.3826	ENSG00000105676	ARMC6
ENSG00000105677	110.38	73.135	42.2066	20.8193	ENSG00000105677	TMEM147
ENSG00000105679	6.14178	9.69909	13.0494	2.6298	ENSG00000105679	GAPDHS
ENSG00000105694	1.0386	0.793512	0.460474	2.00999	ENSG00000105694	ELOCP28
ENSG00000105695	0.134358	0.25783	0.02072	0.288164	ENSG00000105695	MAG
ENSG00000105696	0.071476	0.30987	0.182248	0.243993	ENSG00000105696	TMEM59L

ENSG00000105697	1.81568	3.69438	2.78428	6.11589	ENSG00000105697	HAMP
ENSG00000105698	44.5036	33.0473	40.5	36.3948	ENSG00000105698	USF2
ENSG00000105699	118.598	93.7515	77.3083	36.7509	ENSG00000105699	LSR
ENSG00000105700	51.7641	53.3665	56.5875	60.6251	ENSG00000105700	KXD1
ENSG00000105701	92.7719	72.2056	72.3117	63.1936	ENSG00000105701	FKBP8
ENSG00000105705	22.2087	20.8318	21.4886	20.8107	ENSG00000105705	SUGP1
ENSG00000105707	3.32724	9.03729	6.43965	10.4069	ENSG00000105707	HPN
ENSG00000105708	3.37808	3.79623	3.78117	3.30722	ENSG00000105708	ZNF14
ENSG00000105711	0.993002	2.1246	1.71894	4.90584	ENSG00000105711	SCN1B
ENSG00000105717	2.03567	3.9891	2.41292	4.45573	ENSG00000105717	PBX4
ENSG00000105722	41.0792	48.834	63.2939	36.3037	ENSG00000105722	ERF
ENSG00000105723	17.7148	15.4005	15.4481	12.5763	ENSG00000105723	GSK3A
ENSG00000105726	44.6609	49.1728	45.5013	32.6926	ENSG00000105726	ATP13A1
ENSG00000105732	7.50418	8.1839	6.88096	6.65357	ENSG00000105732	ZNF574
ENSG00000105737	0.036254	0.17709	0.0989798	0.154913	ENSG00000105737	GRIK5
ENSG00000105738	14.6443	21.2733	25.214	56.3989	ENSG00000105738	SIPA1L3
ENSG00000105750	6.37536	14.5404	11.4962	14.4179	ENSG00000105750	ZNF85
ENSG00000105755	137.501	81.2927	41.2383	34.0098	ENSG00000105755	ETHE1
ENSG00000105767	6.85867	5.9259	5.19886	3.27438	ENSG00000105767	CADM4
ENSG00000105771	24.6434	47.1308	33.0691	46.1856	ENSG00000105771	SMG9
ENSG00000105778	27.4105	25.7433	22.2304	24.8729	ENSG00000105778	AVL9
ENSG00000105784	1.05246	2.36229	2.64784	5.48473	ENSG00000105784	RUNDC3B
ENSG00000105792	6.77767	13.4527	12.315	28.4496	ENSG00000105792	CFAP69
ENSG00000105793	13.4867	19.0203	15.0869	16.4363	ENSG00000105793	GTPBP10
ENSG00000105808	6.92562	6.70974	11.9547	11.4082	ENSG00000105808	RASA4
ENSG00000105810	72.276	54.2018	84.8605	76.8098	ENSG00000105810	CDK6
ENSG00000105819	20.1299	23.746	20.0861	16.5615	ENSG00000105819	PMPCB
ENSG00000105821	11.2938	15.0603	21.9543	19.7533	ENSG00000105821	DNAJC2
ENSG00000105825	241.917	265.393	4.47132	74.8287	ENSG00000105825	TFPI2
ENSG00000105829	14.9285	19.8457	23.3873	26.2816	ENSG00000105829	BET1
ENSG00000105835	135.465	61.9303	100.516	56.3584	ENSG00000105835	NAMPT
ENSG00000105849	11.9373	6.66648	8.65087	7.67572	ENSG00000105849	TWISTNB
ENSG00000105851	0.207826	0.633547	0.932137	0.916391	ENSG00000105851	PIK3CG
ENSG00000105852	2.07584	5.27602	4.10355	7.81473	ENSG00000105852	PON3
ENSG00000105854	62.937	81.5557	92.8074	65.1822	ENSG00000105854	PON2
ENSG00000105855	67.0835	26.2089	22.2917	13.5737	ENSG00000105855	ITGB8
ENSG00000105856	37.1598	27.9417	25.466	24.8473	ENSG00000105856	HBP1
ENSG00000105865	8.77223	15.4875	12.6044	11.2688	ENSG00000105865	DUS4L
ENSG00000105866	1.64166	3.37933	3.30545	2.85111	ENSG00000105866	SP4
ENSG00000105875	21.5889	36.972	38.4979	34.8829	ENSG00000105875	WDR91
ENSG00000105877	18.2021	51.1144	38.8408	70.6719	ENSG00000105877	DNAH11
ENSG00000105879	17.3072	12.5381	11.8471	9.71215	ENSG00000105879	CBLL1
ENSG00000105880	1.09174	0.915842	0.450029	0.731752	ENSG00000105880	DLX5
ENSG00000105887	62.929	39.6487	37.9473	42.4953	ENSG00000105887	MTPN
ENSG00000105889	7.50386	6.16131	2.25121	6.86263	ENSG00000105889	STEAP1B
ENSG00000105894	0	0.818087	0.462441	1.68023	ENSG00000105894	PTN
ENSG00000105926	7.13342	9.82275	8.86715	14.6949	ENSG00000105926	MPP6
ENSG00000105928	28.2449	43.2172	47.6989	34.0746	ENSG00000105928	DFNA5
ENSG00000105929	0.366165	0.352764	0.423988	0.116787	ENSG00000105929	ATP6V0A4
ENSG00000105939	18.2621	17.3026	9.64975	24.7442	ENSG00000105939	ZC3HAV1
ENSG00000105948	2.94866	3.91978	3.46228	4.03275	ENSG00000105948	TTC26
ENSG00000105953	49.6898	53.709	39.8042	43.4526	ENSG00000105953	OGDH
ENSG00000105954	0	0.0969397	0.131425	0.109945	ENSG00000105954	NPVF
ENSG00000105963	4.03112	7.72321	9.27158	3.14926	ENSG00000105963	ADAP1

ENSG00000105967	1.37589	1.85198	0.599944	3.46355	ENSG00000105967	TFEC
ENSG00000105968	20.6356	40.086	20.8398	31.4577	ENSG00000105968	H2AFV
ENSG00000105971	174.234	126.639	88.5503	92.2453	ENSG00000105971	CAV2
ENSG00000105974	468.939	350.56	157.445	236.328	ENSG00000105974	CAV1
ENSG00000105976	113.877	187.987	87.7845	47.0497	ENSG00000105976	MET
ENSG00000105982	1.94665	4.96515	6.13549	4.21731	ENSG00000105982	RNF32
ENSG00000105983	32.9503	37.2744	35.3971	30.0061	ENSG00000105983	LMBR1
ENSG00000105988	0	0	0.472379	0	ENSG00000105988	NHP2P1
ENSG00000105989	0.192197	0.0360035	0.0879691	0.392854	ENSG00000105989	WNT2
ENSG00000105991	3.10845	2.07955	2.99606	1.46853	ENSG00000105991	HOXA1
ENSG00000105993	82.7605	40.6819	55.5542	83.8304	ENSG00000105993	DNAJB6
ENSG00000105996	2.24479	2.76073	2.53714	1.77571	ENSG00000105996	HOXA2
ENSG00000105997	4.86809	5.59504	5.40296	3.98174	ENSG00000105997	HOXA3
ENSG00000106003	8.15907	14.9831	21.2019	12.7646	ENSG00000106003	LFNG
ENSG00000106004	1.22525	4.48298	3.09684	2.1454	ENSG00000106004	HOXA5
ENSG00000106006	2.51655	5.76642	4.42751	4.29767	ENSG00000106006	HOXA6
ENSG00000106009	11.6214	16.7628	13.1535	11.3747	ENSG00000106009	BRAT1
ENSG00000106012	10.4089	9.53011	7.65206	13.5144	ENSG00000106012	IQCE
ENSG00000106013	0.375567	0.848375	1.90104	0.612059	ENSG00000106013	ANKRD7
ENSG00000106018	0.210945	0.303389	0.335349	0.536624	ENSG00000106018	VIPR2
ENSG00000106025	0.834652	0.561244	0.575461	1.34504	ENSG00000106025	TSPAN12
ENSG00000106028	41.5505	36.7423	33.1949	26.796	ENSG00000106028	SSBP1
ENSG00000106031	0.197143	0.344417	0.355992	0.723481	ENSG00000106031	HOXA13
ENSG00000106034	0.747451	1.97936	1.51787	21.3042	ENSG00000106034	CPED1
ENSG00000106038	0.116096	0.274261	0.369302	0.320845	ENSG00000106038	EVX1
ENSG00000106049	9.09671	14.1159	8.35014	9.22232	ENSG00000106049	HIBADH
ENSG00000106052	51.0929	37.9991	42.5098	38.8142	ENSG00000106052	TAX1BP1
ENSG00000106066	0.410162	1.15882	0.966548	2.01303	ENSG00000106066	CPVL
ENSG00000106069	8.75254	16.9317	18.0772	28.6919	ENSG00000106069	CHN2
ENSG00000106070	16.7701	55.4858	53.2467	67.4079	ENSG00000106070	GRB10
ENSG00000106077	5.9857	6.44069	3.76178	6.84619	ENSG00000106077	ABHD11
ENSG00000106078	1.34739	0.905782	1.07329	1.68197	ENSG00000106078	COBL
ENSG00000106080	28.4316	26.3534	23.8853	23.5949	ENSG00000106080	FKBP14
ENSG00000106086	8.41509	9.35874	8.06648	8.59942	ENSG00000106086	PLEKHA8
ENSG00000106089	12.1127	15.5984	7.06571	13.8636	ENSG00000106089	STX1A
ENSG00000106100	6.43584	12.9651	10.8353	8.60873	ENSG00000106100	NOD1
ENSG00000106105	66.3904	162.202	195.25	98.1861	ENSG00000106105	GARS
ENSG00000106113	1.54875	2.68448	3.64734	3.44685	ENSG00000106113	CRHR2
ENSG00000106123	0.709513	0.677726	1.04073	0.675559	ENSG00000106123	EPHB6
ENSG00000106125	2.55488	4.50869	4.06618	4.08317	ENSG00000106125	MINDY4
ENSG00000106128	0	0.385356	0.370101	0.453734	ENSG00000106128	GHRHR
ENSG00000106133	8.39332	5.02893	5.58149	7.58893	ENSG00000106133	NSUN5P2
ENSG00000106144	9.51859	10.8257	11.0976	15.017	ENSG00000106144	CASP2
ENSG00000106153	136.144	110.811	74.4163	60.2091	ENSG00000106153	CHCHD2
ENSG00000106178	0	0	0	0	ENSG00000106178	CCL24
ENSG00000106211	713.654	105.335	383.752	112.27	ENSG00000106211	HSPB1
ENSG00000106236	0.0816584	0	0.0663783	28.456	ENSG00000106236	NPTX2
ENSG00000106244	46.7169	39.4997	47.9268	36.8063	ENSG00000106244	PDAP1
ENSG00000106245	51.3114	42.4275	46.3997	36.8027	ENSG00000106245	BUD31
ENSG00000106246	11.1399	8.8521	10.2129	6.69359	ENSG00000106246	PTCD1
ENSG00000106258	37.1035	59.0875	41.9086	82.6451	ENSG00000106258	CYP3A5
ENSG00000106261	36.1753	48.117	45.128	45.4199	ENSG00000106261	ZKSCAN1
ENSG00000106263	96.2326	89.8984	112.607	78.6163	ENSG00000106263	EIF3B
ENSG00000106266	11.7326	8.63619	9.75351	11.8297	ENSG00000106266	SNX8

ENSG00000106268	18.4593	38.6327	26.3323	40.2601	ENSG00000106268	NUDT1
ENSG00000106278	28.8717	81.4315	71.323	53.5868	ENSG00000106278	PTPRZ1
ENSG00000106290	20.7184	27.8336	28.444	34.275	ENSG00000106290	TAF6
ENSG00000106299	28.9632	17.077	17.9823	12.4899	ENSG00000106299	WASL
ENSG00000106302	0.611351	2.886	4.12725	5.72836	ENSG00000106302	HYAL4
ENSG00000106304	0.100988	0.19659	0.219359	0.454277	ENSG00000106304	SPAM1
ENSG00000106305	20.478	18.9757	21.7803	11.4974	ENSG00000106305	AIMP2
ENSG00000106327	2.67215	4.15091	5.08723	19.2347	ENSG00000106327	TFR2
ENSG00000106328	0.53442	0.239827	0.302092	0.399198	ENSG00000106328	FSCN3
ENSG00000106330	5.4376	4.06084	3.08222	4.75466	ENSG00000106330	MOSPD3
ENSG00000106331	0.421768	1.02635	0.856134	1.66803	ENSG00000106331	PAX4
ENSG00000106333	2.7123	6.70453	5.46526	88.9612	ENSG00000106333	PCOLCE
ENSG00000106336	2.30585	4.6293	3.81049	7.19236	ENSG00000106336	FBXO24
ENSG00000106341	0.253673	0.364261	0.32972	0.72678	ENSG00000106341	PPP1R17
ENSG00000106344	16.8319	16.7215	18.1345	19.911	ENSG00000106344	RBM28
ENSG00000106346	5.90812	7.62073	8.14414	11.5975	ENSG00000106346	USP42
ENSG00000106348	33.3299	52.151	37.2721	27.4466	ENSG00000106348	IMPDH1
ENSG00000106351	7.25374	6.44033	4.63484	6.72614	ENSG00000106351	AGFG2
ENSG00000106355	15.9214	17.5651	13.7133	13.3549	ENSG00000106355	LSM5
ENSG00000106366	988.644	562.95	171.371	1058.25	ENSG00000106366	SERPINE1
ENSG00000106367	56.4639	50.0637	31.9187	27.1376	ENSG00000106367	AP1S1
ENSG00000106384	2.19077	2.81812	2.73036	5.47221	ENSG00000106384	MOGAT3
ENSG00000106392	53.0007	35.5637	34.1305	30.035	ENSG00000106392	C1GALT1
ENSG00000106397	63.226	84.8353	72.8052	102.188	ENSG00000106397	PLOD3
ENSG00000106399	13.9329	23.5551	7.16882	9.18738	ENSG00000106399	RPA3
ENSG00000106400	37.1131	25.2586	21.3211	20.9477	ENSG00000106400	ZNHIT1
ENSG00000106404	3.90137	5.01181	7.6996	5.45814	ENSG00000106404	CLDN15
ENSG00000106410	0.0662688	0.127703	0.0288604	0.0363174	ENSG00000106410	NOBOX
ENSG00000106415	2.87419	4.21753	5.04912	8.30931	ENSG00000106415	GLCCI1
ENSG00000106436	1.59465	1.85254	2.26486	5.06034	ENSG00000106436	MYL10
ENSG00000106443	7.79176	22.477	20.0187	21.8481	ENSG00000106443	PHF14
ENSG00000106459	8.33419	10.0879	9.68208	10.7905	ENSG00000106459	NRF1
ENSG00000106460	51.5857	32.0682	26.8113	21.2711	ENSG00000106460	TMEM106B
ENSG00000106462	5.82703	11.48	7.39541	12.4148	ENSG00000106462	EZH2
ENSG00000106477	2.8898	6.07195	5.02118	7.74472	ENSG00000106477	CEP41
ENSG00000106479	9.45177	16.268	17.7885	14.8431	ENSG00000106479	ZNF862
ENSG00000106483	0.714369	1.6497	1.82708	1.60684	ENSG00000106483	SFRP4
ENSG00000106484	4.80407	3.43389	3.79086	2.29573	ENSG00000106484	MEST
ENSG00000106511	0.0704471	0.198764	0.141561	0.949577	ENSG00000106511	MEOX2
ENSG00000106524	4.00544	6.187	3.33861	4.38454	ENSG00000106524	ANKMY2
ENSG00000106526	2.7191	2.73786	3.75556	3.54723	ENSG00000106526	ACTR3C
ENSG00000106536	0.585612	1.11656	1.82952	3.10722	ENSG00000106536	POU6F2
ENSG00000106537	15.6056	13.1461	7.23262	7.55192	ENSG00000106537	TSPAN13
ENSG00000106538	0.268105	0.234863	0.254386	1.28012	ENSG00000106538	RARRES2
ENSG00000106540	0.317952	0.112092	0.77959	0.355841	ENSG00000106540	AC004837.1
ENSG00000106541	5.21204	3.40554	1.05122	2.229	ENSG00000106541	AGR2
ENSG00000106546	31.965	32.1145	71.3022	19.9511	ENSG00000106546	AHR
ENSG00000106554	16.859	23.2048	19.065	22.4971	ENSG00000106554	CHCHD3
ENSG00000106560	4.5149	15.9093	13.0541	28.6105	ENSG00000106560	GIMAP2
ENSG00000106565	0.168799	0.303334	0.139681	4.98841	ENSG00000106565	TMEM176B
ENSG00000106571	2.52661	9.03558	7.44611	11.3271	ENSG00000106571	GLI3
ENSG00000106588	52.512	48.5704	26.2308	29.6919	ENSG00000106588	PSMA2
ENSG00000106591	33.1741	36.5172	33.1429	21.4159	ENSG00000106591	MRPL32
ENSG00000106603	24.7278	49.0495	39.8659	55.1034	ENSG00000106603	COA1

ENSG00000106605	9.66422	13.0236	9.86428	11.9451	ENSG00000106605	BLVRA
ENSG00000106608	17.0292	20.1533	25.4828	23.8694	ENSG00000106608	URGCP
ENSG00000106609	62.1567	48.7397	36.2829	27.9963	ENSG00000106609	TMEM248
ENSG00000106610	8.29618	6.69438	9.51922	4.51065	ENSG00000106610	STAG3L4
ENSG00000106615	38.995	35.2822	40.3072	33.473	ENSG00000106615	RHEB
ENSG00000106617	17.9222	15.5788	11.5566	15.4246	ENSG00000106617	PRKAG2
ENSG00000106624	2.43072	2.47617	17.9042	96.0105	ENSG00000106624	AEBP1
ENSG00000106628	32.1516	57.8573	52.3583	38.2973	ENSG00000106628	POLD2
ENSG00000106631	0.777798	0	0.44251	0.503901	ENSG00000106631	MYL7
ENSG00000106633	0.0450542	0.468632	0.27812	0.870073	ENSG00000106633	GCK
ENSG00000106635	8.73537	6.30907	8.51348	6.10502	ENSG00000106635	BCL7B
ENSG00000106636	43.4387	31.4812	43.1737	26.1634	ENSG00000106636	YKT6
ENSG00000106638	20.9602	17.935	15.7131	11.79	ENSG00000106638	TBL2
ENSG00000106648	0.987784	0.866394	1.31707	1.58902	ENSG00000106648	GALNTL5
ENSG00000106665	5.97855	7.87627	7.09289	16.7336	ENSG00000106665	CLIP2
ENSG00000106682	59.0382	44.9789	48.8949	34.2798	ENSG00000106682	EIF4H
ENSG00000106683	8.75641	8.71624	8.0739	8.46538	ENSG00000106683	LIMK1
ENSG00000106686	6.6917	14.4873	11.1657	17.9592	ENSG00000106686	SPATA6L
ENSG00000106688	0.291668	0.354202	0.306369	0.391925	ENSG00000106688	SLC1A1
ENSG00000106689	0.304724	0.425673	1.28162	1.11872	ENSG00000106689	LHX2
ENSG00000106692	16.9932	36.4859	28.2561	21.1237	ENSG00000106692	FKTN
ENSG00000106701	4.02414	9.42879	7.77962	11.3711	ENSG00000106701	FSD1L
ENSG00000106714	13.7108	35.2376	17.4281	14.3692	ENSG00000106714	CNTNAP3
ENSG00000106723	21.1557	25.0531	24.9692	22.9087	ENSG00000106723	SPIN1
ENSG00000106733	13.9744	16.6362	19.3856	17.2389	ENSG00000106733	NMRK1
ENSG00000106771	25.6877	38.2004	18.7697	18.0715	ENSG00000106771	TMEM245
ENSG00000106772	1.02326	1.43145	1.10347	2.08702	ENSG00000106772	PRUNE2
ENSG00000106780	10.4996	6.06104	6.39966	5.56205	ENSG00000106780	MEGF9
ENSG00000106785	7.35063	12.2656	11.1478	12.51	ENSG00000106785	TRIM14
ENSG00000106789	11.9881	13.2141	11.8084	7.13095	ENSG00000106789	CORO2A
ENSG00000106799	34.428	30.1905	22.2555	20.8156	ENSG00000106799	TGFBR1
ENSG00000106803	69.6445	56.5479	50.6745	41.8101	ENSG00000106803	SEC61B
ENSG00000106804	2.6006	7.83791	7.12651	16.759	ENSG00000106804	C5
ENSG00000106809	0.300358	1.05531	0.486967	1.47126	ENSG00000106809	OGN
ENSG00000106819	0.954441	2.98382	2.60386	5.99416	ENSG00000106819	ASPN
ENSG00000106823	0.677167	2.70702	5.61413	3.39438	ENSG00000106823	ECM2
ENSG00000106829	10.2414	18.0206	15.982	22.6037	ENSG00000106829	TLE4
ENSG00000106852	0.48436	1.14217	0.912659	1.75111	ENSG00000106852	LHX6
ENSG00000106853	27.8504	32.4495	26.124	38.5181	ENSG00000106853	PTGR1
ENSG00000106868	2.45756	3.96551	1.59607	3.35124	ENSG00000106868	SUSD1
ENSG00000106927	0.0433588	0.122716	0.213795	0.234201	ENSG00000106927	AMBP
ENSG00000106948	4.66334	13.1653	9.78654	10.0847	ENSG00000106948	AKNA
ENSG00000106952	0.148496	1.04245	0.340941	0.993548	ENSG00000106952	TNFSF8
ENSG00000106976	0.457918	2.1311	2.34171	29.4054	ENSG00000106976	DNM1
ENSG00000106991	3.72603	12.3813	8.4753	13.9521	ENSG00000106991	ENG
ENSG00000106992	41.8439	18.811	18.8374	15.5812	ENSG00000106992	AK1
ENSG00000106993	10.324	7.35954	11.7607	7.0564	ENSG00000106993	CDC37L1
ENSG00000107014	0.542649	1.12983	0.530855	0.587215	ENSG00000107014	RLN2
ENSG00000107018	0.172743	0.164956	0.166839	0	ENSG00000107018	RLN1
ENSG00000107020	14.8566	26.8769	10.9478	13.5914	ENSG00000107020	PLGRKT
ENSG00000107021	11.4348	5.36385	7.10964	5.76419	ENSG00000107021	TBC1D13
ENSG00000107036	14.4595	21.3262	19.4539	19.577	ENSG00000107036	RIC1
ENSG00000107077	15.0426	27.2537	26.3489	26.3647	ENSG00000107077	KDM4C
ENSG00000107099	2.60445	3.48925	3.25393	7.2054	ENSG00000107099	DOCK8

ENSG00000107104	50.4286	35.4258	27.6224	26.6313	ENSG00000107104	KANK1
ENSG00000107105	4.05516	8.03513	7.15734	8.81476	ENSG00000107105	ELAVL2
ENSG00000107130	6.34865	4.67594	7.28136	6.32849	ENSG00000107130	NCS1
ENSG00000107140	9.69439	9.17637	12.5069	9.36023	ENSG00000107140	TESK1
ENSG00000107147	0.403634	0.237316	0.626975	0.25117	ENSG00000107147	KCNT1
ENSG00000107159	0.602089	2.65171	4.30548	3.52638	ENSG00000107159	CA9
ENSG00000107164	33.1471	28.8314	42.0245	36.0645	ENSG00000107164	FUBP3
ENSG00000107165	21.9904	6.53733	3.6464	2.896	ENSG00000107165	TYRP1
ENSG00000107175	17.594	15.643	18.1975	10.4231	ENSG00000107175	CREB3
ENSG00000107185	11.3121	11.9296	14.5895	10.0321	ENSG00000107185	RGP1
ENSG00000107186	4.19874	9.47154	7.72994	21.5766	ENSG00000107186	MPDZ
ENSG00000107187	0.0235466	0.136017	0.0412324	0.258311	ENSG00000107187	LHX3
ENSG00000107201	12.1663	20.2355	15.9128	17.8683	ENSG00000107201	DDX58
ENSG00000107223	150.21	85.6555	93.1396	66.5653	ENSG00000107223	EDF1
ENSG00000107242	0.566135	0.899655	0.69727	0.902688	ENSG00000107242	PIP5K1B
ENSG00000107249	0.920932	0.603315	1.89005	15.5474	ENSG00000107249	GLIS3
ENSG00000107262	32.4229	25.4278	33.8455	33.9496	ENSG00000107262	BAG1
ENSG00000107263	10.5338	18.4731	20.8228	17.8981	ENSG00000107263	RAPGEF1
ENSG00000107281	25.2816	28.4067	20.6738	10.1333	ENSG00000107281	NPDC1
ENSG00000107282	2.16403	6.19344	3.53304	14.773	ENSG00000107282	APBA1
ENSG00000107290	25.3941	32.2359	29.7489	36.9404	ENSG00000107290	SETX
ENSG00000107295	0.150924	0.189922	0.334973	0.30896	ENSG00000107295	SH3GL2
ENSG00000107317	0.885282	1.9894	2.29888	16.071	ENSG00000107317	PTGDS
ENSG00000107331	4.18469	6.33627	5.3224	11.824	ENSG00000107331	ABCA2
ENSG00000107338	12.6573	14.9296	16.7958	11.0457	ENSG00000107338	SHB
ENSG00000107341	17.2637	12.6892	13.1549	16.0181	ENSG00000107341	UBE2R2
ENSG00000107362	15.2242	8.18007	8.75939	9.28073	ENSG00000107362	ABHD17B
ENSG00000107371	20.7772	19.0469	22.7501	19.9836	ENSG00000107371	EXOSC3
ENSG00000107372	72.852	65.2167	63.6282	55.0442	ENSG00000107372	ZFAND5
ENSG00000107404	80.0267	92.9795	54.3792	46.85	ENSG00000107404	DVL1
ENSG00000107438	36.8078	46.9014	48.5154	31.4741	ENSG00000107438	PDLIM1
ENSG00000107443	3.39189	3.19966	4.48649	3.44857	ENSG00000107443	CCNJ
ENSG00000107447	0	0.0827392	0.0498654	0.0941944	ENSG00000107447	DNTT
ENSG00000107485	5.88157	3.93709	5.50672	4.11549	ENSG00000107485	GATA3
ENSG00000107518	1.63467	2.16845	2.18029	2.96321	ENSG00000107518	ATRNL1
ENSG00000107521	30.9487	30.1576	35.0446	26.6817	ENSG00000107521	HPS1
ENSG00000107537	9.89586	10.4628	10.5614	14.7931	ENSG00000107537	PHYH
ENSG00000107551	1.45403	4.41311	4.71551	12.3673	ENSG00000107551	RASSF4
ENSG00000107554	13.0747	18.7615	7.22608	18.0556	ENSG00000107554	DNMBP
ENSG00000107560	5.69277	11.4655	11.6883	10.0541	ENSG00000107560	RAB11FIP2
ENSG00000107562	0.356222	1.8081	0.860389	4.43525	ENSG00000107562	CXCL12
ENSG00000107566	11.8783	22.9831	18.4915	12.3121	ENSG00000107566	ERLIN1
ENSG00000107581	78.2788	68.8818	77.4209	78.5326	ENSG00000107581	EIF3A
ENSG00000107593	0.0194497	0.0937656	0.0426911	0	ENSG00000107593	PKD2L1
ENSG00000107611	0.25514	0.817603	0.511397	0.951973	ENSG00000107611	CUBN
ENSG00000107614	3.53713	5.64131	4.77849	6.16135	ENSG00000107614	TRDMT1
ENSG00000107618	0.0190393	0.0689638	0.0227986	0.0912868	ENSG00000107618	RBP3
ENSG00000107623	0.014048	0.0479073	0.0295439	0	ENSG00000107623	GDF10
ENSG00000107625	16.252	20.2546	17.8762	18.1355	ENSG00000107625	DDX50
ENSG00000107643	16.9027	22.6683	18.3678	22.6343	ENSG00000107643	MAPK8
ENSG00000107651	18.0174	21.1464	21.9351	22.7185	ENSG00000107651	SEC23IP
ENSG00000107669	42.3107	101.755	98.3031	111.358	ENSG00000107669	ATE1
ENSG00000107672	16.8269	32.324	25.5052	18.5314	ENSG00000107672	NSMCE4A
ENSG00000107679	36.9746	28.3422	31.0908	25.0916	ENSG00000107679	PLEKHA1

ENSG00000107719	0.502632	0.454344	0.874605	0.98533	ENSG00000107719	PALD1
ENSG00000107731	9.50479	13.6547	30.2096	8.81146	ENSG00000107731	UNC5B
ENSG00000107736	0.660655	0.860204	0.909371	1.39686	ENSG00000107736	CDH23
ENSG00000107738	38.5452	13.1708	8.75476	4.25003	ENSG00000107738	VSIR
ENSG00000107742	0.325016	0.616625	0.51577	0.744439	ENSG00000107742	SPOCK2
ENSG00000107745	25.583	38.0051	28.7118	44.2729	ENSG00000107745	MICU1
ENSG00000107758	11.0118	17.4912	17.591	25.0242	ENSG00000107758	PPP3CB
ENSG00000107771	19.6756	20.2881	21.185	23.1946	ENSG00000107771	CCSER2
ENSG00000107779	14.3172	15.5759	10.6478	10.9134	ENSG00000107779	BMPR1A
ENSG00000107789	12.3524	15.3848	10.0945	11.4801	ENSG00000107789	MINPP1
ENSG00000107796	10.9966	21.6134	22.5461	42.6249	ENSG00000107796	ACTA2
ENSG00000107798	37.7746	50.204	31.7742	27.5101	ENSG00000107798	LIPA
ENSG00000107807	0.209797	0.264864	0.590596	0.657788	ENSG00000107807	TLX1
ENSG00000107815	7.15556	4.7718	15.264	7.00109	ENSG00000107815	TWNK
ENSG00000107816	36.3567	29.5315	33.7007	24.0365	ENSG00000107816	LZTS2
ENSG00000107819	32.0123	40.5676	34.1696	29.8712	ENSG00000107819	SFXN3
ENSG00000107821	0.506649	1.13802	0.631363	0.843435	ENSG00000107821	KAZALD1
ENSG00000107829	9.71239	14.0305	15.0692	15.87	ENSG00000107829	FBXW4
ENSG00000107831	0.566171	0.726518	0.735	1.67355	ENSG00000107831	FGF8
ENSG00000107833	15.7907	32.5916	27.3954	12.9488	ENSG00000107833	NPM3
ENSG00000107854	16.6921	18.6468	21.3056	15.3703	ENSG00000107854	TNKS2
ENSG00000107859	0.0421259	0.0405711	0.132004	0.184319	ENSG00000107859	PITX3
ENSG00000107862	26.7457	27.4739	24.3636	30.3753	ENSG00000107862	GBF1
ENSG00000107863	57.9917	66.8961	58.0563	71.3162	ENSG00000107863	ARHGAP21
ENSG00000107864	1.8208	0.955766	1.54072	1.26147	ENSG00000107864	CPEB3
ENSG00000107872	6.16775	4.85526	3.67034	4.04492	ENSG00000107872	FBXL15
ENSG00000107874	15.3604	18.0137	17.3407	14.9615	ENSG00000107874	CUEDC2
ENSG00000107882	2.72902	2.99541	3.06428	4.9878	ENSG00000107882	SUFU
ENSG00000107890	14.0718	30.1153	28.5969	47.8535	ENSG00000107890	ANKRD26
ENSG00000107897	9.59306	8.22968	8.55104	7.70266	ENSG00000107897	ACBD5
ENSG00000107902	6.45284	9.51773	7.84218	8.92352	ENSG00000107902	LHPP
ENSG00000107929	47.7279	47.3801	51.172	53.2692	ENSG00000107929	LARP4B
ENSG00000107937	38.8511	35.3796	40.9184	33.7915	ENSG00000107937	GTPBP4
ENSG00000107938	15.1901	19.0358	23.8304	24.7693	ENSG00000107938	EDRF1
ENSG00000107949	20.6193	16.3777	17.8296	12.9876	ENSG00000107949	BCCIP
ENSG00000107951	13.7223	15.3245	16.4499	11.4968	ENSG00000107951	MTPAP
ENSG00000107954	3.763	4.16531	8.19382	29.1342	ENSG00000107954	NEURL1
ENSG00000107957	72.5672	86.1901	81.3803	99.0306	ENSG00000107957	SH3PXD2A
ENSG00000107959	41.2968	52.3108	46.2355	38.5723	ENSG00000107959	PITRM1
ENSG00000107960	19.6228	14.5896	12.1374	8.02518	ENSG00000107960	STN1
ENSG00000107968	9.11294	2.03493	2.12895	2.68497	ENSG00000107968	MAP3K8
ENSG00000107984	97.538	58.7052	1.68451	23.6231	ENSG00000107984	DKK1
ENSG00000108001	0.199928	0.3392	0.329169	0.711104	ENSG00000108001	EBF3
ENSG00000108010	70.7319	72.4741	85.2522	71.977	ENSG00000108010	GLRX3
ENSG00000108018	0.736959	0.292437	0.882118	0.968331	ENSG00000108018	SORCS1
ENSG00000108021	41.3339	50.5117	65.6527	57.9837	ENSG00000108021	FAM208B
ENSG00000108039	54.2123	57.8886	52.2692	49.1347	ENSG00000108039	XPNPEP1
ENSG00000108055	10.8622	17.0987	13.6482	16.6548	ENSG00000108055	SMC3
ENSG00000108061	19.1988	23.9482	23.3718	32.9189	ENSG00000108061	SHOC2
ENSG00000108064	11.6454	14.3033	16.255	10.6137	ENSG00000108064	TFAM
ENSG00000108091	12.94	12.9812	18.225	12.1446	ENSG00000108091	CCDC6
ENSG00000108094	22.3246	18.4313	14.7739	15.2594	ENSG00000108094	CUL2
ENSG00000108100	21.2752	27.0168	25.2107	23.8202	ENSG00000108100	CCNY
ENSG00000108106	27.46	95.4112	28.3872	63.6705	ENSG00000108106	UBE2S

ENSG00000108107	117.346	140.322	148.241	108.218	ENSG00000108107	RPL28
ENSG00000108175	9.76228	12.3122	18.9405	20.0338	ENSG00000108175	ZMIZ1
ENSG00000108176	0.632436	0.864935	1.56405	2.27858	ENSG00000108176	DNAJC12
ENSG00000108179	34.3531	33.2235	38.37	36.1846	ENSG00000108179	PPIF
ENSG00000108187	11.4558	11.4039	13.1301	13.1417	ENSG00000108187	PBLD
ENSG00000108219	134.301	92.8093	80.4424	77.6978	ENSG00000108219	TSPAN14
ENSG00000108231	0.541587	1.48309	1.04228	1.47542	ENSG00000108231	LGI1
ENSG00000108239	6.05575	5.61295	5.77777	6.31504	ENSG00000108239	TBC1D12
ENSG00000108242	0.0991795	0.448255	0.31843	0.400214	ENSG00000108242	CYP2C18
ENSG00000108244	22.7456	3.26158	5.62023	2.91007	ENSG00000108244	KRT23
ENSG00000108255	0.66568	0.954003	0.662035	1.53306	ENSG00000108255	CRYBA1
ENSG00000108256	41.023	32.5096	34.4423	24.9534	ENSG00000108256	NUFIP2
ENSG00000108262	19.2202	28.9942	30.8797	16.1447	ENSG00000108262	GIT1
ENSG00000108264	10.5815	21.6951	18.2776	27.7724	ENSG00000108264	TADA2A
ENSG00000108270	15.2921	19.135	20.0274	17.9635	ENSG00000108270	AATF
ENSG00000108272	8.5721	3.86839	4.63422	1.77124	ENSG00000108272	DHRS11
ENSG00000108278	19.3323	31.5992	29.0808	45.6408	ENSG00000108278	ZNHIT3
ENSG00000108292	29.2721	48.013	52.8158	57.5779	ENSG00000108292	MLLT6
ENSG00000108294	71.2751	56.2094	34.3465	35.4052	ENSG00000108294	PSMB3
ENSG00000108296	8.62224	9.30246	11.944	11.7866	ENSG00000108296	CWC25
ENSG00000108298	702.477	552.324	442.564	259.361	ENSG00000108298	RPL19
ENSG00000108306	9.90834	8.98689	9.60038	9.68496	ENSG00000108306	FBXL20
ENSG00000108309	2.97823	2.02102	2.84253	2.32739	ENSG00000108309	RUNDC3A
ENSG00000108312	32.2759	49.015	45.9277	48.4848	ENSG00000108312	UBTF
ENSG00000108342	1.12649	17.4146	7.98307	36.6683	ENSG00000108342	CSF3
ENSG00000108344	66.2279	53.7528	50.6597	34.599	ENSG00000108344	PSMD3
ENSG00000108349	15.4175	19.5736	25.1863	24.6578	ENSG00000108349	CASC3
ENSG00000108352	38.4949	27.5359	43.9704	12.4064	ENSG00000108352	RAPGEFL1
ENSG00000108370	0.578652	1.41853	0.545953	1.04701	ENSG00000108370	RGS9
ENSG00000108375	19.1774	12.9948	10.2275	8.67522	ENSG00000108375	RNF43
ENSG00000108379	1.13374	2.02088	2.01023	1.35831	ENSG00000108379	WNT3
ENSG00000108381	5.22288	11.6034	10.2033	17.7863	ENSG00000108381	ASPA
ENSG00000108384	5.70507	10.3995	11.842	8.04106	ENSG00000108384	RAD51C
ENSG00000108387	1.23191	2.45533	4.101	4.16704	ENSG00000108387	SEPT4
ENSG00000108389	16.0203	23.8467	13.801	21.2425	ENSG00000108389	MTMR4
ENSG00000108395	14.1729	19.2202	18.1657	19.6056	ENSG00000108395	TRIM37
ENSG00000108405	0.760954	1.03791	1.39571	0.935629	ENSG00000108405	P2RX1
ENSG00000108406	12.3298	12.2976	14.9629	12.3966	ENSG00000108406	DHX40
ENSG00000108417	0.414538	0.151937	0.120172	0.402665	ENSG00000108417	KRT37
ENSG00000108423	8.64835	15.702	12.7969	22.0661	ENSG00000108423	TUBD1
ENSG00000108424	127.335	143.756	146.186	125.65	ENSG00000108424	KPNB1
ENSG00000108433	31.7162	23.4099	32.6952	25.9116	ENSG00000108433	GOSR2
ENSG00000108439	19.1455	17.8128	25.2945	15.2183	ENSG00000108439	PNPO
ENSG00000108442	0	0.327687	0.295968	0.122545	ENSG00000108442	TVP23BP2
ENSG00000108443	25.3864	33.3997	37.3045	44.6758	ENSG00000108443	RPS6KB1
ENSG00000108448	26.6116	19.5057	21.6478	19.7566	ENSG00000108448	TRIM16L
ENSG00000108452	1.34202	6.02895	9.2597	3.66442	ENSG00000108452	ZNF29P
ENSG00000108465	51.8475	60.604	50.3495	56.4113	ENSG00000108465	CDK5RAP3
ENSG00000108468	17.3473	20.4405	21.6571	21.2935	ENSG00000108468	CBX1
ENSG00000108469	25.9367	38.2014	40.6829	24.5429	ENSG00000108469	RECQL5
ENSG00000108474	79.0124	131.227	138.807	168.531	ENSG00000108474	PIGL
ENSG00000108479	13.0472	16.0707	11.3801	15.7139	ENSG00000108479	GALK1
ENSG00000108506	9.53677	12.9098	11.4249	9.9129	ENSG00000108506	INTS2
ENSG00000108509	17.7913	30.7184	40.6995	42.4172	ENSG00000108509	CAMTA2

ENSG00000108510	30.2198	41.7469	40.7689	49.4896	ENSG00000108510	MED13
ENSG00000108511	1.05797	1.90149	3.88478	8.79869	ENSG00000108511	HOXB6
ENSG00000108515	16.9793	34.7079	20.6499	17.7953	ENSG00000108515	ENO3
ENSG00000108516	0	0	0	0	ENSG00000108516	AC003958.1
ENSG00000108518	411.201	530.43	322.342	250.732	ENSG00000108518	PFN1
ENSG00000108523	48.7808	52.7879	53.6615	36.2251	ENSG00000108523	RNF167
ENSG00000108528	19.6715	18.3036	14.4655	11.0781	ENSG00000108528	SLC25A11
ENSG00000108551	0.359652	0.226744	0.427184	1.01755	ENSG00000108551	RASD1
ENSG00000108556	1.56902	0.866808	1.2441	0.880399	ENSG00000108556	CHRNE
ENSG00000108557	15.7661	25.379	22.3983	33.4993	ENSG00000108557	RAI1
ENSG00000108559	39.9874	59.1706	52.0843	47.2566	ENSG00000108559	NUP88
ENSG00000108561	57.902	69.2931	52.0222	36.8325	ENSG00000108561	C1QBP
ENSG00000108576	0.637859	0.784826	1.15851	1.65242	ENSG00000108576	SLC6A4
ENSG00000108578	9.81193	30.1816	20.4335	33.3532	ENSG00000108578	BLMH
ENSG00000108582	34.3068	75.5702	58.2535	54.4152	ENSG00000108582	CPD
ENSG00000108587	20.831	24.0563	30.0923	35.3347	ENSG00000108587	GOSR1
ENSG00000108588	50.9091	52.5582	53.1233	42.175	ENSG00000108588	CCDC47
ENSG00000108590	21.5876	8.98872	16.2454	8.09716	ENSG00000108590	MED31
ENSG00000108591	27.0712	28.527	24.9301	19.2172	ENSG00000108591	DRG2
ENSG00000108592	19.9522	17.3866	21.3049	15.821	ENSG00000108592	FTSJ3
ENSG00000108599	17.8203	25.2454	27.1915	26.9823	ENSG00000108599	AKAP10
ENSG00000108602	1.32374	2.36408	1.38201	0.711388	ENSG00000108602	ALDH3A1
ENSG00000108604	61.6084	55.488	41.2397	30.098	ENSG00000108604	SMARCD2
ENSG00000108622	2.93491	7.30264	6.16485	11.1166	ENSG00000108622	ICAM2
ENSG00000108639	69.2779	33.4552	32.0035	9.43234	ENSG00000108639	SYNGR2
ENSG00000108641	7.84965	12.077	14.3734	9.35599	ENSG00000108641	B9D1
ENSG00000108651	40.4629	47.618	48.617	44.4062	ENSG00000108651	UTP6
ENSG00000108654	141.313	189.075	265.121	206.393	ENSG00000108654	DDX5
ENSG00000108666	13.8897	17.9699	17.2077	13.1507	ENSG00000108666	C17orf75
ENSG00000108669	23.7323	26.0344	34.1469	21.5926	ENSG00000108669	CYTH1
ENSG00000108671	41.4357	34.5403	34.6384	33.974	ENSG00000108671	PSMD11
ENSG00000108679	125.043	344.574	122.384	141.688	ENSG00000108679	LGALS3BP
ENSG00000108684	0.0789709	0.0609252	0.273222	0.56899	ENSG00000108684	ASIC2
ENSG00000108688	0	0	0	1.27466	ENSG00000108688	CCL7
ENSG00000108691	0.178429	0.0857193	0	49.2179	ENSG00000108691	CCL2
ENSG00000108700	0.0471007	0.136473	0.206101	0.104537	ENSG00000108700	CCL8
ENSG00000108702	0	0	0	0.12889	ENSG00000108702	CCL1
ENSG00000108733	2.68878	3.37819	4.69722	2.18336	ENSG00000108733	PEX12
ENSG00000108753	0.233667	0.578716	0.530446	0.618394	ENSG00000108753	HNF1B
ENSG00000108759	0.0979092	0.0314251	0	0	ENSG00000108759	KRT32
ENSG00000108771	5.34288	18.0183	13.2337	13.7318	ENSG00000108771	DHX58
ENSG00000108773	7.95674	14.4018	14.5177	12.8721	ENSG00000108773	KAT2A
ENSG00000108774	24.8847	19.3012	21.1003	21.9314	ENSG00000108774	RAB5C
ENSG00000108784	11.5128	20.4245	18.924	15.7356	ENSG00000108784	NAGLU
ENSG00000108785	0.523963	0.719653	1.23813	0.606022	ENSG00000108785	HSD17B1P1
ENSG00000108786	15.8208	16.8545	23.2185	11.6149	ENSG00000108786	HSD17B1
ENSG00000108788	17.9323	14.1805	14.037	15.5894	ENSG00000108788	MLX
ENSG00000108797	3.9937	12.2773	11.3579	24.975	ENSG00000108797	CNTNAP1
ENSG00000108798	0.220287	0.307722	0.382666	0.403495	ENSG00000108798	ABI3
ENSG00000108799	23.8425	39.5742	28.1571	41.6001	ENSG00000108799	EZH1
ENSG00000108813	0.113643	0.320363	0.532297	0.230771	ENSG00000108813	DLX4
ENSG00000108819	16.1686	22.3009	23.5794	24.4006	ENSG00000108819	PPP1R9B
ENSG00000108821	8.48304	19.2686	98.2457	3287.78	ENSG00000108821	COL1A1
ENSG00000108823	0.103005	0.580202	0.511158	0.718347	ENSG00000108823	SGCA

ENSG00000108825	0.197232	0	0.590487	0.179815	ENSG00000108825	PTGES3L-AARSD1
ENSG00000108826	24.8215	23.4618	20.2304	15.0067	ENSG00000108826	MRPL27
ENSG00000108828	67.8926	37.5712	38.3539	34.6682	ENSG00000108828	VAT1
ENSG00000108829	60.5809	43.1918	45.1489	34.7546	ENSG00000108829	LRRC59
ENSG00000108830	0.490061	1.03922	0.988096	1.77736	ENSG00000108830	RND2
ENSG00000108839	2.43004	3.97934	2.79071	2.92282	ENSG00000108839	ALOX12
ENSG00000108840	14.7176	14.171	10.3964	20.0987	ENSG00000108840	HDAC5
ENSG00000108846	21.7953	111.049	59.0348	61.2952	ENSG00000108846	ABCC3
ENSG00000108848	33.7253	81.829	67.4863	78.9373	ENSG00000108848	LUC7L3
ENSG00000108849	0	0.147353	0.257073	0.48346	ENSG00000108849	PPY
ENSG00000108852	0.34337	0.522529	0.637983	1.70705	ENSG00000108852	MPP2
ENSG00000108854	38.4465	50.3841	17.1627	92.1013	ENSG00000108854	SMURF2
ENSG00000108861	33.0673	28.4038	29.1375	36.8019	ENSG00000108861	DUSP3
ENSG00000108878	0.0941158	0.13593	0.12301	0.205673	ENSG00000108878	CACNG1
ENSG00000108883	60.7182	90.8972	72.4889	103.535	ENSG00000108883	EFTUD2
ENSG00000108924	0.28833	0.460915	0.781465	0.601623	ENSG00000108924	HLF
ENSG00000108932	0.736239	1.42103	0.775694	1.97886	ENSG00000108932	SLC16A6
ENSG00000108946	97.762	91.7796	92.7283	81.9924	ENSG00000108946	PRKAR1A
ENSG00000108947	0.730753	2.84599	1.64219	1.35272	ENSG00000108947	EFNB3
ENSG00000108950	1.40042	3.49852	2.93341	4.09184	ENSG00000108950	FAM20A
ENSG00000108953	136.963	101.703	97.7679	114.864	ENSG00000108953	YWHAE
ENSG00000108958	0.292494	0.487447	0.861029	2.25725	ENSG00000108958	AC130689.1
ENSG00000108960	3.93094	4.39321	4.22487	3.5616	ENSG00000108960	MMD
ENSG00000108961	4.37613	4.44998	5.78481	4.25782	ENSG00000108961	RANGRF
ENSG00000108963	18.7265	22.4352	24.8098	22.1941	ENSG00000108963	DPH1
ENSG00000108984	1.19155	2.726	1.98086	3.51751	ENSG00000108984	MAP2K6
ENSG00000109016	24.2669	25.83	19.7963	15.7878	ENSG00000109016	DHRS7B
ENSG00000109046	114.396	127.979	124.512	104.582	ENSG00000109046	WSB1
ENSG00000109047	0.683999	1.14955	1.68485	2.3295	ENSG00000109047	RCVRN
ENSG00000109061	0.00884227	0.0511806	0.0311649	0.326123	ENSG00000109061	MYH1
ENSG00000109062	19.9511	23.9132	10.7353	8.40971	ENSG00000109062	SLC9A3R1
ENSG00000109063	4.53307	10.4223	9.56013	18.9513	ENSG00000109063	MYH3
ENSG00000109065	41.1978	45.417	52.472	36.2967	ENSG00000109065	NAT9
ENSG00000109066	13.6201	11.1335	10.5751	8.00812	ENSG00000109066	TMEM104
ENSG00000109072	0.707657	0.848025	1.49823	1.08256	ENSG00000109072	VTN
ENSG00000109079	23.842	16.2692	18.5598	9.49109	ENSG00000109079	TNFAIP1
ENSG00000109083	8.01135	9.43236	11.6274	16.8596	ENSG00000109083	IFT20
ENSG00000109084	4.89421	7.94985	3.06178	7.80549	ENSG00000109084	TMEM97
ENSG00000109089	10.1553	4.03645	8.20089	7.78047	ENSG00000109089	CDR2L
ENSG00000109099	1.94982	1.2426	1.30532	11.1718	ENSG00000109099	PMP22
ENSG00000109101	0.208322	1.07805	1.83054	0.594803	ENSG00000109101	FOXN1
ENSG00000109103	22.9008	23.0971	19.1045	11.3597	ENSG00000109103	UNC119
ENSG00000109107	13.267	12.7754	3.99792	9.44479	ENSG00000109107	ALDOC
ENSG00000109111	26.7502	31.5552	43.46	42.8736	ENSG00000109111	SUPT6H
ENSG00000109113	38.8572	53.0568	40.608	37.8096	ENSG00000109113	RAB34
ENSG00000109118	12.9164	15.9565	19.4096	21.8498	ENSG00000109118	PHF12
ENSG00000109132	1.16721	0.262566	0.640335	0.900286	ENSG00000109132	PHOX2B
ENSG00000109133	76.1243	77.3807	71.8677	39.5191	ENSG00000109133	TMEM33
ENSG00000109158	0.461168	0.614665	0.370422	0.997407	ENSG00000109158	GABRA4
ENSG00000109163	1.20475	1.09738	0.794739	0.971092	ENSG00000109163	GNRHR
ENSG00000109171	28.5592	25.9411	29.0569	26.6867	ENSG00000109171	SLAIN2
ENSG00000109180	100.88	106.769	93.922	62.6861	ENSG00000109180	OCIAD1
ENSG00000109181	0	0	0	0	ENSG00000109181	UGT2B10
ENSG00000109182	101.901	35.557	58.8554	45.7991	ENSG00000109182	CWH43

ENSG00000109184	13.7853	36.0397	39.1857	35.4392	ENSG00000109184	DCUN1D4
ENSG00000109189	8.94445	8.36035	8.16853	9.67857	ENSG00000109189	USP46
ENSG00000109193	1.30847	3.3169	11.1395	3.42606	ENSG00000109193	SULT1E1
ENSG00000109205	0	0.111666	0.113753	0.140933	ENSG00000109205	ODAM
ENSG00000109208	0.410231	0.098518	0.533855	0.812621	ENSG00000109208	SMR3A
ENSG00000109220	25.6756	20.6594	17.0786	16.8997	ENSG00000109220	CHIC2
ENSG00000109255	2.24607	5.98258	0.453032	0.234523	ENSG00000109255	NMU
ENSG00000109265	0.284729	0.182417	0.343908	1.41096	ENSG00000109265	KIAA1211
ENSG00000109270	26.9671	9.53601	15.227	9.22045	ENSG00000109270	LAMTOR3
ENSG00000109272	0	0	0	0	ENSG00000109272	PF4V1
ENSG00000109320	18.0928	33.5003	32.9979	31.3424	ENSG00000109320	NFKB1
ENSG00000109321	980.172	1036.57	489.993	246.878	ENSG00000109321	AREG
ENSG00000109323	9.39835	15.6114	20.6481	15.9412	ENSG00000109323	MANBA
ENSG00000109332	179.655	137.838	106.789	129.527	ENSG00000109332	UBE2D3
ENSG00000109339	17.6389	29.9141	23.4041	29.4047	ENSG00000109339	MAPK10
ENSG00000109381	16.6394	23.5416	17.8534	25.492	ENSG00000109381	ELF2
ENSG00000109390	36.722	34.986	26.6192	18.2394	ENSG00000109390	NDUFC1
ENSG00000109424	0.119485	0.116718	0.24748	0.130767	ENSG00000109424	UCP1
ENSG00000109436	8.69157	13.0001	12.5196	13.3184	ENSG00000109436	TBC1D9
ENSG00000109445	18.5665	25.1949	29.4882	17.5523	ENSG00000109445	ZNF330
ENSG00000109452	137.55	71.3546	32.3758	74.8481	ENSG00000109452	INPP4B
ENSG00000109458	22.2575	24.1721	23.4344	30.6986	ENSG00000109458	GAB1
ENSG00000109466	17.7032	18.1275	13.8012	15.4013	ENSG00000109466	KLHL2
ENSG00000109471	0	0.057425	0	0	ENSG00000109471	IL2
ENSG00000109472	11.6429	3.94995	12.9691	23.6248	ENSG00000109472	CPE
ENSG00000109475	426.2	365.357	258.264	199.397	ENSG00000109475	RPL34
ENSG00000109501	12.7111	12.6052	12.4519	12.2324	ENSG00000109501	WFS1
ENSG00000109511	0.0412544	1.85618	0.667437	1.3587	ENSG00000109511	ANXA10
ENSG00000109519	25.7721	17.0567	20.2141	10.7272	ENSG00000109519	GRPEL1
ENSG00000109534	6.22937	4.0666	5.25365	3.86118	ENSG00000109534	GAR1
ENSG00000109536	12.1828	20.4479	17.3609	15.2594	ENSG00000109536	FRG1
ENSG00000109572	39.1887	31.361	26.0038	30.1283	ENSG00000109572	CLCN3
ENSG00000109576	2.32503	2.72318	3.58038	6.43938	ENSG00000109576	AADAT
ENSG00000109586	15.9029	25.4813	20.538	15.7988	ENSG00000109586	GALNT7
ENSG00000109606	97.321	116.731	88.5759	96.2298	ENSG00000109606	DHX15
ENSG00000109610	0.190418	0.460724	0.286462	1.20535	ENSG00000109610	SOD3
ENSG00000109618	6.83611	13.1554	11.8859	11.4142	ENSG00000109618	SEPSECS
ENSG00000109625	1.33749	2.27787	0.898783	2.8076	ENSG00000109625	CPZ
ENSG00000109654	16.6962	7.21237	6.76907	9.45154	ENSG00000109654	TRIM2
ENSG00000109667	27.1499	55.554	81.4589	33.3155	ENSG00000109667	SLC2A9
ENSG00000109670	30.2076	34.2882	31.3184	27.6891	ENSG00000109670	FBXW7
ENSG00000109674	1.56232	7.92027	1.33939	4.47246	ENSG00000109674	NEIL3
ENSG00000109680	7.46937	14.9097	11.91	17.5227	ENSG00000109680	TBC1D19
ENSG00000109684	2.3418	3.81445	3.62277	5.71446	ENSG00000109684	CLNK
ENSG00000109685	19.3072	74.2844	26.5824	65.7197	ENSG00000109685	NSD2
ENSG00000109686	28.8062	31.7642	33.6352	33.4909	ENSG00000109686	SH3D19
ENSG00000109689	15.8277	37.866	35.9267	18.9847	ENSG00000109689	STIM2
ENSG00000109705	0.196792	0.15323	0.258311	0.108484	ENSG00000109705	NKX3-2
ENSG00000109736	104.735	131.715	93.4073	66.4801	ENSG00000109736	MFSD10
ENSG00000109738	0.681879	1.14469	0.621107	1.21023	ENSG00000109738	GLRB
ENSG00000109743	3.98708	7.99231	7.7883	14.4594	ENSG00000109743	BST1
ENSG00000109756	52.9826	43.7826	37.0147	50.865	ENSG00000109756	RAPGEF2
ENSG00000109758	0.364431	0.209454	0.248165	0.347685	ENSG00000109758	HGFAC
ENSG00000109762	12.3866	9.86148	7.35575	11.953	ENSG00000109762	SNX25

ENSG00000109771	1.43876	2.53535	2.41529	3.75782	ENSG00000109771	LRP2BP
ENSG00000109775	11.5845	13.012	12.2389	7.57424	ENSG00000109775	UFSP2
ENSG00000109787	37.1719	31.0714	39.673	28.9079	ENSG00000109787	KLF3
ENSG00000109790	12.6895	25.9115	23.7299	26.7089	ENSG00000109790	KLHL5
ENSG00000109794	3.32891	5.54394	4.03014	7.4067	ENSG00000109794	FAM149A
ENSG00000109805	4.51562	36.3317	4.19208	14.59	ENSG00000109805	NCAPG
ENSG00000109814	10.5953	16.097	20.8668	20.7951	ENSG00000109814	UGDH
ENSG00000109819	1.08979	0.898642	1.93882	1.53336	ENSG00000109819	PPARGC1A
ENSG00000109832	0.276069	1.20151	0.98494	2.4132	ENSG00000109832	DDX25
ENSG00000109846	18.4616	3.01475	5.31211	6.6403	ENSG00000109846	CRYAB
ENSG00000109851	0.0850115	0.163745	0.0826214	0.0572254	ENSG00000109851	DBX1
ENSG00000109854	14.2683	10.063	9.76582	6.68501	ENSG00000109854	HTATIP2
ENSG00000109861	778.57	329.712	259.899	176.466	ENSG00000109861	CTSC
ENSG00000109881	2.2274	4.35257	4.15477	7.46902	ENSG00000109881	CCDC34
ENSG00000109906	2.70213	3.37731	10.8443	11.1626	ENSG00000109906	ZBTB16
ENSG00000109911	6.27752	9.97906	7.21807	7.01215	ENSG00000109911	ELP4
ENSG00000109917	34.7488	33.9622	26.8936	19.159	ENSG00000109917	ZPR1
ENSG00000109919	45.2567	43.5971	41.8396	25.7237	ENSG00000109919	MTCH2
ENSG00000109920	61.9285	90.0611	102.28	103.838	ENSG00000109920	FNBP4
ENSG00000109927	0.180838	0.182388	0.756199	0.253681	ENSG00000109927	TECTA
ENSG00000109929	63.8129	54.7669	28.051	27.3966	ENSG00000109929	SC5D
ENSG00000109943	2.96853	1.9771	1.51163	3.67683	ENSG00000109943	CRTAM
ENSG00000109944	3.13818	4.39924	4.8248	5.01049	ENSG00000109944	C11orf63
ENSG00000109956	1.0821	2.23176	2.13594	3.67568	ENSG00000109956	B3GAT1
ENSG00000109971	1145.7	414.308	327.403	416.38	ENSG00000109971	HSPA8
ENSG00000109991	1.64908	2.61734	3.7496	5.90308	ENSG00000109991	P2RX3
ENSG00000110002	20.5526	16.8669	8.19371	5.19455	ENSG00000110002	VWA5A
ENSG00000110011	8.70006	10.6439	12.9016	9.70314	ENSG00000110011	DNAJC4
ENSG00000110013	8.04283	17.348	12.685	12.2745	ENSG00000110013	SIAE
ENSG00000110025	6.49573	6.44817	8.63333	5.32415	ENSG00000110025	SNX15
ENSG00000110031	4.63901	4.5145	7.30556	11.0824	ENSG00000110031	LPXN
ENSG00000110042	9.3884	4.40228	5.47558	6.1386	ENSG00000110042	DTX4
ENSG00000110046	16.8029	15.7664	17.9328	21.9955	ENSG00000110046	ATG2A
ENSG00000110047	70.9425	47.0361	16.3451	37.2308	ENSG00000110047	EHD1
ENSG00000110048	15.1334	22.6253	20.6857	18.6329	ENSG00000110048	OSBP
ENSG00000110057	11.6295	19.9226	13.273	11.5313	ENSG00000110057	UNC93B1
ENSG00000110060	8.14252	9.63617	10.972	7.96086	ENSG00000110060	PUS3
ENSG00000110063	5.4523	5.55006	5.18936	6.11992	ENSG00000110063	DCPS
ENSG00000110066	13.9821	22.079	21.428	26.7599	ENSG00000110066	KMT5B
ENSG00000110074	10.6547	23.3757	18.3957	24.4463	ENSG00000110074	FOXRED1
ENSG00000110075	63.1427	76.5589	65.4344	77.0969	ENSG00000110075	PPP6R3
ENSG00000110076	0.495067	0.597348	0.920777	11.5844	ENSG00000110076	NRXN2
ENSG00000110077	2.35209	4.53027	3.93569	6.04837	ENSG00000110077	MS4A6A
ENSG00000110079	0.146382	0.243523	0.289971	0.456637	ENSG00000110079	MS4A4A
ENSG00000110080	12.0934	17.6854	7.24054	22.7602	ENSG00000110080	ST3GAL4
ENSG00000110090	14.2377	29.595	19.1285	21.097	ENSG00000110090	CPT1A
ENSG00000110092	143.803	57.4792	73.4136	163.411	ENSG00000110092	CCND1
ENSG00000110104	7.77046	4.79907	9.67324	7.32282	ENSG00000110104	CCDC86
ENSG00000110107	15.7632	18.3909	24.0362	18.7231	ENSG00000110107	PRPF19
ENSG00000110108	35.9981	26.1031	7.65558	15.3313	ENSG00000110108	TMEM109
ENSG00000110148	0	0.0317436	0.0286957	0	ENSG00000110148	CCKBR
ENSG00000110169	4.45662	3.24223	5.45451	3.73194	ENSG00000110169	HPX
ENSG00000110171	10.2223	12.5228	12.6758	14.5005	ENSG00000110171	TRIM3
ENSG00000110172	17.9395	17.9953	23.5603	26.4847	ENSG00000110172	CHORDC1

ENSG00000110195	0.132854	0.216876	0.380558	0.143388	ENSG00000110195	FOLR1
ENSG00000110200	17.6169	26.1993	17.1966	26.5957	ENSG00000110200	ANAPC15
ENSG00000110203	16.77	17.4902	15.1351	11.8276	ENSG00000110203	FOLR3
ENSG00000110218	36.9427	37.3795	30.6204	25.4214	ENSG00000110218	PANX1
ENSG00000110237	7.04228	9.51253	17.2707	24.6581	ENSG00000110237	ARHGEF17
ENSG00000110243	0.0597061	0.0287689	0.0780222	0.151302	ENSG00000110243	APOA5
ENSG00000110244	0.197926	0.114387	0.206794	0.173301	ENSG00000110244	APOA4
ENSG00000110245	0	0	0	0	ENSG00000110245	APOC3
ENSG00000110274	16.7367	38.8291	54.5666	29.0333	ENSG00000110274	CEP164
ENSG00000110315	36.9152	23.0943	26.3429	14.8447	ENSG00000110315	RNF141
ENSG00000110318	0.862431	2.20741	2.28598	3.80111	ENSG00000110318	CEP126
ENSG00000110321	330.15	246.988	304.25	171.128	ENSG00000110321	EIF4G2
ENSG00000110324	0.856164	1.80927	1.02952	2.19525	ENSG00000110324	IL10RA
ENSG00000110328	17.3841	28.5002	21.9802	13.2472	ENSG00000110328	GALNT18
ENSG00000110330	32.3439	36.4501	31.6208	27.9422	ENSG00000110330	BIRC2
ENSG00000110344	13.5031	12.8116	9.88327	7.05416	ENSG00000110344	UBE4A
ENSG00000110367	30.1833	26.2826	22.7935	31.8829	ENSG00000110367	DDX6
ENSG00000110375	2.02624	1.01515	1.79551	1.63462	ENSG00000110375	UPK2
ENSG00000110395	7.18991	10.826	8.82981	10.0209	ENSG00000110395	CBL
ENSG00000110400	72.8724	129.445	129.865	46.3687	ENSG00000110400	NECTIN1
ENSG00000110422	34.3178	29.7934	32.677	26.0305	ENSG00000110422	HIPK3
ENSG00000110427	12.0581	12.8538	3.91914	12.5164	ENSG00000110427	KIAA1549L
ENSG00000110429	41.1665	22.2712	17.8081	18.8397	ENSG00000110429	FBXO3
ENSG00000110435	23.4719	25.4472	28.7682	35.2124	ENSG00000110435	PDHX
ENSG00000110436	0.268585	0.386822	0.367635	0.553897	ENSG00000110436	SLC1A2
ENSG00000110442	17.6117	10.2953	12.1644	10.0215	ENSG00000110442	COMMD9
ENSG00000110446	0.748124	2.8594	4.00987	6.08621	ENSG00000110446	SLC15A3
ENSG00000110448	0.169397	0.392042	0.458833	0.652291	ENSG00000110448	CD5
ENSG00000110455	8.70488	14.0022	15.1954	19.6168	ENSG00000110455	ACCS
ENSG00000110484	1.97977	2.83533	2.19763	3.20812	ENSG00000110484	SCGB2A2
ENSG00000110492	22.2254	18.1595	12.2614	14.8618	ENSG00000110492	MDK
ENSG00000110497	20.8812	23.5593	18.9601	23.5895	ENSG00000110497	AMBRA1
ENSG00000110514	9.97191	18.0942	16.311	19.0991	ENSG00000110514	MADD
ENSG00000110536	47.7191	31.1342	22.8596	10.2029	ENSG00000110536	PTPMT1
ENSG00000110583	10.9508	15.9046	13.5427	13.013	ENSG00000110583	NAA40
ENSG00000110619	25.6391	77.4507	69.3676	45.7959	ENSG00000110619	CARS
ENSG00000110628	15.1184	50.1375	27.983	17.2311	ENSG00000110628	SLC22A18
ENSG00000110651	176.81	236.796	145.675	157.77	ENSG00000110651	CD81
ENSG00000110660	47.1784	55.1671	29.8162	14.2938	ENSG00000110660	SLC35F2
ENSG00000110665	1.23529	2.60224	1.97644	4.33407	ENSG00000110665	C11orf21
ENSG00000110675	2.03838	2.07915	2.26865	3.48446	ENSG00000110675	ELMOD1
ENSG00000110680	0.121156	0.106168	0.08	0.208871	ENSG00000110680	CALCA
ENSG00000110693	6.59871	6.78719	9.77251	7.14405	ENSG00000110693	SOX6
ENSG00000110696	65.1001	52.5227	82.2292	70.783	ENSG00000110696	C11orf58
ENSG00000110697	29.3337	39.0454	36.1142	36.7072	ENSG00000110697	PITPNM1
ENSG00000110700	328.251	288.546	247.301	167.675	ENSG00000110700	RPS13
ENSG00000110711	12.2064	14.5682	8.83933	11.6588	ENSG00000110711	AIP
ENSG00000110713	53.7137	64.4155	63.9495	73.7817	ENSG00000110713	NUP98
ENSG00000110717	68.5938	56.0826	52.1925	42.5102	ENSG00000110717	NDUFS8
ENSG00000110719	65.6222	99.1694	45.6402	66.1358	ENSG00000110719	TCIRG1
ENSG00000110721	5.25634	4.53867	6.02402	9.59261	ENSG00000110721	CHKA
ENSG00000110723	9.1559	19.949	16.3824	6.05775	ENSG00000110723	EXPH5
ENSG00000110756	23.8288	17.1118	24.7259	25.2289	ENSG00000110756	HPS5
ENSG00000110768	28.5938	23.4906	35.7069	19.808	ENSG00000110768	GTF2H1

ENSG00000110777	3.1129	5.10347	4.71053	8.12915	ENSG00000110777	POU2AF1
ENSG00000110786	1.03961	1.56754	1.38155	2.03009	ENSG00000110786	PTPN5
ENSG00000110799	0.344263	0.485707	0.355833	0.456195	ENSG00000110799	VWF
ENSG00000110801	43.4098	45.7475	40.1243	49.236	ENSG00000110801	PSMD9
ENSG00000110811	3.08693	8.15854	4.57589	17.4918	ENSG00000110811	P3H3
ENSG00000110841	45.2541	73.2244	45.1432	102.363	ENSG00000110841	PPFIBP1
ENSG00000110844	7.55933	23.958	24.648	17.8784	ENSG00000110844	PRPF40B
ENSG00000110848	0.068411	0.860375	0.251461	0.867299	ENSG00000110848	CD69
ENSG00000110851	18.977	23.4599	21.7291	14.9044	ENSG00000110851	PRDM4
ENSG00000110852	5.07532	2.5714	1.30925	4.8016	ENSG00000110852	CLEC2B
ENSG00000110871	14.7281	26.9718	23.0954	32.116	ENSG00000110871	COQ5
ENSG00000110876	1.6521	1.15957	1.86436	2.49605	ENSG00000110876	SELPLG
ENSG00000110880	59.3556	55.0852	43.3506	89.3405	ENSG00000110880	CORO1C
ENSG00000110881	1.76818	4.16824	4.06861	4.30027	ENSG00000110881	ASIC1
ENSG00000110887	0.275455	0.374357	0.391042	0.505486	ENSG00000110887	DAO
ENSG00000110888	16.5777	37.9705	20.2109	36.4119	ENSG00000110888	CAPRIN2
ENSG00000110900	0.803944	2.36753	1.25134	2.19092	ENSG00000110900	TSPAN11
ENSG00000110906	20.4423	18.2317	21.8454	25.8301	ENSG00000110906	KCTD10
ENSG00000110911	42.3179	54.1295	51.8568	82.9557	ENSG00000110911	SLC11A2
ENSG00000110917	55.8578	53.3478	30.3799	35.0876	ENSG00000110917	MLEC
ENSG00000110921	26.7715	17.8981	10.0773	12.385	ENSG00000110921	MVK
ENSG00000110925	12.0387	10.4607	23.5167	14.5674	ENSG00000110925	CSRNP2
ENSG00000110931	7.77432	11.265	15.5938	12.0075	ENSG00000110931	CAMKK2
ENSG00000110934	1.62943	5.1489	4.84517	7.6944	ENSG00000110934	BIN2
ENSG00000110944	2.77404	5.15469	1.4491	1.6679	ENSG00000110944	IL23A
ENSG00000110955	174.046	164.727	158.512	104.477	ENSG00000110955	ATP5B
ENSG00000110958	42.377	38.2066	38.2103	40.9821	ENSG00000110958	PTGES3
ENSG00000110975	0.375818	0.469414	0.795742	1.01696	ENSG00000110975	SYT10
ENSG00000110987	9.83908	13.5742	14.814	16.3326	ENSG00000110987	BCL7A
ENSG00000111011	48.6752	59.0552	52.8084	57.6539	ENSG00000111011	RSRC2
ENSG00000111012	6.41432	23.8245	7.05012	15.4587	ENSG00000111012	CYP27B1
ENSG00000111046	0	0	0	0	ENSG00000111046	MYF6
ENSG00000111049	0.0784304	0.149923	0.133423	0.453002	ENSG00000111049	MYF5
ENSG00000111052	0.804065	2.18593	3.94697	3.32066	ENSG00000111052	LIN7A
ENSG00000111057	88.2275	180.242	37.8838	33.9938	ENSG00000111057	KRT18
ENSG00000111058	1.06848	1.44164	1.29438	2.46007	ENSG00000111058	ACSS3
ENSG00000111077	8.12955	19.3946	12.9223	32.7111	ENSG00000111077	TNS2
ENSG00000111087	0.280882	2.49885	5.54828	1.20721	ENSG00000111087	GLI1
ENSG00000111110	0.73243	0.225152	0.633269	0.84568	ENSG00000111110	PPM1H
ENSG00000111142	40.5251	47.2026	44.4973	51.5221	ENSG00000111142	METAP2
ENSG00000111144	75.7884	50.6424	35.0438	34.9408	ENSG00000111144	LTA4H
ENSG00000111145	55.7371	42.3877	13.951	61.9024	ENSG00000111145	ELK3
ENSG00000111181	1.46845	1.89328	1.37765	2.05511	ENSG00000111181	SLC6A12
ENSG00000111186	21.1098	24.6124	4.66641	58.4984	ENSG00000111186	WNT5B
ENSG00000111196	9.87221	12.8668	11.8162	10.0704	ENSG00000111196	MAGOHB
ENSG00000111199	0.539955	0.893573	1.37787	1.92673	ENSG00000111199	TRPV4
ENSG00000111203	13.2989	16.5368	19.2789	18.7582	ENSG00000111203	ITFG2
ENSG00000111206	4.96802	14.6978	6.11535	14.6561	ENSG00000111206	FOXM1
ENSG00000111215	1.73473	11.9529	7.87543	21.2434	ENSG00000111215	PRR4
ENSG00000111218	0.899074	0.504544	3.45621	1.56747	ENSG00000111218	PRMT8
ENSG00000111224	2.58444	4.19188	4.52521	7.45901	ENSG00000111224	PARP11
ENSG00000111229	183.471	107.019	87.6417	86.1931	ENSG00000111229	ARPC3
ENSG00000111231	9.68746	9.50196	6.43964	9.67462	ENSG00000111231	GPN3
ENSG00000111237	56.9647	47.1398	52.3865	42.494	ENSG00000111237	VPS29

ENSG00000111241	0	0	0.494518	0.602491	ENSG00000111241	FGF6
ENSG00000111245	0	0.742945	0.513659	0.651683	ENSG00000111245	MYL2
ENSG00000111247	3.426	12.3167	3.40237	7.71455	ENSG00000111247	RAD51AP1
ENSG00000111249	0.101067	0.120886	0.203517	0.275827	ENSG00000111249	CUX2
ENSG00000111252	4.5842	13.1539	10.1946	20.4453	ENSG00000111252	SH2B3
ENSG00000111254	1.32897	2.03938	2.2096	0.143375	ENSG00000111254	AKAP3
ENSG00000111261	7.08617	4.9568	3.65973	3.67352	ENSG00000111261	MANSC1
ENSG00000111262	0.142334	0.226869	0.663455	0.201136	ENSG00000111262	KCNA1
ENSG00000111266	17.5728	10.7	18.612	10.1485	ENSG00000111266	DUSP16
ENSG00000111269	6.22624	4.78902	5.92517	4.17132	ENSG00000111269	CREBL2
ENSG00000111271	15.7262	27.3852	26.7367	24.2234	ENSG00000111271	ACAD10
ENSG00000111275	3.29382	17.9728	22.1073	5.11405	ENSG00000111275	ALDH2
ENSG00000111276	12.5272	10.7629	7.52287	5.93669	ENSG00000111276	CDKN1B
ENSG00000111291	2.52055	1.35673	1.0963	2.24518	ENSG00000111291	GPRC5D
ENSG00000111300	26.3515	26.2784	28.7435	32.8827	ENSG00000111300	NAA25
ENSG00000111305	2.59402	6.07344	4.26274	7.17607	ENSG00000111305	GSG1
ENSG00000111319	72.1453	78.5888	19.4843	34.812	ENSG00000111319	SCNN1A
ENSG00000111321	154.922	176.234	139.539	129.396	ENSG00000111321	LTBR
ENSG00000111325	15.3138	22.3107	21.5258	14.6227	ENSG00000111325	OGFOD2
ENSG00000111328	51.4252	37.8104	37.0218	32.9167	ENSG00000111328	CDK2AP1
ENSG00000111331	13.1883	43.6312	25.6873	28.0536	ENSG00000111331	OAS3
ENSG00000111335	17.7516	60.3787	16.0118	26.7589	ENSG00000111335	OAS2
ENSG00000111339	0.760948	0.713497	0.512307	0.895988	ENSG00000111339	ART4
ENSG00000111341	1.91573	4.22332	4.15679	5.70671	ENSG00000111341	MGP
ENSG00000111344	1.91722	1.73454	1.61782	1.92194	ENSG00000111344	RASAL1
ENSG00000111348	14.732	20.1787	2.81262	9.39195	ENSG00000111348	ARHGDIB
ENSG00000111358	20.0581	20.0436	32.7157	17.491	ENSG00000111358	GTF2H3
ENSG00000111361	17.9833	13.8677	20.2744	14.0378	ENSG00000111361	EIF2B1
ENSG00000111364	19.3712	25.9908	29.822	26.7723	ENSG00000111364	DDX55
ENSG00000111371	84.7917	191.067	168.181	58.6428	ENSG00000111371	SLC38A1
ENSG00000111404	0.0907582	0.348853	0.599311	0.722491	ENSG00000111404	RERGL
ENSG00000111405	0.551685	0.812226	0.696208	0.936528	ENSG00000111405	ENDOU
ENSG00000111412	17.2626	10.1036	8.09619	6.99521	ENSG00000111412	C12orf49
ENSG00000111424	13.2069	15.8582	13.7428	10.8964	ENSG00000111424	VDR
ENSG00000111432	1.69644	1.29368	0.684836	0.634143	ENSG00000111432	FZD10
ENSG00000111445	14.7483	24.9235	13.6126	23.7083	ENSG00000111445	RFC5
ENSG00000111450	14.5205	23.1565	9.13515	19.1318	ENSG00000111450	STX2
ENSG00000111452	0.766488	1.64799	1.68832	2.70712	ENSG00000111452	ADGRD1
ENSG00000111481	51.5883	35.1767	35.4105	28.568	ENSG00000111481	COPZ1
ENSG00000111490	6.64992	12.067	12.8475	19.5595	ENSG00000111490	TBC1D30
ENSG00000111530	81.0002	81.0134	71.2602	69.0991	ENSG00000111530	CAND1
ENSG00000111536	0.113354	0.109206	0.0530941	0.0635074	ENSG00000111536	IL26
ENSG00000111537	0.0490153	0.14157	0.0853045	0.0535335	ENSG00000111537	IFNG
ENSG00000111540	56.3443	40.1518	38.4359	50.4638	ENSG00000111540	RAB5B
ENSG00000111554	8.92453	13.1842	11.4708	11.4763	ENSG00000111554	MDM1
ENSG00000111581	25.0463	47.2151	23.7296	27.957	ENSG00000111581	NUP107
ENSG00000111596	63.9219	93.1586	85.0354	103.965	ENSG00000111596	CNOT2
ENSG00000111602	1.84577	5.98841	3.08489	5.2911	ENSG00000111602	TIMELESS
ENSG00000111605	30.2189	39.3756	34.0016	45.5654	ENSG00000111605	CPSF6
ENSG00000111615	29.5423	32.0992	29.5349	22.0912	ENSG00000111615	KRR1
ENSG00000111639	57.3867	42.8009	31.1017	30.8688	ENSG00000111639	MRPL51
ENSG00000111640	1215.73	1321.63	635.334	531.304	ENSG00000111640	GAPDH
ENSG00000111641	39.4361	41.9441	43.7306	42.4519	ENSG00000111641	NOP2
ENSG00000111642	70.812	92.8867	97.5473	98.5672	ENSG00000111642	CHD4

ENSG00000111644	0.387162	0.334046	0.99637	0.316495	ENSG00000111644	ACRBP
ENSG00000111647	9.94169	10.9946	9.3844	14.7667	ENSG00000111647	UHRF1BP1L
ENSG00000111652	28.8237	26.9554	23.1344	22.4609	ENSG00000111652	COPS7A
ENSG00000111653	14.0532	12.7646	14.6293	9.10875	ENSG00000111653	ING4
ENSG00000111664	0.4579	1.02511	1.5768	2.27283	ENSG00000111664	GNB3
ENSG00000111665	3.3447	13.6975	3.83343	7.31988	ENSG00000111665	CDCA3
ENSG00000111666	9.20017	21.9956	10.7315	25.8648	ENSG00000111666	CHPT1
ENSG00000111667	21.5686	18.03	17.7095	15.3011	ENSG00000111667	USP5
ENSG00000111669	142.848	117.095	79.5247	75.1267	ENSG00000111669	TPI1
ENSG00000111670	21.2981	30.106	24.8455	28.9578	ENSG00000111670	GNPTAB
ENSG00000111671	4.2073	4.89946	4.82358	2.79618	ENSG00000111671	SPSB2
ENSG00000111674	1.53277	2.05405	1.22862	8.47759	ENSG00000111674	ENO2
ENSG00000111676	3.3068	6.27533	6.05689	10.979	ENSG00000111676	ATN1
ENSG00000111678	8.07904	17.7375	12.5828	12.0531	ENSG00000111678	C12orf57
ENSG00000111679	4.53221	6.3694	4.0226	2.96146	ENSG00000111679	PTPN6
ENSG00000111684	13.1502	26.3354	22.9278	13.4304	ENSG00000111684	LPCAT3
ENSG00000111696	17.65	19.023	17.2021	26.9325	ENSG00000111696	NT5DC3
ENSG00000111700	0.450635	1.14402	0.925292	1.47275	ENSG00000111700	SLCO1B3
ENSG00000111701	0	0	0	0.160642	ENSG00000111701	APOBEC1
ENSG00000111704	0.759844	2.12294	2.00976	3.74344	ENSG00000111704	NANOG
ENSG00000111707	20.1216	36.4955	28.178	31.5903	ENSG00000111707	SUDS3
ENSG00000111711	35.5169	37.2622	26.789	25.715	ENSG00000111711	GOLT1B
ENSG00000111713	0.122129	0.0672954	0.106476	0.0576153	ENSG00000111713	GYS2
ENSG00000111716	140.074	178.984	100.342	124.709	ENSG00000111716	LDHB
ENSG00000111725	21.9217	33.0389	35.48	32.4353	ENSG00000111725	PRKAB1
ENSG00000111726	24.656	23.4329	19.4052	15.9366	ENSG00000111726	CMAS
ENSG00000111727	8.37468	8.56907	11.568	9.79312	ENSG00000111727	HCFC2
ENSG00000111728	10.3734	36.9941	27.966	34.7979	ENSG00000111728	ST8SIA1
ENSG00000111729	0.964189	0.901798	1.62995	1.86906	ENSG00000111729	CLEC4A
ENSG00000111731	7.509	19.1207	16.9507	27.7178	ENSG00000111731	C2CD5
ENSG00000111732	0.77749	1.97665	1.77308	2.45623	ENSG00000111732	AICDA
ENSG00000111737	17.0442	15.6049	19.8442	12.9712	ENSG00000111737	RAB35
ENSG00000111752	4.90841	10.0062	6.65522	9.80812	ENSG00000111752	PHC1
ENSG00000111775	318.252	357.568	162.911	153.341	ENSG00000111775	COX6A1
ENSG00000111780	0.363362	0.226015	0	0	ENSG00000111780	AL021546.1
ENSG00000111783	5.36384	9.96901	7.50462	14.613	ENSG00000111783	RFX4
ENSG00000111785	4.737	9.85126	6.72808	9.60911	ENSG00000111785	RIC8B
ENSG00000111786	72.1076	72.5137	69.8366	52.126	ENSG00000111786	SRSF9
ENSG00000111788	2.55167	4.97497	1.30957	5.58155	ENSG00000111788	RP11-22B23.1
ENSG00000111790	15.6923	19.7233	17.7251	20.7998	ENSG00000111790	FGFR1OP2
ENSG00000111796	0.121175	1.15136	0.634158	0.661885	ENSG00000111796	KLRB1
ENSG00000111799	39.8037	100.482	94.4666	151.697	ENSG00000111799	COL12A1
ENSG00000111801	1.93132	5.67211	6.62323	6.57038	ENSG00000111801	BTN3A3
ENSG00000111802	8.76351	9.55879	14.1324	9.97929	ENSG00000111802	TDP2
ENSG00000111816	14.1729	27.308	26.6597	55.1125	ENSG00000111816	FRK
ENSG00000111817	76.283	95.9959	90.5346	55.2415	ENSG00000111817	DSE
ENSG00000111832	19.5253	18.0836	13.3519	14.4869	ENSG00000111832	RWDD1
ENSG00000111834	0.252941	0.321428	0.609513	0.689846	ENSG00000111834	RSPH4A
ENSG00000111837	0.412708	1.29795	1.53591	3.48006	ENSG00000111837	MAK
ENSG00000111843	46.5929	49.2789	34.2618	30.7409	ENSG00000111843	TMEM14C
ENSG00000111845	9.26302	9.46792	9.34431	7.27342	ENSG00000111845	PAK1IP1
ENSG00000111846	11.9819	13.12	13.0313	21.1673	ENSG00000111846	GCNT2
ENSG00000111850	2.14231	4.38318	4.21584	3.46417	ENSG00000111850	SMIM8
ENSG00000111859	7.25294	13.1796	12.8146	24.258	ENSG00000111859	NEDD9

ENSG00000111860	4.7368	10.0432	7.84821	14.5346	ENSG00000111860	CEP85L
ENSG00000111863	17.8107	40.492	56.1561	18.1073	ENSG00000111863	ADTRP
ENSG00000111875	8.58752	12.1317	11.536	6.70807	ENSG00000111875	ASF1A
ENSG00000111877	8.05428	12.7567	8.84618	10.9904	ENSG00000111877	MCM9
ENSG00000111879	0.735838	1.433	0.978306	2.19368	ENSG00000111879	FAM184A
ENSG00000111880	12.1892	15.3917	9.85251	14.3022	ENSG00000111880	RNGTT
ENSG00000111885	8.85887	20.2666	10.6314	18.6722	ENSG00000111885	MAN1A1
ENSG00000111886	0.13648	0.130939	0.0885003	0.658069	ENSG00000111886	GABRR2
ENSG00000111897	110.671	97.833	86.245	63.2084	ENSG00000111897	SERINC1
ENSG00000111906	16.9929	21.6494	17.6876	14.8351	ENSG00000111906	HDDC2
ENSG00000111907	43.5604	35.9734	50.9874	24.9725	ENSG00000111907	TPD52L1
ENSG00000111911	9.84556	6.28115	7.63831	6.94861	ENSG00000111911	HINT3
ENSG00000111912	6.76574	39.0367	35.0627	14.0531	ENSG00000111912	NCOA7
ENSG00000111913	0.905888	1.39999	1.12021	2.01275	ENSG00000111913	RIPOR2
ENSG00000111961	6.85649	3.34201	4.89351	18.6121	ENSG00000111961	SASH1
ENSG00000111962	5.47824	17.5558	11.5462	7.74692	ENSG00000111962	UST
ENSG00000111971	0.0973281	0.0758412	0	0.0644326	ENSG00000111971	LY6G5C
ENSG00000111981	4.31301	11.3113	13.1366	8.47272	ENSG00000111981	ULBP1
ENSG00000112029	2.98034	8.21516	2.5455	5.19224	ENSG00000112029	FBXO5
ENSG00000112031	10.677	14.7263	12.0651	12.5652	ENSG00000112031	MTRF1L
ENSG00000112033	28.1561	14.4992	12.8066	30.9192	ENSG00000112033	PPARD
ENSG00000112038	2.01825	4.86583	4.04499	6.03249	ENSG00000112038	OPRM1
ENSG00000112039	4.09136	11.9695	10.7753	3.379	ENSG00000112039	FANCE
ENSG00000112041	1.8591	3.10854	4.28748	8.01147	ENSG00000112041	TULP1
ENSG00000112053	1.20353	2.53444	2.10029	3.98432	ENSG00000112053	SLC26A8
ENSG00000112062	29.2442	35.7801	26.4705	30.3366	ENSG00000112062	MAPK14
ENSG00000112077	0.0486931	0.0285229	0.0257851	0.0324664	ENSG00000112077	RHAG
ENSG00000112078	15.71	14.915	13.3754	18.8332	ENSG00000112078	KCTD20
ENSG00000112079	16.4892	11.4594	12.6647	10.3325	ENSG00000112079	STK38
ENSG00000112081	80.7266	60.0474	125.314	41.8672	ENSG00000112081	SRSF3
ENSG00000112096	37.9372	81.2954	87.6256	207.362	ENSG00000112096	SOD2
ENSG00000112110	28.5792	24.1471	22.4169	15.2138	ENSG00000112110	MRPL18
ENSG00000112115	0.0305208	0	0	0.0335327	ENSG00000112115	IL17A
ENSG00000112116	0	0	0	0	ENSG00000112116	IL17F
ENSG00000112118	13.5343	30.7947	9.48381	20.2594	ENSG00000112118	MCM3
ENSG00000112130	23.6582	19.3301	18.0407	12.2223	ENSG00000112130	RNF8
ENSG00000112137	3.32713	6.07871	6.24085	13.9625	ENSG00000112137	PHACTR1
ENSG00000112139	1.73363	3.28805	1.26578	6.53374	ENSG00000112139	MDGA1
ENSG00000112144	2.68584	2.77782	2.99601	3.79121	ENSG00000112144	ICK
ENSG00000112146	39.6448	36.4062	39.5574	27.8341	ENSG00000112146	FBXO9
ENSG00000112149	2.64471	2.17693	0.802354	2.40591	ENSG00000112149	CD83
ENSG00000112159	11.7503	16.836	14.587	18.8166	ENSG00000112159	MDN1
ENSG00000112164	0.0184157	0.122697	0.135325	0.148738	ENSG00000112164	GLP1R
ENSG00000112167	6.55859	7.58246	7.25917	7.46007	ENSG00000112167	SAYSD1
ENSG00000112175	0.0773188	0.306441	0.237202	0.663758	ENSG00000112175	BMP5
ENSG00000112182	1.15418	1.94296	2.18755	2.08405	ENSG00000112182	BACH2
ENSG00000112183	0.346148	0.753811	0.698742	1.81361	ENSG00000112183	RBM24
ENSG00000112186	2.49314	5.22683	4.99829	3.91689	ENSG00000112186	CAP2
ENSG00000112195	0.412469	0.641642	0.759627	0.910661	ENSG00000112195	TREML2
ENSG00000112200	33.1661	47.4794	46.8302	45.8664	ENSG00000112200	ZNF451
ENSG00000112208	1.5747	2.11177	2.29452	4.9831	ENSG00000112208	BAG2
ENSG00000112210	6.33776	7.17027	7.08344	8.89026	ENSG00000112210	RAB23
ENSG00000112212	0.384457	0.671254	0.33892	0.844242	ENSG00000112212	TSPO2
ENSG00000112214	0	0.0286536	0.0777096	0.0652287	ENSG00000112214	FHL5

ENSG00000112218	0.936808	2.70734	2.16624	2.74107	ENSG00000112218	GPR63
ENSG00000112232	0.122261	0.246838	0.179834	0.308602	ENSG00000112232	KHDRBS2
ENSG00000112234	9.63126	13.0648	13.1983	11.913	ENSG00000112234	FBXL4
ENSG00000112237	64.5668	63.1002	58.0306	44.9664	ENSG00000112237	CCNC
ENSG00000112238	0	0	0.0445724	0.0513252	ENSG00000112238	PRDM13
ENSG00000112242	5.28335	5.62691	7.49571	6.93345	ENSG00000112242	E2F3
ENSG00000112245	31.1284	41.2305	49.1944	26.0604	ENSG00000112245	PTP4A1
ENSG00000112246	0.125594	0.397105	0.66311	2.17368	ENSG00000112246	SIM1
ENSG00000112249	44.6806	60.845	54.7965	62.9331	ENSG00000112249	ASCC3
ENSG00000112273	77.4504	7.18459	5.2887	7.55556	ENSG00000112273	HDGFL1
ENSG00000112276	6.78477	4.74056	4.18429	6.19827	ENSG00000112276	BVES
ENSG00000112280	1.28554	1.97635	2.10798	4.4317	ENSG00000112280	COL9A1
ENSG00000112282	18.9322	25.2994	23.5269	17.8309	ENSG00000112282	MED23
ENSG00000112290	5.43133	9.67545	13.376	9.34467	ENSG00000112290	WASF1
ENSG00000112293	3.51831	5.63891	4.74365	8.80992	ENSG00000112293	GPLD1
ENSG00000112294	0.751154	1.26262	1.12041	1.48522	ENSG00000112294	ALDH5A1
ENSG00000112297	47.9523	107.47	55.3234	49.1326	ENSG00000112297	CRYBG1
ENSG00000112299	3.49375	8.57906	3.74414	5.0741	ENSG00000112299	VNN1
ENSG00000112303	0.504762	1.00753	1.63255	0.678215	ENSG00000112303	VNN2
ENSG00000112304	12.3246	11.2725	8.81991	6.75062	ENSG00000112304	ACOT13
ENSG00000112305	8.68042	6.42683	6.97338	8.14291	ENSG00000112305	SMAP1
ENSG00000112306	526.895	443.841	390.178	216.767	ENSG00000112306	RPS12
ENSG00000112308	58.3341	61.5994	71.2856	43.5849	ENSG00000112308	C6orf62
ENSG00000112309	0.199876	0.540467	0.390601	0.462198	ENSG00000112309	B3GAT2
ENSG00000112312	3.89431	15.2847	4.40586	9.09365	ENSG00000112312	GMNN
ENSG00000112319	0.318586	0.16648	0.15506	0.583172	ENSG00000112319	EYA4
ENSG00000112320	0.131561	0.169572	0.303854	1.65081	ENSG00000112320	SOBP
ENSG00000112333	0.327311	0.505673	0.574286	0.446871	ENSG00000112333	NR2E1
ENSG00000112335	46.7795	27.9236	24.6353	21.8229	ENSG00000112335	SNX3
ENSG00000112337	0.0245753	0.023689	0.0643805	0.054005	ENSG00000112337	SLC17A2
ENSG00000112339	36.8328	29.6969	34.2613	34.4742	ENSG00000112339	HBS1L
ENSG00000112343	14.3206	14.4077	9.33109	11.492	ENSG00000112343	TRIM38
ENSG00000112357	5.77397	5.43693	5.25348	4.12514	ENSG00000112357	PEX7
ENSG00000112365	3.02459	4.09522	5.98386	4.61563	ENSG00000112365	ZBTB24
ENSG00000112367	6.36962	6.95564	6.49608	4.68283	ENSG00000112367	FIG4
ENSG00000112378	1169.43	397.437	397.086	172.441	ENSG00000112378	PERP
ENSG00000112379	0.8455	0.864115	0.436474	0.510529	ENSG00000112379	ARFGEF3
ENSG00000112394	1.53161	2.99105	3.39128	4.064	ENSG00000112394	SLC16A10
ENSG00000112406	9.82028	8.99465	10.6184	7.88176	ENSG00000112406	HECA
ENSG00000112414	23.197	43.6702	11.3232	13.7789	ENSG00000112414	ADGRG6
ENSG00000112419	15.5361	16.7561	20.2499	16.5131	ENSG00000112419	PHACTR2
ENSG00000112425	1.03561	2.05385	2.56246	2.53917	ENSG00000112425	EPM2A
ENSG00000112459	0	0	0	0	ENSG00000112459	OR14J1
ENSG00000112461	0	0	0	0.0254603	ENSG00000112461	OR5V1
ENSG00000112462	0.0151711	0.0536059	0.0442655	0.0942871	ENSG00000112462	OR12D3
ENSG00000112473	8.10034	7.04224	6.12923	6.51393	ENSG00000112473	SLC39A7
ENSG00000112474	1.5288	1.62628	2.07747	0.55839	ENSG00000112474	HSD17B8
ENSG00000112486	0.263685	0.373619	0.386405	0.643227	ENSG00000112486	CCR6
ENSG00000112493	3.00406	0.67659	3.06109	13.8232	ENSG00000112493	TAPBP
ENSG00000112494	0.0628546	0.394446	0.305893	0.206757	ENSG00000112494	UNC93A
ENSG00000112499	0.811167	1.90321	1.76524	2.44511	ENSG00000112499	SLC22A2
ENSG00000112511	1.60958	3.61529	2.09651	3.13526	ENSG00000112511	PHF1
ENSG00000112514	49.1436	56.471	25.1091	33.9326	ENSG00000112514	CUTA
ENSG00000112530	0.327506	0.643446	0.785306	0.89193	ENSG00000112530	PACRG

ENSG00000112531	33.5441	39.555	44.1595	63.6591	ENSG00000112531	QKI
ENSG00000112539	0.321007	0.241051	0.162159	0.169442	ENSG00000112539	C6orf118
ENSG00000112541	1.20348	3.77504	3.83806	6.2043	ENSG00000112541	PDE10A
ENSG00000112559	72.3491	111.798	63.8205	49.292	ENSG00000112559	MDFI
ENSG00000112561	6.66447	15.032	29.0874	7.47133	ENSG00000112561	TFEB
ENSG00000112562	1.17827	1.54159	0.983164	1.42246	ENSG00000112562	SMOC2
ENSG00000112576	17.3779	25.4162	19.4991	18.8435	ENSG00000112576	CCND3
ENSG00000112578	8.34494	10.4318	12.0019	8.78559	ENSG00000112578	BYSL
ENSG00000112584	5.68712	11.2234	12.014	13.5455	ENSG00000112584	FAM120B
ENSG00000112592	8.50717	9.70491	9.47111	5.76989	ENSG00000112592	TBP
ENSG00000112599	1.14579	1.51891	1.3846	0.955146	ENSG00000112599	GUCA1B
ENSG00000112619	0.118505	0.465817	0.291952	0.366878	ENSG00000112619	PRPH2
ENSG00000112624	1.89	2.50926	3.15463	2.67067	ENSG00000112624	BICRAL
ENSG00000112640	21.0123	18.3776	15.1112	18.9687	ENSG00000112640	PPP2R5D
ENSG00000112651	12.0272	21.255	20.7408	12.5134	ENSG00000112651	MRPL2
ENSG00000112655	48.9877	113.144	132.72	119.724	ENSG00000112655	PTK7
ENSG00000112658	12.9688	10.4077	15.1912	9.38212	ENSG00000112658	SRF
ENSG00000112659	23.5755	39.7577	52.3371	28.8892	ENSG00000112659	CUL9
ENSG00000112667	23.327	26.4301	21.1986	14.6509	ENSG00000112667	DNPH1
ENSG00000112679	14.2364	25.055	23.4155	16.4033	ENSG00000112679	DUSP22
ENSG00000112685	19.512	22.2282	17.4095	17.7519	ENSG00000112685	EXOC2
ENSG00000112695	163.97	145.338	70.2177	72.7758	ENSG00000112695	COX7A2
ENSG00000112697	69.2659	61.9265	46.4142	52.6525	ENSG00000112697	TMEM30A
ENSG00000112699	3.76006	11.339	14.9136	9.59416	ENSG00000112699	GMDS
ENSG00000112701	42.0817	70.5906	75.8493	84.3463	ENSG00000112701	SENP6
ENSG00000112706	0.691207	1.47675	1.00067	1.0837	ENSG00000112706	IMPG1
ENSG00000112715	27.2013	217.367	253.306	82.1161	ENSG00000112715	VEGFA
ENSG00000112739	29.4693	41.1754	39.5739	37.8558	ENSG00000112739	PRPF4B
ENSG00000112742	4.19019	20.6303	2.01011	6.62644	ENSG00000112742	TTK
ENSG00000112759	7.62803	18.8399	7.69511	6.75887	ENSG00000112759	SLC29A1
ENSG00000112761	0.421391	1.30057	5.78407	1.5397	ENSG00000112761	WISP3
ENSG00000112763	9.22575	12.9485	14.7837	8.67562	ENSG00000112763	BTN2A1
ENSG00000112769	1.51626	2.50672	2.40967	18.8968	ENSG00000112769	LAMA4
ENSG00000112773	3.6377	2.28406	5.20184	5.88527	ENSG00000112773	FAM46A
ENSG00000112782	0.868635	1.14683	0.912872	1.24712	ENSG00000112782	CLIC5
ENSG00000112787	44.3995	35.6176	47.7536	23.3646	ENSG00000112787	FBRSL1
ENSG00000112796	2.628	3.07735	0.553972	2.4614	ENSG00000112796	ENPP5
ENSG00000112799	0	0	0	0	ENSG00000112799	LY86
ENSG00000112812	3.68582	6.00698	4.18372	5.29375	ENSG00000112812	PRSS16
ENSG00000112818	0.54111	0.443182	0.184322	0.455683	ENSG00000112818	MEP1A
ENSG00000112837	0.430285	0.280071	0.841053	40.0064	ENSG00000112837	TBX18
ENSG00000112851	48.6453	55.6675	42.6784	51.7707	ENSG00000112851	ERBIN
ENSG00000112852	0.773595	0.227065	0.263211	0.489048	ENSG00000112852	PCDHB2
ENSG00000112855	24.2251	18.9925	21.5314	18.2154	ENSG00000112855	HARS2
ENSG00000112874	11.8674	10.283	9.89	8.21712	ENSG00000112874	NUDT12
ENSG00000112877	5.98361	8.26254	11.1921	9.89153	ENSG00000112877	CEP72
ENSG00000112893	56.6088	65.8901	60.2487	51.547	ENSG00000112893	MAN2A1
ENSG00000112902	1.09472	2.31051	1.12684	10.0277	ENSG00000112902	SEMA5A
ENSG00000112936	0.24728	0.347591	0.319016	0.387951	ENSG00000112936	C7
ENSG00000112941	13.2777	22.4124	24.0241	27.6689	ENSG00000112941	PAPD7
ENSG00000112964	4.665	7.47784	8.66617	11.85	ENSG00000112964	GHR
ENSG00000112972	168.577	187.85	29.8626	169.867	ENSG00000112972	HMGCS1
ENSG00000112977	5.18279	12.8643	6.68099	20.5717	ENSG00000112977	DAP
ENSG00000112981	5.29798	11.8042	11.0753	23.2574	ENSG00000112981	NME5

ENSG00000112983	25.7185	38.9333	39.2181	42.9163	ENSG00000112983	BRD8
ENSG00000112984	4.78388	32.023	1.76327	10.6458	ENSG00000112984	KIF20A
ENSG00000112992	17.361	22.7853	20.9781	26.0055	ENSG00000112992	NNT
ENSG00000112996	19.8944	28.3515	30.1389	15.5543	ENSG00000112996	MRPS30
ENSG00000113013	79.7399	142.348	171.1	91.5177	ENSG00000113013	HSPA9
ENSG00000113048	29.4855	37.0576	30.1781	33.304	ENSG00000113048	MRPS27
ENSG00000113068	21.8142	21.4134	18.6695	13.7971	ENSG00000113068	PFDN1
ENSG00000113070	26.3559	80.1172	40.3875	17.5221	ENSG00000113070	HBEGF
ENSG00000113073	0.345128	0.31599	0.442807	0.294715	ENSG00000113073	SLC4A9
ENSG00000113083	0.638601	0.949686	1.79092	44.0902	ENSG00000113083	LOX
ENSG00000113088	0.153762	0.411767	0.502072	0.596874	ENSG00000113088	GZMK
ENSG00000113100	3.04577	1.99234	2.71797	6.81551	ENSG00000113100	CDH9
ENSG00000113108	6.06899	14.613	19.1505	11.0369	ENSG00000113108	APBB3
ENSG00000113119	20.162	28.5166	22.7543	35.2266	ENSG00000113119	TMCO6
ENSG00000113140	70.699	297.778	114.753	741.612	ENSG00000113140	SPARC
ENSG00000113141	48.6139	34.5496	37.8982	38.8764	ENSG00000113141	IK
ENSG00000113161	169.995	174.684	61.1505	122.632	ENSG00000113161	HMGCR
ENSG00000113163	19.7966	20.5419	18.103	21.783	ENSG00000113163	COL4A3BP
ENSG00000113194	41.499	38.0882	28.8214	23.8386	ENSG00000113194	FAF2
ENSG00000113196	0.280516	0.593543	0.324837	0.555608	ENSG00000113196	HAND1
ENSG00000113205	0.0853093	0.0812371	0.0651443	0.0979091	ENSG00000113205	PCDHB3
ENSG00000113209	0.324602	0.203527	0.538471	0.247105	ENSG00000113209	PCDHB5
ENSG00000113211	0.0378828	0.178853	0	0	ENSG00000113211	PCDHB6
ENSG00000113212	0.0306789	0.0604342	0.0831789	0.084722	ENSG00000113212	PCDHB7
ENSG00000113231	1.31689	2.74434	3.06036	2.62253	ENSG00000113231	PDE8B
ENSG00000113240	12.051	22.1868	21.277	17.9044	ENSG00000113240	CLK4
ENSG00000113248	0.140585	0.0717563	0.220912	0.141507	ENSG00000113248	PCDHB15
ENSG00000113249	0.194351	0.352481	0.480657	1.23813	ENSG00000113249	HAVCR1
ENSG00000113262	0.427934	1.08616	0.986833	1.851	ENSG00000113262	GRM6
ENSG00000113263	2.33227	7.1406	6.75677	12.2288	ENSG00000113263	ITK
ENSG00000113269	10.2602	11.542	9.32642	8.93876	ENSG00000113269	RNF130
ENSG00000113272	3.92628	7.64234	7.01624	4.15352	ENSG00000113272	THG1L
ENSG00000113273	4.54849	6.56848	5.46287	9.0821	ENSG00000113273	ARSB
ENSG00000113282	60.6418	42.6975	61.9109	42.6332	ENSG00000113282	CLINT1
ENSG00000113296	0.293337	1.47915	1.56726	2.37647	ENSG00000113296	THBS4
ENSG00000113300	7.63977	10.2885	15.4979	13.233	ENSG00000113300	CNOT6
ENSG00000113302	0.433437	1.25431	0.779189	1.31154	ENSG00000113302	IL12B
ENSG00000113303	1.12089	1.36683	1.43926	2.68778	ENSG00000113303	BTNL8
ENSG00000113312	19.0625	12.1432	14.0436	9.31425	ENSG00000113312	TTC1
ENSG00000113318	4.41446	9.68557	9.54274	8.85961	ENSG00000113318	MSH3
ENSG00000113319	0.299457	0.521594	0.40032	0.812238	ENSG00000113319	RASGRF2
ENSG00000113327	0.177131	0.397436	0.334965	0.606277	ENSG00000113327	GABRG2
ENSG00000113328	45.6764	45.5635	40.4963	34.7782	ENSG00000113328	CCNG1
ENSG00000113356	8.98938	12.2498	9.99565	15.0914	ENSG00000113356	POLR3G
ENSG00000113360	21.2774	39.6379	40.3587	47.7898	ENSG00000113360	DROSHA
ENSG00000113361	0.42726	1.0361	1.12131	1.7725	ENSG00000113361	CDH6
ENSG00000113368	5.11108	31.5899	1.77104	15.6743	ENSG00000113368	LMNB1
ENSG00000113369	53.0337	52.1052	39.2976	21.4371	ENSG00000113369	ARRDC3
ENSG00000113384	26.3413	16.027	18.4539	18.783	ENSG00000113384	GOLPH3
ENSG00000113387	105.577	88.9158	87.3878	88.4845	ENSG00000113387	SUB1
ENSG00000113389	1.79051	2.437	2.4243	4.96836	ENSG00000113389	NPR3
ENSG00000113391	6.82281	8.87948	9.57977	14.6167	ENSG00000113391	FAM172A
ENSG00000113396	3.77181	7.26975	4.26431	3.1669	ENSG00000113396	SLC27A6
ENSG00000113407	81.9256	146.284	139.897	67.1408	ENSG00000113407	TARS

ENSG00000113430	40.5859	32.8654	70.3378	66.4601	ENSG00000113430	IRX4
ENSG00000113441	36.8021	54.958	34.081	31.6284	ENSG00000113441	LNPEP
ENSG00000113448	4.59944	13.844	6.74041	19.599	ENSG00000113448	PDE4D
ENSG00000113456	13.0041	13.8076	11.5835	12.2055	ENSG00000113456	RAD1
ENSG00000113460	19.3348	17.046	18.4071	15.8488	ENSG00000113460	BRIX1
ENSG00000113492	0.150857	0.266488	0.361813	0.683835	ENSG00000113492	AGXT2
ENSG00000113494	0.614668	0.382542	1.26935	1.83864	ENSG00000113494	PRLR
ENSG00000113504	6.64796	7.7578	5.59775	6.21243	ENSG00000113504	SLC12A7
ENSG00000113520	0.340621	0.327006	0.791649	0.628256	ENSG00000113520	IL4
ENSG00000113522	30.7622	43.4554	51.9861	48.0382	ENSG00000113522	RAD50
ENSG00000113525	0	0.597151	0.834363	1.66055	ENSG00000113525	IL5
ENSG00000113532	0.668651	2.08396	1.16953	2.11452	ENSG00000113532	ST8SIA4
ENSG00000113552	15.8058	15.2657	14.7995	10.0345	ENSG00000113552	GNPDA1
ENSG00000113555	2.44083	3.00974	2.1436	3.23066	ENSG00000113555	PCDH12
ENSG00000113558	177.256	91.0158	67.5117	78.1328	ENSG00000113558	SKP1
ENSG00000113569	20.3004	30.3517	23.3321	20.4182	ENSG00000113569	NUP155
ENSG00000113575	74.7404	55.5593	57.9827	46.4738	ENSG00000113575	PPP2CA
ENSG00000113578	4.10197	9.74288	12.05	23.7165	ENSG00000113578	FGF1
ENSG00000113580	42.3623	44.0383	35.144	36.6615	ENSG00000113580	NR3C1
ENSG00000113583	39.7753	36.6513	28.7943	23.3544	ENSG00000113583	C5orf15
ENSG00000113593	21.6328	34.6487	30.2838	33.6726	ENSG00000113593	PPWD1
ENSG00000113594	4.44146	9.97367	9.57747	10.6874	ENSG00000113594	LIFR
ENSG00000113595	8.65342	9.50879	9.88529	11.8387	ENSG00000113595	TRIM23
ENSG00000113597	10.8143	9.89796	12.8979	8.11399	ENSG00000113597	TRAPPC13
ENSG00000113600	0.982811	1.70982	1.83003	3.26353	ENSG00000113600	C9
ENSG00000113615	15.171	9.01649	8.7675	18.5114	ENSG00000113615	SEC24A
ENSG00000113621	28.8989	43.3979	38.0026	54.2658	ENSG00000113621	TXNDC15
ENSG00000113638	4.67867	3.53242	3.34275	4.81001	ENSG00000113638	TTC33
ENSG00000113643	72.6442	56.495	58.5153	59.8197	ENSG00000113643	RARS
ENSG00000113645	20.5207	13.1379	19.4165	19.9535	ENSG00000113645	WWC1
ENSG00000113648	111.531	117.462	98.5953	78.6248	ENSG00000113648	H2AFY
ENSG00000113649	57.5801	75.6332	73.7234	81.6809	ENSG00000113649	TCERG1
ENSG00000113657	1.06368	5.18269	2.14857	12.6765	ENSG00000113657	DPYSL3
ENSG00000113658	37.0461	54.5724	35.5542	37.239	ENSG00000113658	SMAD5
ENSG00000113712	242.28	286.474	315.516	188.233	ENSG00000113712	CSNK1A1
ENSG00000113716	19.0777	26.4039	24.2732	24.9809	ENSG00000113716	HMGXB3
ENSG00000113719	62.3257	50.3381	42.0474	42.952	ENSG00000113719	ERGIC1
ENSG00000113721	1.64482	5.77256	6.81229	138.662	ENSG00000113721	PDGFRB
ENSG00000113722	0.259768	0.18839	0.227781	0.998095	ENSG00000113722	CDX1
ENSG00000113732	205.734	58.5823	49.7597	36.5457	ENSG00000113732	ATP6V0E1
ENSG00000113734	5.90925	7.43481	7.10551	5.03027	ENSG00000113734	BNIP1
ENSG00000113739	3.41931	77.1953	114.833	42.6189	ENSG00000113739	STC2
ENSG00000113742	27.9382	12.3319	17.1878	15.39	ENSG00000113742	CPEB4
ENSG00000113749	0.887148	1.2131	1.34775	1.50874	ENSG00000113749	HRH2
ENSG00000113758	60.6295	68.6751	66.7135	54.5853	ENSG00000113758	DBN1
ENSG00000113761	6.96292	10.0957	12.445	13.8827	ENSG00000113761	ZNF346
ENSG00000113763	0.116953	0.0794402	0.155336	0.156806	ENSG00000113763	UNC5A
ENSG00000113790	5.52402	7.38454	6.02115	5.9601	ENSG00000113790	EHHADH
ENSG00000113805	1.33816	2.00086	3.8991	4.79681	ENSG00000113805	CNTN3
ENSG00000113810	27.274	95.1834	28.4275	68.8574	ENSG00000113810	SMC4
ENSG00000113811	20.3535	15.6062	13.9616	8.31923	ENSG00000113811	SELENOK
ENSG00000113812	17.437	16.3969	13.8203	10.0059	ENSG00000113812	ACTR8
ENSG00000113838	7.454	11.5434	9.30136	13.503	ENSG00000113838	TBCCD1
ENSG00000113845	43.5618	45.2372	41.4565	30.8515	ENSG00000113845	TIMMDC1

ENSG00000113851	15.287	18.5688	17.1769	17.2569	ENSG00000113851	CRBN
ENSG00000113889	0.250532	0.279318	0.279549	0.450069	ENSG00000113889	KNG1
ENSG00000113905	1.71515	3.00488	2.72598	7.80815	ENSG00000113905	HRG
ENSG00000113916	9.7183	8.50646	15.9658	18.0253	ENSG00000113916	BCL6
ENSG00000113924	1.12801	1.58758	1.72888	1.97001	ENSG00000113924	HGD
ENSG00000113946	1.91961	0.862466	3.44783	2.86756	ENSG00000113946	CLDN16
ENSG00000113966	5.75554	8.83537	7.20902	12.7269	ENSG00000113966	ARL6
ENSG00000113971	17.0624	27.2603	25.4313	38.8823	ENSG00000113971	NPHP3
ENSG00000114013	4.20729	0.370541	0.913183	0.875083	ENSG00000114013	CD86
ENSG00000114019	86.121	42.6345	50.4788	57.8514	ENSG00000114019	AMOTL2
ENSG00000114021	35.9429	28.2627	26.8375	16.7257	ENSG00000114021	NIT2
ENSG00000114023	23.0585	18.2916	16.9059	14.2982	ENSG00000114023	FAM162A
ENSG00000114026	9.64219	15.315	13.3895	14.7832	ENSG00000114026	OGG1
ENSG00000114030	35.825	30.5716	35.088	25.6467	ENSG00000114030	KPNA1
ENSG00000114054	15.061	21.3422	16.7805	12.2895	ENSG00000114054	PCCB
ENSG00000114062	23.4568	31.9824	34.6427	26.0091	ENSG00000114062	UBE3A
ENSG00000114098	26.7073	31.9823	25.8337	29.4208	ENSG00000114098	ARMC8
ENSG00000114107	6.27489	13.3437	8.75434	8.1083	ENSG00000114107	CEP70
ENSG00000114113	0.291011	1.53603	3.29605	2.30305	ENSG00000114113	RBP2
ENSG00000114115	6.66776	12.3481	25.3533	24.2015	ENSG00000114115	RBP1
ENSG00000114120	35.0609	64.7422	54.1306	47.4835	ENSG00000114120	SLC25A36
ENSG00000114124	0.357252	0.484121	0.607841	1.09034	ENSG00000114124	GRK7
ENSG00000114125	42.9006	39.5086	43.778	42.699	ENSG00000114125	RNF7
ENSG00000114126	20.1449	25.226	27.4759	32.5912	ENSG00000114126	TFDP2
ENSG00000114127	26.1711	41.1452	36.9229	59.6464	ENSG00000114127	XRN1
ENSG00000114166	7.52801	5.8094	3.6227	9.17801	ENSG00000114166	KAT2B
ENSG00000114200	1.49214	2.75393	3.55195	2.59829	ENSG00000114200	BCHE
ENSG00000114204	0.629517	1.60964	1.44178	1.21115	ENSG00000114204	SERPINI2
ENSG00000114209	41.709	46.4511	35.9239	37.7915	ENSG00000114209	PDCD10
ENSG00000114248	0.202402	0.357698	0.381329	0.495909	ENSG00000114248	LRRC31
ENSG00000114251	6.70799	12.7077	12.1487	151.972	ENSG00000114251	WNT5A
ENSG00000114268	24.235	27.4466	30.9151	58.2999	ENSG00000114268	PFKFB4
ENSG00000114270	145.826	468.634	279.076	386.043	ENSG00000114270	COL7A1
ENSG00000114279	0.711714	1.52804	0.768386	2.29642	ENSG00000114279	FGF12
ENSG00000114302	17.9281	14.4331	15.2087	15.2123	ENSG00000114302	PRKAR2A
ENSG00000114315	66.6428	36.6289	37.5979	22.0959	ENSG00000114315	HES1
ENSG00000114316	17.1857	28.3553	30.2361	46.8348	ENSG00000114316	USP4
ENSG00000114331	39.2665	70.5201	68.6819	77.922	ENSG00000114331	ACAP2
ENSG00000114346	20.8571	58.0007	21.5516	49.1653	ENSG00000114346	ECT2
ENSG00000114349	0.35977	0.0442956	0.0600697	0.10647	ENSG00000114349	GNAT1
ENSG00000114353	62.6122	54.4145	36.6234	39.4743	ENSG00000114353	GNAI2
ENSG00000114354	49.0156	42.6403	71.6581	52.2982	ENSG00000114354	TFG
ENSG00000114374	19.0034	24.5646	20.2659	1.4442	ENSG00000114374	USP9Y
ENSG00000114378	11.6361	4.01475	1.56871	2.61249	ENSG00000114378	HYAL1
ENSG00000114383	5.99091	3.76077	4.78971	1.98391	ENSG00000114383	TUSC2
ENSG00000114388	7.12679	6.9697	5.58217	5.79091	ENSG00000114388	NPRL2
ENSG00000114391	345.964	228.316	149.831	148.257	ENSG00000114391	RPL24
ENSG00000114395	16.2591	12.6774	8.33284	7.73268	ENSG00000114395	CYB561D2
ENSG00000114405	8.28304	10.2252	7.82853	9.88256	ENSG00000114405	C3orf14
ENSG00000114416	46.7655	56.5044	53.9473	78.0403	ENSG00000114416	FXR1
ENSG00000114423	9.07071	17.617	16.8495	18.9649	ENSG00000114423	CBLB
ENSG00000114439	33.8637	60.2664	62.7589	59.1322	ENSG00000114439	BBX
ENSG00000114446	14.8142	21.4162	17.3377	15.4986	ENSG00000114446	IFT57
ENSG00000114450	20.3906	28.7786	23.0724	39.2909	ENSG00000114450	GNB4

ENSG00000114455	0.51098	0.799523	1.16718	1.53133	ENSG00000114455	HHLA2
ENSG00000114473	9.71383	15.0261	16.4347	26.4043	ENSG00000114473	IQCG
ENSG00000114480	12.4828	16.2394	13.2495	30.3713	ENSG00000114480	GBE1
ENSG00000114487	0.0431621	0.166866	0.252968	0.335923	ENSG00000114487	MORC1
ENSG00000114491	21.5761	15.2879	14.4881	14.5767	ENSG00000114491	UMPS
ENSG00000114503	25.7482	21.9332	28.515	23.5894	ENSG00000114503	NCBP2
ENSG00000114520	15.4108	13.8849	11.4269	16.2209	ENSG00000114520	SNX4
ENSG00000114529	19.2405	15.1592	14.4748	14.5328	ENSG00000114529	C3orf52
ENSG00000114541	49.7767	105.288	69.6174	106.311	ENSG00000114541	FRMD4B
ENSG00000114544	30.7551	52.4394	33.2507	36.162	ENSG00000114544	SLC41A3
ENSG00000114547	0.340312	0.475375	0.446542	0.534892	ENSG00000114547	ROPN1B
ENSG00000114554	59.6696	86.0612	78.354	70.4273	ENSG00000114554	PLXNA1
ENSG00000114573	41.975	20.0052	19.285	21.6628	ENSG00000114573	ATP6V1A
ENSG00000114626	2.7376	6.83854	6.88448	8.78747	ENSG00000114626	ABTB1
ENSG00000114631	5.22599	2.34706	2.09894	1.18022	ENSG00000114631	PODXL2
ENSG00000114638	37.8603	4.37817	12.9373	8.27254	ENSG00000114638	UPK1B
ENSG00000114646	1.02959	4.11602	1.49231	2.9798	ENSG00000114646	CSPG5
ENSG00000114648	15.582	9.00361	13.483	10.1984	ENSG00000114648	KLHL18
ENSG00000114650	40.5719	55.2826	67.8471	34.1735	ENSG00000114650	SCAP
ENSG00000114654	0.0862805	0.194021	0.142123	0.378646	ENSG00000114654	EFCC1
ENSG00000114656	1.96427	3.69708	3.49809	5.78558	ENSG00000114656	KIAA1257
ENSG00000114670	5.18022	5.1057	7.51515	5.75101	ENSG00000114670	NEK11
ENSG00000114686	62.34	90.7201	98.6637	124.295	ENSG00000114686	MRPL3
ENSG00000114698	0.669867	1.13741	1.12839	6.55119	ENSG00000114698	PLSCR4
ENSG00000114735	11.9117	19.0756	15.9354	11.8953	ENSG00000114735	HEMK1
ENSG00000114737	1.35754	2.66643	1.84387	1.44398	ENSG00000114737	CISH
ENSG00000114738	54.9222	38.181	25.4082	19.009	ENSG00000114738	MAPKAPK3
ENSG00000114739	1.47573	2.45888	2.07623	3.00867	ENSG00000114739	ACVR2B
ENSG00000114742	18.3846	24.5016	19.5917	22.4522	ENSG00000114742	WDR48
ENSG00000114744	17.2177	20.0779	16.8773	12.6572	ENSG00000114744	COMMD2
ENSG00000114745	35.4085	39.5367	33.8264	29.8509	ENSG00000114745	GORASP1
ENSG00000114757	1.81287	5.63409	1.60852	9.22168	ENSG00000114757	PEX5L
ENSG00000114767	8.70361	11.8614	14.6695	7.10548	ENSG00000114767	RRP9
ENSG00000114770	13.9289	26.7355	28.5287	28.311	ENSG00000114770	ABCC5
ENSG00000114771	0.0349903	0.101133	0.218504	0.153343	ENSG00000114771	AADAC
ENSG00000114779	10.572	12.7229	10.0386	9.9474	ENSG00000114779	ABHD14B
ENSG00000114784	6.72627	11.0048	10.9601	10.5399	ENSG00000114784	EIF1B
ENSG00000114786	0.703686	1.43279	1.35805	0.672788	ENSG00000114786	ABHD14A-ACY1
ENSG00000114790	2.3306	3.21181	2.98043	3.01609	ENSG00000114790	ARHGEF26
ENSG00000114796	15.5412	17.9836	22.0459	23.761	ENSG00000114796	KLHL24
ENSG00000114805	0.0581609	0.282227	0.153369	0.12034	ENSG00000114805	PLCH1
ENSG00000114812	3.44015	8.37609	9.14625	6.94457	ENSG00000114812	VIPR1
ENSG00000114841	1.98307	1.79258	3.39464	3.67105	ENSG00000114841	DNAH1
ENSG00000114850	305.001	283.829	107.515	149.713	ENSG00000114850	SSR3
ENSG00000114853	6.53353	5.57564	7.55023	7.19452	ENSG00000114853	ZBTB47
ENSG00000114854	0	0.0878255	0.158674	0.303464	ENSG00000114854	TNNC1
ENSG00000114857	34.3194	65.3072	56.9866	83.6284	ENSG00000114857	NKTR
ENSG00000114859	3.41994	5.28747	4.73104	6.41962	ENSG00000114859	CLCN2
ENSG00000114861	11.5246	31.0528	18.0307	26.1668	ENSG00000114861	FOXP1
ENSG00000114867	225.098	191.868	158.638	196.074	ENSG00000114867	EIF4G1
ENSG00000114902	65.9523	46.2052	44.8046	28.3117	ENSG00000114902	SPCS1
ENSG00000114904	14.8223	13.0447	10.5139	14.6261	ENSG00000114904	NEK4
ENSG00000114923	21.3681	18.8502	19.8166	20.0932	ENSG00000114923	SLC4A3
ENSG00000114933	8.68088	12.274	10.5968	10.1522	ENSG00000114933	INO80D

ENSG00000114942	181.718	160.726	142.22	89.8402	ENSG00000114942	EEF1B2
ENSG00000114948	0.515883	1.35352	1.04066	2.85522	ENSG00000114948	ADAM23
ENSG00000114956	27.3027	28.9914	20.7728	16.7231	ENSG00000114956	DGUOK
ENSG00000114978	58.0585	44.8453	41.8431	38.8527	ENSG00000114978	MOB1A
ENSG00000114982	31.3355	42.4234	47.6701	57.2072	ENSG00000114982	KANSL3
ENSG00000114988	12.925	16.0817	12.4321	7.05582	ENSG00000114988	LMAN2L
ENSG00000114993	125.52	82.548	94.704	87.1603	ENSG00000114993	RTKN
ENSG00000114999	14.8911	23.208	23.6182	27.0177	ENSG00000114999	TTL
ENSG00000115008	122.788	124.903	131.555	60.9434	ENSG00000115008	IL1A
ENSG00000115009	3.82917	5.05844	8.42982	5.54643	ENSG00000115009	CCL20
ENSG00000115020	17.5969	23.3292	19.7084	20.8208	ENSG00000115020	PIKFYVE
ENSG00000115041	4.6909	1.09219	2.48725	7.76701	ENSG00000115041	KCNIP3
ENSG00000115042	14.2898	25.0574	21.8254	16.8098	ENSG00000115042	FAHD2A
ENSG00000115053	103.95	113.605	162.68	154.228	ENSG00000115053	NCL
ENSG00000115073	24.2752	28.2938	21.7795	20.7588	ENSG00000115073	ACTR1B
ENSG00000115084	66.1309	67.5757	54.3301	51.0028	ENSG00000115084	SLC35F5
ENSG00000115085	0.201137	0.386463	0.566477	0.655219	ENSG00000115085	ZAP70
ENSG00000115091	181.956	140.047	126.793	120.876	ENSG00000115091	ACTR3
ENSG00000115107	28.5778	25.0628	14.1846	24.0211	ENSG00000115107	STEAP3
ENSG00000115109	27.9573	24.2594	19.1858	27.1777	ENSG00000115109	EPB41L5
ENSG00000115112	30.3835	17.2382	10.172	20.4552	ENSG00000115112	TFCP2L1
ENSG00000115128	55.3388	49.5143	55.1268	29.3017	ENSG00000115128	SF3B6
ENSG00000115129	89.2703	22.3453	24.3609	24.2152	ENSG00000115129	TP53I3
ENSG00000115137	2.8045	6.09212	4.05632	5.83853	ENSG00000115137	DNAJC27
ENSG00000115138	0.365516	0.167386	0.225665	0.311665	ENSG00000115138	POMC
ENSG00000115145	18.2286	15.2894	14.658	16.326	ENSG00000115145	STAM2
ENSG00000115155	0.015302	0.249595	0.337292	0.410051	ENSG00000115155	OTOF
ENSG00000115159	37.644	43.5881	16.4684	23.9881	ENSG00000115159	GPD2
ENSG00000115163	2.17353	11.8939	2.40712	5.23846	ENSG00000115163	CENPA
ENSG00000115165	1.05772	1.52718	1.48121	2.61588	ENSG00000115165	CYTIP
ENSG00000115170	15.6192	33.0316	28.1278	22.8607	ENSG00000115170	ACVR1
ENSG00000115183	13.2204	23.2121	23.3147	24.0276	ENSG00000115183	TANC1
ENSG00000115194	0.600126	0.860396	0.96065	2.04686	ENSG00000115194	SLC30A3
ENSG00000115204	34.7373	50.3468	40.4016	49.089	ENSG00000115204	MPV17
ENSG00000115207	21.6033	29.1219	27.0494	24.0644	ENSG00000115207	GTF3C2
ENSG00000115211	17.2506	15.4196	17.5707	17.2549	ENSG00000115211	EIF2B4
ENSG00000115216	43.4213	40.8196	36.7068	36.5093	ENSG00000115216	NRBP1
ENSG00000115221	117.126	89.8348	44.1584	60.2438	ENSG00000115221	ITGB6
ENSG00000115226	16.4015	8.20929	3.55671	7.15131	ENSG00000115226	FNDC4
ENSG00000115232	0.670541	9.44848	7.90994	17.0245	ENSG00000115232	ITGA4
ENSG00000115233	52.856	49.7003	37.7862	31.8559	ENSG00000115233	PSMD14
ENSG00000115234	36.7644	38.8009	39.1267	31.2802	ENSG00000115234	SNX17
ENSG00000115239	34.763	77.7255	70.3514	128.355	ENSG00000115239	ASB3
ENSG00000115241	39.1536	44.8086	32.7358	35.2701	ENSG00000115241	PPM1G
ENSG00000115252	0.252145	0.339165	0.281989	0.543764	ENSG00000115252	PDE1A
ENSG00000115255	5.97304	1.60307	1.84813	1.30271	ENSG00000115255	REEP6
ENSG00000115257	3.40847	4.01556	2.59725	1.89042	ENSG00000115257	PCSK4
ENSG00000115263	0	0.233221	0.313181	0.525473	ENSG00000115263	GCG
ENSG00000115266	5.05524	20.9718	11.4039	23.8789	ENSG00000115266	APC2
ENSG00000115267	10.4497	14.3796	12.6316	10.9983	ENSG00000115267	IFIH1
ENSG00000115268	380.798	242.531	144.788	143.006	ENSG00000115268	RPS15
ENSG00000115271	8.77139	8.02951	4.75979	5.27161	ENSG00000115271	GCA
ENSG00000115274	19.3402	20.15	25.6261	15.0824	ENSG00000115274	INO80B
ENSG00000115275	66.3568	75.7655	57.428	51.2157	ENSG00000115275	MOGS

ENSG00000115282	7.76285	10.897	10.2596	9.69364	ENSG00000115282	TTC31
ENSG00000115286	31.5537	32.8319	28.2331	18.3825	ENSG00000115286	NDUFS7
ENSG00000115289	23.6368	27.4334	26.8574	14.8931	ENSG00000115289	PCGF1
ENSG00000115290	2.15846	3.30438	2.02729	2.37112	ENSG00000115290	GRB14
ENSG00000115295	57.3381	62.3801	55.1788	44.7878	ENSG00000115295	CLIP4
ENSG00000115297	0.237112	0.430085	0.504433	0.653903	ENSG00000115297	TLX2
ENSG00000115306	99.7553	177.149	158.163	105.482	ENSG00000115306	SPTBN1
ENSG00000115307	95.4635	84.2293	60.7392	43.4627	ENSG00000115307	AUP1
ENSG00000115310	355.329	296.4	193.273	201.488	ENSG00000115310	RTN4
ENSG00000115317	16.5574	14.6148	12.4675	7.38818	ENSG00000115317	HTRA2
ENSG00000115318	1.22824	0.918055	0.971154	12.0469	ENSG00000115318	LOXL3
ENSG00000115325	0.851889	1.75417	1.31483	3.60902	ENSG00000115325	DOK1
ENSG00000115339	90.7915	96.2835	40.6128	28.6696	ENSG00000115339	GALNT3
ENSG00000115350	14.7953	14.5433	11.3824	9.21024	ENSG00000115350	POLE4
ENSG00000115353	0.440724	0.730746	0.967382	2.77032	ENSG00000115353	TACR1
ENSG00000115355	14.4848	26.7778	14.3163	30.5962	ENSG00000115355	CCDC88A
ENSG00000115361	1.10898	3.52897	3.95734	4.49215	ENSG00000115361	ACADL
ENSG00000115363	17.8578	13.6735	8.6946	36.7068	ENSG00000115363	EVA1A
ENSG00000115364	28.2146	24.8845	20.095	19.0855	ENSG00000115364	MRPL19
ENSG00000115365	15.6317	21.2708	17.0109	16.1453	ENSG00000115365	LANCL1
ENSG00000115368	23.5261	30.843	32.3734	24.5352	ENSG00000115368	WDR75
ENSG00000115380	67.5475	110.713	42.2616	36.1542	ENSG00000115380	EFEMP1
ENSG00000115386	0	0	0	0.264108	ENSG00000115386	REG1A
ENSG00000115392	12.2259	22.9407	13.4631	18.4429	ENSG00000115392	FANCL
ENSG00000115414	2829.53	1066.74	3734.94	11817.4	ENSG00000115414	FN1
ENSG00000115415	34.7449	72.5087	82.1716	93.2667	ENSG00000115415	STAT1
ENSG00000115419	121.824	130.555	108.31	189.092	ENSG00000115419	GLS
ENSG00000115421	11.799	13.089	9.55978	10.2585	ENSG00000115421	PAPOLG
ENSG00000115423	1.27787	2.53096	1.50153	2.69511	ENSG00000115423	DNAH6
ENSG00000115425	6.27099	9.42675	7.25784	11.4657	ENSG00000115425	PECR
ENSG00000115446	36.4698	35.542	30.1904	17.8796	ENSG00000115446	UNC50
ENSG00000115457	3.91163	17.4457	8.56859	14.0685	ENSG00000115457	IGFBP2
ENSG00000115459	12.3186	20.0624	22.0986	19.573	ENSG00000115459	ELMOD3
ENSG00000115461	0.134622	0.558042	1.08535	6.37823	ENSG00000115461	IGFBP5
ENSG00000115464	43.3205	74.0144	72.6661	104.51	ENSG00000115464	USP34
ENSG00000115468	1.45741	3.50125	3.03085	5.58878	ENSG00000115468	EFHD1
ENSG00000115474	1.43309	3.88573	3.33157	4.24792	ENSG00000115474	KCNJ13
ENSG00000115484	99.0052	85.2955	67.0255	56.9593	ENSG00000115484	CCT4
ENSG00000115486	23.2783	31.6264	25.1039	26.9382	ENSG00000115486	GGCX
ENSG00000115488	0	0.0507817	0.13769	0.115141	ENSG00000115488	NEU2
ENSG00000115504	72.3912	90.3493	46.6388	72.133	ENSG00000115504	EHBP1
ENSG00000115507	4.56656	3.25596	2.70154	3.28821	ENSG00000115507	OTX1
ENSG00000115514	32.6779	25.4783	22.5601	16.7873	ENSG00000115514	TXNDC9
ENSG00000115520	17.6712	11.3432	12.1198	13.4161	ENSG00000115520	COQ10B
ENSG00000115523	1.33205	3.09081	1.88018	4.52669	ENSG00000115523	GNLY
ENSG00000115524	126.802	155.948	134.124	128.185	ENSG00000115524	SF3B1
ENSG00000115525	12.6422	18.5251	9.43868	17.0863	ENSG00000115525	ST3GAL5
ENSG00000115526	2.95296	4.81033	3.66583	5.86049	ENSG00000115526	CHST10
ENSG00000115539	7.80676	6.06445	6.06419	3.8651	ENSG00000115539	PDCL3
ENSG00000115540	17.9282	13.6613	13.567	10.4392	ENSG00000115540	MOB4
ENSG00000115541	36.3323	37.0491	27.894	25.6565	ENSG00000115541	HSPE1
ENSG00000115548	19.8728	23.5598	29.496	22.1432	ENSG00000115548	KDM3A
ENSG00000115556	2.37073	14.6528	6.20566	11.1341	ENSG00000115556	PLCD4
ENSG00000115561	43.1989	40.1561	42.4647	44.9866	ENSG00000115561	CHMP3

ENSG00000115568	9.16892	11.5114	14.6547	11.3124	ENSG00000115568	ZNF142
ENSG00000115590	11.6242	10.2713	3.90253	24.2357	ENSG00000115590	IL1R2
ENSG00000115592	0.441092	1.21536	1.45416	2.03952	ENSG00000115592	PRKAG3
ENSG00000115593	0.331049	0.723007	0.787292	0.935206	ENSG00000115593	SMYD1
ENSG00000115594	2.63057	3.06548	3.21972	21.1844	ENSG00000115594	IL1R1
ENSG00000115596	0.207032	0.226662	0.966507	0.152407	ENSG00000115596	WNT6
ENSG00000115598	2.49968	3.40098	3.97685	1.07245	ENSG00000115598	IL1RL2
ENSG00000115602	3.89556	2.49218	2.14354	5.82374	ENSG00000115602	IL1RL1
ENSG00000115604	3.47001	4.07319	7.06076	5.28466	ENSG00000115604	IL18R1
ENSG00000115607	0	0	0.131097	0.0986296	ENSG00000115607	IL18RAP
ENSG00000115616	0.610358	0.390618	0.146467	0.141536	ENSG00000115616	SLC9A2
ENSG00000115641	31.343	39.9424	42.0579	43.2984	ENSG00000115641	FHL2
ENSG00000115648	9.97896	5.25463	5.8864	35.2523	ENSG00000115648	MLPH
ENSG00000115649	22.819	19.7242	18.4045	9.381	ENSG00000115649	CNPPD1
ENSG00000115652	24.6987	30.5148	28.0557	34.7392	ENSG00000115652	UXS1
ENSG00000115657	6.65446	14.8569	12.4088	8.13388	ENSG00000115657	ABCB6
ENSG00000115661	13.8109	22.9025	18.3368	10.9897	ENSG00000115661	STK16
ENSG00000115665	0.206946	0.142452	0.12233	0.164998	ENSG00000115665	SLC5A7
ENSG00000115677	228.167	238.755	210.302	278.936	ENSG00000115677	HDLBP
ENSG00000115685	32.0232	16.9139	22.6513	20.6018	ENSG00000115685	PPP1R7
ENSG00000115687	4.92298	9.84849	6.20207	10.8649	ENSG00000115687	PASK
ENSG00000115694	116.907	133.066	123.896	105.071	ENSG00000115694	STK25
ENSG00000115705	0.426139	0.867652	0.552762	0.688152	ENSG00000115705	TPO
ENSG00000115718	1.26951	1.30572	1.02835	0.840521	ENSG00000115718	PROC
ENSG00000115738	6.94035	1.92466	2.46642	4.28074	ENSG00000115738	ID2
ENSG00000115750	12.3087	36.0772	15.0144	28.521	ENSG00000115750	TAF1B
ENSG00000115756	7.7653	15.4175	6.51417	17.0255	ENSG00000115756	HPCAL1
ENSG00000115758	58.368	68.6645	48.2219	25.93	ENSG00000115758	ODC1
ENSG00000115760	56.8717	88.5126	73.1273	84.7206	ENSG00000115760	BIRC6
ENSG00000115761	14.5201	17.29	18.5845	19.4942	ENSG00000115761	NOL10
ENSG00000115762	44.5994	26.6072	29.33	29.2807	ENSG00000115762	PLEKHB2
ENSG00000115806	31.5325	23.3477	23.513	20.7274	ENSG00000115806	GORASP2
ENSG00000115808	22.0417	15.8857	13.3318	16.1979	ENSG00000115808	STRN
ENSG00000115816	19.6208	27.6063	24.1958	18.7723	ENSG00000115816	CEBPZ
ENSG00000115825	12.9687	25.0837	15.2242	24.8464	ENSG00000115825	PRKD3
ENSG00000115827	13.7676	16.2877	23.5888	15.9745	ENSG00000115827	DCAF17
ENSG00000115828	6.27748	11.5286	6.65945	8.17379	ENSG00000115828	QPCT
ENSG00000115839	36.7349	53.7952	46.6412	29.7774	ENSG00000115839	RAB3GAP1
ENSG00000115840	9.47403	15.1097	18.626	13.6766	ENSG00000115840	SLC25A12
ENSG00000115841	2.83335	3.65077	3.16422	3.03303	ENSG00000115841	RMDN2
ENSG00000115844	1.49617	1.27961	2.21852	1.25851	ENSG00000115844	DLX2
ENSG00000115850	0.0683866	0.137632	0.143716	0.225434	ENSG00000115850	LCT
ENSG00000115866	45.2999	49.895	46.8943	40.2423	ENSG00000115866	DARS
ENSG00000115875	53.522	70.1219	61.2012	41.9802	ENSG00000115875	SRSF7
ENSG00000115884	1443.68	1175.83	411.645	526.228	ENSG00000115884	SDC1
ENSG00000115896	0.21692	0.254547	0.197172	0.38284	ENSG00000115896	PLCL1
ENSG00000115902	4.42103	43.8738	23.7916	16.6495	ENSG00000115902	SLC1A4
ENSG00000115904	18.8819	20.0122	20.7202	19.473	ENSG00000115904	SOS1
ENSG00000115919	6.50648	4.40889	5.89511	5.48172	ENSG00000115919	KYNU
ENSG00000115935	5.98525	15.0732	9.11425	33.1559	ENSG00000115935	WIPF1
ENSG00000115942	21.4666	26.024	22.3885	27.1628	ENSG00000115942	ORC2
ENSG00000115944	38.7781	42.2982	50.6623	29.7154	ENSG00000115944	COX7A2L
ENSG00000115946	12.1336	15.6526	19.0737	19.3836	ENSG00000115946	PNO1
ENSG00000115947	20.5157	39.9917	30.4449	54.9504	ENSG00000115947	ORC4

ENSG00000115956	0.019141	0.111011	0.100501	0.168365	ENSG00000115956	PLEK
ENSG00000115963	121.026	62.5264	103.91	65.1759	ENSG00000115963	RND3
ENSG00000115966	16.7232	30.5513	20.9457	33.4312	ENSG00000115966	ATF2
ENSG00000115970	11.8106	30.5361	25.1544	31.9962	ENSG00000115970	THADA
ENSG00000115977	16.2653	21.9671	29.2285	24.8413	ENSG00000115977	AAK1
ENSG00000115993	8.5837	12.1035	10.542	14.6868	ENSG00000115993	TRAK2
ENSG00000115998	7.18282	18.4327	11.7544	18.2156	ENSG00000115998	C2orf42
ENSG00000116001	50.9147	81.907	77.7797	77.244	ENSG00000116001	TIA1
ENSG00000116005	37.177	39.7238	26.9392	33.863	ENSG00000116005	PCYOX1
ENSG00000116014	0.271325	0.133993	0.297383	0.297156	ENSG00000116014	KISS1R
ENSG00000116016	24.3609	43.5805	76.3145	42.775	ENSG00000116016	EPAS1
ENSG00000116017	14.9835	16.3742	10.1677	22.59	ENSG00000116017	ARID3A
ENSG00000116030	41.509	36.5684	34.5233	30.7021	ENSG00000116030	SUMO1
ENSG00000116031	0.0151889	0.0585476	0.0396956	0.0999496	ENSG00000116031	CD207
ENSG00000116032	9.42011	2.13502	5.45381	2.95926	ENSG00000116032	GRIN3B
ENSG00000116035	0.10834	0.0760753	0.120245	0.216199	ENSG00000116035	VAX2
ENSG00000116039	0.283739	0.397602	0.569339	1.18897	ENSG00000116039	ATP6V1B1
ENSG00000116044	42.7693	68.3801	83.9945	51.3418	ENSG00000116044	NFE2L2
ENSG00000116062	23.1725	36.9537	23.522	39.587	ENSG00000116062	MSH6
ENSG00000116095	7.90112	7.07843	5.70264	4.0193	ENSG00000116095	PLEKHA3
ENSG00000116096	7.59317	5.41121	4.5376	2.49399	ENSG00000116096	SPR
ENSG00000116106	3.69131	5.07043	16.317	8.82647	ENSG00000116106	EPHA4
ENSG00000116117	2.19351	2.58298	2.70515	6.31056	ENSG00000116117	PARD3B
ENSG00000116120	22.2421	26.3766	26.0629	19.5261	ENSG00000116120	FARSB
ENSG00000116127	5.48382	11.1082	8.94065	10.718	ENSG00000116127	ALMS1
ENSG00000116128	1.33896	0.8595	2.65965	0.337235	ENSG00000116128	BCL9
ENSG00000116132	0.653428	1.86898	2.93295	57.3344	ENSG00000116132	PRRX1
ENSG00000116133	196.822	173.77	97.0327	62.9894	ENSG00000116133	DHCR24
ENSG00000116138	14.2004	19.5351	18.0546	17.985	ENSG00000116138	DNAJC16
ENSG00000116141	4.08702	10.955	10.8072	7.90987	ENSG00000116141	MARK1
ENSG00000116147	0.25975	0.467793	0.593856	0.897622	ENSG00000116147	TNR
ENSG00000116151	9.02032	10.7375	15.4165	14.6754	ENSG00000116151	MORN1
ENSG00000116157	1.26246	1.78568	1.16057	2.37549	ENSG00000116157	GPX7
ENSG00000116161	32.1074	31.1887	14.2556	25.3112	ENSG00000116161	CACYBP
ENSG00000116171	45.1332	25.6883	21.4741	20.4188	ENSG00000116171	SCP2
ENSG00000116176	0	0	0	0.125226	ENSG00000116176	TPSG1
ENSG00000116183	0.206069	0.568826	12.3836	1.4707	ENSG00000116183	PAPPA2
ENSG00000116191	25.1893	17.8514	11.3083	21.2624	ENSG00000116191	RALGPS2
ENSG00000116194	1.28969	1.39353	0.926544	2.57098	ENSG00000116194	ANGPTL1
ENSG00000116198	17.9725	18.2554	24.7118	20.7279	ENSG00000116198	CEP104
ENSG00000116199	24.359	17.6133	10.4176	13.3753	ENSG00000116199	FAM20B
ENSG00000116205	2.84906	4.58123	4.91302	5.99217	ENSG00000116205	TCEANC2
ENSG00000116209	133.557	82.2397	64.5769	34.629	ENSG00000116209	TMEM59
ENSG00000116212	22.0064	21.6388	22.5622	12.8534	ENSG00000116212	LRRC42
ENSG00000116213	7.50135	9.19788	10.5753	5.73087	ENSG00000116213	WRAP73
ENSG00000116218	0	0	0	0	ENSG00000116218	NPHS2
ENSG00000116221	25.5701	25.9594	21.4786	14.6941	ENSG00000116221	MRPL37
ENSG00000116237	46.0901	41.7379	20.9221	17.6734	ENSG00000116237	ICMT
ENSG00000116251	124.038	92.1744	64.6339	46.4711	ENSG00000116251	RPL22
ENSG00000116254	0.571387	0.310906	0.247433	0.319321	ENSG00000116254	CHD5
ENSG00000116260	91.1949	117.974	94.7564	113.781	ENSG00000116260	QSOX1
ENSG00000116266	23.2934	30.7155	33.1663	36.6972	ENSG00000116266	STXBP3
ENSG00000116273	6.60355	6.12181	5.58616	5.7835	ENSG00000116273	PHF13
ENSG00000116285	38.533	75.6636	82.9986	41.2433	ENSG00000116285	ERRFI1

ENSG00000116288	63.5621	72.4072	53.6637	74.207	ENSG00000116288	PARK7
ENSG00000116299	1.17294	1.69323	1.50853	2.72038	ENSG00000116299	KIAA1324
ENSG00000116329	0.0321284	0	0.0279858	0.105668	ENSG00000116329	OPRD1
ENSG00000116337	21.8002	27.7653	38.7196	38.9335	ENSG00000116337	AMPD2
ENSG00000116350	24.3242	37.6408	40.8886	46.7213	ENSG00000116350	SRSF4
ENSG00000116353	20.8026	21.2375	23.7064	18.2823	ENSG00000116353	MECR
ENSG00000116396	7.65997	17.0612	12.2063	20.4301	ENSG00000116396	KCNC4
ENSG00000116406	25.2191	36.7097	27.2256	25.549	ENSG00000116406	EDEM3
ENSG00000116455	30.3085	27.0006	32.784	17.9111	ENSG00000116455	WDR77
ENSG00000116459	124.952	76.2695	52.4044	31.6207	ENSG00000116459	ATP5F1
ENSG00000116473	11.5507	12.3453	10.1378	14.9079	ENSG00000116473	RAP1A
ENSG00000116478	40.242	39.6283	28.0206	32.8025	ENSG00000116478	HDAC1
ENSG00000116489	103.015	87.8335	78.9344	73.8087	ENSG00000116489	CAPZA1
ENSG00000116497	19.8598	45.9567	34.4825	45.6118	ENSG00000116497	S100PBP
ENSG00000116514	24.3749	17.1192	10.8561	9.05592	ENSG00000116514	RNF19B
ENSG00000116521	16.3168	10.1038	11.5246	8.22023	ENSG00000116521	SCAMP3
ENSG00000116525	4.42704	4.59297	4.93182	3.83356	ENSG00000116525	TRIM62
ENSG00000116539	19.9418	29.9164	29.6725	39.9025	ENSG00000116539	ASH1L
ENSG00000116544	0.109687	0.271068	0.337338	0.21324	ENSG00000116544	DLGAP3
ENSG00000116560	132.492	165.026	160.504	171.195	ENSG00000116560	SFPQ
ENSG00000116574	0.236298	0.529966	0.758809	0.997323	ENSG00000116574	RHOU
ENSG00000116580	20.6804	31.219	36.3434	43.5274	ENSG00000116580	GON4L
ENSG00000116584	40.76	81.6583	100.578	67.3971	ENSG00000116584	ARHGEF2
ENSG00000116586	24.9882	20.067	16.1354	12.1118	ENSG00000116586	LAMTOR2
ENSG00000116604	18.2546	17.8116	19.0878	21.107	ENSG00000116604	MEF2D
ENSG00000116641	20.1712	30.6271	21.733	38.6027	ENSG00000116641	DOCK7
ENSG00000116649	26.0749	16.9157	34.3744	28.85	ENSG00000116649	SRM
ENSG00000116652	3.89136	11.8523	6.10812	8.85364	ENSG00000116652	DLEU2L
ENSG00000116661	12.758	23.9347	23.8994	10.7805	ENSG00000116661	FBXO2
ENSG00000116663	12.9661	8.67247	7.87412	8.32855	ENSG00000116663	FBXO6
ENSG00000116667	11.8614	27.4385	20.0245	17.9686	ENSG00000116667	C1orf21
ENSG00000116668	2.10082	3.03656	2.11707	3.3636	ENSG00000116668	SWT1
ENSG00000116670	14.1348	18.9231	14.2607	10.9976	ENSG00000116670	MAD2L2
ENSG00000116675	1.66356	3.48414	4.02692	7.50645	ENSG00000116675	DNAJC6
ENSG00000116678	9.60995	7.58501	7.4889	10.0419	ENSG00000116678	LEPR
ENSG00000116679	83.5971	56.8754	58.9847	125.601	ENSG00000116679	IVNS1ABP
ENSG00000116685	27.7583	28.1794	22.5255	17.108	ENSG00000116685	KIAA2013
ENSG00000116688	42.8158	53.6497	56.8298	26.2803	ENSG00000116688	MFN2
ENSG00000116690	0.105763	0.17573	0.144775	0.100418	ENSG00000116690	PRG4
ENSG00000116691	23.396	22.5295	14.0096	14.3624	ENSG00000116691	MIIP
ENSG00000116698	23.2176	28.1129	31.0255	26.3944	ENSG00000116698	SMG7
ENSG00000116701	22.816	7.93703	5.89418	5.3959	ENSG00000116701	NCF2
ENSG00000116703	0.0513417	0.263899	0.614294	1.33757	ENSG00000116703	PDC
ENSG00000116704	14.9096	15.6091	10.9801	10.3186	ENSG00000116704	SLC35D1
ENSG00000116711	5.35579	6.08477	4.2535	3.46544	ENSG00000116711	PLA2G4A
ENSG00000116717	147.101	81.3769	77.8885	62.9326	ENSG00000116717	GADD45A
ENSG00000116721	0.236449	0.518659	0.143144	0.500833	ENSG00000116721	PRAMEF1
ENSG00000116726	0.0429638	0	0	0	ENSG00000116726	PRAMEF12
ENSG00000116729	33.9846	91.3036	51.9073	55.6859	ENSG00000116729	WLS
ENSG00000116731	13.7031	17.2583	19.4696	25.9204	ENSG00000116731	PRDM2
ENSG00000116741	59.2882	6.50074	5.7939	2.15321	ENSG00000116741	RGS2
ENSG00000116745	0.931242	0.306072	0.295164	0.512268	ENSG00000116745	RPE65
ENSG00000116747	48.0205	39.5266	44.1918	38.0093	ENSG00000116747	TROVE2
ENSG00000116748	0.183412	0	0	0	ENSG00000116748	AMPD1

ENSG00000116750	16.3409	20.7546	24.1433	21.6359	ENSG00000116750	UCHL5
ENSG00000116752	17.8798	13.0581	12.5551	7.48075	ENSG00000116752	BCAS2
ENSG00000116754	70.4683	101.883	108.289	110.898	ENSG00000116754	SRSF11
ENSG00000116761	5.40824	17.7713	19.8533	15.8267	ENSG00000116761	CTH
ENSG00000116771	1.37493	2.63815	2.43788	4.2607	ENSG00000116771	AGMAT
ENSG00000116774	3.53313	3.20773	0.620176	17.3711	ENSG00000116774	OLFML3
ENSG00000116783	0.869486	1.76831	0.899882	2.40784	ENSG00000116783	TNNI3K
ENSG00000116785	0.165887	0.640254	1.23743	0.515637	ENSG00000116785	CFHR3
ENSG00000116786	26.0098	26.4423	30.3796	20.6874	ENSG00000116786	PLEKHM2
ENSG00000116791	9.48727	19.4711	6.96135	12.8984	ENSG00000116791	CRYZ
ENSG00000116793	12.1914	22.8443	13.1031	25.4269	ENSG00000116793	PHTF1
ENSG00000116809	30.7741	39.7761	34.102	33.462	ENSG00000116809	ZBTB17
ENSG00000116815	16.5433	28.8984	19.6105	11.9568	ENSG00000116815	CD58
ENSG00000116819	0.408903	0.640474	0.8908	0.785654	ENSG00000116819	TFAP2E
ENSG00000116824	0.0357873	0	0	0	ENSG00000116824	CD2
ENSG00000116830	14.2243	31.0958	17.9126	17.9511	ENSG00000116830	TTF2
ENSG00000116833	1.64622	2.8575	1.82932	5.21882	ENSG00000116833	NR5A2
ENSG00000116852	0.621701	3.05276	4.2027	2.77658	ENSG00000116852	KIF21B
ENSG00000116857	44.8048	41.5045	32.8186	16.1605	ENSG00000116857	TMEM9
ENSG00000116863	17.5368	11.9963	16.1932	6.63164	ENSG00000116863	ADPRHL2
ENSG00000116871	133.931	121.097	115.373	104.291	ENSG00000116871	MAP7D1
ENSG00000116874	4.5974	6.77271	6.31331	4.07879	ENSG00000116874	WARS2
ENSG00000116882	0.123526	0.118544	0	0.105439	ENSG00000116882	HAO2
ENSG00000116883	8.23487	8.14586	11.7809	8.49117	ENSG00000116883	RP11-268J15.5
ENSG00000116885	6.36977	3.3084	4.91807	8.48223	ENSG00000116885	OSCP1
ENSG00000116898	56.6195	43.6146	32.4459	30.1007	ENSG00000116898	MRPS15
ENSG00000116903	8.63887	7.01615	7.41689	6.27583	ENSG00000116903	EXOC8
ENSG00000116906	20.931	21.7427	15.5148	17.3905	ENSG00000116906	GNPAT
ENSG00000116918	21.8326	14.0693	16.2167	15.6733	ENSG00000116918	TSNAX
ENSG00000116922	18.0417	16.5919	28.6003	16.291	ENSG00000116922	C1orf109
ENSG00000116954	12.9559	12.5687	13.2638	10.6814	ENSG00000116954	RRAGC
ENSG00000116957	22.4623	25.668	28.7174	18.8564	ENSG00000116957	TBCE
ENSG00000116962	1.0115	1.3417	5.168	44.565	ENSG00000116962	NID1
ENSG00000116977	25.154	33.7758	40.1401	32.3305	ENSG00000116977	LGALS8
ENSG00000116981	0	0	0	0	ENSG00000116981	NT5C1A
ENSG00000116983	0	0.0213139	0.0096382	0.0972998	ENSG00000116983	HPCAL4
ENSG00000116984	16.5256	27.2898	25.1369	27.1772	ENSG00000116984	MTR
ENSG00000116985	70.8086	24.4183	36.7255	32.5849	ENSG00000116985	BMP8B
ENSG00000116990	4.44242	4.96329	4.20992	1.84609	ENSG00000116990	MYCL
ENSG00000116991	3.98211	2.48808	4.37912	3.21396	ENSG00000116991	SIPA1L2
ENSG00000116996	0.126553	0.335352	0.137798	0.763161	ENSG00000116996	ZP4
ENSG00000117000	11.4563	9.08519	9.18948	9.24409	ENSG00000117000	RLF
ENSG00000117009	0.813972	1.34122	2.06249	2.11725	ENSG00000117009	KMO
ENSG00000117010	2.09262	7.514	6.17909	9.50169	ENSG00000117010	ZNF684
ENSG00000117013	0.453401	0.113189	0.102582	0.194529	ENSG00000117013	KCNQ4
ENSG00000117016	3.63393	2.09656	1.41402	2.29678	ENSG00000117016	RIMS3
ENSG00000117020	11.8627	20.0947	20.9458	65.1741	ENSG00000117020	AKT3
ENSG00000117036	11.1027	12.7479	10.5275	12.8713	ENSG00000117036	ETV3
ENSG00000117054	18.4784	27.6255	22.6184	25.932	ENSG00000117054	ACADM
ENSG00000117069	6.59995	7.15527	2.95444	3.2553	ENSG00000117069	ST6GALNAC5
ENSG00000117090	0.118525	0.0856665	0.0835944	0.133711	ENSG00000117090	SLAMF1
ENSG00000117091	0.0320688	0.476255	0.242676	0.696714	ENSG00000117091	CD48
ENSG00000117114	33.3381	15.1878	20.937	18.5202	ENSG00000117114	ADGRL2
ENSG00000117115	3.67968	1.45585	0.949852	2.24323	ENSG00000117115	PADI2

ENSG00000117118	50.0153	40.6958	27.7614	18.1071	ENSG00000117118	SDHB
ENSG00000117122	60.1593	60.2515	75.1937	42.4636	ENSG00000117122	MFAP2
ENSG00000117133	19.9985	16.9774	15.891	10.6739	ENSG00000117133	RPF1
ENSG00000117139	60.7393	63.6522	73.1631	59.4974	ENSG00000117139	KDM5B
ENSG00000117143	88.5014	79.912	47.9091	51.8864	ENSG00000117143	UAP1
ENSG00000117148	0	0	0	0	ENSG00000117148	ACTL8
ENSG00000117151	7.95976	9.83633	6.62155	6.78589	ENSG00000117151	CTBS
ENSG00000117152	0.875441	1.14959	1.36895	2.22908	ENSG00000117152	RGS4
ENSG00000117153	13.1744	12.9237	13.1535	8.89728	ENSG00000117153	KLHL12
ENSG00000117154	1.18176	1.36394	1.26239	2.3626	ENSG00000117154	IGSF21
ENSG00000117155	5.60731	12.8601	10.2224	8.78008	ENSG00000117155	SSX2IP
ENSG00000117174	5.69955	8.08667	9.05955	9.65368	ENSG00000117174	ZNHIT6
ENSG00000117215	0.607338	1.93193	1.97774	3.88394	ENSG00000117215	PLA2G2D
ENSG00000117222	6.15502	7.69425	7.24792	9.06495	ENSG00000117222	RBBP5
ENSG00000117226	24.9449	18.3569	18.5072	17.1044	ENSG00000117226	GBP3
ENSG00000117228	6.20035	8.86446	17.0989	15.4397	ENSG00000117228	GBP1
ENSG00000117245	2.6159	8.33183	3.9799	10.01	ENSG00000117245	KIF17
ENSG00000117262	12.9821	16.5172	12.4663	11.7393	ENSG00000117262	GPR89A
ENSG00000117266	11.8294	17.4917	17.3096	17.2278	ENSG00000117266	CDK18
ENSG00000117280	13.1808	17.0566	14.8793	14.9389	ENSG00000117280	RAB29
ENSG00000117281	0.753519	2.14575	2.25517	3.08596	ENSG00000117281	CD160
ENSG00000117289	48.208	62.8905	172.609	40.1313	ENSG00000117289	TXNIP
ENSG00000117298	26.9451	69.5963	72.89	56.7349	ENSG00000117298	ECE1
ENSG00000117305	15.4608	16.557	19.5932	17.4741	ENSG00000117305	HMGCL
ENSG00000117308	50.136	54.8725	30.0255	24.5688	ENSG00000117308	GALE
ENSG00000117318	10.2486	8.97784	21.1824	13.2392	ENSG00000117318	ID3
ENSG00000117322	1.2381	3.3101	3.53946	4.40636	ENSG00000117322	CR2
ENSG00000117335	117.707	141.313	96.5967	83.6162	ENSG00000117335	CD46
ENSG00000117360	18.93	23.0615	25.4913	26.693	ENSG00000117360	PRPF3
ENSG00000117362	44.5299	39.9657	28.2028	12.453	ENSG00000117362	APH1A
ENSG00000117385	41.3115	69.4529	60.3812	109.403	ENSG00000117385	P3H1
ENSG00000117394	553.886	594.007	669.038	274.415	ENSG00000117394	SLC2A1
ENSG00000117395	57.423	65.0212	61.8742	44.4005	ENSG00000117395	EBNA1BP2
ENSG00000117399	11.7473	61.7612	8.28305	15.4799	ENSG00000117399	CDC20
ENSG00000117400	0.126112	0.26925	0.319623	0.430889	ENSG00000117400	MPL
ENSG00000117407	132.481	209.136	195.638	92.2456	ENSG00000117407	ARTN
ENSG00000117408	24.3043	27.4834	43.0574	17.3068	ENSG00000117408	IPO13
ENSG00000117410	109.649	71.7834	55.6078	32.5014	ENSG00000117410	ATP6V0B
ENSG00000117411	32.1785	40.0298	36.5035	20.8402	ENSG00000117411	B4GALT2
ENSG00000117419	23.9812	29.5188	32.5832	28.5561	ENSG00000117419	ERI3
ENSG00000117425	11.429	21.5633	20.8057	10.2654	ENSG00000117425	PTCH2
ENSG00000117448	40.6991	48.1479	31.9308	37.8898	ENSG00000117448	AKR1A1
ENSG00000117450	239.46	168.717	65.6397	94.9751	ENSG00000117450	PRDX1
ENSG00000117461	3.55269	7.15494	11.3507	9.57091	ENSG00000117461	PIK3R3
ENSG00000117472	241.697	95.7069	5.65565	32.5357	ENSG00000117472	TSPAN1
ENSG00000117475	33.7173	23.5742	20.5454	24.7016	ENSG00000117475	BLZF1
ENSG00000117477	0.815271	0.943855	0.793081	0.962747	ENSG00000117477	CCDC181
ENSG00000117479	10.5115	7.17732	5.9314	3.966	ENSG00000117479	SLC19A2
ENSG00000117480	7.67994	10.539	11.9137	4.30591	ENSG00000117480	FAAH
ENSG00000117481	8.03738	12.7332	14.0061	11.0797	ENSG00000117481	NSUN4
ENSG00000117500	35.1261	35.2541	25.7956	19.8838	ENSG00000117500	TMED5
ENSG00000117501	0.0172554	0.099913	0.341247	0.63733	ENSG00000117501	MROH9
ENSG00000117505	23.7486	22.7689	28.7319	18.1398	ENSG00000117505	DR1
ENSG00000117507	0.208154	0.248113	0.313083	0.885073	ENSG00000117507	FMO6P

ENSG00000117519	56.2259	45.6009	15.8107	54.5261	ENSG00000117519	CNN3
ENSG00000117523	60.2114	94.8919	97.7839	117.431	ENSG00000117523	PRRC2C
ENSG00000117525	1629.78	470.362	358.591	563.69	ENSG00000117525	F3
ENSG00000117528	28.7966	28.2637	22.6529	21.3388	ENSG00000117528	ABCD3
ENSG00000117533	4.83409	5.55097	4.11047	4.80012	ENSG00000117533	VAMP4
ENSG00000117543	11.5225	24.4475	21.3381	22.2914	ENSG00000117543	DPH5
ENSG00000117560	0.0944407	0.400114	0.201521	0.389741	ENSG00000117560	FASLG
ENSG00000117569	10.1996	19.4666	17.6477	19.0765	ENSG00000117569	PTBP2
ENSG00000117586	0.239151	1.4731	0.846521	1.78107	ENSG00000117586	TNFSF4
ENSG00000117592	65.3515	70.5542	53.8083	46.8822	ENSG00000117592	PRDX6
ENSG00000117593	11.983	18.2664	11.7319	14.1716	ENSG00000117593	DARS2
ENSG00000117594	2.00127	37.3832	0.281352	2.13097	ENSG00000117594	HSD11B1
ENSG00000117595	367.404	171.326	162.518	108.061	ENSG00000117595	IRF6
ENSG00000117597	6.419	6.20159	6.59452	7.13429	ENSG00000117597	DIEXF
ENSG00000117598	0.848877	0.954713	0.251005	0.830099	ENSG00000117598	PLPPR5
ENSG00000117600	0.0358009	0.149637	0.25501	0.749738	ENSG00000117600	PLPPR4
ENSG00000117601	0.21697	0.13935	0.157457	0.469095	ENSG00000117601	SERPINC1
ENSG00000117602	9.90634	9.25443	8.30789	6.95643	ENSG00000117602	RCAN3
ENSG00000117614	19.367	14.5909	15.474	11.9826	ENSG00000117614	SYF2
ENSG00000117616	69.6578	126.547	94.7376	130.431	ENSG00000117616	RSRP1
ENSG00000117620	56.6046	26.8133	16.3832	15.3363	ENSG00000117620	SLC35A3
ENSG00000117625	26.4451	32.6305	28.8491	44.5409	ENSG00000117625	RCOR3
ENSG00000117632	21.5995	48.877	22.6581	49.7887	ENSG00000117632	STMN1
ENSG00000117640	15.6083	13.9891	17.4291	14.8203	ENSG00000117640	MTFR1L
ENSG00000117643	3.4021	7.35226	5.24087	10.5635	ENSG00000117643	MAN1C1
ENSG00000117650	3.34465	15.9458	3.2958	7.09157	ENSG00000117650	NEK2
ENSG00000117676	30.6454	64.2434	42.4862	27.2166	ENSG00000117676	RPS6KA1
ENSG00000117682	29.7978	25.8257	31.4631	31.717	ENSG00000117682	DHDDS
ENSG00000117691	44.2803	32.4694	16.9409	13.7641	ENSG00000117691	NENF
ENSG00000117697	6.67869	11.4944	7.01148	9.32981	ENSG00000117697	NSL1
ENSG00000117707	2.82933	3.7532	3.32291	8.4281	ENSG00000117707	PROX1
ENSG00000117713	17.7638	21.8093	26.2241	26.4075	ENSG00000117713	ARID1A
ENSG00000117724	6.63244	51.5864	5.00516	27.8945	ENSG00000117724	CENPF
ENSG00000117748	7.69751	7.47663	5.45562	5.47905	ENSG00000117748	RPA2
ENSG00000117751	16.5509	13.452	15.3711	9.20676	ENSG00000117751	PPP1R8
ENSG00000117758	33.0738	18.4199	22.1641	27.1273	ENSG00000117758	STX12
ENSG00000117791	0.965677	2.14727	0.833003	3.20787	ENSG00000117791	MARC2
ENSG00000117834	0.53128	1.09809	1.512	3.56846	ENSG00000117834	SLC5A9
ENSG00000117859	57.2745	74.6752	52.9913	78.4743	ENSG00000117859	OSBPL9
ENSG00000117862	22.8458	39.5243	24.0988	16.2679	ENSG00000117862	TXNDC12
ENSG00000117868	69.1927	71.5866	41.3019	38.6133	ENSG00000117868	ESYT2
ENSG00000117877	8.11817	7.7978	9.17678	11.9953	ENSG00000117877	CD3EAP
ENSG00000117899	16.8143	22.6193	15.3461	12.6315	ENSG00000117899	MESD
ENSG00000117906	50.3018	46.9523	27.2761	28.3272	ENSG00000117906	RCN2
ENSG00000117971	4.23116	8.94476	8.73526	12.2115	ENSG00000117971	CHRNB4
ENSG00000117983	1.08605	2.19978	1.3749	1.90469	ENSG00000117983	MUC5B
ENSG00000117984	633.684	279.909	253.179	144.266	ENSG00000117984	CTSD
ENSG00000118004	1.16146	3.05922	1.87931	2.92508	ENSG00000118004	COLEC11
ENSG00000118007	10.7858	17.1327	15.9055	20.3466	ENSG00000118007	STAG1
ENSG00000118017	0.0643764	0.310156	0.196265	0.282302	ENSG00000118017	A4GNT
ENSG00000118046	34.7566	46.4059	49.322	27.7163	ENSG00000118046	STK11
ENSG00000118058	11.0642	21.0045	17.85	27.5622	ENSG00000118058	KMT2A
ENSG00000118094	0.139851	0.424699	0.484079	1.24052	ENSG00000118094	TREH
ENSG00000118096	6.98574	9.29196	10.4838	9.08705	ENSG00000118096	IFT46

ENSG00000118113	2.21127	2.98979	3.56072	6.12113	ENSG00000118113	MMP8
ENSG00000118137	0.202911	0.0650447	0.10115	0.192351	ENSG00000118137	APOA1
ENSG00000118156	0.123526	0.0137384	0.107047	0.195495	ENSG00000118156	ZNF541
ENSG00000118160	1.06156	1.45023	1.1187	2.45316	ENSG00000118160	SLC8A2
ENSG00000118162	6.40568	5.43438	6.76498	6.83149	ENSG00000118162	KPTN
ENSG00000118181	179.463	162.219	111.06	86.8003	ENSG00000118181	RPS25
ENSG00000118193	2.12831	14.3052	1.41772	5.32841	ENSG00000118193	KIF14
ENSG00000118194	12.2054	4.80939	5.30412	11.334	ENSG00000118194	TNNT2
ENSG00000118197	9.55574	14.4569	9.69661	10.4746	ENSG00000118197	DDX59
ENSG00000118200	39.0123	45.1422	69.1323	36.3506	ENSG00000118200	CAMSAP2
ENSG00000118217	16.4378	23.0659	20.7516	12.387	ENSG00000118217	ATF6
ENSG00000118231	0.112799	0	0.245418	0.121517	ENSG00000118231	CRYGD
ENSG00000118242	18.6277	12.412	14.264	6.7949	ENSG00000118242	MREG
ENSG00000118245	0.207841	0	0	0.220175	ENSG00000118245	TNP1
ENSG00000118246	27.81	24.4782	18.7773	12.9886	ENSG00000118246	FASTKD2
ENSG00000118257	17.3311	50.7401	56.4551	41.0261	ENSG00000118257	NRP2
ENSG00000118260	24.4914	37.6529	25.2583	32.8413	ENSG00000118260	CREB1
ENSG00000118263	45.441	72.9383	64.7259	90.5173	ENSG00000118263	KLF7
ENSG00000118271	0	0.398135	0.0565572	0.59209	ENSG00000118271	TTR
ENSG00000118276	5.9638	7.19222	4.87766	6.97636	ENSG00000118276	B4GALT6
ENSG00000118292	1.01353	0.820569	1.31338	1.9679	ENSG00000118292	C1orf54
ENSG00000118298	2.35892	5.85295	5.61713	8.75898	ENSG00000118298	CA14
ENSG00000118307	0.945308	1.65917	1.11247	2.82741	ENSG00000118307	CASC1
ENSG00000118308	0.647969	0.655845	0.484037	1.62592	ENSG00000118308	LRMP
ENSG00000118322	6.7329	9.69524	10.5275	17.8399	ENSG00000118322	ATP10B
ENSG00000118363	30.7314	25.5642	23.3444	23.3541	ENSG00000118363	SPCS2
ENSG00000118369	7.71423	6.22379	9.23951	6.84825	ENSG00000118369	USP35
ENSG00000118402	34.7069	12.0171	10.7954	7.30293	ENSG00000118402	ELOVL4
ENSG00000118407	0.380995	0.661976	0.753619	1.42213	ENSG00000118407	FILIP1
ENSG00000118418	22.5295	21.6778	34.1487	19.7543	ENSG00000118418	HMGN3
ENSG00000118420	4.00794	7.17491	7.8744	11.8053	ENSG00000118420	UBE3D
ENSG00000118432	0.365962	0.0705683	0.140431	0.296335	ENSG00000118432	CNR1
ENSG00000118434	0.202848	0.195072	0.117509	0.44117	ENSG00000118434	SPACA1
ENSG00000118454	12.6178	8.78528	10.3083	11.1936	ENSG00000118454	ANKRD13C
ENSG00000118473	1.03702	1.93322	2.38504	73.91	ENSG00000118473	SGIP1
ENSG00000118482	19.2348	35.1742	28.5932	34.1607	ENSG00000118482	PHF3
ENSG00000118491	0.404115	0.518171	0.748511	1.09526	ENSG00000118491	ZC2HC1B
ENSG00000118492	1.38657	3.75544	4.02937	3.82651	ENSG00000118492	ADGB
ENSG00000118495	67.9046	39.0697	70.8858	392.698	ENSG00000118495	PLAGL1
ENSG00000118496	3.68518	4.38387	5.61452	5.2557	ENSG00000118496	FBXO30
ENSG00000118503	51.1281	42.1667	50.8241	62.7063	ENSG00000118503	TNFAIP3
ENSG00000118507	3.0083	5.69656	4.6475	8.20122	ENSG00000118507	AKAP7
ENSG00000118508	13.6184	15.6177	18.253	9.32364	ENSG00000118508	RAB32
ENSG00000118513	0.308127	0.789221	0.713612	2.10201	ENSG00000118513	MYB
ENSG00000118514	3.89706	9.52207	6.15415	11.1481	ENSG00000118514	ALDH8A1
ENSG00000118515	53.9483	33.0503	37.2032	38.2324	ENSG00000118515	SGK1
ENSG00000118518	14.6758	23.4824	30.1145	23.9217	ENSG00000118518	RNF146
ENSG00000118520	0.918858	1.13055	1.68242	2.44938	ENSG00000118520	ARG1
ENSG00000118523	24.3173	15.8192	8.43369	248.664	ENSG00000118523	CTGF
ENSG00000118526	0.262219	0.630454	0.435465	0.687059	ENSG00000118526	TCF21
ENSG00000118557	2.92181	6.42967	5.55173	5.67792	ENSG00000118557	PMFBP1
ENSG00000118564	32.4695	47.6196	37.7529	25.5191	ENSG00000118564	FBXL5
ENSG00000118579	8.72233	9.52336	15.0899	14.7969	ENSG00000118579	MED28
ENSG00000118596	12.5114	26.2433	33.0681	44.0146	ENSG00000118596	SLC16A7

ENSG00000118600	16.6827	26.1209	23.0843	23.6037	ENSG00000118600	TMEM5
ENSG00000118620	22.8911	35.6994	26.1541	43.0044	ENSG00000118620	ZNF430
ENSG00000118640	49.9963	17.7275	21.0415	16.0481	ENSG00000118640	VAMP8
ENSG00000118655	2.47758	2.96936	2.98475	2.35573	ENSG00000118655	DCLRE1B
ENSG00000118680	267.298	231.675	150.587	106.364	ENSG00000118680	MYL12B
ENSG00000118689	24.2838	13.8938	18.6407	19.655	ENSG00000118689	FOXO3
ENSG00000118690	2.23303	2.14692	2.06666	4.09257	ENSG00000118690	ARMC2
ENSG00000118702	0	0.122311	0.148179	0.182544	ENSG00000118702	GHRH
ENSG00000118705	146.723	186.231	120.295	85.1229	ENSG00000118705	RPN2
ENSG00000118707	2.41268	4.4436	6.77983	4.89991	ENSG00000118707	TGIF2
ENSG00000118729	0.864965	1.76976	4.54476	10.4448	ENSG00000118729	CASQ2
ENSG00000118733	0.106282	0.282286	0.443543	0.673946	ENSG00000118733	OLFM3
ENSG00000118762	15.3062	28.1053	18.3557	28.9751	ENSG00000118762	PKD2
ENSG00000118777	0.886869	2.37249	1.22544	1.343	ENSG00000118777	ABCG2
ENSG00000118785	0.692644	0.214125	0.130666	0.500559	ENSG00000118785	SPP1
ENSG00000118804	2.85499	1.60638	1.31496	1.08157	ENSG00000118804	STBD1
ENSG00000118816	74.6245	90.3043	65.0565	83.0214	ENSG00000118816	CCNI
ENSG00000118849	12.5912	0.529855	5.12674	3.26215	ENSG00000118849	RARRES1
ENSG00000118855	53.8163	42.3101	42.0429	28.731	ENSG00000118855	MFSD1
ENSG00000118873	24.562	33.1811	34.4525	37.1233	ENSG00000118873	RAB3GAP2
ENSG00000118894	10.2033	10.6384	13.5111	6.53732	ENSG00000118894	EEF2KMT
ENSG00000118898	154.108	62.1244	66.162	35.521	ENSG00000118898	PPL
ENSG00000118900	22.9125	24.7608	27.6705	20.5869	ENSG00000118900	UBN1
ENSG00000118903	0	0.156038	0.281715	0	ENSG00000118903	BTF3P11
ENSG00000118922	5.07294	8.5797	6.38707	10.44	ENSG00000118922	KLF12
ENSG00000118939	29.4776	29.4795	26.6508	21.0887	ENSG00000118939	UCHL3
ENSG00000118946	0.102692	0.156881	0.234134	0.435823	ENSG00000118946	PCDH17
ENSG00000118960	13.3662	17.9392	14.6398	16.9332	ENSG00000118960	HS1BP3
ENSG00000118961	9.75869	12.5082	9.18921	8.20854	ENSG00000118961	LDAH
ENSG00000118965	3.32194	9.00304	8.30361	8.39287	ENSG00000118965	WDR35
ENSG00000118971	146.012	169.455	241.22	109.765	ENSG00000118971	CCND2
ENSG00000118972	0.300093	0.362876	0.552419	0.371161	ENSG00000118972	FGF23
ENSG00000118976	0.0383384	0.357201	0.341285	0.258802	ENSG00000118976	HIN1L
ENSG00000118985	63.853	93.5354	87.4311	88.4105	ENSG00000118985	ELL2
ENSG00000118990	0	0	0	0	ENSG00000118990	GLRXP3
ENSG00000118997	2.45248	4.42948	4.39422	6.31258	ENSG00000118997	DNAH7
ENSG00000119004	13.3549	14.6219	14.4248	15.6527	ENSG00000119004	CYP20A1
ENSG00000119013	45.4381	30.3657	17.1148	21.4856	ENSG00000119013	NDUFB3
ENSG00000119041	45.4866	64.9702	69.9677	68.7063	ENSG00000119041	GTF3C3
ENSG00000119042	4.14205	9.46495	8.63253	20.4481	ENSG00000119042	SATB2
ENSG00000119048	18.8253	22.5538	28.1973	27.2241	ENSG00000119048	UBE2B
ENSG00000119121	1.92191	2.31778	2.35038	4.16959	ENSG00000119121	TRPM6
ENSG00000119125	4.85434	6.72448	6.79819	10.1986	ENSG00000119125	GDA
ENSG00000119138	2.47808	4.80328	5.08967	11.1362	ENSG00000119138	KLF9
ENSG00000119139	92.9388	64.2359	41.8977	55.6842	ENSG00000119139	TJP2
ENSG00000119147	5.34823	12.6586	10.9415	14.9417	ENSG00000119147	C2orf40
ENSG00000119185	42.1877	25.1604	26.5492	28.9164	ENSG00000119185	ITGB1BP1
ENSG00000119203	21.4626	23.0314	20.8432	15.5839	ENSG00000119203	CPSF3
ENSG00000119227	1.97928	2.48654	3.92683	2.88855	ENSG00000119227	PIGZ
ENSG00000119231	20.5402	19.7091	25.493	24.4681	ENSG00000119231	SENP5
ENSG00000119242	7.15059	7.15665	11.7924	10.1555	ENSG00000119242	CCDC92
ENSG00000119280	10.2346	9.16049	10.4627	24.5452	ENSG00000119280	C1orf198
ENSG00000119283	0.207848	0.392567	0.25269	0.687623	ENSG00000119283	TRIM67
ENSG00000119285	22.1168	29.6243	36.2814	26.9638	ENSG00000119285	HEATR1

ENSG00000119314	36.3459	32.6878	28.569	30.1361	ENSG00000119314	PTBP3
ENSG00000119318	97.2764	74.1202	69.375	47.5288	ENSG00000119318	RAD23B
ENSG00000119321	22.0704	19.4927	20.0802	17.7227	ENSG00000119321	FKBP15
ENSG00000119326	17.8238	40.6905	12.5718	23.8099	ENSG00000119326	CTNNAL1
ENSG00000119328	11.2408	11.1061	12.4289	7.49436	ENSG00000119328	FAM206A
ENSG00000119333	14.9476	28.6951	11.6205	13.6179	ENSG00000119333	WDR34
ENSG00000119335	195.57	184.27	173.817	122.11	ENSG00000119335	SET
ENSG00000119383	44.4111	49.6272	45.194	51.5529	ENSG00000119383	PTPA
ENSG00000119392	9.76072	12.7784	9.21547	7.86315	ENSG00000119392	GLE1
ENSG00000119396	14.1852	15.9681	15.7985	16.9666	ENSG00000119396	RAB14
ENSG00000119397	3.10458	17.2307	8.12444	9.96255	ENSG00000119397	CNTRL
ENSG00000119401	7.68914	9.80001	10.9103	8.83219	ENSG00000119401	TRIM32
ENSG00000119402	18.7726	27.4833	29.7846	24.287	ENSG00000119402	FBXW2
ENSG00000119403	8.18171	22.8729	9.16721	14.5759	ENSG00000119403	PHF19
ENSG00000119408	9.25214	15.3123	8.87224	26.4057	ENSG00000119408	NEK6
ENSG00000119411	4.12779	1.89912	1.76949	2.51624	ENSG00000119411	BSPRY
ENSG00000119414	29.764	21.2508	16.1206	9.90319	ENSG00000119414	PPP6C
ENSG00000119421	15.3855	9.95604	8.93549	10.2319	ENSG00000119421	NDUFA8
ENSG00000119431	11.9602	8.00583	9.10045	3.99932	ENSG00000119431	HDHD3
ENSG00000119440	0	0	0	0	ENSG00000119440	LCN1P1
ENSG00000119446	11.5302	8.66206	8.77137	5.82639	ENSG00000119446	RBM18
ENSG00000119457	0.0477741	0.201188	0.141883	0.0333555	ENSG00000119457	SLC46A2
ENSG00000119471	9.72432	11.7923	9.55917	8.30692	ENSG00000119471	HSDL2
ENSG00000119487	68.2356	64.9266	40.1304	56.8947	ENSG00000119487	MAPKAP1
ENSG00000119508	0.275015	0.207648	0.192618	0.501672	ENSG00000119508	NR4A3
ENSG00000119509	10.5303	13.5444	13.4035	16.1213	ENSG00000119509	INVS
ENSG00000119514	1.30251	1.37829	0.763032	0.555484	ENSG00000119514	GALNT12
ENSG00000119522	5.7191	11.8533	11.1571	16.8359	ENSG00000119522	DENND1A
ENSG00000119523	27.9072	26.2858	28.8425	11.275	ENSG00000119523	ALG2
ENSG00000119535	3.40168	6.86962	6.49944	13.8536	ENSG00000119535	CSF3R
ENSG00000119537	59.4871	53.3609	33.6306	29.7516	ENSG00000119537	KDSR
ENSG00000119541	90.0807	42.4406	37.258	37.0243	ENSG00000119541	VPS4B
ENSG00000119547	0.115287	0.499869	0.176918	0.790506	ENSG00000119547	ONECUT2
ENSG00000119559	32.5457	42.8997	48.2858	52.7641	ENSG00000119559	C19orf25
ENSG00000119574	8.43269	7.47764	8.05342	6.17333	ENSG00000119574	ZBTB45
ENSG00000119596	17.1647	34.0058	29.2532	46.5882	ENSG00000119596	YLPM1
ENSG00000119599	8.26283	16.3037	23.6603	21.4154	ENSG00000119599	DCAF4
ENSG00000119608	0.977256	1.2648	1.33885	1.68391	ENSG00000119608	PROX2
ENSG00000119614	0.0182988	0.0529085	0	0.0201141	ENSG00000119614	VSX2
ENSG00000119616	12.88	16.9888	19.5242	20.3285	ENSG00000119616	FCF1
ENSG00000119630	10.2876	34.8671	30.8113	17.9003	ENSG00000119630	PGF
ENSG00000119632	50.4196	43.7955	29.0196	21.7441	ENSG00000119632	IFI27L2
ENSG00000119636	1.76021	2.88418	3.7017	4.99606	ENSG00000119636	BBOF1
ENSG00000119638	10.4568	22.0147	18.7739	24.2095	ENSG00000119638	NEK9
ENSG00000119640	9.85664	18.2955	14.1279	20.6616	ENSG00000119640	ACYP1
ENSG00000119650	23.1727	28.2131	27.8524	26.1533	ENSG00000119650	IFT43
ENSG00000119655	152.508	144.114	33.8468	40.1305	ENSG00000119655	NPC2
ENSG00000119660	0	0	0	0	ENSG00000119660	DPPA5P4
ENSG00000119661	11.2496	13.9893	13.8158	21.2101	ENSG00000119661	DNAL1
ENSG00000119669	10.914	25.8457	16.8298	15.2629	ENSG00000119669	IRF2BPL
ENSG00000119673	3.02587	3.1675	4.184	5.39442	ENSG00000119673	ACOT2
ENSG00000119681	77.2844	75.7256	69.0373	159.424	ENSG00000119681	LTBP2
ENSG00000119682	30.9688	39.4095	35.9468	47.8193	ENSG00000119682	AREL1
ENSG00000119684	9.77808	11.0688	12.892	8.09688	ENSG00000119684	MLH3

ENSG00000119685	19.4283	27.0408	18.5977	41.4794	ENSG00000119685	TTLL5
ENSG00000119686	2.05904	0.944088	1.69821	1.22891	ENSG00000119686	FLVCR2
ENSG00000119688	24.9786	34.5812	30.9062	34.1611	ENSG00000119688	ABCD4
ENSG00000119689	41.7749	73.671	53.6764	71.1743	ENSG00000119689	DLST
ENSG00000119698	4.4826	19.1167	16.0876	9.84603	ENSG00000119698	PPP4R4
ENSG00000119699	2.57732	5.48405	3.36759	8.44168	ENSG00000119699	TGFB3
ENSG00000119703	0.838874	1.38667	0.916258	1.5346	ENSG00000119703	ZC2HC1C
ENSG00000119705	75.0784	84.7529	73.1427	75.5286	ENSG00000119705	SLIRP
ENSG00000119707	31.9368	43.8432	47.79	40.9765	ENSG00000119707	RBM25
ENSG00000119711	6.75163	10.4975	5.29928	11.0784	ENSG00000119711	ALDH6A1
ENSG00000119714	3.58024	11.5413	5.7831	6.36873	ENSG00000119714	GPR68
ENSG00000119715	0.604375	0.226218	0.361036	0.303429	ENSG00000119715	ESRRB
ENSG00000119718	21.9064	23.401	22.7914	18.329	ENSG00000119718	EIF2B2
ENSG00000119720	6.26988	8.74462	10.2286	13.7045	ENSG00000119720	NRDE2
ENSG00000119723	20.6803	32.3981	32.537	39.5489	ENSG00000119723	COQ6
ENSG00000119725	35.074	40.8815	45.0322	33.9295	ENSG00000119725	ZNF410
ENSG00000119729	23.1645	28.72	36.0907	45.4181	ENSG00000119729	RHOQ
ENSG00000119737	2.05828	2.0656	2.03545	2.6507	ENSG00000119737	GPR75
ENSG00000119760	17.5094	20.8293	21.1225	14.2099	ENSG00000119760	SUPT7L
ENSG00000119771	5.94067	6.04344	9.05993	5.38454	ENSG00000119771	KLHL29
ENSG00000119772	5.06752	9.17468	10.388	11.2046	ENSG00000119772	DNMT3A
ENSG00000119777	40.1897	41.0002	32.8308	36.3173	ENSG00000119777	TMEM214
ENSG00000119778	19.3961	42.2313	38.2654	49.3891	ENSG00000119778	ATAD2B
ENSG00000119782	6.13733	4.77383	2.07711	2.52676	ENSG00000119782	FKBP1B
ENSG00000119787	119.505	92.2838	72.8078	71.7454	ENSG00000119787	ATL2
ENSG00000119801	41.3117	26.7817	34.1585	24.6003	ENSG00000119801	YPEL5
ENSG00000119812	17.585	13.9083	13.7413	28.4712	ENSG00000119812	FAM98A
ENSG00000119820	30.6501	27.4153	24.1537	16.8387	ENSG00000119820	YIPF4
ENSG00000119844	14.7124	12.3807	14.5451	9.06455	ENSG00000119844	AFTPH
ENSG00000119862	32.1868	9.80056	12.6345	6.13152	ENSG00000119862	LGALSL
ENSG00000119865	0.230715	0.634787	1.19555	5.45988	ENSG00000119865	CNRIP1
ENSG00000119866	3.78086	10.7471	13.3292	8.02119	ENSG00000119866	BCL11A
ENSG00000119878	5.57999	3.70207	3.67459	5.43583	ENSG00000119878	CRIPT
ENSG00000119888	6.84329	22.0306	3.38125	1.82568	ENSG00000119888	EPCAM
ENSG00000119899	14.2387	8.01208	3.67734	8.37832	ENSG00000119899	SLC17A5
ENSG00000119900	7.30795	8.39478	14.6625	11.0289	ENSG00000119900	OGFRL1
ENSG00000119906	12.3525	23.4173	20.3591	25.479	ENSG00000119906	SLF2
ENSG00000119912	20.8609	27.9686	20.6622	23.2156	ENSG00000119912	IDE
ENSG00000119913	1.18918	0.881128	0.583352	2.04951	ENSG00000119913	TECTB
ENSG00000119915	0.342574	0.536146	0.596424	0.328749	ENSG00000119915	ELOVL3
ENSG00000119917	5.12871	10.9565	11.125	12.2011	ENSG00000119917	IFIT3
ENSG00000119919	0.801056	0.832232	0.31739	9.78213	ENSG00000119919	NKX2-3
ENSG00000119922	1.13704	1.12657	8.42691	0.94503	ENSG00000119922	IFIT2
ENSG00000119927	6.34621	5.70359	4.99812	5.98588	ENSG00000119927	GPAM
ENSG00000119929	6.93031	8.6556	6.92118	8.74054	ENSG00000119929	CUTC
ENSG00000119938	0.965315	1.35394	7.91135	2.10754	ENSG00000119938	PPP1R3C
ENSG00000119943	8.09147	20.1312	12.8359	18.5324	ENSG00000119943	PYROXD2
ENSG00000119946	0.50735	0.647482	0.743443	1.84335	ENSG00000119946	CNNM1
ENSG00000119950	10.8876	6.53397	9.74861	8.36154	ENSG00000119950	MXI1
ENSG00000119953	8.32652	11.253	11.3279	12.1677	ENSG00000119953	SMNDC1
ENSG00000119965	9.32539	5.73152	7.7559	10.8972	ENSG00000119965	C10orf88
ENSG00000119969	8.52717	27.544	10.5043	29.814	ENSG00000119969	HELLS
ENSG00000119973	0	0.0305424	0.0248233	0.0347523	ENSG00000119973	PRLHR
ENSG00000119977	18.1023	22.1366	16.6338	11.0327	ENSG00000119977	TCTN3

ENSG00000119979	42.3773	26.5771	23.6929	23.4539	ENSG00000119979	FAM45A
ENSG00000119986	42.9392	11.8612	14.7669	6.21497	ENSG00000119986	AVPI1
ENSG00000120008	44.9423	58.6801	50.9857	54.2929	ENSG00000120008	WDR11
ENSG00000120029	5.2314	7.94297	8.47229	11.6812	ENSG00000120029	C10orf76
ENSG00000120049	1.38677	2.14387	2.86397	4.40067	ENSG00000120049	KCNIP2
ENSG00000120051	0.230236	0.508616	0.630891	0.669434	ENSG00000120051	CFAP58
ENSG00000120053	10.2954	22.7928	21.1747	10.4613	ENSG00000120053	GOT1
ENSG00000120054	0.101753	0	0.0882815	0.0341362	ENSG00000120054	CPN1
ENSG00000120055	3.02998	2.73298	3.33396	0.887801	ENSG00000120055	C10orf95
ENSG00000120057	0.748919	0.490973	0.622679	0.644643	ENSG00000120057	SFRP5
ENSG00000120063	13	16.4453	12.6599	9.31865	ENSG00000120063	GNA13
ENSG00000120068	0.151079	0.496272	0.523099	0.403907	ENSG00000120068	HOXB8
ENSG00000120071	28.8315	45.6647	85.1361	69.1373	ENSG00000120071	KANSL1
ENSG00000120075	0.388696	0.388079	0.393346	1.5076	ENSG00000120075	HOXB5
ENSG00000120088	0.248086	0.157127	0.154641	0.0430247	ENSG00000120088	CRHR1
ENSG00000120093	1.57918	1.71022	4.62608	36.9063	ENSG00000120093	HOXB3
ENSG00000120094	0.195151	0.147304	0.121451	0.389596	ENSG00000120094	HOXB1
ENSG00000120129	24.231	11.1028	8.38465	9.60921	ENSG00000120129	DUSP1
ENSG00000120137	43.0771	26.5187	34.1728	31.9361	ENSG00000120137	PANK3
ENSG00000120149	0.946876	1.18074	1.08015	1.96552	ENSG00000120149	MSX2
ENSG00000120156	0.271326	0.222962	0.175609	0.334086	ENSG00000120156	TEK
ENSG00000120158	7.19941	12.8556	18.2405	14.0368	ENSG00000120158	RCL1
ENSG00000120159	7.3512	11.2168	13.8439	6.79856	ENSG00000120159	CAAP1
ENSG00000120160	0.161579	0.721306	0.940948	0.427256	ENSG00000120160	EQTN
ENSG00000120162	8.86293	12.0692	12.4191	12.8822	ENSG00000120162	MOB3B
ENSG00000120210	5.23397	15.3691	15.4737	15.4041	ENSG00000120210	INSL6
ENSG00000120211	0.565815	1.84033	2.16365	3.43244	ENSG00000120211	INSL4
ENSG00000120215	6.2307	9.10103	10.1306	11.5547	ENSG00000120215	MLANA
ENSG00000120217	9.20001	23.9348	14.8108	18.2844	ENSG00000120217	CD274
ENSG00000120235	0.113731	0.576125	0.338693	0.505485	ENSG00000120235	IFNA6
ENSG00000120242	0.0589988	0.0567735	0	0	ENSG00000120242	IFNA8
ENSG00000120251	1.61895	1.72469	1.88076	2.52666	ENSG00000120251	GRIA2
ENSG00000120253	13.018	19.2193	16.4906	16.92	ENSG00000120253	NUP43
ENSG00000120254	14.8949	40.6768	55.4573	34.1549	ENSG00000120254	MTHFD1L
ENSG00000120256	101.224	81.1491	65.2602	38.5343	ENSG00000120256	LRP11
ENSG00000120262	0.386331	0.932086	0.629858	1.25071	ENSG00000120262	CCDC170
ENSG00000120265	41.0774	50.3686	34.8495	30.2044	ENSG00000120265	PCMT1
ENSG00000120278	4.82152	3.60425	7.09651	2.81278	ENSG00000120278	PLEKHG1
ENSG00000120279	1.33916	3.35897	2.17818	4.54243	ENSG00000120279	MYCT1
ENSG00000120280	0.228362	0.62704	0.804978	1.30066	ENSG00000120280	CXorf21
ENSG00000120289	0.0762011	0.0490258	0.175966	0.0555962	ENSG00000120289	MAGEB4
ENSG00000120306	16.7141	19.3801	13.8607	13.9013	ENSG00000120306	CYSTM1
ENSG00000120314	13.2912	12.1713	13.8288	12.9743	ENSG00000120314	WDR55
ENSG00000120318	2.5884	8.78059	7.77886	9.53102	ENSG00000120318	ARAP3
ENSG00000120322	0	0.0109423	0	0.0702223	ENSG00000120322	PCDHB8
ENSG00000120324	0.0890643	0.059008	0.110826	0.184549	ENSG00000120324	PCDHB10
ENSG00000120327	0.422639	0.159446	0.510084	0.263305	ENSG00000120327	PCDHB14
ENSG00000120328	0.137383	0.0578632	0.120017	0.111703	ENSG00000120328	PCDHB12
ENSG00000120329	0.0412544	0.238401	0.107747	0.180542	ENSG00000120329	SLC25A2
ENSG00000120332	0.0855716	0.0619013	0.0995348	0.0942746	ENSG00000120332	TNN
ENSG00000120333	10.6556	9.55355	8.09858	5.02132	ENSG00000120333	MRPS14
ENSG00000120334	6.23803	9.97241	6.42903	8.12007	ENSG00000120334	CENPL
ENSG00000120337	0.116293	0.273239	0.201311	0.72654	ENSG00000120337	TNFSF18
ENSG00000120341	3.49583	8.29803	5.92598	10.4795	ENSG00000120341	SEC16B

ENSG00000120370	5.55101	7.55019	6.5305	8.09794	ENSG00000120370	GORAB
ENSG00000120436	0.0546122	0.315814	0.190338	0.329652	ENSG00000120436	GPR31
ENSG00000120437	56.4299	40.9828	5.23881	24.7699	ENSG00000120437	ACAT2
ENSG00000120438	135.404	98.4563	89.5776	82.639	ENSG00000120438	TCP1
ENSG00000120440	0.0621225	0.207266	0.145015	0.275823	ENSG00000120440	TTLL2
ENSG00000120451	50.9655	56.6928	61.0575	42.5927	ENSG00000120451	SNX19
ENSG00000120457	1.06966	4.5049	15.4308	3.11843	ENSG00000120457	KCNJ5
ENSG00000120458	4.17373	9.41938	7.09457	9.05967	ENSG00000120458	MSANTD2
ENSG00000120471	3.5683	22.2551	28.5615	6.50751	ENSG00000120471	TP53AIP1
ENSG00000120498	0.0716389	0.174637	0.236535	0.378998	ENSG00000120498	TEX11
ENSG00000120500	1.64466	2.02158	1.29337	2.64147	ENSG00000120500	ARR3
ENSG00000120509	19.1585	14.325	10.2258	10.7648	ENSG00000120509	PDZD11
ENSG00000120519	11.4636	16.3881	9.74952	12.0405	ENSG00000120519	SLC10A7
ENSG00000120526	16.1368	17.3727	10.6502	13.1255	ENSG00000120526	NUDCD1
ENSG00000120533	32.8109	33.2469	26.1459	32.8017	ENSG00000120533	ENY2
ENSG00000120539	5.1512	10.7568	4.97016	7.09998	ENSG00000120539	MASTL
ENSG00000120549	22.9341	37.5634	48.3882	37.6506	ENSG00000120549	KIAA1217
ENSG00000120555	1.88893	3.91148	3.34121	2.65135	ENSG00000120555	SEPT7P9
ENSG00000120563	0	0	0	0	ENSG00000120563	LYZL1
ENSG00000120586	0.0550266	0.0225683	0.0497898	0.0569968	ENSG00000120586	MRC1
ENSG00000120594	3.58896	3.55075	14.8201	2.80004	ENSG00000120594	PLXDC2
ENSG00000120616	12.6393	20.787	17.7694	19.7116	ENSG00000120616	EPC1
ENSG00000120645	0.172798	0.250039	0.205375	0.302439	ENSG00000120645	IQSEC3
ENSG00000120647	11.8426	22.8793	19.826	24.7756	ENSG00000120647	CCDC77
ENSG00000120656	11.5675	13.8615	11.309	10.7071	ENSG00000120656	TAF12
ENSG00000120658	0.497225	0.955189	1.08163	2.25271	ENSG00000120658	ENOX1
ENSG00000120659	0.203676	0.462986	1.12657	1.03804	ENSG00000120659	TNFSF11
ENSG00000120662	12.0534	15.4886	15.6305	13.4737	ENSG00000120662	MTRF1
ENSG00000120664	0.272686	0.686501	1.1004	0.767559	ENSG00000120664	SPG20-AS1
ENSG00000120669	0.764456	1.52505	1.16659	1.66032	ENSG00000120669	SOHLH2
ENSG00000120675	12.7456	10.7213	5.97081	9.21594	ENSG00000120675	DNAJC15
ENSG00000120685	14.529	20.1213	27.4696	21.1215	ENSG00000120685	PROSER1
ENSG00000120686	49.1827	44.3113	47.9743	36.4266	ENSG00000120686	UFM1
ENSG00000120688	7.32126	7.80455	6.71366	6.81803	ENSG00000120688	WBP4
ENSG00000120690	28.7191	27.4341	32.5871	18.5648	ENSG00000120690	ELF1
ENSG00000120693	1.02243	1.29416	1.83039	1.93271	ENSG00000120693	SMAD9
ENSG00000120694	57.7647	30.1581	34.7145	41.9647	ENSG00000120694	HSPH1
ENSG00000120696	2.32039	2.597	2.03101	2.21942	ENSG00000120696	KBTBD7
ENSG00000120697	25.3276	31.9044	20.2399	18.0852	ENSG00000120697	ALG5
ENSG00000120699	14.6121	43.1535	36.1419	22.5769	ENSG00000120699	EXOSC8
ENSG00000120705	68.0346	53.7492	68.7081	34.8371	ENSG00000120705	ETF1
ENSG00000120708	333.927	194.093	652.762	354.157	ENSG00000120708	TGFBI
ENSG00000120709	14.4491	18.9282	18.8494	20.0222	ENSG00000120709	FAM53C
ENSG00000120725	42.5928	74.5934	64.0595	58.7471	ENSG00000120725	SIL1
ENSG00000120727	13.8212	10.6631	14.7996	18.6016	ENSG00000120727	PAIP2
ENSG00000120729	2.34395	3.27241	4.33347	2.30699	ENSG00000120729	MYOT
ENSG00000120733	22.5874	29.0845	28.0007	31.7076	ENSG00000120733	KDM3B
ENSG00000120738	5.24448	54.8398	18.5438	38.7413	ENSG00000120738	EGR1
ENSG00000120742	62.8108	44.8611	42.6636	43.4072	ENSG00000120742	SERP1
ENSG00000120756	11.9076	15.3993	5.41303	9.6225	ENSG00000120756	PLS1
ENSG00000120784	11.8555	19.0973	16.5365	22.6079	ENSG00000120784	ZFP30
ENSG00000120798	23.1712	30.6671	26.405	37.3226	ENSG00000120798	NR2C1
ENSG00000120800	13.897	17.5355	12.9575	15.4176	ENSG00000120800	UTP20
ENSG00000120802	23.8259	60.5426	17.1462	33.6827	ENSG00000120802	TMPO

ENSG00000120805	45.0652	41.5295	35.1454	47.4681	ENSG00000120805	ARL1
ENSG00000120820	1.65193	3.27029	7.7004	13.2225	ENSG00000120820	GLT8D2
ENSG00000120832	3.38904	7.04237	5.28741	5.52949	ENSG00000120832	MTERF2
ENSG00000120833	5.5989	7.16943	8.31723	5.38925	ENSG00000120833	SOCS2
ENSG00000120837	9.24869	13.8681	13.3739	9.65716	ENSG00000120837	NFYB
ENSG00000120860	24.7629	31.0102	29.8278	25.5128	ENSG00000120860	WASHC3
ENSG00000120868	9.59518	15.3009	9.4006	19.7492	ENSG00000120868	APAF1
ENSG00000120875	45.2686	23.703	6.32746	28.3218	ENSG00000120875	DUSP4
ENSG00000120885	12.604	12.1561	3.89262	6.4951	ENSG00000120885	CLU
ENSG00000120889	90.2892	161.145	151.083	86.812	ENSG00000120889	TNFRSF10B
ENSG00000120896	31.419	34.9107	35.0175	29.4433	ENSG00000120896	SORBS3
ENSG00000120899	36.5518	32.5396	22.5482	22.218	ENSG00000120899	PTK2B
ENSG00000120903	10.3635	16.9212	22.0187	33.1438	ENSG00000120903	CHRNA2
ENSG00000120907	2.20053	3.47217	3.51736	4.97329	ENSG00000120907	ADRA1A
ENSG00000120910	17.4346	12.8726	11.9553	12.9245	ENSG00000120910	PPP3CC
ENSG00000120913	40.4498	35.2498	25.2638	21.6564	ENSG00000120913	PDLIM2
ENSG00000120915	12.1688	19.099	16.1633	20.9187	ENSG00000120915	EPHX2
ENSG00000120925	20.3748	13.7294	11.7617	12.033	ENSG00000120925	RNF170
ENSG00000120937	0.0970036	0.314684	0	0.278893	ENSG00000120937	NPPB
ENSG00000120942	5.71524	9.00704	8.44299	5.65357	ENSG00000120942	UBIAD1
ENSG00000120948	32.5788	38.7391	43.7428	48.2482	ENSG00000120948	TARDBP
ENSG00000120949	0.0756018	0.141823	0.180609	0.177063	ENSG00000120949	TNFRSF8
ENSG00000120952	0.0349903	0	0	0	ENSG00000120952	PRAMEF2
ENSG00000120963	36.8944	41.2837	41.6123	30.8581	ENSG00000120963	ZNF706
ENSG00000120992	80.8016	53.9537	45.5682	47.7289	ENSG00000120992	LYPLA1
ENSG00000121005	1.34531	0.581132	1.17399	0.744926	ENSG00000121005	CRISPLD1
ENSG00000121022	27.5775	25.6877	26.3249	18.1392	ENSG00000121022	COPS5
ENSG00000121039	20.0276	15.9224	11.7655	7.89812	ENSG00000121039	RDH10
ENSG00000121053	0.122103	0.294312	0.301564	0.0894779	ENSG00000121053	EPX
ENSG00000121057	17.5724	25.5199	21.1393	15.3726	ENSG00000121057	AKAP1
ENSG00000121058	7.17983	7.33826	5.9327	5.75746	ENSG00000121058	COIL
ENSG00000121060	27.9726	71.8662	55.4344	53.6899	ENSG00000121060	TRIM25
ENSG00000121064	30.204	61.543	66.5508	41.9123	ENSG00000121064	SCPEP1
ENSG00000121067	17.6572	32.1001	29.5496	40.7364	ENSG00000121067	SPOP
ENSG00000121068	0.204003	0.197849	0.213357	8.22371	ENSG00000121068	TBX2
ENSG00000121073	45.0117	57.4295	28.2855	21.0345	ENSG00000121073	SLC35B1
ENSG00000121075	1.01847	2.28506	2.51848	2.85935	ENSG00000121075	TBX4
ENSG00000121089	0.43436	0.313915	0.546011	0.494938	ENSG00000121089	NACA3P
ENSG00000121101	2.23582	5.49421	6.98645	8.39085	ENSG00000121101	TEX14
ENSG00000121104	4.78233	5.45685	3.986	9.68718	ENSG00000121104	FAM117A
ENSG00000121152	1.87324	7.27374	1.33278	6.15386	ENSG00000121152	NCAPH
ENSG00000121207	13.1176	3.20815	4.62143	3.83933	ENSG00000121207	LRAT
ENSG00000121210	8.47166	13.6123	28.2877	15.0707	ENSG00000121210	TMEM131L
ENSG00000121211	1.9188	6.99026	0.894524	5.31371	ENSG00000121211	MND1
ENSG00000121236	1.89105	2.99302	3.9701	2.81427	ENSG00000121236	TRIM6
ENSG00000121270	0.901484	2.01923	1.97544	3.06842	ENSG00000121270	ABCC11
ENSG00000121274	8.17685	6.17994	7.55766	7.71465	ENSG00000121274	PAPD5
ENSG00000121281	42.9336	41.1728	48.8017	43.6846	ENSG00000121281	ADCY7
ENSG00000121289	12.6162	17.1611	16.2143	19.0808	ENSG00000121289	CEP89
ENSG00000121297	1.93299	5.64877	5.21296	12.9648	ENSG00000121297	TSHZ3
ENSG00000121310	37.5017	53.1034	70.7345	44.3847	ENSG00000121310	ECHDC2
ENSG00000121314	0	0	0.0277802	0.0174369	ENSG00000121314	TAS2R8
ENSG00000121316	32.4509	4.52201	1.69301	4.3039	ENSG00000121316	PLBD1
ENSG00000121318	0.137195	0.226324	0.340901	0.448548	ENSG00000121318	TAS2R10

ENSG00000121335	3.18891	7.751	5.75483	4.22407	ENSG00000121335	PRB2
ENSG00000121350	19.4827	28.3456	28.3171	20.0412	ENSG00000121350	PYROXD1
ENSG00000121351	1.04146	1.86433	1.19248	3.41421	ENSG00000121351	IAPP
ENSG00000121361	0.0465263	0.112129	0.0405488	0.255544	ENSG00000121361	KCNJ8
ENSG00000121377	0	0.03555	0	0.0201421	ENSG00000121377	TAS2R7
ENSG00000121380	1.90953	6.29497	6.66349	9.94402	ENSG00000121380	BCL2L14
ENSG00000121381	0	0	0	0	ENSG00000121381	TAS2R9
ENSG00000121388	0	0	0	0	ENSG00000121388	RP11-408E5.4
ENSG00000121390	17.9001	18.186	21.9759	21.6246	ENSG00000121390	PSPC1
ENSG00000121406	5.45768	6.9448	8.36014	8.29292	ENSG00000121406	ZNF549
ENSG00000121410	4.66564	10.9014	11.8455	15.9393	ENSG00000121410	A1BG
ENSG00000121413	32.0653	39.4088	36.6061	24.4023	ENSG00000121413	ZSCAN18
ENSG00000121417	11.7584	14.2213	18.673	9.84109	ENSG00000121417	ZNF211
ENSG00000121440	1.04936	0.59287	0.503377	18.6356	ENSG00000121440	PDZRN3
ENSG00000121446	0.625119	1.41264	1.49158	1.82563	ENSG00000121446	RGSL1
ENSG00000121454	1.65326	3.42157	4.08026	2.93545	ENSG00000121454	LHX4
ENSG00000121481	7.10441	10.7888	10.0181	11.7086	ENSG00000121481	RNF2
ENSG00000121486	7.21436	14.4382	7.77672	9.60696	ENSG00000121486	TRMT1L
ENSG00000121542	20.1962	21.9993	16.7291	9.40839	ENSG00000121542	SEC22A
ENSG00000121552	916.71	174.278	133.099	107.905	ENSG00000121552	CSTA
ENSG00000121570	3.92395	4.95905	5.41505	9.76752	ENSG00000121570	DPPA4
ENSG00000121577	38.724	44.3838	18.254	54.9652	ENSG00000121577	POPDC2
ENSG00000121578	40.1178	22.3909	18.7734	19.163	ENSG00000121578	B4GALT4
ENSG00000121579	60.1788	44.5253	56.1555	44.974	ENSG00000121579	NAA50
ENSG00000121594	0.143943	0.144002	0.239381	0.17576	ENSG00000121594	CD80
ENSG00000121621	1.67107	15.5453	2.50449	8.53873	ENSG00000121621	KIF18A
ENSG00000121634	0	0	0	0	ENSG00000121634	GJA8
ENSG00000121644	13.7008	19.645	15.989	9.21513	ENSG00000121644	DESI2
ENSG00000121653	1.06064	0.974231	1.04923	1.8872	ENSG00000121653	MAPK8IP1
ENSG00000121671	7.51405	9.96855	13.4631	8.47947	ENSG00000121671	CRY2
ENSG00000121680	27.1835	32.6033	43.7405	27.4164	ENSG00000121680	PEX16
ENSG00000121690	6.41115	8.86583	3.80846	6.29976	ENSG00000121690	DEPDC7
ENSG00000121691	19.0884	26.8016	30.1151	17.1347	ENSG00000121691	CAT
ENSG00000121716	36.1884	25.3228	29.7299	25.9933	ENSG00000121716	PILRB
ENSG00000121741	50.625	67.4008	78.2524	66.6795	ENSG00000121741	ZMYM2
ENSG00000121742	34.0932	61.0816	116.804	14.6095	ENSG00000121742	GJB6
ENSG00000121743	0.27717	0.376293	0.322331	0.180954	ENSG00000121743	GJA3
ENSG00000121749	7.27992	12.9843	11.3787	19.8476	ENSG00000121749	TBC1D15
ENSG00000121753	1.81061	3.94671	2.64933	7.39462	ENSG00000121753	ADGRB2
ENSG00000121764	0.586848	0.82865	0.826069	0.498856	ENSG00000121764	HCRTR1
ENSG00000121766	16.0628	14.0387	15.8747	12.8319	ENSG00000121766	ZCCHC17
ENSG00000121769	2.66938	6.44174	6.34479	9.73343	ENSG00000121769	FABP3
ENSG00000121774	21.9518	29.7682	23.1255	36.727	ENSG00000121774	KHDRBS1
ENSG00000121775	3.88062	8.40516	8.76817	7.01069	ENSG00000121775	TMEM39B
ENSG00000121797	0.144748	0.724782	0.497429	0.405875	ENSG00000121797	CCRL2
ENSG00000121807	0	0.172703	0.130851	0.0775995	ENSG00000121807	CCR2
ENSG00000121848	5.39821	11.5753	11.4409	20.6865	ENSG00000121848	RNF115
ENSG00000121851	3.14077	3.8456	2.59059	2.67382	ENSG00000121851	POLR3GL
ENSG00000121853	0	0	0	0.0749726	ENSG00000121853	GHSR
ENSG00000121858	17.0936	24.2128	52.0903	15.6525	ENSG00000121858	TNFSF10
ENSG00000121864	14.4062	17.4203	17.715	17.28	ENSG00000121864	ZNF639
ENSG00000121871	0.112947	0.179737	0.138699	0.373247	ENSG00000121871	SLITRK3
ENSG00000121879	16.1402	16.001	13.387	17.2078	ENSG00000121879	PIK3CA
ENSG00000121892	48.4699	56.22	49.7189	89.0719	ENSG00000121892	PDS5A

ENSG00000121895	1.89713	5.65416	4.87372	7.446	ENSG00000121895	TMEM156
ENSG00000121897	6.46104	13.1863	12.9273	10.8769	ENSG00000121897	LIAS
ENSG00000121898	0.482154	0.80707	0.953694	7.77992	ENSG00000121898	CPXM2
ENSG00000121900	51.2176	40.4853	22.5122	15.2565	ENSG00000121900	TMEM54
ENSG00000121903	4.00822	4.76786	4.41194	4.7882	ENSG00000121903	ZSCAN20
ENSG00000121904	0.901673	9.3327	3.65638	13.8426	ENSG00000121904	CSMD2
ENSG00000121905	0.973949	2.38656	1.66593	1.70233	ENSG00000121905	HPCA
ENSG00000121931	15.5344	11.0857	12.9127	7.0044	ENSG00000121931	LRIF1
ENSG00000121933	0.359704	0.240397	0.33616	0.320095	ENSG00000121933	TMIGD3
ENSG00000121940	23.6374	27.125	20.4341	22.976	ENSG00000121940	CLCC1
ENSG00000121957	28.8376	48.3626	28.7659	24.2211	ENSG00000121957	GPSM2
ENSG00000121964	4.96598	8.14851	7.86245	14.6426	ENSG00000121964	GTDC1
ENSG00000121966	0.059775	0.14401	0.182261	0.271464	ENSG00000121966	CXCR4
ENSG00000121988	5.4193	12.422	8.05698	9.84604	ENSG00000121988	ZRANB3
ENSG00000121989	10.9454	10.9556	14.1877	9.6959	ENSG00000121989	ACVR2A
ENSG00000122008	14.483	27.5124	24.2032	29.9009	ENSG00000122008	POLK
ENSG00000122012	1.25893	3.44853	3.47564	2.78911	ENSG00000122012	SV2C
ENSG00000122025	0.0844954	0.594768	0.135432	0.251892	ENSG00000122025	FLT3
ENSG00000122026	73.4228	117.942	104.513	72.9263	ENSG00000122026	RPL21
ENSG00000122033	21.9576	35.1131	25.9401	27.2303	ENSG00000122033	MTIF3
ENSG00000122034	19.3278	21.0531	17.4424	11.7589	ENSG00000122034	GTF3A
ENSG00000122035	0.613315	0.571087	0.386774	0.455106	ENSG00000122035	RASL11A
ENSG00000122042	11.4734	10.4224	8.96585	23.7515	ENSG00000122042	UBL3
ENSG00000122068	33.4035	19.351	24.8124	19.6548	ENSG00000122068	FYTTD1
ENSG00000122085	17.2704	24.248	32.6554	21.5643	ENSG00000122085	MTERF4
ENSG00000122121	0.252457	0.215022	0.280963	0.427992	ENSG00000122121	XPNPEP2
ENSG00000122122	2.48652	0.626216	2.02661	1.64121	ENSG00000122122	SASH3
ENSG00000122126	10.2873	10.516	11.4205	8.30925	ENSG00000122126	OCRL
ENSG00000122133	1.16042	4.18641	2.1636	3.76048	ENSG00000122133	PAEP
ENSG00000122136	0	0.129919	0.234535	0	ENSG00000122136	OBP2A
ENSG00000122140	12.6847	15.3787	17.4414	10.8489	ENSG00000122140	MRPS2
ENSG00000122145	0.149353	0.0555575	0.129293	0.0948707	ENSG00000122145	TBX22
ENSG00000122176	0.247327	0.178788	0.426318	1.56201	ENSG00000122176	FMOD
ENSG00000122180	0.269455	0.456302	0.573872	0.872749	ENSG00000122180	MYOG
ENSG00000122188	1.39221	3.38682	3.11883	5.42303	ENSG00000122188	LAX1
ENSG00000122194	3.17541	4.57302	3.17985	6.68868	ENSG00000122194	PLG
ENSG00000122203	31.5937	22.3149	29.9653	26.5948	ENSG00000122203	KIAA1191
ENSG00000122218	58.8322	61.2463	62.2879	90.8804	ENSG00000122218	COPA
ENSG00000122223	0.274405	0	0.0196238	0	ENSG00000122223	CD244
ENSG00000122224	1.82047	3.76647	4.1287	5.95613	ENSG00000122224	LY9
ENSG00000122254	3.28379	4.0702	0.86379	2.28237	ENSG00000122254	HS3ST2
ENSG00000122257	45.0183	59.0336	48.9564	52.9516	ENSG00000122257	RBBP6
ENSG00000122299	23.7422	39.0819	37.2752	44.6162	ENSG00000122299	ZC3H7A
ENSG00000122304	0	0	0	0.107619	ENSG00000122304	PRM2
ENSG00000122335	7.18765	7.46143	7.38315	9.35011	ENSG00000122335	SERAC1
ENSG00000122359	241.697	82.431	41.6568	80.9296	ENSG00000122359	ANXA11
ENSG00000122367	0.644618	2.21306	1.17621	1.56589	ENSG00000122367	LDB3
ENSG00000122375	0.0347325	0.066926	0	0.0380554	ENSG00000122375	OPN4
ENSG00000122376	7.34513	8.99589	6.4285	8.82293	ENSG00000122376	FAM35A
ENSG00000122378	25.5974	47.9864	25.0184	17.2874	ENSG00000122378	FAM213A
ENSG00000122386	10.4916	8.35755	11.6932	5.54969	ENSG00000122386	ZNF205
ENSG00000122390	29.8444	50.4474	59.2838	64.7341	ENSG00000122390	NAA60
ENSG00000122406	447.807	304.648	299.314	193.611	ENSG00000122406	RPL5
ENSG00000122417	41.8259	76.7762	67.7753	105.23	ENSG00000122417	ODF2L

ENSG00000122420	0.157541	0.312873	0.0979603	4.43386	ENSG00000122420	PTGFR
ENSG00000122432	2.97072	5.87162	7.18183	10.2373	ENSG00000122432	SPATA1
ENSG00000122435	8.20436	8.97462	12.6769	8.70556	ENSG00000122435	TRMT13
ENSG00000122477	0.621234	0.577564	0.713364	0.837964	ENSG00000122477	LRRC39
ENSG00000122481	17.7222	12.2245	13.4	12.4493	ENSG00000122481	RWDD3
ENSG00000122482	24.0355	42.105	34.3389	50.9851	ENSG00000122482	ZNF644
ENSG00000122483	4.03329	15.7726	8.95422	10.9401	ENSG00000122483	CCDC18
ENSG00000122484	15.6213	33.9373	33.6019	67.6153	ENSG00000122484	RPAP2
ENSG00000122490	42.1369	37.5289	33.378	34.6666	ENSG00000122490	PQLC1
ENSG00000122497	22.4002	12.6765	26.2026	21.3242	ENSG00000122497	NBPF14
ENSG00000122507	5.67838	5.73078	7.44949	12.6786	ENSG00000122507	BBS9
ENSG00000122512	10.84	16.4267	18.9109	14.5793	ENSG00000122512	PMS2
ENSG00000122515	17.4564	31.4226	27.0171	36.1242	ENSG00000122515	ZMIZ2
ENSG00000122543	0.111826	0	0.0969647	0.120494	ENSG00000122543	OCM
ENSG00000122545	69.8457	58.7602	54.9696	74.4295	ENSG00000122545	SEPT7
ENSG00000122547	1.78606	1.42589	1.76057	8.71469	ENSG00000122547	EEPD1
ENSG00000122548	0.344161	0.573218	0.769349	0.877513	ENSG00000122548	KIAA0087
ENSG00000122550	22.5575	30.8914	24.1081	34.4245	ENSG00000122550	KLHL7
ENSG00000122557	21.1746	19.5252	19.8969	12.8852	ENSG00000122557	HERPUD2
ENSG00000122565	62.5245	85.778	66.1035	65.4632	ENSG00000122565	CBX3
ENSG00000122566	56.6676	104.228	87.7128	131.928	ENSG00000122566	HNRNPA2B1
ENSG00000122574	0.947333	1.3618	1.12646	1.98229	ENSG00000122574	WIPF3
ENSG00000122584	0.0657302	0.0724337	0.114396	0.368664	ENSG00000122584	NXPH1
ENSG00000122585	0	0.122611	0	0	ENSG00000122585	NPY
ENSG00000122591	13.9172	29.799	14.8509	43.8954	ENSG00000122591	FAM126A
ENSG00000122592	3.0313	4.3218	5.36027	1.6282	ENSG00000122592	HOXA7
ENSG00000122641	61.4417	65.4516	56.9982	128.655	ENSG00000122641	INHBA
ENSG00000122642	103.262	196.486	191.815	141.706	ENSG00000122642	FKBP9
ENSG00000122643	19.2302	31.9598	22.1822	18.3834	ENSG00000122643	NT5C3A
ENSG00000122644	9.00426	9.92736	16.509	6.29276	ENSG00000122644	ARL4A
ENSG00000122674	34.7672	24.77	33.9918	24.1365	ENSG00000122674	CCZ1
ENSG00000122678	12.7999	14.2245	12.92	17.8504	ENSG00000122678	POLM
ENSG00000122679	0.0445893	0.171754	0.228774	0.243739	ENSG00000122679	RAMP3
ENSG00000122687	11.0836	8.4854	10.5243	6.02019	ENSG00000122687	MRM2
ENSG00000122691	0.600174	1.70663	1.80514	13.8353	ENSG00000122691	TWIST1
ENSG00000122692	37.3068	32.8152	30.5601	20.5124	ENSG00000122692	SMU1
ENSG00000122694	1.9186	2.13239	2.27025	4.72096	ENSG00000122694	GLIPR2
ENSG00000122696	14.4717	17.0525	17.2226	18.4037	ENSG00000122696	SLC25A51
ENSG00000122705	102.864	63.945	55.8639	46.2167	ENSG00000122705	CLTA
ENSG00000122707	2.51249	4.01655	3.77092	11.1486	ENSG00000122707	RECK
ENSG00000122711	0.84811	0	0.182948	0.673135	ENSG00000122711	SPINK4
ENSG00000122718	0	0	0.152544	0.127443	ENSG00000122718	OR2S2
ENSG00000122728	0.056629	0.0897227	0.0588977	0.15832	ENSG00000122728	TAF1L
ENSG00000122729	9.67296	11.6905	8.40006	16.5917	ENSG00000122729	ACO1
ENSG00000122733	2.19515	0.950088	0.884541	0.43925	ENSG00000122733	PHF24
ENSG00000122735	0.216146	0.655306	0.586353	1.44199	ENSG00000122735	DNAI1
ENSG00000122741	15.4483	17.9542	20.2152	15.1654	ENSG00000122741	DCAF10
ENSG00000122756	0.0888938	0.142777	0.0774436	0.514159	ENSG00000122756	CNTFR
ENSG00000122778	1.17086	2.69473	2.80549	3.73042	ENSG00000122778	KIAA1549
ENSG00000122779	7.22758	8.26495	6.56789	8.38045	ENSG00000122779	TRIM24
ENSG00000122783	46.1555	55.0769	54.011	40.694	ENSG00000122783	C7orf49
ENSG00000122786	93.0686	103.96	136.058	199.013	ENSG00000122786	CALD1
ENSG00000122787	0.66588	0.890931	0.880096	1.75404	ENSG00000122787	AKR1D1
ENSG00000122824	0.311287	0.541821	0.832236	0.666906	ENSG00000122824	NUDT10

ENSG00000122852	0.246048	0.302757	0.843426	0.402465	ENSG00000122852	SFTPA1
ENSG00000122859	0.0426456	0	0.0742472	0	ENSG00000122859	NEUROG3
ENSG00000122861	538.65	1077.06	328.322	372.307	ENSG00000122861	PLAU
ENSG00000122862	0.322994	0.698551	0.861211	3.19057	ENSG00000122862	SRGN
ENSG00000122863	11.206	26.9182	21.9997	10.3143	ENSG00000122863	CHST3
ENSG00000122870	2.00377	2.47003	5.62293	14.5167	ENSG00000122870	BICC1
ENSG00000122872	0.389372	1.66921	0.421035	0.774048	ENSG00000122872	ARL4P
ENSG00000122873	11.4492	12.8837	11.7445	6.98402	ENSG00000122873	CISD1
ENSG00000122877	0.464612	1.45898	0.608572	2.45497	ENSG00000122877	EGR2
ENSG00000122882	21.4847	35.4492	31.0636	50.3198	ENSG00000122882	ECD
ENSG00000122884	39.0503	57.0986	30.1558	52.5569	ENSG00000122884	P4HA1
ENSG00000122912	14.3375	20.5514	14.1568	21.2928	ENSG00000122912	SLC25A16
ENSG00000122952	4.65592	9.75251	2.30062	5.34707	ENSG00000122952	ZWINT
ENSG00000122958	15.0228	13.9206	14.2456	12.9918	ENSG00000122958	VPS26A
ENSG00000122965	13.5036	19.9899	18.1056	17.4036	ENSG00000122965	RBM19
ENSG00000122966	3.1965	33.3229	3.17524	23.4263	ENSG00000122966	CIT
ENSG00000122970	9.61807	11.886	15.2967	22.2514	ENSG00000122970	IFT81
ENSG00000122971	4.25705	3.8439	2.80317	2.88991	ENSG00000122971	ACADS
ENSG00000122986	4.12794	7.68236	5.57894	8.59866	ENSG00000122986	HVCN1
ENSG00000123009	0.106393	0.4191	0.270102	0.67638	ENSG00000123009	NME2P1
ENSG00000123064	28.521	32.6724	37.5095	27.7939	ENSG00000123064	DDX54
ENSG00000123066	34.0387	56.1525	54.0433	64.2462	ENSG00000123066	MED13L
ENSG00000123080	0.269233	1.05965	0.218948	2.75873	ENSG00000123080	CDKN2C
ENSG00000123091	65.6393	22.1878	27.9021	25.5912	ENSG00000123091	RNF11
ENSG00000123094	8.39988	23.3177	14.5561	39.3324	ENSG00000123094	RASSF8
ENSG00000123095	3.80226	0.71942	3.05874	4.09665	ENSG00000123095	BHLHE41
ENSG00000123096	1.54904	1.4331	1.33923	1.9313	ENSG00000123096	SSPN
ENSG00000123104	7.01576	19.2895	13.5651	22.0784	ENSG00000123104	ITPR2
ENSG00000123106	34.2621	55.9772	53.8438	51.7464	ENSG00000123106	CCDC91
ENSG00000123119	0.552927	1.64518	1.12428	1.6245	ENSG00000123119	NECAB1
ENSG00000123124	25.8424	36.8316	38.7241	41.978	ENSG00000123124	WWP1
ENSG00000123130	42.757	48.6119	37.3701	42.4107	ENSG00000123130	ACOT9
ENSG00000123131	62.4421	68.0589	32.6982	26.3772	ENSG00000123131	PRDX4
ENSG00000123136	35.7456	45.8362	36.2946	35.417	ENSG00000123136	DDX39A
ENSG00000123143	12.6084	11.949	8.61638	28.7338	ENSG00000123143	PKN1
ENSG00000123144	65.487	39.9687	42.3587	38.7612	ENSG00000123144	TRIR
ENSG00000123146	30.9385	23.0673	15.1011	16.1984	ENSG00000123146	ADGRE5
ENSG00000123154	8.27259	11.0054	12.7222	14.3925	ENSG00000123154	WDR83
ENSG00000123159	189.29	92.5038	96.7828	64.7283	ENSG00000123159	GIPC1
ENSG00000123165	0	0.0390209	0.0356805	0.0886632	ENSG00000123165	ACTRT1
ENSG00000123171	0.0524886	0.101051	0	0	ENSG00000123171	CCDC70
ENSG00000123178	10.8351	10.436	9.14358	8.80337	ENSG00000123178	SPRYD7
ENSG00000123179	33.0025	50.3002	33.3482	27.0732	ENSG00000123179	EBPL
ENSG00000123191	4.19539	3.95536	4.87399	5.80988	ENSG00000123191	ATP7B
ENSG00000123200	14.3594	19.1581	19.0763	31.6495	ENSG00000123200	ZC3H13
ENSG00000123201	0.264979	1.09483	0.413637	1.38392	ENSG00000123201	GUCY1B2
ENSG00000123213	12.1817	19.9139	20.9259	19.6376	ENSG00000123213	NLN
ENSG00000123219	13.7495	42.4186	20.1334	47.9387	ENSG00000123219	CENPK
ENSG00000123240	57.7673	65.7729	85.5625	76.3043	ENSG00000123240	OPTN
ENSG00000123243	2.18425	3.24537	4.58726	7.24914	ENSG00000123243	ITIH5
ENSG00000123268	15.8952	14.7817	19.5283	14.2831	ENSG00000123268	ATF1
ENSG00000123297	12.3888	14.3699	13.4922	16.8478	ENSG00000123297	TSFM
ENSG00000123307	0.0273409	0.0663886	0.0238419	0.0601969	ENSG00000123307	NEUROD4

ENSG00000123329	0.430019	0.683975	0.762683	1.16315	ENSG00000123329	ARHGAP9
ENSG00000123338	6.70901	9.61182	9.30791	12.6354	ENSG00000123338	NCKAP1L
ENSG00000123342	3.58278	6.15287	3.60513	22.9842	ENSG00000123342	MMP19
ENSG00000123349	174.508	126.163	92.364	81.8338	ENSG00000123349	PFDN5
ENSG00000123352	21.5377	42.7229	32.0454	52.8379	ENSG00000123352	SPATS2
ENSG00000123353	96.7274	53.8631	26.9805	17.6957	ENSG00000123353	ORMDL2
ENSG00000123358	2.28722	4.62751	3.21265	5.20993	ENSG00000123358	NR4A1
ENSG00000123360	0.504081	1.74323	1.69204	2.55572	ENSG00000123360	PDE1B
ENSG00000123364	4.13043	1.32625	3.46512	1.0567	ENSG00000123364	HOXC13
ENSG00000123374	21.2385	28.0047	11.5555	16.1142	ENSG00000123374	CDK2
ENSG00000123384	22.9233	40.2429	42.5572	122.541	ENSG00000123384	LRP1
ENSG00000123388	4.02705	3.35698	3.59302	3.00755	ENSG00000123388	HOXC11
ENSG00000123395	23.7821	18.9666	21.734	14.5901	ENSG00000123395	ATG101
ENSG00000123405	0.546046	0.142948	0.218664	0.148506	ENSG00000123405	NFE2
ENSG00000123407	0.947225	0.110243	1.43843	0.919188	ENSG00000123407	HOXC12
ENSG00000123411	1.68205	1.55668	1.83447	3.23135	ENSG00000123411	IKZF4
ENSG00000123415	31.0484	36.1594	34.953	29.7037	ENSG00000123415	SMUG1
ENSG00000123416	341.167	398.767	72.8736	178.615	ENSG00000123416	TUBA1B
ENSG00000123427	3.95842	4.88345	4.40985	5.66125	ENSG00000123427	EEF1AKMT3
ENSG00000123444	6.17658	4.48501	4.99448	4.40929	ENSG00000123444	KBTBD4
ENSG00000123447	0	0.383301	0.252154	0	ENSG00000123447	TYRL
ENSG00000123453	0.341463	1.12789	1.23079	2.97953	ENSG00000123453	SARDH
ENSG00000123454	0.0597615	0.134446	0.138917	0.306584	ENSG00000123454	DBH
ENSG00000123472	13.8291	14.3834	12.3842	10.7188	ENSG00000123472	ATPAF1
ENSG00000123473	8.30308	19.2262	9.95693	18.099	ENSG00000123473	STIL
ENSG00000123485	6.18435	32.3369	5.55734	16.8636	ENSG00000123485	HJURP
ENSG00000123496	0.931283	0.900284	0.298212	0.586977	ENSG00000123496	IL13RA2
ENSG00000123500	1.90976	5.43556	2.51641	13.385	ENSG00000123500	COL10A1
ENSG00000123505	35.5722	26.6987	29.1947	20.6036	ENSG00000123505	AMD1
ENSG00000123545	8.9926	9.59448	11.6305	4.82198	ENSG00000123545	NDUFAF4
ENSG00000123552	12.5822	21.6714	20.0022	24.1418	ENSG00000123552	USP45
ENSG00000123560	1.62131	0.265088	0.815782	2.6835	ENSG00000123560	PLP1
ENSG00000123561	0.0301833	0	0.18818	0.0993139	ENSG00000123561	SERPINA7
ENSG00000123562	173.061	114.84	99.7938	113.726	ENSG00000123562	MORF4L2
ENSG00000123569	0.0353247	0.0829495	0.0959269	0.0500352	ENSG00000123569	H2BFWT
ENSG00000123570	0.103923	0.186195	0.273915	0.404415	ENSG00000123570	RAB9B
ENSG00000123572	0.170952	0.444995	0.201023	1.36205	ENSG00000123572	NRK
ENSG00000123575	5.61269	5.68962	7.00043	4.92844	ENSG00000123575	FAM199X
ENSG00000123576	0.0194219	0.0935406	0	0.0212604	ENSG00000123576	ESX1
ENSG00000123584	0	0	0	1.23E-08	ENSG00000123584	MAGEA9
ENSG00000123594	0.358973	0.440221	0.198977	0.652213	ENSG00000123594	ATXN3L
ENSG00000123595	23.3338	10.891	18.6842	7.75736	ENSG00000123595	RAB9A
ENSG00000123600	26.1237	27.8258	32.699	24.8853	ENSG00000123600	METTL8
ENSG00000123607	4.98219	16.8905	9.36485	14.306	ENSG00000123607	TTC21B
ENSG00000123609	2.15233	5.20304	2.90147	3.23954	ENSG00000123609	NMI
ENSG00000123610	0.164364	0.277035	0.537576	3.0032	ENSG00000123610	TNFAIP6
ENSG00000123612	0.23202	0.307336	0.420247	1.28843	ENSG00000123612	ACVR1C
ENSG00000123636	47.8495	66.3254	66.2736	67.0103	ENSG00000123636	BAZ2B
ENSG00000123643	7.70239	7.95042	11.1616	8.39713	ENSG00000123643	SLC36A1
ENSG00000123684	26.1052	33.0706	17.9933	22.738	ENSG00000123684	LPGAT1
ENSG00000123685	0.116343	0.997168	0.758332	1.4825	ENSG00000123685	BATF3
ENSG00000123689	31.9417	270.343	104.425	40.32	ENSG00000123689	G0S2
ENSG00000123700	0.149924	0.336071	0.229157	0.574919	ENSG00000123700	KCNJ2
ENSG00000123728	16.1535	13.0117	16.4364	8.9201	ENSG00000123728	RAP2C

ENSG00000123737	12.1729	18.0008	11.4789	15.5582	ENSG00000123737	EXOSC9
ENSG00000123739	26.6651	18.0418	14.298	8.9104	ENSG00000123739	PLA2G12A
ENSG00000123810	3.06419	5.69833	5.45346	5.85741	ENSG00000123810	B9D2
ENSG00000123815	22.2535	22.8534	19.2077	21.5692	ENSG00000123815	COQ8B
ENSG00000123836	18.6112	15.7827	16.8586	12.5465	ENSG00000123836	PFKFB2
ENSG00000123838	0.325772	0.600577	0.704701	0.675226	ENSG00000123838	C4BPA
ENSG00000123843	5.11937	13.1115	12.9033	17.1472	ENSG00000123843	C4BPB
ENSG00000123870	5.95175	5.49095	2.4369	3.58985	ENSG00000123870	ZNF137P
ENSG00000123892	29.2628	56.3241	57.6662	11.2956	ENSG00000123892	RAB38
ENSG00000123901	0.81329	1.89058	1.64972	2.53464	ENSG00000123901	GPR83
ENSG00000123908	27.8501	40.8284	33.4286	45.4784	ENSG00000123908	AGO2
ENSG00000123933	21.2699	14.6494	26.7828	19.8753	ENSG00000123933	MXD4
ENSG00000123965	6.78857	9.03024	12.7362	11.4025	ENSG00000123965	PMS2P5
ENSG00000123975	18.2501	54.9116	9.11609	13.9072	ENSG00000123975	CKS2
ENSG00000123977	1.27889	0.463183	1.27112	2.72381	ENSG00000123977	DAW1
ENSG00000123983	179.698	218.078	109.978	145.814	ENSG00000123983	ACSL3
ENSG00000123989	89.2502	82.1607	61.903	37.891	ENSG00000123989	CHPF
ENSG00000123992	19.4642	27.0997	32.6822	22.03	ENSG00000123992	DNPEP
ENSG00000123999	1.41962	1.27151	1.86236	1.5862	ENSG00000123999	INHA
ENSG00000124003	0	0.256152	0.0550426	0.301564	ENSG00000124003	MOGAT1
ENSG00000124006	17.2806	20.7448	24.4754	19.8642	ENSG00000124006	OBSL1
ENSG00000124019	0.465789	0.793853	0.813403	1.30742	ENSG00000124019	FAM124B
ENSG00000124067	73.4211	84.0559	72.1262	79.3295	ENSG00000124067	SLC12A4
ENSG00000124074	6.54258	13.6026	11.4672	7.81983	ENSG00000124074	ENKD1
ENSG00000124089	0	0.108031	0.0488182	0.0612015	ENSG00000124089	MC3R
ENSG00000124091	0.301331	1.10394	1.1167	1.5459	ENSG00000124091	GCNT7
ENSG00000124092	3.85254	6.82277	7.00894	12.5168	ENSG00000124092	CTCFL
ENSG00000124097	0	0	0	0	ENSG00000124097	HMGB1P1
ENSG00000124098	14.4348	10.7097	11.4893	12.8655	ENSG00000124098	FAM210B
ENSG00000124102	395.175	35.7326	45.7114	80.3953	ENSG00000124102	PI3
ENSG00000124103	0.190069	0.664045	0.487685	0.51819	ENSG00000124103	FAM209A
ENSG00000124104	8.18103	11.3888	8.63971	11.1983	ENSG00000124104	SNX21
ENSG00000124107	2058.98	116.388	163.308	144.45	ENSG00000124107	SLPI
ENSG00000124116	2.76389	4.64152	3.85095	6.24299	ENSG00000124116	WFDC3
ENSG00000124120	31.0195	13.0578	19.664	17.8492	ENSG00000124120	TTPAL
ENSG00000124126	3.73303	9.71946	10.0449	14.1176	ENSG00000124126	PREX1
ENSG00000124134	0.578655	1.38125	1.36764	1.92391	ENSG00000124134	KCNS1
ENSG00000124140	0.578716	2.19236	2.2885	2.00201	ENSG00000124140	SLC12A5
ENSG00000124143	4.39546	2.09783	7.53753	2.44542	ENSG00000124143	ARHGAP40
ENSG00000124145	277.666	181.881	125.16	70.8038	ENSG00000124145	SDC4
ENSG00000124151	30.3974	31.0962	28.9139	36.6314	ENSG00000124151	NCOA3
ENSG00000124155	30.617	35.5854	24.5008	20.1981	ENSG00000124155	PIGT
ENSG00000124157	0.109687	0	0.0477854	0	ENSG00000124157	SEMG2
ENSG00000124159	0.305767	0.352455	0.294487	0.260445	ENSG00000124159	MATN4
ENSG00000124160	6.02651	4.8781	6.37748	6.67753	ENSG00000124160	NCOA5
ENSG00000124164	11.2733	13.2042	9.88932	13.211	ENSG00000124164	VAPB
ENSG00000124171	16.9184	9.07081	4.28891	5.87818	ENSG00000124171	PARD6B
ENSG00000124172	32.2167	23.7304	17.0691	14.8378	ENSG00000124172	ATP5E
ENSG00000124177	18.4515	31.8019	26.0369	33.4067	ENSG00000124177	CHD6
ENSG00000124181	43.6255	50.3119	53.1116	68.3263	ENSG00000124181	PLCG1
ENSG00000124191	0.162208	0.657538	0.48935	2.26866	ENSG00000124191	TOX2
ENSG00000124193	35.808	45.4617	55.0632	33.1492	ENSG00000124193	SRSF6
ENSG00000124194	1.34234	0.681032	0.900105	1.69527	ENSG00000124194	GDAP1L1
ENSG00000124196	0	0.147675	0.133423	0	ENSG00000124196	GTSF1L

ENSG00000124198	17.0875	19.0323	21.683	23.2554	ENSG00000124198	ARFGEF2
ENSG00000124201	18.3899	16.4657	22.5417	22.2176	ENSG00000124201	ZNFX1
ENSG00000124203	0.0448731	0.0865912	0.0735221	0.136415	ENSG00000124203	ZNF831
ENSG00000124205	0.0463599	0.111728	0.0908719	0.0509269	ENSG00000124205	EDN3
ENSG00000124207	43.5376	60.941	31.4719	32.4216	ENSG00000124207	CSE1L
ENSG00000124208	0	0	1.23771	0	ENSG00000124208	TMEM189-UBE2V1
ENSG00000124209	12.619	11.3047	11.0269	11.9027	ENSG00000124209	RAB22A
ENSG00000124212	0.655224	1.37981	1.11855	1.92004	ENSG00000124212	PTGIS
ENSG00000124214	24.0303	18.8003	17.7529	20.2202	ENSG00000124214	STAU1
ENSG00000124215	2.76204	4.82906	2.60971	4.49409	ENSG00000124215	CDH26
ENSG00000124216	0.441757	0	0.147983	0.782011	ENSG00000124216	SNAI1
ENSG00000124217	6.99279	5.31955	6.75153	4.22052	ENSG00000124217	MOCS3
ENSG00000124222	18.1279	23.5029	29.8578	42.2887	ENSG00000124222	STX16
ENSG00000124224	10.9869	18.7766	13.2705	17.6624	ENSG00000124224	PPP4R1L
ENSG00000124225	107.286	37.0373	49.2942	61.2485	ENSG00000124225	PMEPA1
ENSG00000124226	11.9401	12.5839	11.4648	8.80922	ENSG00000124226	RNF114
ENSG00000124227	0.120581	0	0	0.130791	ENSG00000124227	ANKRD60
ENSG00000124228	23.1921	20.9608	22.975	15.8569	ENSG00000124228	DDX27
ENSG00000124232	0.0677327	0	0.0926055	0.0388297	ENSG00000124232	RBPJL
ENSG00000124233	0.103573	0	0	0.102468	ENSG00000124233	SEMG1
ENSG00000124237	0.0806223	0	0.280058	0	ENSG00000124237	C20orf85
ENSG00000124243	12.4069	10.9966	10.9564	12.4868	ENSG00000124243	BCAS4
ENSG00000124249	0.268228	0.0860984	0.194556	0.19549	ENSG00000124249	KCNK15
ENSG00000124251	1.15225	1.67025	2.76073	2.53233	ENSG00000124251	TP53TG5
ENSG00000124253	0.40273	0.366021	0.154157	0.771594	ENSG00000124253	PCK1
ENSG00000124256	26.2133	47.1754	49.6053	79.1194	ENSG00000124256	ZBP1
ENSG00000124257	0.970821	1.39267	2.86958	2.54889	ENSG00000124257	NEURL2
ENSG00000124260	1.65335	2.57885	2.33337	3.84568	ENSG00000124260	MAGEA10
ENSG00000124275	20.7578	36.662	44.4267	26.5056	ENSG00000124275	MTRR
ENSG00000124279	5.37162	6.34446	6.90831	4.40372	ENSG00000124279	FASTKD3
ENSG00000124299	18.3992	11.829	16.7852	16.9407	ENSG00000124299	PEPD
ENSG00000124302	0.026293	0	0.10544	0.049135	ENSG00000124302	CHST8
ENSG00000124313	1.49144	1.48042	2.19863	2.02854	ENSG00000124313	IQSEC2
ENSG00000124333	12.3603	7.30281	7.58502	6.76262	ENSG00000124333	VAMP7
ENSG00000124334	0.668572	0.0327869	0.359726	0.110835	ENSG00000124334	IL9R
ENSG00000124343	33.6928	27.508	55.0975	30.9123	ENSG00000124343	XG
ENSG00000124356	34.0678	25.8221	23.9054	18.9083	ENSG00000124356	STAMBP
ENSG00000124357	23.5242	28.7554	36.7815	30.473	ENSG00000124357	NAGK
ENSG00000124370	5.82502	9.04804	7.1453	12.6315	ENSG00000124370	MCEE
ENSG00000124374	1.3473	1.57582	1.54651	1.69878	ENSG00000124374	PAIP2B
ENSG00000124380	14.8396	14.4828	12.6271	14.1105	ENSG00000124380	SNRNP27
ENSG00000124383	9.88042	12.3717	13.5586	12.7762	ENSG00000124383	MPHOSPH10
ENSG00000124391	0.779479	1.0808	1.21264	0.574557	ENSG00000124391	IL17C
ENSG00000124399	0	0	0	0	ENSG00000124399	RP11-663P9.2
ENSG00000124406	0.21887	0.697875	0.378795	0.569451	ENSG00000124406	ATP8A1
ENSG00000124422	74.1865	86.9702	86.9603	73.5312	ENSG00000124422	USP22
ENSG00000124429	24.3037	6.71556	7.55183	6.40017	ENSG00000124429	POF1B
ENSG00000124440	2.4038	3.90858	4.51978	9.02618	ENSG00000124440	HIF3A
ENSG00000124444	4.45965	4.19005	6.24901	4.10845	ENSG00000124444	ZNF576
ENSG00000124449	0.135409	0	0.120274	0.151317	ENSG00000124449	IRGC
ENSG00000124459	8.58175	12.5607	9.79071	11.0365	ENSG00000124459	ZNF45
ENSG00000124466	98.2582	36.8734	40.6443	25.4676	ENSG00000124466	LYPD3
ENSG00000124467	0.408922	0.151557	0.346628	0.827468	ENSG00000124467	PSG8
ENSG00000124469	0.732424	1.16897	1.26428	2.0105	ENSG00000124469	CEACAM8

ENSG00000124479	0.140082	0.432745	0.113402	0.815784	ENSG00000124479	NDP
ENSG00000124486	46.3457	63.6493	55.6732	90.9547	ENSG00000124486	USP9X
ENSG00000124490	0	0	0	0	ENSG00000124490	CRISP2
ENSG00000124491	0.0675331	0.258318	0.292836	1.15077	ENSG00000124491	F13A1
ENSG00000124493	0.733481	1.01614	0.939455	1.96437	ENSG00000124493	GRM4
ENSG00000124496	4.68723	7.75061	5.0604	5.79283	ENSG00000124496	TRERF1
ENSG00000124507	0.549433	1.57668	0.260166	1.6873	ENSG00000124507	PACSIN1
ENSG00000124508	8.82142	13.4647	14.5393	11.447	ENSG00000124508	BTN2A2
ENSG00000124523	7.94155	17.9152	15.7844	16.0612	ENSG00000124523	SIRT5
ENSG00000124529	28.3616	84.3237	35.7935	24.9345	ENSG00000124529	HIST1H4B
ENSG00000124532	17.7897	13.2091	12.8488	13.951	ENSG00000124532	MRS2
ENSG00000124535	26.6541	28.1205	23.5836	17.6011	ENSG00000124535	WRNIP1
ENSG00000124541	43.2382	31.8605	35.7995	35.502	ENSG00000124541	RRP36
ENSG00000124549	2.55629	5.12508	5.10588	6.01436	ENSG00000124549	BTN2A3P
ENSG00000124557	0.075836	0.109683	0.0495825	0.0833857	ENSG00000124557	BTN1A1
ENSG00000124562	33.3066	29.7843	26.22	16.4004	ENSG00000124562	SNRPC
ENSG00000124564	0.374746	0.221542	0.173851	1.03278	ENSG00000124564	SLC17A3
ENSG00000124568	0.0671703	0.161797	0.0877565	0.257654	ENSG00000124568	SLC17A1
ENSG00000124570	29.9327	19.3201	16.2124	24.9258	ENSG00000124570	SERPINB6
ENSG00000124571	34.1773	46.5342	60.5157	45.8968	ENSG00000124571	XPO5
ENSG00000124574	34.7658	58.1424	47.3538	76.4702	ENSG00000124574	ABCC10
ENSG00000124575	18.5682	120.585	36.1096	34.8686	ENSG00000124575	HIST1H1D
ENSG00000124578	0	0	0	0	ENSG00000124578	HIST1H4G
ENSG00000124587	8.55411	7.03917	9.31545	9.26702	ENSG00000124587	PEX6
ENSG00000124588	8.34671	15.0365	8.51812	10.6857	ENSG00000124588	NQO2
ENSG00000124593	8.36417	8.17741	5.47761	4.50168	ENSG00000124593	PRICKLE4
ENSG00000124596	7.92359	11.293	11.1617	10.6562	ENSG00000124596	OARD1
ENSG00000124602	0.90833	1.61253	1.21184	1.14819	ENSG00000124602	UNC5CL
ENSG00000124608	11.3968	14.9975	11.6132	11.0504	ENSG00000124608	AARS2
ENSG00000124610	1.66956	2.80805	1.52212	4.7047	ENSG00000124610	HIST1H1A
ENSG00000124613	5.18398	4.61548	6.62236	7.08041	ENSG00000124613	ZNF391
ENSG00000124614	541.74	388.429	311.452	190.424	ENSG00000124614	RPS10
ENSG00000124615	0.859063	1.3741	1.44534	3.53298	ENSG00000124615	MOCS1
ENSG00000124635	19.5857	50.6343	16.2223	17.5762	ENSG00000124635	HIST1H2BJ
ENSG00000124641	23.441	32.5472	23.8968	33.883	ENSG00000124641	MED20
ENSG00000124657	0.997872	0	0	0	ENSG00000124657	OR2B6
ENSG00000124659	12.402	9.79963	9.47023	4.80579	ENSG00000124659	TBCC
ENSG00000124664	0.418766	0.263475	0.416805	0.262205	ENSG00000124664	SPDEF
ENSG00000124678	0	0.374213	0.219667	0.642453	ENSG00000124678	TCP11
ENSG00000124688	11.3038	8.61212	11.2491	6.73882	ENSG00000124688	MAD2L1BP
ENSG00000124693	17.5566	86.1023	13.7541	27.92	ENSG00000124693	HIST1HB
ENSG00000124701	0.523297	1.54867	1.36582	1.01582	ENSG00000124701	APOBEC2
ENSG00000124702	16.4903	12.176	13.6378	10.3851	ENSG00000124702	KLHDC3
ENSG00000124713	0.284318	0.0547246	0.296751	0.125308	ENSG00000124713	GNMT
ENSG00000124721	0.32617	0.201035	0.363071	0.36468	ENSG00000124721	DNAH8
ENSG00000124731	0.895469	1.97071	3.73221	3.94059	ENSG00000124731	TREM1
ENSG00000124733	23.2905	18.5142	13.9353	11.3086	ENSG00000124733	MEA1
ENSG00000124743	0.456393	0.658655	2.03604	0.565558	ENSG00000124743	KLHL31
ENSG00000124749	0.407125	1.3916	2.22677	3.45109	ENSG00000124749	COL21A1
ENSG00000124762	227.542	114.249	181.558	114.449	ENSG00000124762	CDKN1A
ENSG00000124766	33.6141	14.6192	32.8124	22.4776	ENSG00000124766	SOX4
ENSG00000124767	89.1082	45.9837	40.8904	42.3407	ENSG00000124767	GLO1
ENSG00000124772	0.0555755	0.261177	0.198611	0.0919202	ENSG00000124772	CPNE5
ENSG00000124780	0.400515	0.993748	0.700211	0.729515	ENSG00000124780	KCNK17

ENSG00000124782	23.0092	30.5178	30.2875	27.8641	ENSG00000124782	RREB1
ENSG00000124783	66.5705	104.568	61.7368	52.9188	ENSG00000124783	SSR1
ENSG00000124784	9.84557	14.0727	15.8126	14.1153	ENSG00000124784	RIOK1
ENSG00000124785	0.473431	0.883698	0.444989	4.84051	ENSG00000124785	NRN1
ENSG00000124786	9.07337	15.1426	12.6327	12.4896	ENSG00000124786	SLC35B3
ENSG00000124787	6.55951	5.44334	7.3907	3.791	ENSG00000124787	RPP40
ENSG00000124788	11.7536	21.2386	21.4214	32.06	ENSG00000124788	ATXN1
ENSG00000124789	18.0394	18.1933	16.5214	20.7979	ENSG00000124789	NUP153
ENSG00000124795	29.8871	57.1282	26.0125	48.4131	ENSG00000124795	DEK
ENSG00000124802	19.8712	33.2762	31.4609	33.4074	ENSG00000124802	EEF1E1
ENSG00000124812	0	0.127898	0.174976	0.110069	ENSG00000124812	CRISP1
ENSG00000124813	2.37359	7.17922	3.50607	19.0067	ENSG00000124813	RUNX2
ENSG00000124818	0.109205	0.38852	0.458617	0.613462	ENSG00000124818	OPN5
ENSG00000124827	0.0227409	0.109742	0.13915	0.388316	ENSG00000124827	GCM2
ENSG00000124831	60.0896	114.987	105.783	126.487	ENSG00000124831	LRRFIP1
ENSG00000124839	1.70013	0.823933	0.847671	1.18997	ENSG00000124839	RAB17
ENSG00000124875	0.463347	0.360229	0.174042	14.7526	ENSG00000124875	CXCL6
ENSG00000124882	18.7814	18.4538	67.866	38.5499	ENSG00000124882	EREG
ENSG00000124900	0	0	0	0	ENSG00000124900	TRIM51
ENSG00000124920	0.945918	1.80958	2.41689	2.20227	ENSG00000124920	MYRF
ENSG00000124935	0	0	0	0	ENSG00000124935	SCGB1D2
ENSG00000124939	0.866434	0.143526	0.250064	0.310693	ENSG00000124939	SCGB2A1
ENSG00000124942	708.36	619.168	400.896	614.088	ENSG00000124942	AHNAK
ENSG00000125037	63.3314	55.5728	30.9918	34.9288	ENSG00000125037	EMC3
ENSG00000125046	6.37222	12.4253	24.2721	19.3443	ENSG00000125046	SSUH2
ENSG00000125084	0	0	0.0440215	0	ENSG00000125084	WNT1
ENSG00000125089	81.7655	82.2748	73.8732	100.381	ENSG00000125089	SH3TC1
ENSG00000125107	94.6003	106.901	102.059	95.2309	ENSG00000125107	CNOT1
ENSG00000125122	1.56442	4.58414	4.44789	3.06656	ENSG00000125122	LRRC29
ENSG00000125124	30.3159	38.7823	34.8498	34.0129	ENSG00000125124	BBS2
ENSG00000125144	0.852669	1.03054	0.44647	0.734813	ENSG00000125144	MT1G
ENSG00000125148	268.294	671.681	32.0367	556.793	ENSG00000125148	MT2A
ENSG00000125149	20.3143	19.0305	19.5842	27.0965	ENSG00000125149	C16orf70
ENSG00000125166	47.3694	55.5349	40.4603	36.8125	ENSG00000125166	GOT2
ENSG00000125170	15.1151	12.1195	14.5917	8.79446	ENSG00000125170	DOK4
ENSG00000125207	0.219405	0.490269	0.383979	0.616176	ENSG00000125207	PIWIL1
ENSG00000125245	1.1249	2.8239	3.0156	5.30108	ENSG00000125245	GPR18
ENSG00000125246	4.34403	6.81316	5.10069	5.60939	ENSG00000125246	CLYBL
ENSG00000125247	11.804	14.7564	6.14443	11.3148	ENSG00000125247	TMTC4
ENSG00000125249	9.0535	9.24375	7.97637	6.13091	ENSG00000125249	RAP2A
ENSG00000125255	0.0860139	0.0832305	0.162507	0.191472	ENSG00000125255	SLC10A2
ENSG00000125257	7.18081	19.4691	15.8875	20.6268	ENSG00000125257	ABCC4
ENSG00000125266	46.9809	27.6537	29.1275	21.6514	ENSG00000125266	EFNB2
ENSG00000125285	0.15541	0.128964	0.251322	0.373497	ENSG00000125285	SOX21
ENSG00000125304	164.838	131.65	84.8867	77.7526	ENSG00000125304	TM9SF2
ENSG00000125319	1.05658	5.10975	1.3468	1.97078	ENSG00000125319	C17orf53
ENSG00000125337	1.40726	2.95489	2.09623	3.80455	ENSG00000125337	KIF25
ENSG00000125347	7.93612	15.7414	14.0585	12.9256	ENSG00000125347	IRF1
ENSG00000125351	2.6582	3.4667	4.36096	3.95562	ENSG00000125351	UPF3B
ENSG00000125352	4.82257	3.14359	3.72295	2.49691	ENSG00000125352	RNF113A
ENSG00000125354	4.27179	4.60021	6.53356	6.52286	ENSG00000125354	SEPT6
ENSG00000125355	0.0774689	0.0930421	0.168105	0.493846	ENSG00000125355	TMEM255A
ENSG00000125356	47.692	38.5272	23.834	20.5386	ENSG00000125356	NDUFA1
ENSG00000125363	0.0898238	0	0	0.0972143	ENSG00000125363	AMELX

ENSG00000125375	7.40991	10.2171	11.4137	10.4616	ENSG00000125375	ATP5S
ENSG00000125378	0.244689	1.21998	0.509993	1.18647	ENSG00000125378	BMP4
ENSG00000125384	0.214426	0.102967	0.185959	0.640575	ENSG00000125384	PTGER2
ENSG00000125385	0	0.201806	0.189788	0	ENSG00000125385	AL161781.1
ENSG00000125386	11.5871	17.1651	18.2672	20.2762	ENSG00000125386	FAM193A
ENSG00000125388	4.33546	5.44358	8.62332	10.4649	ENSG00000125388	GRK4
ENSG00000125398	43.6808	15.3855	9.02824	21.7015	ENSG00000125398	SOX9
ENSG00000125409	1.1108	1.52097	0.735551	1.26421	ENSG00000125409	TEKT3
ENSG00000125414	0.555119	0.490624	0.590437	1.11235	ENSG00000125414	MYH2
ENSG00000125430	2.32704	0.608563	1.83029	10.9899	ENSG00000125430	HS3ST3B1
ENSG00000125434	3.48022	7.35625	6.39819	13.6692	ENSG00000125434	SLC25A35
ENSG00000125445	31.0655	28.1191	22.6126	15.0879	ENSG00000125445	MRPS7
ENSG00000125447	21.3656	19.318	26.6297	17.9674	ENSG00000125447	GGA3
ENSG00000125449	2.26206	4.01656	3.37172	3.05729	ENSG00000125449	ARMC7
ENSG00000125450	36.7049	63.386	41.8317	54.9913	ENSG00000125450	NUP85
ENSG00000125454	5.07622	7.89261	5.89745	8.9737	ENSG00000125454	SLC25A19
ENSG00000125457	8.35842	7.34182	9.52127	5.91762	ENSG00000125457	MIF4GD
ENSG00000125458	30.9512	60.7981	44.0396	22.5945	ENSG00000125458	NT5C
ENSG00000125459	34.9324	39.792	50.6818	33.463	ENSG00000125459	MSTO1
ENSG00000125462	1.7657	3.66722	3.3501	7.48629	ENSG00000125462	C1orf61
ENSG00000125482	7.52897	7.12791	6.53913	9.48891	ENSG00000125482	TTF1
ENSG00000125484	4.93896	5.34248	10.4272	5.73316	ENSG00000125484	GTF3C4
ENSG00000125485	10.79	12.987	15.6025	12.1997	ENSG00000125485	DDX31
ENSG00000125492	0.0968199	0.337005	0.2072	0.327634	ENSG00000125492	BARHL1
ENSG00000125498	0	0	0.0108934	0	ENSG00000125498	KIR2DL1
ENSG00000125503	48.6605	37.1835	47.1176	46.0835	ENSG00000125503	PPP1R12C
ENSG00000125505	5.20344	3.88437	1.75536	1.72367	ENSG00000125505	MBOAT7
ENSG00000125508	0.803084	1.28932	0.399588	0.628018	ENSG00000125508	SRMS
ENSG00000125510	0.329829	0.246285	0.151345	0.420078	ENSG00000125510	OPRL1
ENSG00000125520	20.2554	63.0212	52.8856	26.7764	ENSG00000125520	SLC2A4RG
ENSG00000125522	0	0	0	0	ENSG00000125522	NPBWR2
ENSG00000125531	2.00565	1.49198	0.785023	0.235977	ENSG00000125531	FNDC11
ENSG00000125533	0.117515	0.182266	0.0502828	0	ENSG00000125533	BHLHE23
ENSG00000125534	82.5333	62.2138	54.1779	44.9702	ENSG00000125534	PPDPF
ENSG00000125538	81.7358	71.6767	92.9113	35.633	ENSG00000125538	IL1B
ENSG00000125551	0.654546	1.13298	0.980374	4.17262	ENSG00000125551	PLGLB2
ENSG00000125571	0.120675	0.707667	0.196114	0.795021	ENSG00000125571	IL37
ENSG00000125611	5.93904	6.89969	5.47551	4.52096	ENSG00000125611	CHCHD5
ENSG00000125618	10.9248	25.8597	27.3309	11.4165	ENSG00000125618	PAX8
ENSG00000125629	16.8343	14.6957	10.1781	15.5104	ENSG00000125629	INSIG2
ENSG00000125630	18.1511	27.1802	35.0433	27.0535	ENSG00000125630	POLR1B
ENSG00000125631	1.44821	1.30686	1.62692	1.36159	ENSG00000125631	HTR5BP
ENSG00000125633	25.6709	27.2184	22.8072	30.0322	ENSG00000125633	CCDC93
ENSG00000125637	27.1391	22.0681	17.3876	14.9838	ENSG00000125637	PSD4
ENSG00000125648	20.6461	10.8824	9.32307	18.4232	ENSG00000125648	SLC25A23
ENSG00000125650	1.60785	1.54066	2.23579	2.95777	ENSG00000125650	PSPN
ENSG00000125651	24.0058	22.3961	27.2519	21.1123	ENSG00000125651	GTF2F1
ENSG00000125652	12.1929	9.90365	8.75859	9.64119	ENSG00000125652	ALKBH7
ENSG00000125656	20.9564	22.9409	17.4549	20.8232	ENSG00000125656	CLPP
ENSG00000125657	24.0064	12.9618	5.90532	9.32311	ENSG00000125657	TNFSF9
ENSG00000125675	0.15706	0.515379	1.93772	10.3975	ENSG00000125675	GRIA3
ENSG00000125676	28.3465	50.8761	44.1843	55.2819	ENSG00000125676	THOC2
ENSG00000125686	20.8673	22.6672	25.4744	28.9858	ENSG00000125686	MED1
ENSG00000125691	512.832	446.488	283.541	255.228	ENSG00000125691	RPL23

ENSG00000125695	0	0	0	0	ENSG00000125695	AC046185.1
ENSG00000125703	4.11741	5.14383	3.61492	6.28611	ENSG00000125703	ATG4C
ENSG00000125726	2.39653	3.88081	3.25327	5.39867	ENSG00000125726	CD70
ENSG00000125730	24.4594	31.7314	119.953	64.5408	ENSG00000125730	C3
ENSG00000125731	35.5607	37.4968	35.6917	28.9376	ENSG00000125731	SH2D3A
ENSG00000125733	60.6312	38.5503	42.0607	36.7587	ENSG00000125733	TRIP10
ENSG00000125734	53.7566	58.2922	55.508	15.9299	ENSG00000125734	GPR108
ENSG00000125735	0.535327	1.12694	1.03456	1.80408	ENSG00000125735	TNFSF14
ENSG00000125740	2.31139	3.27475	0.759471	1.64147	ENSG00000125740	FOSB
ENSG00000125741	7.90636	8.66784	9.41156	11.235	ENSG00000125741	OPA3
ENSG00000125743	135.19	128.02	49.8055	67.9215	ENSG00000125743	SNRPD2
ENSG00000125744	8.70106	7.65195	4.5503	8.33743	ENSG00000125744	RTN2
ENSG00000125746	53.2495	97.0766	55.0131	55.992	ENSG00000125746	EML2
ENSG00000125753	100.479	87.1291	66.5793	77.8345	ENSG00000125753	VASP
ENSG00000125755	30.2894	44.914	52.4171	67.3842	ENSG00000125755	SYMPK
ENSG00000125772	21.4858	26.3714	28.0447	13.4568	ENSG00000125772	GPCPD1
ENSG00000125775	64.4713	14.3578	8.33298	9.45596	ENSG00000125775	SDCBP2
ENSG00000125779	18.1569	24.6375	21.3019	24.0284	ENSG00000125779	PANK2
ENSG00000125780	0.0417834	0.10071	0.091051	0.0459231	ENSG00000125780	TGM3
ENSG00000125787	0.742113	1.80101	1.45733	1.91209	ENSG00000125787	GNRH2
ENSG00000125788	0	0	0	0.368346	ENSG00000125788	DEFB126
ENSG00000125798	0.0694666	2.31731	4.81725	0.708606	ENSG00000125798	FOXA2
ENSG00000125810	0.10531	0.124235	0.122984	0.186497	ENSG00000125810	CD93
ENSG00000125812	5.67637	9.78071	10.8568	5.67592	ENSG00000125812	GZF1
ENSG00000125813	0.206416	0.224933	0.434219	0.499353	ENSG00000125813	PAX1
ENSG00000125814	5.55339	9.35072	10.3596	11.9773	ENSG00000125814	NAPB
ENSG00000125815	0	0.105787	0	0.356235	ENSG00000125815	CST8
ENSG00000125816	0.0250886	0.0240656	0.0652645	0.0548022	ENSG00000125816	NKX2-4
ENSG00000125817	23.5153	18.6373	18.1257	17.265	ENSG00000125817	CENPB
ENSG00000125818	30.3047	28.2362	27.8673	19.6906	ENSG00000125818	PSMF1
ENSG00000125820	0.801752	1.35282	0.753975	2.19439	ENSG00000125820	NKX2-2
ENSG00000125821	22.5292	25.7147	23.4948	16.2567	ENSG00000125821	DTD1
ENSG00000125823	2.44765	6.31697	2.75424	6.85294	ENSG00000125823	CSTL1
ENSG00000125826	20.3537	58.7336	176.254	44.7036	ENSG00000125826	RBCK1
ENSG00000125827	6.92547	11.2944	7.35468	6.97151	ENSG00000125827	TMX4
ENSG00000125831	0	0	0	0	ENSG00000125831	CST11
ENSG00000125834	9.09888	10.1842	10.1914	10.0176	ENSG00000125834	STK35
ENSG00000125835	88.4647	78.5239	53.9799	41.6988	ENSG00000125835	SNRPB
ENSG00000125841	6.78396	16.5514	20.0592	18.1728	ENSG00000125841	NRSN2
ENSG00000125843	5.95096	7.16048	7.69756	5.47493	ENSG00000125843	AP5S1
ENSG00000125844	137.463	146.748	118.435	209.008	ENSG00000125844	RRBP1
ENSG00000125845	6.41225	4.90879	9.10275	6.81728	ENSG00000125845	BMP2
ENSG00000125846	10.8939	17.3877	17.7132	11.8685	ENSG00000125846	ZNF133
ENSG00000125848	122.21	107.993	55.2406	35.6483	ENSG00000125848	FLRT3
ENSG00000125850	6.21263	6.63386	3.93244	3.62533	ENSG00000125850	OVOL2
ENSG00000125851	0.729168	1.75318	1.61996	2.67222	ENSG00000125851	PCSK2
ENSG00000125861	2.19968	1.94377	0.904701	1.62761	ENSG00000125861	GFRA4
ENSG00000125863	4.34867	9.14696	10.8515	4.84182	ENSG00000125863	MKKS
ENSG00000125864	6.85001	5.95021	4.9651	3.33478	ENSG00000125864	BFSP1
ENSG00000125868	119.178	68.9345	60.8807	69.4281	ENSG00000125868	DSTN
ENSG00000125869	0	0	0	0	ENSG00000125869	LAMP5
ENSG00000125870	20.191	20.3023	12.4122	10.7494	ENSG00000125870	SNRPB2
ENSG00000125871	8.17622	11.3283	12.8366	8.11304	ENSG00000125871	MGME1
ENSG00000125872	0.286708	1.24401	0.249914	0.675305	ENSG00000125872	LRRN4

ENSG00000125875	11.5643	13.3667	17.5238	11.9037	ENSG00000125875	TBC1D20
ENSG00000125877	27.9862	28.8134	37.4965	25.8459	ENSG00000125877	ITPA
ENSG00000125878	0.299449	0.223689	0.327223	0.368966	ENSG00000125878	TCF15
ENSG00000125879	0.0584665	0.11378	0.102849	0.254887	ENSG00000125879	OTOR
ENSG00000125885	4.89842	10.9226	6.17328	9.67624	ENSG00000125885	MCM8
ENSG00000125888	0.387243	0.800085	1.32	2.75142	ENSG00000125888	BANF2
ENSG00000125895	6.30598	2.25691	3.05095	2.51259	ENSG00000125895	TMEM74B
ENSG00000125898	7.72021	14.784	14.0525	6.77897	ENSG00000125898	FAM110A
ENSG00000125899	0	2.06514	0.155739	0	ENSG00000125899	C20orf187
ENSG00000125900	0.401524	0.111177	0.0251265	0.158205	ENSG00000125900	SIRPD
ENSG00000125901	17.9795	21.7358	17.5466	16.4707	ENSG00000125901	MRPS26
ENSG00000125903	0.0962927	0.0925352	0	0	ENSG00000125903	DEFB129
ENSG00000125910	1.22432	0.716794	0.490348	0.785021	ENSG00000125910	S1PR4
ENSG00000125912	71.1288	68.4048	41.0014	35.7493	ENSG00000125912	NCLN
ENSG00000125931	0.362882	0.669578	0.393716	0.34999	ENSG00000125931	CITED1
ENSG00000125944	38.6547	60.1991	60.2583	68.9234	ENSG00000125944	HNRNPR
ENSG00000125945	7.28782	9.97868	11.6915	4.34351	ENSG00000125945	ZNF436
ENSG00000125952	23.4731	21.9337	26.7189	22.6783	ENSG00000125952	MAX
ENSG00000125954	0.303735	0	0	0	ENSG00000125954	CHURC1-FNTB
ENSG00000125962	6.72065	8.38299	8.17981	5.55549	ENSG00000125962	ARMCX5
ENSG00000125965	0.125757	0.479698	0.512928	0.578969	ENSG00000125965	GDF5
ENSG00000125966	7.88992	4.57008	4.65015	8.14205	ENSG00000125966	MMP24
ENSG00000125967	8.73155	18.574	14.4053	16.1313	ENSG00000125967	NECAB3
ENSG00000125968	97.5003	61.4888	39.357	12.4881	ENSG00000125968	ID1
ENSG00000125970	40.3124	66.8173	45.6161	43.8853	ENSG00000125970	RALY
ENSG00000125971	63.2016	34.5486	23.975	32.9207	ENSG00000125971	DYNLRB1
ENSG00000125975	0	0.0570974	0	0.16657	ENSG00000125975	C20orf173
ENSG00000125977	42.9041	46.7363	50.0094	23.2201	ENSG00000125977	EIF2S2
ENSG00000125991	97.1834	105.021	89.3569	69.656	ENSG00000125991	ERGIC3
ENSG00000125995	108.821	62.6475	38.3861	31.38	ENSG00000125995	ROMO1
ENSG00000125997	0.101883	1.48368	2.60581	1.76486	ENSG00000125997	BPIFB9P
ENSG00000125998	7.98735	2.96211	4.47639	2.77421	ENSG00000125998	FAM83C
ENSG00000125999	1.68784	2.54021	2.71636	4.96781	ENSG00000125999	BPIFB1
ENSG00000126001	12.9824	20.8989	14.8634	24.7923	ENSG00000126001	CEP250
ENSG00000126003	4.24534	3.61174	5.75455	2.68938	ENSG00000126003	PLAGL2
ENSG00000126010	0.029313	0.112997	0.178764	0.192938	ENSG00000126010	GRPR
ENSG00000126012	23.7859	24.5446	31.5579	32.0976	ENSG00000126012	KDM5C
ENSG00000126016	0.203209	0.321128	1.0376	2.09101	ENSG00000126016	AMOT
ENSG00000126062	34.2336	29.2269	24.0529	15.7305	ENSG00000126062	TMEM115
ENSG00000126067	17.2193	15.8479	14.6962	16.3161	ENSG00000126067	PSMB2
ENSG00000126070	8.38336	16.4633	13.9878	19.0205	ENSG00000126070	AGO3
ENSG00000126088	30.4416	33.33	32.1146	24.0473	ENSG00000126088	UROD
ENSG00000126091	5.53363	15.5863	10.8839	15.2458	ENSG00000126091	ST3GAL3
ENSG00000126106	3.99619	6.3846	4.32468	4.17308	ENSG00000126106	TMEM53
ENSG00000126107	15.3106	9.66248	16.4584	13.8901	ENSG00000126107	HECTD3
ENSG00000126214	130.565	162.033	164.981	182.684	ENSG00000126214	KLC1
ENSG00000126215	19.177	42.3065	33.6514	32.2032	ENSG00000126215	XRCC3
ENSG00000126216	7.29531	15.4414	10.7267	14.1206	ENSG00000126216	TUBGCP3
ENSG00000126217	1.87238	4.65763	3.36816	6.82602	ENSG00000126217	MCF2L
ENSG00000126218	0.256181	0.491647	0.213498	0.666163	ENSG00000126218	F10
ENSG00000126226	24.1038	33.221	28.8935	24.6065	ENSG00000126226	PCID2
ENSG00000126231	0.50878	0.838803	0.680395	1.00077	ENSG00000126231	PROZ
ENSG00000126233	0.411607	0.263256	0.831647	1.17634	ENSG00000126233	SLURP1
ENSG00000126243	8.31974	10.1174	6.92419	11.5052	ENSG00000126243	LRFN3

ENSG00000126246	10.6043	36.3102	22.9364	32.5253	ENSG00000126246	IGFLR1
ENSG00000126247	135.409	113.59	83.3365	58.5782	ENSG00000126247	CAPNS1
ENSG00000126249	6.55714	7.32828	7.08073	3.33924	ENSG00000126249	PDCD2L
ENSG00000126251	0	0	0	0.0293442	ENSG00000126251	GPR42
ENSG00000126254	28.5516	21.2194	23.6057	17.1352	ENSG00000126254	RBM42
ENSG00000126259	0.0859943	0.165753	0.0749219	0.220149	ENSG00000126259	KIRREL2
ENSG00000126261	46.3686	43.6142	42.2921	32.2753	ENSG00000126261	UBA2
ENSG00000126262	6.16277	10.9469	7.81392	23.0758	ENSG00000126262	FFAR2
ENSG00000126264	0.361778	0.173097	0.312554	0.246144	ENSG00000126264	HCST
ENSG00000126266	0.135941	0.339189	0.295306	0.223676	ENSG00000126266	FFAR1
ENSG00000126267	113.634	71.654	33.6927	43.6336	ENSG00000126267	COX6B1
ENSG00000126337	0.0698864	0	0	0.0382844	ENSG00000126337	KRT36
ENSG00000126351	4.67592	6.09543	4.02574	7.5466	ENSG00000126351	THRA
ENSG00000126353	0.248038	0.312964	0.27048	0.324181	ENSG00000126353	CCR7
ENSG00000126368	22.4702	5.06941	2.48079	5.32393	ENSG00000126368	NR1D1
ENSG00000126391	48.5175	25.4269	32.2253	20.4782	ENSG00000126391	FRMD8
ENSG00000126432	184.216	110.728	91.8314	57.4025	ENSG00000126432	PRDX5
ENSG00000126453	5.13994	9.28882	3.3214	6.99634	ENSG00000126453	BCL2L12
ENSG00000126456	37.2612	54.0873	50.5592	48.4351	ENSG00000126456	IRF3
ENSG00000126457	123.273	140.368	106.262	82.8309	ENSG00000126457	PRMT1
ENSG00000126458	21.0503	29.0634	21.1564	26.1963	ENSG00000126458	RRAS
ENSG00000126460	12.4456	6.99742	8.41345	2.21241	ENSG00000126460	PRRG2
ENSG00000126461	23.4413	17.8462	21.786	24.6766	ENSG00000126461	SCAF1
ENSG00000126464	4.25812	5.33674	7.90575	10.4333	ENSG00000126464	PRR12
ENSG00000126467	0.0303341	1.05561	1.30575	0.787199	ENSG00000126467	TSKS
ENSG00000126500	0.301168	0.689303	1.2743	1.63915	ENSG00000126500	FLRT1
ENSG00000126522	27.6462	24.9276	18.3215	19.8134	ENSG00000126522	ASL
ENSG00000126524	70.5802	27.7264	41.9528	32.7704	ENSG00000126524	SBDS
ENSG00000126542	0	0	0.597701	0.477821	ENSG00000126542	PTPN20C
ENSG00000126545	0.195949	0.235359	0.20535	0.556826	ENSG00000126545	CSN1S1
ENSG00000126549	0	0.0866094	0.307107	0.336751	ENSG00000126549	STATH
ENSG00000126550	3.98529	9.06959	9.53142	19.617	ENSG00000126550	HTN1
ENSG00000126561	2.24054	2.42324	2.14017	2.94373	ENSG00000126561	STAT5A
ENSG00000126562	1.39658	1.68489	3.0999	4.74994	ENSG00000126562	WNK4
ENSG00000126581	46.7352	33.8085	36.6697	35.2186	ENSG00000126581	BECN1
ENSG00000126583	0	0.233971	0.0364183	0.0893273	ENSG00000126583	PRKCG
ENSG00000126602	35.1672	74.3151	63.339	54.2681	ENSG00000126602	TRAP1
ENSG00000126603	0.997995	2.46477	2.5879	3.14212	ENSG00000126603	GLIS2
ENSG00000126653	40.805	77.9699	89.9061	132.031	ENSG00000126653	NSRP1
ENSG00000126698	33.471	31.9841	30.6381	32.7914	ENSG00000126698	DNAJC8
ENSG00000126705	10.4919	10.5841	10.6769	15.027	ENSG00000126705	AHDC1
ENSG00000126709	144.623	311.829	242.361	167.156	ENSG00000126709	IFI6
ENSG00000126733	0.306386	0.307958	0.501524	0.477876	ENSG00000126733	DACH2
ENSG00000126746	15.3413	15.1849	15.3617	13.1097	ENSG00000126746	ZNF384
ENSG00000126749	16.8301	17.3701	22.6999	13.7126	ENSG00000126749	EMG1
ENSG00000126752	0.0530431	0.171548	0.0341501	0.455038	ENSG00000126752	SSX1
ENSG00000126756	27.4868	33.1075	22.3648	19.5774	ENSG00000126756	UXT
ENSG00000126759	1.08425	1.77604	1.45231	2.28036	ENSG00000126759	CFP
ENSG00000126767	9.71779	8.34391	9.34233	10.1711	ENSG00000126767	ELK1
ENSG00000126768	1.00014	2.84402	13.0584	3.25234	ENSG00000126768	TIMM17B
ENSG00000126773	37.4605	47.7789	43.4798	61.3611	ENSG00000126773	PCNX4
ENSG00000126775	8.10874	5.12562	7.2984	6.41838	ENSG00000126775	ATG14
ENSG00000126777	129.596	165.442	128.577	111.321	ENSG00000126777	KTN1
ENSG00000126778	0.467448	1.08374	1.15678	3.5418	ENSG00000126778	SIX1

ENSG00000126785	0.594466	0.945951	1.4227	1.42725	ENSG00000126785	RHOJ
ENSG00000126787	4.88977	28.1041	1.95124	9.14596	ENSG00000126787	DLGAP5
ENSG00000126790	29.1156	41.5	37.7882	56.1302	ENSG00000126790	L3HYPDH
ENSG00000126803	6.06919	2.6389	3.33807	7.17762	ENSG00000126803	HSPA2
ENSG00000126804	20.6106	24.7904	23.3236	26.3729	ENSG00000126804	ZBTB1
ENSG00000126814	8.96738	10.8392	11.2938	7.79933	ENSG00000126814	TRMT5
ENSG00000126821	25.8473	31.3383	19.6044	11.1441	ENSG00000126821	SGPP1
ENSG00000126822	72.1972	87.6142	68.4575	40.303	ENSG00000126822	PLEKHG3
ENSG00000126838	0.578208	1.31121	3.03446	4.46361	ENSG00000126838	PZP
ENSG00000126856	7.40299	19.2502	19.1648	29.8013	ENSG00000126856	PRDM7
ENSG00000126858	14.057	16.5175	11.8605	14.0787	ENSG00000126858	RHOT1
ENSG00000126860	0.774401	2.03555	1.69074	3.83063	ENSG00000126860	EVI2A
ENSG00000126861	1.24532	6.85781	4.76873	11.4758	ENSG00000126861	OMG
ENSG00000126870	3.04702	4.73424	7.36101	8.21645	ENSG00000126870	WDR60
ENSG00000126878	3.98325	0.917007	4.47474	2.52244	ENSG00000126878	AIF1L
ENSG00000126882	1.02568	1.64063	0.713937	2.96004	ENSG00000126882	FAM78A
ENSG00000126883	22.5167	31.4647	38.0054	45.9939	ENSG00000126883	NUP214
ENSG00000126890	0	0	0	0	ENSG00000126890	CTAG2
ENSG00000126895	0.0354691	0	0.0204954	0	ENSG00000126895	AVPR2
ENSG00000126903	17.7764	3.98036	12.0766	5.28479	ENSG00000126903	SLC10A3
ENSG00000126934	55.1509	49.0652	46.0002	49.2326	ENSG00000126934	MAP2K2
ENSG00000126945	17.0854	9.2679	11.0091	10.0779	ENSG00000126945	HNRNPH2
ENSG00000126947	2.473	3.13176	2.55607	3.3212	ENSG00000126947	ARMCX1
ENSG00000126950	0.124329	0.548467	0.196939	1.00494	ENSG00000126950	TMEM35A
ENSG00000126952	0.184318	0.0628384	0.0999594	0.173823	ENSG00000126952	NXF5
ENSG00000126953	1.44516	1.73928	3.07756	1.7406	ENSG00000126953	TIMM8A
ENSG00000126970	4.39979	5.83468	3.76508	7.2478	ENSG00000126970	ZC4H2
ENSG00000127022	321.883	466.885	349.119	247.547	ENSG00000127022	CANX
ENSG00000127054	59.6334	72.2625	71.8231	60.007	ENSG00000127054	INTS11
ENSG00000127074	0.398696	0.892149	1.01453	1.50279	ENSG00000127074	RGS13
ENSG00000127080	21.0005	10.0702	13.6608	6.48378	ENSG00000127080	IPPK
ENSG00000127081	4.65929	6.54506	5.88007	4.61126	ENSG00000127081	ZNF484
ENSG00000127083	0.13592	0.700122	0.534026	1.26928	ENSG00000127083	OMD
ENSG00000127084	1.04139	1.1001	1.65215	3.02511	ENSG00000127084	FGD3
ENSG00000127124	0.398425	1.907	1.61966	7.27292	ENSG00000127124	HIVEP3
ENSG00000127125	31.8798	25.4624	24.1523	18.533	ENSG00000127125	PPCS
ENSG00000127129	0.929158	1.52315	0.798546	0.753427	ENSG00000127129	EDN2
ENSG00000127152	8.08161	9.05169	9.54944	10.0132	ENSG00000127152	BCL11B
ENSG00000127184	179.829	170.841	105.998	83.7692	ENSG00000127184	COX7C
ENSG00000127191	19.1071	20.6255	20.7432	24.0658	ENSG00000127191	TRAF2
ENSG00000127220	8.81164	4.69214	5.42277	6.09835	ENSG00000127220	ABHD8
ENSG00000127241	0.543057	1.37607	1.17186	4.65032	ENSG00000127241	MASP1
ENSG00000127249	2.61479	1.01957	1.87979	3.90068	ENSG00000127249	ATP13A4
ENSG00000127252	0.0573001	0.0551432	0.132291	0.0624671	ENSG00000127252	HRASLS
ENSG00000127311	1.63415	3.64377	3.60002	5.52212	ENSG00000127311	HELB
ENSG00000127314	56.1169	74.1873	71.1762	110.527	ENSG00000127314	RAP1B
ENSG00000127318	0.157625	0.151729	0.457113	0.22936	ENSG00000127318	IL22
ENSG00000127324	0.511285	0	0	0.0937137	ENSG00000127324	TSPAN8
ENSG00000127325	3.28412	8.02935	6.86922	11.6736	ENSG00000127325	BEST3
ENSG00000127328	11.5838	14.8967	13.7141	9.49502	ENSG00000127328	RAB3IP
ENSG00000127329	2.23938	1.34544	0.858373	1.885	ENSG00000127329	PTPRB
ENSG00000127334	15.1148	11.2754	14.3883	13.5245	ENSG00000127334	DYRK2
ENSG00000127337	7.45901	12.2073	7.13742	6.24668	ENSG00000127337	YEATS4
ENSG00000127362	1.0471	2.88756	4.13023	1.8688	ENSG00000127362	TAS2R3

ENSG00000127364	0.808548	2.13111	4.94986	2.43778	ENSG00000127364	TAS2R4
ENSG00000127366	0.915651	2.13394	4.73752	1.83351	ENSG00000127366	TAS2R5
ENSG00000127377	0.282153	0.342268	0.405774	1.04234	ENSG00000127377	CRYGN
ENSG00000127399	7.8208	15.709	11.6442	15.6162	ENSG00000127399	LRRC61
ENSG00000127412	0.013902	0.0133985	0.0115264	0.0435617	ENSG00000127412	TRPV5
ENSG00000127415	10.9485	8.70166	19.2022	11.2541	ENSG00000127415	IDUA
ENSG00000127418	11.4879	5.37808	5.79051	6.52842	ENSG00000127418	FGFRL1
ENSG00000127419	19.102	23.9527	25.9922	18.5224	ENSG00000127419	TMEM175
ENSG00000127423	1.75881	5.16457	4.56909	1.91114	ENSG00000127423	AUNIP
ENSG00000127445	23.6286	23.9677	15.1021	12.957	ENSG00000127445	PIN1
ENSG00000127452	20.3329	23.5494	24.253	22.2554	ENSG00000127452	FBXL12
ENSG00000127463	50.9771	71.6338	69.235	51.6627	ENSG00000127463	EMC1
ENSG00000127472	0.328223	0.855118	0.796757	1.25809	ENSG00000127472	PLA2G5
ENSG00000127481	43.0822	73.5137	77.2406	93.2475	ENSG00000127481	UBR4
ENSG00000127483	83.2032	133.683	86.1997	125.066	ENSG00000127483	HP1BP3
ENSG00000127507	5.97875	7.0225	8.89075	9.86413	ENSG00000127507	ADGRE2
ENSG00000127511	35.3722	48.4175	64.2139	61.1356	ENSG00000127511	SIN3B
ENSG00000127515	0	0	0.117053	0	ENSG00000127515	OR7A10
ENSG00000127526	48.6799	50.5797	39.1977	46.6292	ENSG00000127526	SLC35E1
ENSG00000127527	12.4098	15.9205	17.0595	18.9102	ENSG00000127527	EPS15L1
ENSG00000127528	0.640453	0.269204	0.392795	2.26378	ENSG00000127528	KLF2
ENSG00000127529	0	0	0	0	ENSG00000127529	OR7C2
ENSG00000127530	0.171721	0.385602	0.19914	0.312011	ENSG00000127530	OR7C1
ENSG00000127533	1.5813	3.62539	3.52089	5.97353	ENSG00000127533	F2RL3
ENSG00000127540	85.8247	68.2304	51.8807	38.614	ENSG00000127540	UQCR11
ENSG00000127554	12.6319	12.4274	10.717	8.42213	ENSG00000127554	GFER
ENSG00000127561	0.48636	1.47212	1.5471	0.735581	ENSG00000127561	SYNGR3
ENSG00000127564	16.0134	53.2548	13.2099	20.4817	ENSG00000127564	PKMYT1
ENSG00000127578	0.470722	0.443965	0.751725	0.599356	ENSG00000127578	WFIKKN1
ENSG00000127580	6.53657	7.41279	11.3843	6.46038	ENSG00000127580	WDR24
ENSG00000127585	1.70018	1.33553	1.79208	2.1531	ENSG00000127585	FBXL16
ENSG00000127586	8.77129	27.8521	10.7932	20.5811	ENSG00000127586	CHTF18
ENSG00000127588	0.188813	0.249876	0.242891	0.150916	ENSG00000127588	GNG13
ENSG00000127589	0.215351	0.337936	0.341674	0.389553	ENSG00000127589	TUBBP1
ENSG00000127603	182.45	252.796	197.264	264.945	ENSG00000127603	MACF1
ENSG00000127616	51.6775	39.7735	46.1167	64.3702	ENSG00000127616	SMARCA4
ENSG00000127663	15.1521	17.5974	24.2902	30.6377	ENSG00000127663	KDM4B
ENSG00000127666	8.44984	5.3689	6.32347	5.7407	ENSG00000127666	TICAM1
ENSG00000127720	7.12335	10.0252	8.99987	9.73695	ENSG00000127720	METTL25
ENSG00000127743	0.94013	0.899481	0.716454	1.12833	ENSG00000127743	IL17B
ENSG00000127774	15.3711	10.1944	8.94162	5.12176	ENSG00000127774	EMC6
ENSG00000127780	0.063868	0	0	0.0886473	ENSG00000127780	OR1E2
ENSG00000127804	9.87216	13.2104	13.7	15.6	ENSG00000127804	METTL16
ENSG00000127824	284.461	77.8114	92.2008	54.1469	ENSG00000127824	TUBA4A
ENSG00000127831	0.10222	0.671524	0.382369	0.6943	ENSG00000127831	VIL1
ENSG00000127837	57.3541	30.739	39.8192	23.7889	ENSG00000127837	AAMP
ENSG00000127838	20.6134	15.7042	15.9573	15.1878	ENSG00000127838	PNKD
ENSG00000127863	5.64514	21.7972	18.6452	30.0801	ENSG00000127863	TNFRSF19
ENSG00000127870	37.2247	26.8153	35.696	18.1291	ENSG00000127870	RNF6
ENSG00000127884	25.016	15.6307	16.0408	10.9623	ENSG00000127884	ECHS1
ENSG00000127903	0.699421	1.57825	1.27739	2.10298	ENSG00000127903	ZNF835
ENSG00000127914	30.7806	48.185	43.1865	59.8289	ENSG00000127914	AKAP9
ENSG00000127920	0.233413	1.45694	0.328826	3.14968	ENSG00000127920	GNG11
ENSG00000127922	43.6903	45.4084	39.1725	42.1504	ENSG00000127922	SEM1

ENSG00000127928	0.276775	0.840918	0.664239	1.61701	ENSG00000127928	GNGT1
ENSG00000127946	0.901213	4.235	3.20657	1.8304	ENSG00000127946	HIP1
ENSG00000127947	60.3885	89.2377	85.4266	149.025	ENSG00000127947	PTPN12
ENSG00000127948	28.5744	27.5319	20.5744	13.5033	ENSG00000127948	POR
ENSG00000127951	0.467201	1.38063	1.69366	1.46634	ENSG00000127951	FGL2
ENSG00000127952	11.7219	8.96171	10.1312	9.13424	ENSG00000127952	STYXL1
ENSG00000127954	15.7293	1.53904	3.43023	3.08542	ENSG00000127954	STEAP4
ENSG00000127955	31.1553	33.1948	45.3196	31.2015	ENSG00000127955	GNAI1
ENSG00000127957	4.81165	5.36461	6.98152	11.0221	ENSG00000127957	PMS2P3
ENSG00000127980	11.1467	14.1568	15.1851	10.1547	ENSG00000127980	PEX1
ENSG00000127989	10.0485	14.2348	15.3881	15.4748	ENSG00000127989	MTERF1
ENSG00000127990	1.22022	25.767	18.3585	21.7035	ENSG00000127990	SGCE
ENSG00000127993	4.9924	4.2038	5.38336	4.47545	ENSG00000127993	RBM48
ENSG00000127995	5.59885	6.65782	6.54267	9.31367	ENSG00000127995	CASD1
ENSG00000128000	6.20806	13.5473	11.449	9.48029	ENSG00000128000	ZNF780B
ENSG00000128011	0.32279	0.268443	0.165647	0.647341	ENSG00000128011	LRFN1
ENSG00000128016	91.1205	91.5133	47.6143	48.6578	ENSG00000128016	ZFP36
ENSG00000128039	11.5965	5.66337	10.5336	5.42288	ENSG00000128039	SRD5A3
ENSG00000128040	0	0.11022	0	0	ENSG00000128040	SPINK2
ENSG00000128045	0.429963	1.00172	0.875532	0.95651	ENSG00000128045	RASL11B
ENSG00000128050	29.5213	46.4974	45.6134	48.2393	ENSG00000128050	PAICS
ENSG00000128052	0.153533	0.363269	0.117213	0.251631	ENSG00000128052	KDR
ENSG00000128059	12.1251	20.0663	18.2935	21.4489	ENSG00000128059	PPAT
ENSG00000128159	25.4958	33.2983	34.3055	27.3716	ENSG00000128159	TUBGCP6
ENSG00000128165	0.485114	6.30317	12.9671	2.57147	ENSG00000128165	ADM2
ENSG00000128185	11.3113	9.05644	8.77953	6.43998	ENSG00000128185	DGCR6L
ENSG00000128191	18.5696	27.2408	32.7216	29.6013	ENSG00000128191	DGCR8
ENSG00000128203	2.27025	3.0097	4.18505	2.8677	ENSG00000128203	ASPHD2
ENSG00000128218	0.30131	0.220869	0.521592	0	ENSG00000128218	VPREB3
ENSG00000128228	22.9865	25.8788	5.67609	10.9711	ENSG00000128228	SDF2L1
ENSG00000128242	2.93719	4.13099	3.39411	4.98682	ENSG00000128242	GAL3ST1
ENSG00000128245	57.6828	45.9517	24.9976	27.6887	ENSG00000128245	YWHAH
ENSG00000128250	0.12325	0.360518	0.32414	0.0915166	ENSG00000128250	RFPL1
ENSG00000128253	0.0854292	0.0240616	0.0661267	0.0591853	ENSG00000128253	RFPL2
ENSG00000128254	1.52796	2.1649	1.63482	2.40658	ENSG00000128254	C22orf24
ENSG00000128262	0.0718818	0.182355	0.0922144	1.02587	ENSG00000128262	POM121L9P
ENSG00000128266	0.845325	0.404235	0.835699	1.8859	ENSG00000128266	GNAZ
ENSG00000128268	2.15687	2.56241	3.18337	4.59908	ENSG00000128268	MGAT3
ENSG00000128271	2.76788	3.79366	5.18905	6.27174	ENSG00000128271	ADORA2A
ENSG00000128272	130.6	230.567	222.54	86.6862	ENSG00000128272	ATF4
ENSG00000128274	24.4234	17.5081	4.41528	7.30987	ENSG00000128274	A4GALT
ENSG00000128276	0	0	0	0	ENSG00000128276	RFPL3
ENSG00000128283	39.468	43.6955	56.5308	24.3767	ENSG00000128283	CDC42EP1
ENSG00000128284	1.3117	2.40076	4.32998	4.82784	ENSG00000128284	APOL3
ENSG00000128285	0.354905	2.37562	2.61252	0.605673	ENSG00000128285	MCHR1
ENSG00000128294	15.4204	21.4771	11.9527	15.7184	ENSG00000128294	TPST2
ENSG00000128298	1.491	1.01959	3.17452	1.62773	ENSG00000128298	BAIAP2L2
ENSG00000128309	19.0359	17.0421	15.9107	11.0208	ENSG00000128309	MPST
ENSG00000128310	0.274314	0.106461	0.0905084	0.113543	ENSG00000128310	GALR3
ENSG00000128311	9.44388	7.22617	8.73825	3.63792	ENSG00000128311	TST
ENSG00000128313	0.202882	0.234491	0.282614	0.0888007	ENSG00000128313	APOL5
ENSG00000128322	0	0	0	0.100798	ENSG00000128322	IGLL1
ENSG00000128335	5.88904	7.47914	13.7176	13.9227	ENSG00000128335	APOL2
ENSG00000128340	36.5995	39.185	16.7689	24.9249	ENSG00000128340	RAC2

ENSG00000128342	6.51287	1.46883	4.61045	7.95048	ENSG00000128342	LIF
ENSG00000128346	41.2321	30.1227	66.7083	20.6345	ENSG00000128346	C22orf23
ENSG00000128383	4.76351	0.791664	0.688664	1.74429	ENSG00000128383	APOBEC3A
ENSG00000128394	5.07059	6.45671	6.33978	5.72547	ENSG00000128394	APOBEC3F
ENSG00000128408	0.501647	1.11932	0.256027	1.16857	ENSG00000128408	RIBC2
ENSG00000128422	8029.63	2424.95	5880.48	1273.55	ENSG00000128422	KRT17
ENSG00000128438	0.821445	0.645985	0.844165	2.08829	ENSG00000128438	TBC1D27
ENSG00000128463	105.624	80.2026	59.5725	65.1712	ENSG00000128463	EMC4
ENSG00000128482	1.35173	1.38488	1.66584	2.60961	ENSG00000128482	RNF112
ENSG00000128487	22.12	30.7084	38.8286	29.6634	ENSG00000128487	SPECC1
ENSG00000128510	110.978	11.9582	35.6997	25.648	ENSG00000128510	CPA4
ENSG00000128512	9.38986	37.6057	7.33607	28.0657	ENSG00000128512	DOCK4
ENSG00000128513	9.65523	19.3058	20.3597	18.9526	ENSG00000128513	POT1
ENSG00000128519	0	0.11937	0	0.0675562	ENSG00000128519	TAS2R16
ENSG00000128524	54.5488	31.0507	32.7795	20.5821	ENSG00000128524	ATP6V1F
ENSG00000128534	13.435	18.0619	18.4881	16.3768	ENSG00000128534	LSM8
ENSG00000128536	8.97077	21.229	14.9019	26.2115	ENSG00000128536	CDHR3
ENSG00000128563	8.49639	6.26754	11.2281	7.25076	ENSG00000128563	PRKRIP1
ENSG00000128564	0.516515	0.4051	0.899442	0.676818	ENSG00000128564	VGF
ENSG00000128567	0.942952	2.35851	2.1165	3.31676	ENSG00000128567	PODXL
ENSG00000128573	4.57931	7.32016	7.20779	10.5788	ENSG00000128573	FOXP2
ENSG00000128578	9.29149	17.8801	8.77058	14.9652	ENSG00000128578	STRIP2
ENSG00000128581	9.44154	15.8564	12.9237	20.8241	ENSG00000128581	IFT22
ENSG00000128585	18.9016	29.8776	26.3364	39.2715	ENSG00000128585	MKLN1
ENSG00000128590	10.9258	9.05464	11.4246	6.61988	ENSG00000128590	DNAJB9
ENSG00000128591	0.827549	0.343346	0.756816	10.47	ENSG00000128591	FLNC
ENSG00000128594	5.97727	6.08068	4.96471	8.48481	ENSG00000128594	LRRC4
ENSG00000128595	141.802	172.436	70.419	197.506	ENSG00000128595	CALU
ENSG00000128596	0.789233	4.71654	2.91307	5.25652	ENSG00000128596	CCDC136
ENSG00000128602	5.63536	5.73182	8.39817	6.07365	ENSG00000128602	SMO
ENSG00000128604	14.7021	5.58202	8.53405	3.74872	ENSG00000128604	IRF5
ENSG00000128606	0.786207	1.66679	1.79884	2.30532	ENSG00000128606	LRRC17
ENSG00000128607	22.854	20.2607	21.722	31.3577	ENSG00000128607	KLHDC10
ENSG00000128609	20.7375	20.8855	23.5188	21.6749	ENSG00000128609	NDUFA5
ENSG00000128610	0.114352	0.221023	0.520096	0.507412	ENSG00000128610	FEZF1
ENSG00000128617	3.04729	4.43553	1.97596	6.94903	ENSG00000128617	OPN1SW
ENSG00000128626	20.655	20.8869	19.8684	17.729	ENSG00000128626	MRPS12
ENSG00000128641	134.383	173.677	282.64	165.582	ENSG00000128641	MYO1B
ENSG00000128645	0.0558921	0.160524	0.14627	0.462804	ENSG00000128645	HOXD1
ENSG00000128652	2.18907	1.45577	1.32724	3.08559	ENSG00000128652	HOXD3
ENSG00000128654	17.1324	17.1881	21.7465	18.3535	ENSG00000128654	MTX2
ENSG00000128655	0.69271	1.5039	1.15837	2.25111	ENSG00000128655	PDE11A
ENSG00000128656	3.02161	1.50133	2.04672	23.0469	ENSG00000128656	CHN1
ENSG00000128683	2.97683	1.45148	1.21079	1.16532	ENSG00000128683	GAD1
ENSG00000128692	0	0.298955	0	0.154592	ENSG00000128692	EIF2S2P4
ENSG00000128694	6.00279	8.88291	5.53577	6.98346	ENSG00000128694	OSGEPL1
ENSG00000128699	35.1622	45.7012	50.9421	28.3012	ENSG00000128699	ORMDL1
ENSG00000128708	14.8532	18.5799	13.0842	14.8218	ENSG00000128708	HAT1
ENSG00000128709	0.467198	0.339232	0.247576	0.558628	ENSG00000128709	HOXD9
ENSG00000128710	0.226062	0.358974	0.117064	0.524231	ENSG00000128710	HOXD10
ENSG00000128713	0.468127	0.266865	0.498988	1.41431	ENSG00000128713	HOXD11
ENSG00000128714	0.0255138	0.120796	0.0868989	0.0827233	ENSG00000128714	HOXD13
ENSG00000128731	23.2701	33.5044	41.887	53.5444	ENSG00000128731	HERC2
ENSG00000128739	11.4708	13.6099	16.5009	17.9245	ENSG00000128739	SNRPN

ENSG00000128789	34.4387	27.0197	23.6086	16.0079	ENSG00000128789	PSMG2
ENSG00000128791	19.0173	27.5132	16.4073	23.3846	ENSG00000128791	TWSG1
ENSG00000128802	0	0	0.0127186	0.0160152	ENSG00000128802	GDF2
ENSG00000128805	21.6615	45.9409	33.6571	104.384	ENSG00000128805	ARHGAP22
ENSG00000128815	0.685296	0.693903	0.537078	0.725792	ENSG00000128815	WDFY4
ENSG00000128829	30.3077	42.8638	35.5889	50.7535	ENSG00000128829	EIF2AK4
ENSG00000128833	0.992202	1.25855	0.783953	1.13425	ENSG00000128833	MYO5C
ENSG00000128849	1.71159	2.8825	3.16336	5.64343	ENSG00000128849	CGNL1
ENSG00000128872	4.85071	5.61148	5.81596	9.2981	ENSG00000128872	TMOD2
ENSG00000128881	9.44601	25.3832	18.5198	20.5524	ENSG00000128881	TTBK2
ENSG00000128886	3.28557	7.07168	12.6338	4.11394	ENSG00000128886	ELL3
ENSG00000128891	10.393	12.5449	12.3215	13.8315	ENSG00000128891	CCDC32
ENSG00000128908	14.3398	22.1716	21.5611	20.1054	ENSG00000128908	INO80
ENSG00000128915	25.3289	40.2915	42.257	45.7973	ENSG00000128915	ICE2
ENSG00000128917	0.260258	0.287958	0.27871	0.662057	ENSG00000128917	DLL4
ENSG00000128918	9.80882	13.4124	11.3359	21.0786	ENSG00000128918	ALDH1A2
ENSG00000128923	17.188	14.815	11.7534	12.4849	ENSG00000128923	MINDY2
ENSG00000128928	8.64212	20.5784	22.971	30.0608	ENSG00000128928	IVD
ENSG00000128944	17.7796	36.3423	19.274	20.9513	ENSG00000128944	KNSTRN
ENSG00000128951	32.3246	49.3111	37.2147	39.4181	ENSG00000128951	DUT
ENSG00000128965	3.51657	31.1641	39.5204	3.27504	ENSG00000128965	CHAC1
ENSG00000128973	21.8136	32.1812	25.6737	28.1779	ENSG00000128973	CLN6
ENSG00000128989	52.0974	37.7737	36.1558	33.287	ENSG00000128989	ARPP19
ENSG00000129003	19.3586	29.4127	28.5018	30.0274	ENSG00000129003	VPS13C
ENSG00000129007	7.76423	12.734	10.8311	11.4882	ENSG00000129007	CALML4
ENSG00000129009	0.187727	0.0744137	0.204393	1.10969	ENSG00000129009	ISLR
ENSG00000129028	0.493388	1.58864	2.26283	1.61747	ENSG00000129028	THAP10
ENSG00000129038	3.11959	8.61102	12.3078	52.6116	ENSG00000129038	LOXL1
ENSG00000129048	0.532147	3.04168	2.77055	6.30651	ENSG00000129048	ACKR4
ENSG00000129055	11.1782	10.6108	15.3739	10.1	ENSG00000129055	ANAPC13
ENSG00000129071	15.9212	22.8348	26.81	12.2276	ENSG00000129071	MBD4
ENSG00000129083	106.827	90.3259	92.023	73.1765	ENSG00000129083	COPB1
ENSG00000129084	96.6434	83.2111	73.0425	60.7679	ENSG00000129084	PSMA1
ENSG00000129103	75.4273	92.7109	89.9244	61.6245	ENSG00000129103	SUMF2
ENSG00000129116	47.8176	78.5251	123.594	95.7871	ENSG00000129116	PALLD
ENSG00000129128	99.4427	122.132	51.6639	51.5121	ENSG00000129128	SPCS3
ENSG00000129151	1.22676	0.623969	4.05539	0.739532	ENSG00000129151	BBOX1
ENSG00000129152	0	0	0	0	ENSG00000129152	MYOD1
ENSG00000129158	15.133	18.9056	15.4725	20.9394	ENSG00000129158	SERGEF
ENSG00000129159	0.212558	0.443965	0.520463	0.704868	ENSG00000129159	KCNC1
ENSG00000129167	0.478936	1.03368	1.93772	1.67457	ENSG00000129167	TPH1
ENSG00000129170	0.0849952	0.206205	0.305768	0.187508	ENSG00000129170	CSRP3
ENSG00000129173	0.790254	2.96792	0.602596	1.9714	ENSG00000129173	E2F8
ENSG00000129187	32.9514	37.7578	32.1797	27.5646	ENSG00000129187	DCTD
ENSG00000129194	44.174	63.6024	55.113	25.7119	ENSG00000129194	SOX15
ENSG00000129195	2.84432	14.482	5.54823	4.85669	ENSG00000129195	PIMREG
ENSG00000129197	16.5675	21.8031	25.3734	21.3298	ENSG00000129197	RPAIN
ENSG00000129204	1.68196	3.02137	3.49718	2.76587	ENSG00000129204	USP6
ENSG00000129214	0.378678	0.326188	0.317988	0.907025	ENSG00000129214	SHBG
ENSG00000129219	33.7245	29.74	39.8979	24.119	ENSG00000129219	PLD2
ENSG00000129221	1.73298	2.29883	2.2888	3.82722	ENSG00000129221	AIPL1
ENSG00000129226	26.1217	47.83	11.4673	20.4306	ENSG00000129226	CD68
ENSG00000129235	166.324	107.499	88.9631	58.1342	ENSG00000129235	TXNDC17
ENSG00000129244	0.578741	1.37897	1.4056	1.82395	ENSG00000129244	ATP1B2

ENSG00000129245	28.3411	30.2775	27.0976	32.8631	ENSG00000129245	FXR2
ENSG00000129250	132.364	72.8685	95.1979	57.2823	ENSG00000129250	KIF1C
ENSG00000129255	47.7706	45.8614	31.0156	37.5649	ENSG00000129255	MPDU1
ENSG00000129270	14.5024	25.8844	18.695	5.80131	ENSG00000129270	MMP28
ENSG00000129277	0	0.0934014	0.228655	0.18982	ENSG00000129277	CCL4
ENSG00000129282	1.34178	2.67563	2.01916	1.33898	ENSG00000129282	MRM1
ENSG00000129292	26.1604	34.88	34.1533	42.2229	ENSG00000129292	PHF20L1
ENSG00000129295	1.76637	2.18505	2.23473	2.3406	ENSG00000129295	LRRC6
ENSG00000129315	18.8824	24.0015	22.562	15.1308	ENSG00000129315	CCNT1
ENSG00000129317	11.7738	13.3718	10.3656	11.8308	ENSG00000129317	PUS7L
ENSG00000129347	9.10608	10.8508	11.7695	10.4042	ENSG00000129347	KRI1
ENSG00000129351	59.4931	83.8727	80.3617	87.1685	ENSG00000129351	ILF3
ENSG00000129353	129.855	92.3879	46.4153	53.476	ENSG00000129353	SLC44A2
ENSG00000129354	51.2963	29.4747	28.5017	18.9344	ENSG00000129354	AP1M2
ENSG00000129355	2.74451	3.30565	2.27197	1.61849	ENSG00000129355	CDKN2D
ENSG00000129422	23.7489	35.7317	31.7749	25.2466	ENSG00000129422	MTUS1
ENSG00000129437	2.36258	0.269621	0.938767	2.38493	ENSG00000129437	KLK14
ENSG00000129450	0.730059	1.49047	1.23387	2.97102	ENSG00000129450	SIGLEC9
ENSG00000129451	586.294	154.487	35.8703	77.8064	ENSG00000129451	KLK10
ENSG00000129455	446.395	89.2266	103.338	80.4422	ENSG00000129455	KLK8
ENSG00000129460	21.0646	21.7682	20.6925	18.3638	ENSG00000129460	NGDN
ENSG00000129465	10.0985	8.83049	5.73297	4.49233	ENSG00000129465	RIPK3
ENSG00000129467	1.45637	3.39498	3.26273	4.62451	ENSG00000129467	ADCY4
ENSG00000129472	10.6094	9.2293	10.0854	10.7521	ENSG00000129472	RAB2B
ENSG00000129473	18.6713	18.5415	30.0217	22.4869	ENSG00000129473	BCL2L2
ENSG00000129474	68.8092	110.999	186.573	58.7086	ENSG00000129474	AJUBA
ENSG00000129480	7.09875	8.90008	9.96475	9.66498	ENSG00000129480	DTD2
ENSG00000129484	10.8448	19.6717	21.1749	19.1282	ENSG00000129484	PARP2
ENSG00000129493	17.5817	17.6989	12.094	26.7123	ENSG00000129493	HEATR5A
ENSG00000129514	1.71432	0.406863	1.15873	2.34967	ENSG00000129514	FOXA1
ENSG00000129515	70.7575	54.0707	43.8687	50.3612	ENSG00000129515	SNX6
ENSG00000129518	18.0479	15.3277	21.7832	15.8029	ENSG00000129518	EAPP
ENSG00000129521	2.06683	4.25781	5.78886	6.13589	ENSG00000129521	EGLN3
ENSG00000129534	12.293	46.3068	21.4993	34.417	ENSG00000129534	MIS18BP1
ENSG00000129535	0.626014	0.893626	1.14627	1.04938	ENSG00000129535	NRL
ENSG00000129538	0.305556	0.0840733	0.0379964	0.225805	ENSG00000129538	RNASE1
ENSG00000129559	134.132	110.239	77.9743	80.2341	ENSG00000129559	NEDD8
ENSG00000129562	155.351	113.975	53.3954	51.3978	ENSG00000129562	DAD1
ENSG00000129566	12.0512	19.9604	14.9421	19.1579	ENSG00000129566	TEP1
ENSG00000129595	30.9936	31.4017	23.2956	47.5576	ENSG00000129595	EPB41L4A
ENSG00000129596	0.782067	3.15987	3.09927	1.78872	ENSG00000129596	CDO1
ENSG00000129625	78.5865	43.8884	37.1976	25.9805	ENSG00000129625	REEP5
ENSG00000129636	55.9401	60.2241	51.5283	38.4596	ENSG00000129636	ITFG1
ENSG00000129646	3.27514	3.45035	2.85178	3.23227	ENSG00000129646	QRICH2
ENSG00000129654	0.168145	0.161543	0.202611	0.279592	ENSG00000129654	FOXJ1
ENSG00000129657	37.7959	31.7454	26.0311	42.2995	ENSG00000129657	SEC14L1
ENSG00000129667	47.7315	69.302	66.3483	69.7189	ENSG00000129667	RHBDF2
ENSG00000129673	1.31137	2.323	1.60795	1.41613	ENSG00000129673	AANAT
ENSG00000129675	0.347983	0.604463	0.418198	3.17098	ENSG00000129675	ARHGEF6
ENSG00000129680	8.66963	11.2474	9.6097	12.1393	ENSG00000129680	MAP7D3
ENSG00000129682	0.657587	0.62788	0.505264	1.74413	ENSG00000129682	FGF13
ENSG00000129691	12.1921	20.8333	17.7023	22.1578	ENSG00000129691	ASH2L
ENSG00000129696	12.386	20.3357	29.9916	16.7662	ENSG00000129696	TTI2
ENSG00000129744	0.313144	1.16223	1.15421	1.74355	ENSG00000129744	ART1

ENSG00000129749	0.728896	1.07776	1.90861	1.37341	ENSG00000129749	CHRNA10
ENSG00000129757	5.61416	3.52035	1.3669	4.71194	ENSG00000129757	CDKN1C
ENSG00000129810	2.10716	6.55969	3.70604	8.17308	ENSG00000129810	SGO1
ENSG00000129824	129.884	110.306	96.3664	1.02228	ENSG00000129824	RPS4Y1
ENSG00000129862	0	0	0	0	ENSG00000129862	VCY1B
ENSG00000129864	0	0	0	0	ENSG00000129864	VCY
ENSG00000129873	0.0288998	0.1114	0.0782432	0.0987723	ENSG00000129873	CDY2B
ENSG00000129910	0.663552	2.27255	1.52934	2.77648	ENSG00000129910	CDH15
ENSG00000129911	10.9899	12.1056	16.0624	9.07757	ENSG00000129911	KLF16
ENSG00000129925	26.1569	31.5634	18.8673	17.9493	ENSG00000129925	TMEM8A
ENSG00000129932	8.03744	6.43638	8.08138	5.54253	ENSG00000129932	DOHH
ENSG00000129933	20.2318	26.5085	33.28	27.4385	ENSG00000129933	MAU2
ENSG00000129946	8.05609	2.17926	3.2341	2.67214	ENSG00000129946	SHC2
ENSG00000129951	0.289395	0.627986	0.600485	1.00885	ENSG00000129951	PLPPR3
ENSG00000129965	0.155211	0	0.275944	0.446202	ENSG00000129965	INS-IGF2
ENSG00000129968	28.8633	22.6036	19.191	16.8809	ENSG00000129968	ABHD17A
ENSG00000129988	0.201545	0.166488	0.354112	0.537008	ENSG00000129988	LBP
ENSG00000129990	4.68865	5.02463	4.0098	5.60071	ENSG00000129990	SYT5
ENSG00000129991	2.48855	3.52711	0.837414	1.45116	ENSG00000129991	TNNI3
ENSG00000129993	0.221691	0.421349	0.674727	1.15788	ENSG00000129993	CBFA2T3
ENSG00000130005	4.55222	4.67826	6.39164	8.7379	ENSG00000130005	GAMT
ENSG00000130021	4.52973	4.14872	3.83567	8.0499	ENSG00000130021	PUDP
ENSG00000130023	20.7047	36.8306	32.5537	25.1689	ENSG00000130023	ERMARD
ENSG00000130024	6.9765	9.47962	8.0179	13.4428	ENSG00000130024	PHF10
ENSG00000130032	3.75828	2.42905	1.12487	1.25869	ENSG00000130032	PRRG3
ENSG00000130035	0.390644	0.169961	0.247314	0.0638991	ENSG00000130035	GALNT8
ENSG00000130037	0.0192024	0.055449	0.0501318	0.126463	ENSG00000130037	KCNA5
ENSG00000130038	1.55032	2.78369	2.54446	6.75617	ENSG00000130038	CRACR2A
ENSG00000130045	11.2986	25.9374	22.9469	36.6901	ENSG00000130045	NXNL2
ENSG00000130052	6.5342	23.599	25.9914	50.626	ENSG00000130052	STARD8
ENSG00000130054	0.0807938	1.54455	0.328593	0.668531	ENSG00000130054	FAM155B
ENSG00000130055	0.333408	1.9589	0.435376	0.682412	ENSG00000130055	GDPD2
ENSG00000130066	405.546	305.297	394.78	218.914	ENSG00000130066	SAT1
ENSG00000130119	12.8316	12.5434	16.3297	18.9945	ENSG00000130119	GNL3L
ENSG00000130147	20.4852	29.1281	33.989	26.4354	ENSG00000130147	SH3BP4
ENSG00000130150	19.3437	51.6905	33.276	60.8605	ENSG00000130150	MOSPD2
ENSG00000130158	25.6419	47.9043	53.2381	49.8704	ENSG00000130158	DOCK6
ENSG00000130159	13.0562	14.4338	10.4693	17.0773	ENSG00000130159	ECSIT
ENSG00000130164	363.126	332.818	100.219	282.833	ENSG00000130164	LDLR
ENSG00000130165	53.2475	40.0847	39.9079	47.7162	ENSG00000130165	ELOF1
ENSG00000130167	1.75915	3.63429	2.94854	3.24117	ENSG00000130167	TSPAN16
ENSG00000130173	0.600874	2.44494	2.05908	1.93643	ENSG00000130173	ANGPTL8
ENSG00000130175	102.625	110.152	97.6959	140.571	ENSG00000130175	PRKCSH
ENSG00000130176	4.0938	6.36958	7.14578	13.2469	ENSG00000130176	CNN1
ENSG00000130177	24.4991	39.3735	39.8429	44.3177	ENSG00000130177	CDC16
ENSG00000130182	0.447679	0.190796	0.764831	0.876656	ENSG00000130182	ZSCAN10
ENSG00000130193	2.3006	4.08715	1.71402	1.12511	ENSG00000130193	THEM6
ENSG00000130201	1.50843	2.45875	2.61837	4.26842	ENSG00000130201	EXOC3L2
ENSG00000130202	54.9011	52.3455	34.0099	31.2916	ENSG00000130202	NECTIN2
ENSG00000130203	47.3332	59.4138	183.561	62.5865	ENSG00000130203	APOE
ENSG00000130204	29.2091	28.498	27.508	18.0186	ENSG00000130204	TOMM40
ENSG00000130208	3.22008	3.03272	3.57851	4.51004	ENSG00000130208	APOC1
ENSG00000130222	3.15169	0.186084	0.348878	0.374821	ENSG00000130222	GADD45G
ENSG00000130224	0.0434986	0.0686276	0.10947	0.310342	ENSG00000130224	LRCH2

ENSG00000130226	0.557783	1.13383	1.29553	2.08903	ENSG00000130226	DPP6
ENSG00000130227	18.4092	27.0508	20.9922	24.99	ENSG00000130227	XPO7
ENSG00000130234	0.45527	0.563824	0.750899	1.3304	ENSG00000130234	ACE2
ENSG00000130244	11.2867	21.9063	16.846	21.606	ENSG00000130244	FAM98C
ENSG00000130254	23.0603	40.0485	48.9561	49.4587	ENSG00000130254	SAFB2
ENSG00000130255	434.789	393.987	340.537	222.214	ENSG00000130255	RPL36
ENSG00000130270	2.19522	13.1423	5.76259	11.6049	ENSG00000130270	ATP8B3
ENSG00000130283	0.228209	0.555203	0.563526	0.65709	ENSG00000130283	GDF1
ENSG00000130287	0.752977	0.726165	0.661502	1.17301	ENSG00000130287	NCAN
ENSG00000130294	0.261393	0.73979	1.52712	1.24684	ENSG00000130294	KIF1A
ENSG00000130299	13.6711	21.1264	21.852	14.9098	ENSG00000130299	GTPBP3
ENSG00000130300	0.421019	0	0.357736	2.59591	ENSG00000130300	PLVAP
ENSG00000130303	0.172533	4.58924	4.71759	3.35434	ENSG00000130303	BST2
ENSG00000130304	21.2812	28.1742	26.7858	34.6327	ENSG00000130304	SLC27A1
ENSG00000130305	11.5978	15.7726	16.6588	8.32822	ENSG00000130305	NSUN5
ENSG00000130307	2.91671	5.85839	4.02537	7.8452	ENSG00000130307	USHBP1
ENSG00000130309	49.2678	63.7765	50.2148	57.3455	ENSG00000130309	COLGALT1
ENSG00000130311	26.8489	12.137	17.5127	14.9406	ENSG00000130311	DDA1
ENSG00000130312	18.8918	27.4142	22.5405	37.5702	ENSG00000130312	MRPL34
ENSG00000130313	41.2845	32.0207	32.4867	20.9939	ENSG00000130313	PGLS
ENSG00000130332	41.8732	53.9148	49.3965	43.6649	ENSG00000130332	LSM7
ENSG00000130338	7.95174	7.83092	14.9242	10.1439	ENSG00000130338	TULP4
ENSG00000130340	28.1566	20.2247	9.68767	18.304	ENSG00000130340	SNX9
ENSG00000130347	7.35565	7.13751	7.52057	7.15804	ENSG00000130347	RTN4IP1
ENSG00000130348	8.21522	13.1153	11.2906	10.7092	ENSG00000130348	QRSL1
ENSG00000130349	5.07486	7.82054	6.91028	9.51424	ENSG00000130349	C6orf203
ENSG00000130363	3.93722	4.55936	5.38575	4.70933	ENSG00000130363	RSPH3
ENSG00000130368	0	0	0	0	ENSG00000130368	MAS1
ENSG00000130377	1.67603	2.31899	2.53006	2.86151	ENSG00000130377	ACSBG2
ENSG00000130382	7.89472	8.43119	9.79414	8.48979	ENSG00000130382	MLLT1
ENSG00000130383	0.34938	0.429688	0.438311	0.566423	ENSG00000130383	FUT5
ENSG00000130385	0	0	0	0	ENSG00000130385	BMP15
ENSG00000130396	95.6234	107.74	89.2626	77.7865	ENSG00000130396	AFDN
ENSG00000130402	514.707	303.339	244.334	257.311	ENSG00000130402	ACTN4
ENSG00000130413	6.44788	18.0664	16.4313	25.244	ENSG00000130413	STK33
ENSG00000130414	38.8507	39.5221	36.127	30.137	ENSG00000130414	NDUFA10
ENSG00000130427	0	0	0.424374	0.0969178	ENSG00000130427	EPO
ENSG00000130429	106.712	162.032	84.9804	107.057	ENSG00000130429	ARPC1B
ENSG00000130433	0.140626	0.101612	0.153089	0.192581	ENSG00000130433	CACNG6
ENSG00000130449	3.70672	5.62924	4.55583	6.86321	ENSG00000130449	ZSWIM6
ENSG00000130475	7.55037	10.4047	11.2284	14.7645	ENSG00000130475	FCHO1
ENSG00000130477	0.368464	0.898717	0.657582	1.12173	ENSG00000130477	UNC13A
ENSG00000130479	17.0241	20.062	13.2196	29.0329	ENSG00000130479	MAP1S
ENSG00000130487	0.0183225	0.0706692	2.52377	0.0201495	ENSG00000130487	KLHDC7B
ENSG00000130489	20.5542	16.1946	40.5535	11.0413	ENSG00000130489	SCO2
ENSG00000130508	60.6419	105.681	67.2256	102.889	ENSG00000130508	PXDN
ENSG00000130511	19.7929	29.4153	25.1504	25.3025	ENSG00000130511	SSBP4
ENSG00000130513	9.57116	9.41733	17.9918	6.81835	ENSG00000130513	GDF15
ENSG00000130517	7.02067	8.19671	5.70042	7.86567	ENSG00000130517	PGPEP1
ENSG00000130518	2.98991	5.99775	6.13141	12.2326	ENSG00000130518	KIAA1683
ENSG00000130520	58.5213	68.108	46.6403	30.1925	ENSG00000130520	LSM4
ENSG00000130522	39.1436	20.2476	25.0361	23.0408	ENSG00000130522	JUND
ENSG00000130528	0.138326	0.51733	0.566578	0.879433	ENSG00000130528	HRC
ENSG00000130529	47.1511	44.5463	41.0553	44.1559	ENSG00000130529	TRPM4

ENSG00000130538	0	0	0	0	ENSG00000130538	OR11H1
ENSG00000130540	1.06152	0.462672	1.64375	0.654038	ENSG00000130540	SULT4A1
ENSG00000130544	5.07385	6.10635	7.12587	6.57758	ENSG00000130544	ZNF557
ENSG00000130545	23.9129	10.2071	9.64382	3.35017	ENSG00000130545	CRB3
ENSG00000130558	0.727267	1.98462	1.56228	3.18972	ENSG00000130558	OLFM1
ENSG00000130559	18.7699	20.9277	20.2883	20.607	ENSG00000130559	CAMSAP1
ENSG00000130560	15.8448	24.3052	22.1111	14.3984	ENSG00000130560	UBAC1
ENSG00000130561	2.13022	4.08066	4.25573	7.52968	ENSG00000130561	SAG
ENSG00000130584	0.951046	2.01489	1.58784	2.96678	ENSG00000130584	ZBTB46
ENSG00000130589	33.7518	55.8532	33.6172	54.5798	ENSG00000130589	HELZ2
ENSG00000130590	2.81131	1.20543	2.25267	1.14234	ENSG00000130590	SAMD10
ENSG00000130592	12.0386	10.8822	19.4112	23.1424	ENSG00000130592	LSP1
ENSG00000130595	0	0	0	0	ENSG00000130595	TNNT3
ENSG00000130598	26.7561	6.19864	16.6589	6.16084	ENSG00000130598	TNNI2
ENSG00000130612	0.245944	0.233895	0.134565	0.563065	ENSG00000130612	CYP2G1P
ENSG00000130635	1.24704	0.421092	22.6672	220.61	ENSG00000130635	COL5A1
ENSG00000130638	40.9097	52.8027	41.3039	66.2089	ENSG00000130638	ATXN10
ENSG00000130640	31.5834	38.4515	35.5315	35.6949	ENSG00000130640	TUBGCP2
ENSG00000130643	0.554515	2.07273	2.51618	0.92742	ENSG00000130643	CALY
ENSG00000130649	2.90232	1.29844	1.94477	2.99212	ENSG00000130649	CYP2E1
ENSG00000130653	0.322369	0.864671	0.609588	0.4839	ENSG00000130653	PNPLA7
ENSG00000130656	0	0	0	0	ENSG00000130656	HBZ
ENSG00000130669	14.5951	19.6928	14.84	21.8398	ENSG00000130669	PAK4
ENSG00000130675	1.43646	1.64373	0.966186	0.710652	ENSG00000130675	MNX1
ENSG00000130684	9.73887	14.4764	16.0247	13.7661	ENSG00000130684	ZNF337
ENSG00000130695	7.42443	16.5554	10.5247	9.65027	ENSG00000130695	CEP85
ENSG00000130699	5.28612	8.94948	7.45729	8.9047	ENSG00000130699	TAF4
ENSG00000130700	0.0106475	0	0.00928064	0.0117013	ENSG00000130700	GATA5
ENSG00000130701	2.56015	0.494552	0.447228	0.90932	ENSG00000130701	RBBP8NL
ENSG00000130702	89.1731	270.136	204.864	121.438	ENSG00000130702	LAMA5
ENSG00000130703	19.9647	17.2619	20.7042	14.0383	ENSG00000130703	OSBPL2
ENSG00000130706	81.1045	71.9644	63.3806	40.683	ENSG00000130706	ADRM1
ENSG00000130707	24.2977	25.4423	82.956	16.4559	ENSG00000130707	ASS1
ENSG00000130711	0.213694	0.70458	0.554268	0.916428	ENSG00000130711	PRDM12
ENSG00000130713	10.4788	20.2598	17.5532	19.0521	ENSG00000130713	EXOSC2
ENSG00000130714	24.6955	24.1547	21.0565	22.4083	ENSG00000130714	POMT1
ENSG00000130717	10.2145	7.89425	13.6346	10.1335	ENSG00000130717	UCK1
ENSG00000130720	1.10797	2.14094	0.628022	1.65836	ENSG00000130720	FIBCD1
ENSG00000130723	34.1235	45.0687	54.0169	57.0604	ENSG00000130723	PRRC2B
ENSG00000130724	34.4242	29.2662	30.5759	23.1015	ENSG00000130724	CHMP2A
ENSG00000130725	27.7933	26.3274	25.367	16.3063	ENSG00000130725	UBE2M
ENSG00000130726	130.686	188.755	155.732	119.69	ENSG00000130726	TRIM28
ENSG00000130731	40.4122	29.3508	23.4922	18.6023	ENSG00000130731	METTL26
ENSG00000130733	47.1146	42.6757	27.0278	20.0743	ENSG00000130733	YIPF2
ENSG00000130734	16.2885	14.6722	14.052	3.61012	ENSG00000130734	ATG4D
ENSG00000130741	73.3462	73.4495	101.404	87.7678	ENSG00000130741	EIF2S3
ENSG00000130748	14.5715	18.8976	7.32508	7.24111	ENSG00000130748	TMEM160
ENSG00000130749	14.7293	16.4442	23.193	18.8919	ENSG00000130749	ZC3H4
ENSG00000130751	1.32519	1.03776	0.958918	0.819347	ENSG00000130751	NPAS1
ENSG00000130755	1.24489	2.78328	2.80205	4.70905	ENSG00000130755	GMFG
ENSG00000130758	13.8949	16.1199	15.3819	18.9126	ENSG00000130758	MAP3K10
ENSG00000130762	11.3563	19.3775	11.4363	7.14215	ENSG00000130762	ARHGEF16
ENSG00000130764	24.8909	20.6991	24.0452	17.4979	ENSG00000130764	LRRC47
ENSG00000130766	16.8056	43.7574	49.1331	8.4902	ENSG00000130766	SESN2

ENSG00000130768	0.904123	1.31285	1.48659	1.05266	ENSG00000130768	SMPDL3B
ENSG00000130770	106.663	65.9299	74.9118	33.2719	ENSG00000130770	ATPIF1
ENSG00000130772	12.3928	9.25365	12.9241	12.4282	ENSG00000130772	MED18
ENSG00000130775	3.72758	3.69279	1.92955	4.10909	ENSG00000130775	THEMIS2
ENSG00000130779	74.9848	48.0712	61.7926	67.4355	ENSG00000130779	CLIP1
ENSG00000130783	0.573311	1.63935	1.1762	3.08685	ENSG00000130783	CCDC62
ENSG00000130787	47.2008	52.2553	38.4224	22.7268	ENSG00000130787	HIP1R
ENSG00000130803	16.8193	13.751	24.1424	11.5473	ENSG00000130803	ZNF317
ENSG00000130810	23.5546	23.9056	34.0164	23.094	ENSG00000130810	PPAN
ENSG00000130811	105.585	78.7393	71.6003	64.0938	ENSG00000130811	EIF3G
ENSG00000130812	0.349119	0.780485	0.737509	1.0156	ENSG00000130812	ANGPTL6
ENSG00000130813	13.6972	24.4042	24.05	27.8627	ENSG00000130813	C19orf66
ENSG00000130816	39.2001	77.226	47.1551	111.345	ENSG00000130816	DNMT1
ENSG00000130818	15.239	10.1151	13.6981	9.47285	ENSG00000130818	ZNF426
ENSG00000130821	33.0071	35.9382	22.9535	17.4518	ENSG00000130821	SLC6A8
ENSG00000130822	0.90601	0.911684	2.22776	2.47073	ENSG00000130822	PNCK
ENSG00000130826	11.7033	15.5968	23.8135	17.2248	ENSG00000130826	DKC1
ENSG00000130827	21.3839	12.1296	41.9163	37.2574	ENSG00000130827	PLXNA3
ENSG00000130829	0.133958	0.2479	0.31226	0.333971	ENSG00000130829	DUSP9
ENSG00000130830	1.3884	2.283	2.40909	5.50363	ENSG00000130830	MPP1
ENSG00000130844	7.60472	15.1878	12.6381	17.3272	ENSG00000130844	ZNF331
ENSG00000130856	11.1135	12.3557	12.224	18.6151	ENSG00000130856	ZNF236
ENSG00000130876	0.422355	0.424588	0.465564	0.57707	ENSG00000130876	SLC7A10
ENSG00000130881	11.7071	4.76736	7.39536	7.49977	ENSG00000130881	LRP3
ENSG00000130921	19.0845	37.6828	38.3664	53.2064	ENSG00000130921	C12orf65
ENSG00000130935	28.7991	37.8752	28.0866	29.8619	ENSG00000130935	NOL11
ENSG00000130939	15.1763	21.8029	17.3664	22.3488	ENSG00000130939	UBE4B
ENSG00000130940	18.7265	7.50675	18.1836	9.05459	ENSG00000130940	CASZ1
ENSG00000130943	0.0978155	0.18009	0.338525	0.26678	ENSG00000130943	PKDREJ
ENSG00000130948	0.832807	1.95248	1.14284	1.71683	ENSG00000130948	HSD17B3
ENSG00000130950	1.61963	3.45322	2.70821	3.67905	ENSG00000130950	NUTM2F
ENSG00000130956	3.63773	4.81963	4.03695	8.22501	ENSG00000130956	HABP4
ENSG00000130957	0	0.043612	0	0	ENSG00000130957	FBP2
ENSG00000130958	18.8023	18.5502	9.69088	9.29677	ENSG00000130958	SLC35D2
ENSG00000130962	7.29543	6.21829	4.39632	5.13537	ENSG00000130962	PRRG1
ENSG00000130985	49.4773	43.219	41.0307	52.1638	ENSG00000130985	UBA1
ENSG00000130988	0.254865	0.292622	0.387346	0.748491	ENSG00000130988	RGN
ENSG00000130997	2.28177	3.95308	2.67825	6.29311	ENSG00000130997	POLN
ENSG00000131002	28.6772	60.5375	51.8286	1.16739	ENSG00000131002	TXLNGY
ENSG00000131013	13.4465	12.7731	15.045	16.9758	ENSG00000131013	PPIL4
ENSG00000131015	11.5243	10.0673	7.90979	4.66195	ENSG00000131015	ULBP2
ENSG00000131016	40.1885	24.4995	2.76163	46.0178	ENSG00000131016	AKAP12
ENSG00000131018	6.71336	19.4145	20.4999	38.1661	ENSG00000131018	SYNE1
ENSG00000131019	6.49636	7.68963	4.83628	1.85336	ENSG00000131019	ULBP3
ENSG00000131023	13.4143	17.3769	16.0504	14.8071	ENSG00000131023	LATS1
ENSG00000131037	13.9514	3.86813	5.63883	3.16433	ENSG00000131037	EPS8L1
ENSG00000131042	0	0.117028	0.124052	0	ENSG00000131042	LILRB2
ENSG00000131043	11.3578	10.1865	10.5388	8.61807	ENSG00000131043	AAR2
ENSG00000131044	0.229791	0.0778935	0.343811	0.209646	ENSG00000131044	TTLL9
ENSG00000131050	0	0	0	0.0637217	ENSG00000131050	BPIFA2
ENSG00000131051	191.058	274.691	264.311	241.605	ENSG00000131051	RBM39
ENSG00000131055	0.388742	0.188965	0.337464	0.118723	ENSG00000131055	COX4I2
ENSG00000131059	0.551474	0.833492	0.635358	0.948057	ENSG00000131059	BPIFA3
ENSG00000131061	1.98199	3.3013	2.26661	4.30295	ENSG00000131061	ZNF341

ENSG00000131067	3.1739	7.67853	7.46073	16.2153	ENSG00000131067	GGT7
ENSG00000131068	0.0531886	0.0511973	0	0.23215	ENSG00000131068	DEFB118
ENSG00000131069	43.8652	108.678	32.848	63.2018	ENSG00000131069	ACSS2
ENSG00000131080	1.58083	5.61988	4.77327	5.17081	ENSG00000131080	EDA2R
ENSG00000131089	3.6298	4.38263	4.71545	5.63971	ENSG00000131089	ARHGEF9
ENSG00000131094	0.0456895	0.307968	0.0411466	0.201199	ENSG00000131094	C1QL1
ENSG00000131095	4.74206	12.2385	13.5438	18.4861	ENSG00000131095	GFAP
ENSG00000131096	0.174221	0.894173	0.454566	0.535024	ENSG00000131096	PYY
ENSG00000131097	0.376389	2.39106	1.31534	0.999548	ENSG00000131097	HIGD1B
ENSG00000131100	81.3835	32.5231	36.7582	46.978	ENSG00000131100	ATP6V1E1
ENSG00000131115	8.40411	18.9659	15.6688	17.0379	ENSG00000131115	ZNF227
ENSG00000131116	10.8557	9.56887	11.3659	8.97476	ENSG00000131116	ZNF428
ENSG00000131126	0.183111	0.137829	0.125154	0.170526	ENSG00000131126	TEX101
ENSG00000131127	8.02876	11.2801	13.3659	17.4726	ENSG00000131127	ZNF141
ENSG00000131142	0.203645	0.341124	0.0770481	0.288217	ENSG00000131142	CCL25
ENSG00000131143	142.217	145.905	102.378	91.911	ENSG00000131143	COX4I1
ENSG00000131148	25.9505	26.9844	26.9572	21.9443	ENSG00000131148	EMC8
ENSG00000131149	11.8785	25.82	26.1261	19.9807	ENSG00000131149	GSE1
ENSG00000131152	0.532526	0.416941	0.216911	0	ENSG00000131152	AC010531.1
ENSG00000131153	4.62642	6.5773	3.01324	4.80133	ENSG00000131153	GINS2
ENSG00000131165	39.9098	32.9778	38.6136	26.3207	ENSG00000131165	CHMP1A
ENSG00000131171	18.3063	17.3454	16.0374	20.0245	ENSG00000131171	SH3BGRL
ENSG00000131174	26.3212	26.6972	17.6537	17.3382	ENSG00000131174	COX7B
ENSG00000131183	0.0874938	0.550866	1.22314	0.450945	ENSG00000131183	SLC34A1
ENSG00000131187	1.81151	4.39976	2.52744	0.975566	ENSG00000131187	F12
ENSG00000131188	1.68529	3.10505	5.12529	3.03463	ENSG00000131188	PRR7
ENSG00000131196	0.528076	1.95905	5.28463	5.15784	ENSG00000131196	NFATC1
ENSG00000131203	0.542468	1.51796	2.17723	1.55845	ENSG00000131203	IDO1
ENSG00000131233	1.03127	1.45322	1.5828	2.27718	ENSG00000131233	GJA9
ENSG00000131236	481.759	277.029	126.918	186.54	ENSG00000131236	CAP1
ENSG00000131238	22.9733	32.4517	21.8698	15.7294	ENSG00000131238	PPT1
ENSG00000131242	9.53582	11.8623	10.9097	4.99915	ENSG00000131242	RAB11FIP4
ENSG00000131263	23.5324	22.9824	21.6695	18.6541	ENSG00000131263	RLIM
ENSG00000131264	0	0.036865	0.0333236	0.0418985	ENSG00000131264	CDX4
ENSG00000131269	7.16442	11.1218	9.80419	7.30361	ENSG00000131269	ABCB7
ENSG00000131323	11.9861	13.8502	24.2547	27.0902	ENSG00000131323	TRAF3
ENSG00000131351	3.26372	7.99661	6.22057	9.92087	ENSG00000131351	HAUS8
ENSG00000131355	0.0286331	0.0827848	0	0.169149	ENSG00000131355	ADGRE3
ENSG00000131368	39.3465	36.4268	49.754	35.2747	ENSG00000131368	MRPS25
ENSG00000131370	8.4191	9.55005	10.6733	14.0941	ENSG00000131370	SH3BP5
ENSG00000131373	5.42399	8.49704	9.03118	7.08648	ENSG00000131373	HACL1
ENSG00000131374	23.2832	50.0458	34.6674	48.7472	ENSG00000131374	TBC1D5
ENSG00000131375	18.813	19.209	20.397	15.5713	ENSG00000131375	CAPN7
ENSG00000131378	14.3414	20.0983	16.2659	25.2299	ENSG00000131378	RFTN1
ENSG00000131379	1.21596	0.692311	1.39763	1.29312	ENSG00000131379	C3orf20
ENSG00000131381	10.9455	16.1116	22.6777	17.9987	ENSG00000131381	RBSN
ENSG00000131386	1.43865	2.37935	3.41791	8.35116	ENSG00000131386	GALNT15
ENSG00000131389	13.1213	25.5793	7.83304	22.3335	ENSG00000131389	SLC6A6
ENSG00000131398	0.58321	0.724394	0.730525	1.31927	ENSG00000131398	KCNC3
ENSG00000131400	1.33466	1.51992	1.0959	0.992592	ENSG00000131400	NAPSA
ENSG00000131401	0.516188	0.185413	0.309569	0.170653	ENSG00000131401	NAPSB
ENSG00000131408	28.6415	23.6466	23.3127	18.1586	ENSG00000131408	NR1H2
ENSG00000131409	0.148257	0.0719341	0.26	0.139621	ENSG00000131409	LRRC4B
ENSG00000131435	56.0138	49.5509	59.1004	37.0183	ENSG00000131435	PDLIM4

ENSG00000131437	8.33095	10.7876	11.4219	13.7183	ENSG00000131437	KIF3A
ENSG00000131446	69.6124	72.7129	58.6987	44.3469	ENSG00000131446	MGAT1
ENSG00000131459	0.123753	0.364972	0.556317	22.8344	ENSG00000131459	GFPT2
ENSG00000131462	39.6078	34.9031	21.9278	25.1349	ENSG00000131462	TUBG1
ENSG00000131467	46.6931	34.724	46.3499	35.5079	ENSG00000131467	PSME3
ENSG00000131469	419.276	370.445	304.323	163.472	ENSG00000131469	RPL27
ENSG00000131470	2.64011	3.97063	3.40144	5.36778	ENSG00000131470	PSMC3IP
ENSG00000131471	1.85212	0.905396	1.27566	0.871068	ENSG00000131471	AOC3
ENSG00000131473	82.6936	72.695	40.0869	77.8096	ENSG00000131473	ACLY
ENSG00000131475	40.963	29.4528	25.7487	18.3937	ENSG00000131475	VPS25
ENSG00000131477	0.722192	0.642871	1.03854	1.07652	ENSG00000131477	RAMP2
ENSG00000131480	2.21191	2.11545	3.86894	0.966434	ENSG00000131480	AOC2
ENSG00000131482	0.655967	1.68071	1.32324	2.48464	ENSG00000131482	G6PC
ENSG00000131495	31.2323	34.0112	29.3457	36.4466	ENSG00000131495	NDUFA2
ENSG00000131503	31.0839	55.2317	53.9282	59.3477	ENSG00000131503	ANKHD1
ENSG00000131504	62.8811	84.2384	47.0301	53.1709	ENSG00000131504	DIAPH1
ENSG00000131507	43.9969	40.1538	25.0042	24.9517	ENSG00000131507	NDFIP1
ENSG00000131508	45.1568	36.2421	39.0414	29.5059	ENSG00000131508	UBE2D2
ENSG00000131558	29.0498	56.3208	50.6268	56.5195	ENSG00000131558	EXOC4
ENSG00000131584	54.4592	62.8928	75.7706	61.4202	ENSG00000131584	ACAP3
ENSG00000131591	16.5377	19.9702	20.1561	15.4605	ENSG00000131591	C1orf159
ENSG00000131620	20.9207	75.0858	5.90828	60.7808	ENSG00000131620	ANO1
ENSG00000131626	33.5109	47.7181	52.8881	62.2551	ENSG00000131626	PPFIA1
ENSG00000131634	1.0874	1.66048	1.21962	6.76411	ENSG00000131634	TMEM204
ENSG00000131650	1.53665	15.8223	10.5866	3.06659	ENSG00000131650	KREMEN2
ENSG00000131652	10.5493	16.7528	9.67039	13.0303	ENSG00000131652	THOC6
ENSG00000131653	37.6185	50.429	48.0628	27.1189	ENSG00000131653	TRAF7
ENSG00000131668	0.226776	0.274682	0.234589	0.523832	ENSG00000131668	BARX1
ENSG00000131669	7.01901	8.78351	13.1245	9.69322	ENSG00000131669	NINJ1
ENSG00000131686	1.4462	3.45471	2.86158	5.19248	ENSG00000131686	CA6
ENSG00000131697	3.68569	8.94289	10.7456	9.84282	ENSG00000131697	NPHP4
ENSG00000131711	2.23797	10.0037	13.5056	51.5451	ENSG00000131711	MAP1B
ENSG00000131721	0.0225664	0	0	0	ENSG00000131721	RHOXF2
ENSG00000131724	27.5524	28.0699	18.2293	18.1259	ENSG00000131724	IL13RA1
ENSG00000131725	18.626	15.2316	9.38639	13.1868	ENSG00000131725	WDR44
ENSG00000131730	1.60079	7.5834	7.30997	7.00083	ENSG00000131730	CKMT2
ENSG00000131732	13.0298	12.8346	12.9219	12.6155	ENSG00000131732	ZCCHC9
ENSG00000131737	3.92203	0.901446	0.515423	1.21239	ENSG00000131737	KRT34
ENSG00000131738	0.0763793	0.160854	0.033048	0.0218248	ENSG00000131738	KRT33B
ENSG00000131746	354.518	187.269	165.63	199.329	ENSG00000131746	TNS4
ENSG00000131747	8.97533	71.2488	6.32318	28.0102	ENSG00000131747	TOP2A
ENSG00000131748	22.8743	29.3677	19.0831	17.4084	ENSG00000131748	STARD3
ENSG00000131759	7.57477	12.8153	11.0617	13.8601	ENSG00000131759	RARA
ENSG00000131771	0.325411	0.857707	0.629918	0.650271	ENSG00000131771	PPP1R1B
ENSG00000131773	4.34826	5.51142	1.79578	8.4198	ENSG00000131773	KHDRBS3
ENSG00000131778	6.16963	8.70137	12.4492	7.27747	ENSG00000131778	CHD1L
ENSG00000131779	5.49905	3.85052	5.19907	2.79975	ENSG00000131779	PEX11B
ENSG00000131781	5.0537	9.9063	10.6196	13.5625	ENSG00000131781	FMO5
ENSG00000131788	2.68474	2.74045	4.13142	2.94205	ENSG00000131788	PIAS3
ENSG00000131791	10.809	21.8352	7.20506	11.3613	ENSG00000131791	PRKAB2
ENSG00000131795	40.4661	26.5023	31.9416	25.5571	ENSG00000131795	RBM8A
ENSG00000131797	17.7472	18.3133	32.9174	10.6754	ENSG00000131797	CLUHP3
ENSG00000131808	0.209817	0.202196	0.10445	0.263012	ENSG00000131808	FSHB
ENSG00000131828	64.6393	79.9957	72.0546	54.5507	ENSG00000131828	PDHA1

ENSG00000131831	0.0276262	0.0680431	0.0241464	0.0611349	ENSG00000131831	RAI2
ENSG00000131844	10.8521	10.5105	11.5313	8.6433	ENSG00000131844	MCCC2
ENSG00000131845	5.77081	5.81043	7.39344	3.67895	ENSG00000131845	ZNF304
ENSG00000131848	23.3675	57.8174	53.6141	71.7595	ENSG00000131848	ZSCAN5A
ENSG00000131849	3.59127	5.44944	7.05403	3.98182	ENSG00000131849	ZNF132
ENSG00000131864	5.78265	7.53467	8.38288	10.67	ENSG00000131864	USP29
ENSG00000131871	59.791	52.7545	34.1719	26.8453	ENSG00000131871	SELENOS
ENSG00000131873	13.5704	32.6156	28.0835	40.6537	ENSG00000131873	CHSY1
ENSG00000131876	15.455	25.4603	25.9209	28.4488	ENSG00000131876	SNRPA1
ENSG00000131885	17.9586	20.0597	58.3799	10.7203	ENSG00000131885	KRT17P1
ENSG00000131899	15.7896	17.0936	16.3728	14.8379	ENSG00000131899	LLGL1
ENSG00000131910	0.052067	0.151226	0.226498	0.170484	ENSG00000131910	NR0B2
ENSG00000131914	1.6538	2.82567	2.67857	4.03188	ENSG00000131914	LIN28A
ENSG00000131931	4.3366	4.84672	5.04068	3.98913	ENSG00000131931	THAP1
ENSG00000131941	6.88027	6.77321	10.2115	7.0869	ENSG00000131941	RHPN2
ENSG00000131943	9.16062	9.12148	12.7659	10.9881	ENSG00000131943	C19orf12
ENSG00000131944	3.97439	9.09192	7.8705	11.7182	ENSG00000131944	FAAP24
ENSG00000131951	0.0227569	0.574129	0.474373	1.8904	ENSG00000131951	LRRC9
ENSG00000131966	35.3095	36.7551	34.091	36.6754	ENSG00000131966	ACTR10
ENSG00000131969	14.0407	21.7872	16.1541	26.7442	ENSG00000131969	ABHD12B
ENSG00000131979	2.82669	1.55685	1.82901	0.864817	ENSG00000131979	GCH1
ENSG00000131981	151.635	54.8979	42.1632	50.5884	ENSG00000131981	LGALS3
ENSG00000131982	0	0	0	0	ENSG00000131982	UBE2L2
ENSG00000132000	5.00081	10.4533	10.9935	17.7862	ENSG00000132000	PODNL1
ENSG00000132002	224.043	64.6583	52.5182	49.8572	ENSG00000132002	DNAJB1
ENSG00000132003	7.4437	4.14765	3.52043	8.46206	ENSG00000132003	ZSWIM4
ENSG00000132004	6.34377	5.43189	6.92911	4.27735	ENSG00000132004	FBXW9
ENSG00000132005	6.09253	10.3237	7.04641	9.78476	ENSG00000132005	RFX1
ENSG00000132010	8.33409	12.7864	10.3105	15.4086	ENSG00000132010	ZNF20
ENSG00000132016	0.655544	1.88609	1.61079	1.15761	ENSG00000132016	C19orf57
ENSG00000132017	23.4447	26.7856	25.1667	16.7833	ENSG00000132017	DCAF15
ENSG00000132024	22.9985	23.1732	30.8552	21.3136	ENSG00000132024	CC2D1A
ENSG00000132026	0.175483	0.61885	0.666919	0.841424	ENSG00000132026	RTBDN
ENSG00000132031	1.79287	2.23794	1.55769	3.22685	ENSG00000132031	MATN3
ENSG00000132109	7.38429	10.4255	8.46972	7.72303	ENSG00000132109	TRIM21
ENSG00000132122	1.48942	5.5915	2.38984	6.6458	ENSG00000132122	SPATA6
ENSG00000132128	33.1847	26.4708	33.7553	27.0636	ENSG00000132128	LRRC41
ENSG00000132130	0.991617	3.25051	1.56238	1.71084	ENSG00000132130	LHX1
ENSG00000132139	0.0818642	0.200377	0.153824	0.182836	ENSG00000132139	GAS2L2
ENSG00000132141	1.44557	2.34968	4.16455	3.23262	ENSG00000132141	CCT6B
ENSG00000132142	57.0795	90.7061	69.4309	83.7856	ENSG00000132142	ACACA
ENSG00000132153	40.7385	46.2854	46.627	45.0279	ENSG00000132153	DHX30
ENSG00000132155	45.3847	48.9748	56.6479	60.0203	ENSG00000132155	RAF1
ENSG00000132164	13.3839	9.20351	9.62779	6.83127	ENSG00000132164	SLC6A11
ENSG00000132170	2.35891	3.84369	1.97973	2.66347	ENSG00000132170	PPARG
ENSG00000132182	0.445141	0.735333	1.00286	1.40652	ENSG00000132182	NUP210
ENSG00000132185	1.97222	3.8112	3.38584	4.6792	ENSG00000132185	FCRLA
ENSG00000132196	31.6206	30.5072	18.7412	28.0859	ENSG00000132196	HSD17B7
ENSG00000132199	19.7489	58.8017	72.8128	46.3124	ENSG00000132199	ENOSF1
ENSG00000132205	0.591193	1.20406	1.87488	6.28883	ENSG00000132205	EMILIN2
ENSG00000132207	25.5215	27.5661	20.7201	14.8211	ENSG00000132207	SLX1A
ENSG00000132254	38.1557	31.7112	49.9943	30.8622	ENSG00000132254	ARFIP2
ENSG00000132256	15.6474	23.5026	18.7078	24.2503	ENSG00000132256	TRIM5
ENSG00000132259	0.334941	0.182532	0.18568	0.368696	ENSG00000132259	CNGA4

ENSG00000132274	140.187	333.846	314.768	654.05	ENSG00000132274	TRIM22
ENSG00000132275	11.9664	14.2402	16.2025	12.0035	ENSG00000132275	RRP8
ENSG00000132286	16.4209	15.4993	16.461	13.6671	ENSG00000132286	TIMM10B
ENSG00000132294	20.7605	25.2529	25.1209	26.8885	ENSG00000132294	EFR3A
ENSG00000132297	5.70672	8.84863	10.5579	17.6957	ENSG00000132297	HHLA1
ENSG00000132300	67.8995	116.29	93.0669	84.6907	ENSG00000132300	PTCD3
ENSG00000132305	29.1112	51.053	41.6394	38.8154	ENSG00000132305	IMMT
ENSG00000132313	19.4315	15.7148	13.8601	7.94901	ENSG00000132313	MRPL35
ENSG00000132321	3.43713	4.08498	6.30787	4.97274	ENSG00000132321	IQCA1
ENSG00000132323	15.7232	27.2196	29.4716	27.5869	ENSG00000132323	ILKAP
ENSG00000132326	3.6496	6.65616	8.21116	2.6405	ENSG00000132326	PER2
ENSG00000132329	0.485801	2.29055	1.41407	1.7104	ENSG00000132329	RAMP1
ENSG00000132330	8.37473	18.3675	20.0432	20.4895	ENSG00000132330	SCLY
ENSG00000132334	19.0945	40.1118	18.0688	28.2344	ENSG00000132334	PTPRE
ENSG00000132341	207.951	204.667	164.367	113.154	ENSG00000132341	RAN
ENSG00000132356	38.5137	48.8746	45.3041	52.8607	ENSG00000132356	PRKAA1
ENSG00000132357	6.95994	8.60113	6.69792	7.06826	ENSG00000132357	CARD6
ENSG00000132359	37.1791	21.6815	15.6143	20.269	ENSG00000132359	RAP1GAP2
ENSG00000132361	62.6277	61.2134	72.4152	40.7693	ENSG00000132361	CLUH
ENSG00000132376	21.6516	14.4098	14.251	17.4944	ENSG00000132376	INPP5K
ENSG00000132382	44.8856	41.9197	64.5392	41.4655	ENSG00000132382	MYBBP1A
ENSG00000132383	7.42824	14.8052	12.2712	16.2554	ENSG00000132383	RPA1
ENSG00000132386	10.3995	31.8635	36.3213	76.5138	ENSG00000132386	SERPINF1
ENSG00000132388	43.6623	31.3146	37.5232	30.1014	ENSG00000132388	UBE2G1
ENSG00000132394	2.43312	3.53211	5.38919	2.93139	ENSG00000132394	EEFSEC
ENSG00000132405	42.9873	36.3217	40.0142	24.8547	ENSG00000132405	TBC1D14
ENSG00000132406	16.4482	16.2297	18.3759	10.2526	ENSG00000132406	TMEM128
ENSG00000132423	6.02763	7.80866	4.31765	4.70015	ENSG00000132423	COQ3
ENSG00000132424	31.7199	56.1795	49.5337	51.0418	ENSG00000132424	PNISR
ENSG00000132429	2.45938	2.84492	2.21654	7.5609	ENSG00000132429	POPDC3
ENSG00000132432	78.0735	58.706	40.3913	43.1767	ENSG00000132432	SEC61G
ENSG00000132434	7.97462	5.7986	8.13504	6.61027	ENSG00000132434	LANCL2
ENSG00000132436	6.84112	14.7533	11.5515	8.10748	ENSG00000132436	FIGNL1
ENSG00000132437	0.0709393	0.545719	0.73017	0.467621	ENSG00000132437	DDC
ENSG00000132446	0	0.0765482	0	0	ENSG00000132446	FTHL17
ENSG00000132463	43.6565	38.1272	34.5322	26.4433	ENSG00000132463	GRSF1
ENSG00000132464	2.71551	9.88237	4.57735	16.1717	ENSG00000132464	ENAM
ENSG00000132465	0.445781	0.673271	0.734903	1.2293	ENSG00000132465	JCHAIN
ENSG00000132466	31.0543	41.6924	45.3285	60.0528	ENSG00000132466	ANKRD17
ENSG00000132467	9.00986	6.66547	8.69609	9.83912	ENSG00000132467	UTP3
ENSG00000132470	875.854	1393.07	827.246	624.239	ENSG00000132470	ITGB4
ENSG00000132471	25.5467	15.8201	12.5553	20.9037	ENSG00000132471	WBP2
ENSG00000132475	380.822	353.793	305.018	168.673	ENSG00000132475	H3F3B
ENSG00000132478	7.77446	14.7237	9.98845	15.6843	ENSG00000132478	UNK
ENSG00000132481	2.46246	19.2872	17.413	8.77138	ENSG00000132481	TRIM47
ENSG00000132485	23.1837	23.6274	37.056	35.8315	ENSG00000132485	ZRANB2
ENSG00000132498	1.87754	2.7087	1.68776	1.10458	ENSG00000132498	ANKRD20A3
ENSG00000132507	164.005	149.306	131.112	107.597	ENSG00000132507	EIF5A
ENSG00000132510	19.7466	19.688	41.7108	28.7775	ENSG00000132510	KDM6B
ENSG00000132514	0.328365	0.694861	0.365591	0.947277	ENSG00000132514	CLEC10A
ENSG00000132517	1.91461	3.55778	3.14239	4.11084	ENSG00000132517	SLC52A1
ENSG00000132518	0.430466	1.5647	1.06538	0.352974	ENSG00000132518	GUCY2D
ENSG00000132522	28.0835	18.6025	19.6181	11.1805	ENSG00000132522	GPS2
ENSG00000132530	28.1488	60.4711	83.3049	178.219	ENSG00000132530	XAF1

ENSG00000132535	3.57774	9.57811	10.0867	12.8851	ENSG00000132535	DLG4
ENSG00000132541	5.14259	7.2961	6.42364	7.7588	ENSG00000132541	RIDA
ENSG00000132549	77.8964	160.54	165.357	376.448	ENSG00000132549	VPS13B
ENSG00000132554	4.14875	7.80841	12.4623	11.7058	ENSG00000132554	RGS22
ENSG00000132561	2.98742	5.06922	10.1758	5.12207	ENSG00000132561	MATN2
ENSG00000132563	4.46773	15.0024	16.0628	21.79	ENSG00000132563	REEP2
ENSG00000132570	6.32314	10.6144	12.093	12.2039	ENSG00000132570	PCBD2
ENSG00000132581	30.1516	24.0343	17.8903	18.0983	ENSG00000132581	SDF2
ENSG00000132589	12.7286	23.4016	15.6357	14.5486	ENSG00000132589	FLOT2
ENSG00000132591	11.1197	11.1425	13.6412	9.67698	ENSG00000132591	ERAL1
ENSG00000132600	14.8133	26.3729	25.242	30.941	ENSG00000132600	PRMT7
ENSG00000132603	20.8988	16.3435	20.1842	15.1479	ENSG00000132603	NIP7
ENSG00000132604	7.14325	16.6048	18.3439	25.0097	ENSG00000132604	TERF2
ENSG00000132612	49.9252	67.2983	55.0319	73.8078	ENSG00000132612	VPS4A
ENSG00000132613	8.73686	23.2822	35.65	22.0475	ENSG00000132613	MTSS1L
ENSG00000132622	0.109202	0.193045	0.224781	0.400533	ENSG00000132622	HSPA12B
ENSG00000132623	4.53731	5.98078	6.14195	5.21695	ENSG00000132623	ANKEF1
ENSG00000132631	0	0	0	0	ENSG00000132631	SCP2D1
ENSG00000132635	8.46931	12.9601	15.408	12.4354	ENSG00000132635	PCED1A
ENSG00000132639	0.109749	0.334928	0.453935	1.13516	ENSG00000132639	SNAP25
ENSG00000132640	12.748	20.9251	14.1161	14.6476	ENSG00000132640	BTBD3
ENSG00000132646	25.8609	32.9378	12.2449	26.3174	ENSG00000132646	PCNA
ENSG00000132661	9.55209	8.80873	11.4775	4.23016	ENSG00000132661	NXT1
ENSG00000132664	9.30349	8.61166	8.85703	7.46582	ENSG00000132664	POLR3F
ENSG00000132669	28.3708	34.7437	24.8567	27.0494	ENSG00000132669	RIN2
ENSG00000132670	24.3144	24.9355	17.3225	13.9473	ENSG00000132670	PTPRA
ENSG00000132671	0	0	0	0	ENSG00000132671	SSTR4
ENSG00000132676	68.7505	79.0405	82.2677	91.2064	ENSG00000132676	DAP3
ENSG00000132677	2.2134	3.35245	3.70273	6.14044	ENSG00000132677	RHBG
ENSG00000132680	35.8442	38.6277	63.0912	53.5361	ENSG00000132680	KIAA0907
ENSG00000132681	0.947565	1.67718	1.56987	3.28938	ENSG00000132681	ATP1A4
ENSG00000132688	0.365606	0.0741293	0.332241	18.1036	ENSG00000132688	NES
ENSG00000132692	0.390586	0.747547	0.422515	0.539943	ENSG00000132692	BCAN
ENSG00000132693	0.0279539	0.281583	0.0488116	0.314228	ENSG00000132693	CRP
ENSG00000132694	14.7697	17.475	19.6269	19.2157	ENSG00000132694	ARHGEF11
ENSG00000132698	64.2907	18.9122	23.662	13.2867	ENSG00000132698	RAB25
ENSG00000132702	0.278116	0.623533	0.101462	0.450574	ENSG00000132702	HAPLN2
ENSG00000132703	0	0	0	0.220869	ENSG00000132703	APCS
ENSG00000132704	4.61409	10.5809	10.3452	20.2793	ENSG00000132704	FCRL2
ENSG00000132716	67.5627	79.3773	95.3554	73.075	ENSG00000132716	DCAF8
ENSG00000132718	1.57544	2.98363	2.88489	9.1444	ENSG00000132718	SYT11
ENSG00000132740	16.1357	22.1444	24.6477	33.666	ENSG00000132740	IGHMBP2
ENSG00000132744	0	0.0645208	0.116601	0.0994428	ENSG00000132744	ACY3
ENSG00000132746	20.5205	4.99129	16.004	4.93884	ENSG00000132746	ALDH3B2
ENSG00000132749	5.36716	6.85934	5.27514	3.8662	ENSG00000132749	TESMIN
ENSG00000132763	4.65946	4.57138	5.19005	7.86081	ENSG00000132763	MMACHC
ENSG00000132768	12.157	12.4799	16.5261	10.9798	ENSG00000132768	DPH2
ENSG00000132773	8.77317	12.3343	6.80776	9.43205	ENSG00000132773	TOE1
ENSG00000132780	17.9147	41.538	33.0602	71.7111	ENSG00000132780	NASP
ENSG00000132781	9.77501	24.4105	22.681	20.4051	ENSG00000132781	MUTYH
ENSG00000132792	12.586	16.3547	12.3701	14.1396	ENSG00000132792	CTNNBL1
ENSG00000132793	23.9207	22.0728	22.2948	21.4315	ENSG00000132793	LPIN3
ENSG00000132801	1.72645	1.5127	2.20074	1.28997	ENSG00000132801	ZSWIM3
ENSG00000132819	3.2227	4.78209	6.87452	2.65725	ENSG00000132819	RBM38

ENSG00000132821	2.58337	0.555575	1.17752	2.1801	ENSG00000132821	VSTM2L
ENSG00000132823	12.5819	13.2313	7.54218	7.25702	ENSG00000132823	OSER1
ENSG00000132824	131.581	82.5947	58.3574	44.1565	ENSG00000132824	SERINC3
ENSG00000132825	5.45185	4.08282	2.06515	1.90246	ENSG00000132825	PPP1R3D
ENSG00000132837	3.73856	9.23333	13.4738	15.2978	ENSG00000132837	DMGDH
ENSG00000132840	1.5344	2.25808	4.82391	9.81924	ENSG00000132840	BHMT2
ENSG00000132842	41.9553	74.3745	53.5945	110.99	ENSG00000132842	AP3B1
ENSG00000132846	0.382829	1.08238	2.68018	1.22824	ENSG00000132846	ZBED3
ENSG00000132849	58.6033	76.4048	50.3825	67.2896	ENSG00000132849	PATJ
ENSG00000132854	2.65345	0.239153	4.4659	1.25126	ENSG00000132854	KANK4
ENSG00000132855	3.17932	6.79214	2.7881	6.82242	ENSG00000132855	ANGPTL3
ENSG00000132872	0.18311	0.268708	0.112063	0.35075	ENSG00000132872	SYT4
ENSG00000132874	1.50306	2.97591	2.81506	4.31865	ENSG00000132874	SLC14A2
ENSG00000132879	17.2917	26.8693	29.4406	28.757	ENSG00000132879	FBXO44
ENSG00000132881	2.59765	3.75639	5.62054	1.6024	ENSG00000132881	RSG1
ENSG00000132906	2.9405	2.67973	2.86673	4.59441	ENSG00000132906	CASP9
ENSG00000132911	6.19154	14.0837	14.1248	26.3933	ENSG00000132911	NMUR2
ENSG00000132912	33.0461	51.7248	53.0687	65.5122	ENSG00000132912	DCTN4
ENSG00000132915	2.27861	4.48748	4.30668	6.08619	ENSG00000132915	PDE6A
ENSG00000132932	0.45007	0.701158	0.49165	0.796875	ENSG00000132932	ATP8A2
ENSG00000132938	0.327631	0.0993454	0.0277466	0.271829	ENSG00000132938	MTUS2
ENSG00000132950	13.4509	12.0289	11.1509	9.34622	ENSG00000132950	ZMYM5
ENSG00000132952	5.6501	7.04483	7.06884	7.88205	ENSG00000132952	USPL1
ENSG00000132953	9.18426	13.1943	13.3092	10.1986	ENSG00000132953	XPO4
ENSG00000132958	0.484349	0.357471	0.241091	0.530136	ENSG00000132958	TPTE2
ENSG00000132963	28.4031	21.2113	16.1215	14.2313	ENSG00000132963	POMP
ENSG00000132964	11.2215	13.0842	11.0189	8.57276	ENSG00000132964	CDK8
ENSG00000132965	0.0703617	0.270646	0.917038	0.0764747	ENSG00000132965	ALOX5AP
ENSG00000132967	11.0424	31.2496	12.0498	12.0619	ENSG00000132967	HMGB1P5
ENSG00000132970	2.80157	3.33593	3.90111	6.22891	ENSG00000132970	WASF3
ENSG00000132972	0.126906	0.0490275	0.155804	0.222815	ENSG00000132972	RNF17
ENSG00000132975	0.140594	0.390206	0.212248	0.596771	ENSG00000132975	GPR12
ENSG00000133019	0.460649	1.03816	0.880097	1.31895	ENSG00000133019	CHRM3
ENSG00000133020	0	0.0171442	0.00769063	0.135923	ENSG00000133020	MYH8
ENSG00000133026	17.7651	35.5332	26.6162	40.7365	ENSG00000133026	MYH10
ENSG00000133027	19.3367	30.5719	18.228	11.5067	ENSG00000133027	PEMT
ENSG00000133028	17.351	21.4618	20.8649	15.8596	ENSG00000133028	SCO1
ENSG00000133030	402.395	226.637	135.531	198.215	ENSG00000133030	MPRIP
ENSG00000133048	1.46382	0.711859	1.32893	1.25666	ENSG00000133048	CHI3L1
ENSG00000133055	0.0315538	0.060751	0.0274593	0.0346405	ENSG00000133055	MYBPH
ENSG00000133056	5.79722	8.48733	11.3166	8.41758	ENSG00000133056	PIK3C2B
ENSG00000133059	5.27581	6.04242	7.72348	7.52175	ENSG00000133059	DSTYK
ENSG00000133063	0.507479	1.36534	2.24745	1.49652	ENSG00000133063	CHIT1
ENSG00000133065	9.36815	18.1114	15.7007	12.9027	ENSG00000133065	SLC41A1
ENSG00000133067	0.751723	0.735532	0.613664	2.25855	ENSG00000133067	LGR6
ENSG00000133069	1.13504	0.959042	1.51614	1.35766	ENSG00000133069	TMCC2
ENSG00000133083	4.87626	7.68903	6.26791	12.7989	ENSG00000133083	DCLK1
ENSG00000133101	3.36085	1.11475	1.73715	0.402082	ENSG00000133101	CCNA1
ENSG00000133103	17.8445	18.647	10.8167	18.1146	ENSG00000133103	COG6
ENSG00000133104	21.7623	31.1862	31.646	29.4268	ENSG00000133104	SPART
ENSG00000133105	0	0.11681	0.0175465	0.129591	ENSG00000133105	RXFP2
ENSG00000133106	1.57746	3.93802	7.27942	8.84823	ENSG00000133106	EPSTI1
ENSG00000133107	0.0223989	0.0215935	0.0492765	0.476518	ENSG00000133107	TRPC4
ENSG00000133110	1.21638	0.718975	15.6221	99.6885	ENSG00000133110	POSTN

ENSG00000133111	0.38744	1.99012	1.1454	1.62986	ENSG00000133111	RFXAP
ENSG00000133112	1099.96	684.506	599.643	407.863	ENSG00000133112	TPT1
ENSG00000133114	16.9228	31.6092	31.09	42.916	ENSG00000133114	GPALPP1
ENSG00000133115	0.0282278	0.0272049	0.0491878	0.185841	ENSG00000133115	STOML3
ENSG00000133116	0.0679142	0.10335	0.0740343	0.213994	ENSG00000133116	KL
ENSG00000133119	4.55134	10.767	3.85786	5.98082	ENSG00000133119	RFC3
ENSG00000133121	13.3979	8.81266	6.7502	35.5582	ENSG00000133121	STARD13
ENSG00000133124	0	0	0.0129286	0	ENSG00000133124	IRS4
ENSG00000133131	90.6969	204.908	192.871	365.334	ENSG00000133131	MORC4
ENSG00000133134	2.9096	2.5784	7.42057	0.535635	ENSG00000133134	BEX2
ENSG00000133135	15.4478	12.4894	9.25697	5.02209	ENSG00000133135	RNF128
ENSG00000133136	0	0	0.138253	0	ENSG00000133136	GNG5P2
ENSG00000133138	38.7928	86.4688	83.1854	211.743	ENSG00000133138	TBC1D8B
ENSG00000133142	25.762	21.4337	24.4512	24.2028	ENSG00000133142	TCEAL4
ENSG00000133149	0	0.167724	0	0.256514	ENSG00000133149	TEX13A
ENSG00000133169	0.147275	0.141629	0.129295	9.35446	ENSG00000133169	BEX1
ENSG00000133193	11.8547	12.7538	11.3256	8.6015	ENSG00000133193	FAM104A
ENSG00000133195	22.6101	36.2927	32.2737	36.0552	ENSG00000133195	SLC39A11
ENSG00000133216	3.38934	4.13934	9.34162	8.49762	ENSG00000133216	EPHB2
ENSG00000133226	52.1701	60.7297	65.1076	98.1077	ENSG00000133226	SRRM1
ENSG00000133243	28.304	28.7128	25.8634	26.8685	ENSG00000133243	BTBD2
ENSG00000133246	1.17185	2.93053	3.77941	6.33169	ENSG00000133246	PRAM1
ENSG00000133247	11.4806	14.3332	16.0494	12.2943	ENSG00000133247	KMT5C
ENSG00000133250	4.30438	7.59709	6.62391	4.52117	ENSG00000133250	ZNF414
ENSG00000133256	1.22123	4.36645	4.48917	6.60724	ENSG00000133256	PDE6B
ENSG00000133265	11.19	12.3946	10.2923	6.30484	ENSG00000133265	HSPBP1
ENSG00000133275	47.8349	58.443	51.2787	37.5436	ENSG00000133275	CSNK1G2
ENSG00000133302	6.80807	9.40506	5.44087	9.09226	ENSG00000133302	SLF1
ENSG00000133313	36.5604	43.6803	68.4371	49.004	ENSG00000133313	CNDP2
ENSG00000133315	13.6481	18.3895	22.2577	19.0712	ENSG00000133315	MACROD1
ENSG00000133316	860.158	1456.82	1576.56	514.88	ENSG00000133316	WDR74
ENSG00000133317	0.351932	0.0696668	0.169256	0.316821	ENSG00000133317	LGALS12
ENSG00000133318	41.8988	49.4303	30.746	22.5316	ENSG00000133318	RTN3
ENSG00000133321	26.6426	1.43767	0.534784	2.66765	ENSG00000133321	RARRES3
ENSG00000133328	4.72025	0.684581	0.386557	1.63873	ENSG00000133328	HRASLS2
ENSG00000133392	11.1978	25.5836	20.4496	34.9954	ENSG00000133392	MYH11
ENSG00000133393	10.5404	15.543	11.5709	9.43474	ENSG00000133393	FOPNL
ENSG00000133398	11.98	12.4138	15.9259	11.9817	ENSG00000133398	MED10
ENSG00000133401	12.381	6.99513	11.071	10.005	ENSG00000133401	PDZD2
ENSG00000133422	11.6864	11.4979	18.458	17.7303	ENSG00000133422	MORC2
ENSG00000133424	19.3422	15.2743	9.60991	18.6082	ENSG00000133424	LARGE1
ENSG00000133433	0.98354	2.34051	0.334042	1.39268	ENSG00000133433	GSTT2B
ENSG00000133454	0.596005	1.33675	1.20286	2.03149	ENSG00000133454	MYO18B
ENSG00000133460	10.8939	16.8497	18.0235	23.604	ENSG00000133460	SLC2A11
ENSG00000133466	19.405	22.4688	17.6678	19.6472	ENSG00000133466	C1QTNF6
ENSG00000133475	0	0	0.0337122	0	ENSG00000133475	GGT2
ENSG00000133477	13.8971	24.2856	28.3576	8.23623	ENSG00000133477	FAM83F
ENSG00000133488	0.67768	1.27582	1.46823	2.93552	ENSG00000133488	SEC14L4
ENSG00000133519	2.54763	3.2568	3.84476	3.14462	ENSG00000133519	ZDHHC8P1
ENSG00000133561	0.11066	0.167697	0.0827025	0.156877	ENSG00000133561	GIMAP6
ENSG00000133574	0.506111	0.31375	0.379527	0.704881	ENSG00000133574	GIMAP4
ENSG00000133597	15.4983	11.688	12.7595	5.44885	ENSG00000133597	ADCK2
ENSG00000133606	40.8491	41.8442	33.5096	37.5461	ENSG00000133606	MKRN1
ENSG00000133612	75.5016	86.731	108.526	73.073	ENSG00000133612	AGAP3

ENSG00000133619	14.3862	18.022	26.9765	14.0992	ENSG00000133619	KRBA1
ENSG00000133624	15.9131	17.5363	32.2119	22.6079	ENSG00000133624	ZNF767P
ENSG00000133627	3.43025	6.35535	6.92615	8.91259	ENSG00000133627	ACTR3B
ENSG00000133636	0	0	0	0	ENSG00000133636	NTS
ENSG00000133639	40.3214	17.096	27.9865	19.9561	ENSG00000133639	BTG1
ENSG00000133640	0.995784	1.97677	1.72563	2.0903	ENSG00000133640	LRRIQ1
ENSG00000133641	27.2571	14.5367	17.5678	10.5736	ENSG00000133641	C12orf29
ENSG00000133657	141.645	134.217	64.4658	174.581	ENSG00000133657	ATP13A3
ENSG00000133661	1.67806	0.225779	0.402614	0.623184	ENSG00000133661	SFTPD
ENSG00000133665	2.22722	3.16217	4.19488	4.67704	ENSG00000133665	DYDC2
ENSG00000133678	17.7283	17.3327	15.0836	10.1316	ENSG00000133678	TMEM254
ENSG00000133687	10.483	2.34561	6.33583	14.1413	ENSG00000133687	TMTC1
ENSG00000133703	9.67168	8.20255	12.4207	11.9894	ENSG00000133703	KRAS
ENSG00000133704	15.8086	28.3487	27.3212	23.9746	ENSG00000133704	IPO8
ENSG00000133706	47.9997	92.4912	111.433	88.7581	ENSG00000133706	LARS
ENSG00000133710	68.4978	11.7309	27.6382	21.8491	ENSG00000133710	SPINK5
ENSG00000133731	9.85522	11.1214	10.5524	9.72904	ENSG00000133731	IMPA1
ENSG00000133739	1.53982	4.09074	1.3632	2.7181	ENSG00000133739	LRRCC1
ENSG00000133740	4.0412	5.77781	7.06078	6.37057	ENSG00000133740	E2F5
ENSG00000133742	1.17062	5.69529	5.1589	6.98692	ENSG00000133742	CA1
ENSG00000133773	13.7192	23.8466	21.8566	15.5057	ENSG00000133773	CCDC59
ENSG00000133789	14.0924	15.0959	17.6102	22.4869	ENSG00000133789	SWAP70
ENSG00000133794	21.5428	30.1602	26.8837	23.6376	ENSG00000133794	ARNTL
ENSG00000133800	0.267308	0.58712	0.290477	0.591204	ENSG00000133800	LYVE1
ENSG00000133805	16.546	25.3197	22.6897	35.7663	ENSG00000133805	AMPD3
ENSG00000133808	13.1696	27.0613	25.2838	26.9824	ENSG00000133808	MICALCL
ENSG00000133812	26.739	44.0185	38.5545	65.7898	ENSG00000133812	SBF2
ENSG00000133816	85.8736	203.771	178.587	308.761	ENSG00000133816	MICAL2
ENSG00000133818	27.5098	32.3602	35.7911	43.8429	ENSG00000133818	RRAS2
ENSG00000133835	46.7343	56.5935	49.7296	55.9385	ENSG00000133835	HSD17B4
ENSG00000133858	20.0053	31.1236	33.8169	50.6364	ENSG00000133858	ZFC3H1
ENSG00000133863	0.705096	0.859223	0.826252	1.01333	ENSG00000133863	TEX15
ENSG00000133872	92.7203	105.548	64.778	38.4866	ENSG00000133872	SARAF
ENSG00000133874	2.15346	2.06375	1.85427	3.13423	ENSG00000133874	RNF122
ENSG00000133878	0	0.147397	0.0541303	0.10221	ENSG00000133878	DUSP26
ENSG00000133884	18.318	23.9419	22.3952	24.6234	ENSG00000133884	DPF2
ENSG00000133895	14.4997	13.4598	15.9258	14.9055	ENSG00000133895	MEN1
ENSG00000133935	13.8154	13.2075	4.75157	6.2269	ENSG00000133935	ERG28
ENSG00000133937	0	0.137952	0.0410653	0.103114	ENSG00000133937	GSC
ENSG00000133943	17.1635	59.0773	25.6342	29.7205	ENSG00000133943	C14orf159
ENSG00000133958	0.378092	0.724171	0.83923	1.56811	ENSG00000133958	UNC79
ENSG00000133961	35.1658	37.6045	40.4166	62.9587	ENSG00000133961	NUMB
ENSG00000133962	4.89032	13.2753	13.7168	17.8152	ENSG00000133962	CATSPERB
ENSG00000133980	0.247598	0.365711	0.181797	0.331644	ENSG00000133980	VRTN
ENSG00000133983	34.6366	22.9553	18.6963	16.9044	ENSG00000133983	COX16
ENSG00000133985	18.0364	1.31793	0.796081	2.66301	ENSG00000133985	TTC9
ENSG00000133997	17.7235	25.4706	23.1724	24.6194	ENSG00000133997	MED6
ENSG00000134001	70.7921	47.0539	53.3719	37.0981	ENSG00000134001	EIF2S1
ENSG00000134007	0.255821	0.853809	1.13511	1.21273	ENSG00000134007	ADAM20
ENSG00000134013	6.19608	32.2846	43.0004	277.804	ENSG00000134013	LOXL2
ENSG00000134014	22.3032	36.9126	34.0493	30.1951	ENSG00000134014	ELP3
ENSG00000134020	0.0710365	0.43101	0.222631	0.61751	ENSG00000134020	PEBP4
ENSG00000134028	0.21735	0.381968	0.501628	0.564874	ENSG00000134028	ADAMDEC1
ENSG00000134030	20.1249	28.7895	60.0783	32.5846	ENSG00000134030	CTIF

ENSG00000134042	0.328969	0.384751	0.379945	1.00899	ENSG00000134042	MRO
ENSG00000134046	49.2624	47.7856	59.3434	39.5015	ENSG00000134046	MBD2
ENSG00000134049	23.8971	15.0017	12.8758	11.2054	ENSG00000134049	IER3IP1
ENSG00000134056	15.6427	8.49881	8.55981	5.23642	ENSG00000134056	MRPS36
ENSG00000134057	22.6911	96.8648	11.1347	22.7639	ENSG00000134057	CCNB1
ENSG00000134058	37.265	14.3162	12.6293	11.6729	ENSG00000134058	CDK7
ENSG00000134061	0.924135	0.781031	0.470491	0.834647	ENSG00000134061	CD180
ENSG00000134070	3.35791	6.77264	5.39	6.53645	ENSG00000134070	IRAK2
ENSG00000134072	3.65347	4.60514	4.42626	6.4734	ENSG00000134072	CAMK1
ENSG00000134077	24.0272	18.8742	25.049	18.1742	ENSG00000134077	THUMPD3
ENSG00000134086	17.5223	23.6958	26.1542	22.1785	ENSG00000134086	VHL
ENSG00000134107	141.225	58.7936	55.0518	57.8962	ENSG00000134107	BHLHE40
ENSG00000134108	64.2543	43.488	44.0376	37.3111	ENSG00000134108	ARL8B
ENSG00000134109	49.6416	73.6101	48.2194	52.2562	ENSG00000134109	EDEM1
ENSG00000134115	0.306159	0.781061	1.26339	0.908265	ENSG00000134115	CNTN6
ENSG00000134121	1.49455	0.797133	0.756195	1.14423	ENSG00000134121	CHL1
ENSG00000134138	33.6718	104.344	69.3484	236.392	ENSG00000134138	MEIS2
ENSG00000134146	9.76191	21.7057	18.3101	22.5929	ENSG00000134146	DPH6
ENSG00000134152	79.5377	92.5474	65.1675	102.761	ENSG00000134152	KATNBL1
ENSG00000134153	22.3131	18.4859	22.2833	13.3772	ENSG00000134153	EMC7
ENSG00000134160	0.404919	0.725118	0.721595	0.874586	ENSG00000134160	TRPM1
ENSG00000134183	1.89466	2.60121	3.86686	3.68417	ENSG00000134183	GNAT2
ENSG00000134184	2.4584	5.273	0.409496	0	ENSG00000134184	GSTM1
ENSG00000134186	17.1319	21.7209	25.0513	24.0498	ENSG00000134186	PRPF38B
ENSG00000134193	0.115423	0.164085	0.251519	0.133337	ENSG00000134193	REG4
ENSG00000134198	0.0521375	0.421951	0.240634	0.421358	ENSG00000134198	TSPAN2
ENSG00000134200	0	0	0	0	ENSG00000134200	TSHB
ENSG00000134201	0.189165	0.360711	0.441313	0.979798	ENSG00000134201	GSTM5
ENSG00000134202	3.28559	12.3607	4.66428	5.97027	ENSG00000134202	GSTM3
ENSG00000134207	0.061846	0.0962848	0.0552121	0.216744	ENSG00000134207	SYT6
ENSG00000134215	17.6909	22.4098	12.3196	14.1032	ENSG00000134215	VAV3
ENSG00000134216	0.207788	0.688015	0.755153	1.09969	ENSG00000134216	CHIA
ENSG00000134222	3.4193	17.8901	4.589	7.44485	ENSG00000134222	PSRC1
ENSG00000134240	0.115487	0.359439	0.120293	0.505034	ENSG00000134240	HMGCS2
ENSG00000134242	4.31626	7.64432	8.40044	7.79781	ENSG00000134242	PTPN22
ENSG00000134243	20.1872	11.7564	11.0427	20.1941	ENSG00000134243	SORT1
ENSG00000134245	2.10399	2.93378	2.12099	3.78362	ENSG00000134245	WNT2B
ENSG00000134247	76.2537	98.0471	104.654	61.5613	ENSG00000134247	PTGFRN
ENSG00000134248	28.083	17.8556	19.8934	20.702	ENSG00000134248	LAMTOR5
ENSG00000134249	0.018499	0.0894051	0.016127	0.081371	ENSG00000134249	ADAM30
ENSG00000134250	69.9448	75.8902	71.2056	70.341	ENSG00000134250	NOTCH2
ENSG00000134253	2.09105	3.67245	2.40023	4.61304	ENSG00000134253	TRIM45
ENSG00000134255	38.2201	54.9198	36.5033	29.1176	ENSG00000134255	CEPT1
ENSG00000134256	1.64024	2.88562	4.62756	2.08166	ENSG00000134256	CD101
ENSG00000134258	1.79821	0.852203	1.2826	1.60098	ENSG00000134258	VTCN1
ENSG00000134259	0.0584665	0.39384	1.62713	0.0637217	ENSG00000134259	NGF
ENSG00000134262	11.4966	20.8087	14.8305	20.9307	ENSG00000134262	AP4B1
ENSG00000134265	30.9302	31.817	32.7631	42.1032	ENSG00000134265	NAPG
ENSG00000134278	17.5093	20.5082	27.8772	22.577	ENSG00000134278	SPIRE1
ENSG00000134283	42.0988	61.8711	53.362	59.9301	ENSG00000134283	PPHLN1
ENSG00000134285	8.5205	19.1188	13.9154	19.9662	ENSG00000134285	FKBP11
ENSG00000134287	45.0899	32.733	30.2345	27.34	ENSG00000134287	ARF3
ENSG00000134291	35.1676	37.2946	18.0303	15.1674	ENSG00000134291	TMEM106C
ENSG00000134294	425.685	1050.84	772.881	318.113	ENSG00000134294	SLC38A2

ENSG00000134297	10.0804	9.95393	7.5753	14.4344	ENSG00000134297	PLEKHA8P1
ENSG00000134308	200.903	123.292	96.9822	78.6306	ENSG00000134308	YWHAQ
ENSG00000134313	26.9002	40.4146	41.8193	32.3267	ENSG00000134313	KIDINS220
ENSG00000134317	47.9971	8.39419	45.4281	8.13382	ENSG00000134317	GRHL1
ENSG00000134318	15.2488	22.3686	15.0333	32.385	ENSG00000134318	ROCK2
ENSG00000134321	6.00651	2.19887	8.24147	3.48278	ENSG00000134321	RSAD2
ENSG00000134323	1.16942	0.0614255	0.0564318	0.0700077	ENSG00000134323	MYCN
ENSG00000134324	87.0473	111.223	30.6544	111.377	ENSG00000134324	LPIN1
ENSG00000134326	1.39536	2.74368	2.44821	2.72775	ENSG00000134326	CMPK2
ENSG00000134330	27.8686	35.0432	21.1723	24.703	ENSG00000134330	IAH1
ENSG00000134333	389.35	235.723	183.283	266.132	ENSG00000134333	LDHA
ENSG00000134339	11.7658	6.12289	17.0999	9.6433	ENSG00000134339	SAA2
ENSG00000134343	0.557207	0.15221	0.104719	0.508394	ENSG00000134343	ANO3
ENSG00000134352	54.5289	84.9273	57.7718	71.1939	ENSG00000134352	IL6ST
ENSG00000134363	218.041	231.235	209.34	144.231	ENSG00000134363	FST
ENSG00000134365	0.0458106	0	0.0562562	0.187206	ENSG00000134365	CFHR4
ENSG00000134369	16.0555	30.2644	21.6257	55.0307	ENSG00000134369	NAV1
ENSG00000134371	12.6747	14.1808	16.6444	21.6819	ENSG00000134371	CDC73
ENSG00000134375	37.4428	27.0643	31.6065	47.6964	ENSG00000134375	TIMM17A
ENSG00000134376	0.313578	0.457508	0.563087	1.62982	ENSG00000134376	CRB1
ENSG00000134389	0.176104	0.386722	0.402077	0.357219	ENSG00000134389	CFHR5
ENSG00000134398	0.795709	1.67429	1.74295	3.99485	ENSG00000134398	ERN2
ENSG00000134419	541.08	448.636	381.65	186.029	ENSG00000134419	RPS15A
ENSG00000134438	0.329838	0.108748	0.0504792	0.177565	ENSG00000134438	RAX
ENSG00000134440	82.1134	95.0669	122.054	55.9009	ENSG00000134440	NARS
ENSG00000134443	0	0.0724549	0.18081	0.443718	ENSG00000134443	GRP
ENSG00000134444	45.8706	56.6472	53.1493	54.6692	ENSG00000134444	KIAA1468
ENSG00000134452	34.692	53.7871	48.9054	60.1885	ENSG00000134452	FBXO18
ENSG00000134453	32.4519	38.1991	43.3272	44.8385	ENSG00000134453	RBM17
ENSG00000134460	0.407136	0.812703	0.807296	1.19932	ENSG00000134460	IL2RA
ENSG00000134461	2.10301	3.81183	5.18605	4.31054	ENSG00000134461	ANKRD16
ENSG00000134463	2.78761	12.9592	6.66242	1.80743	ENSG00000134463	ECHDC3
ENSG00000134470	0.516171	8.67093	2.82674	3.21781	ENSG00000134470	IL15RA
ENSG00000134480	27.225	30.8139	25.0006	29.8194	ENSG00000134480	CCNH
ENSG00000134489	1.00373	1.73735	1.99189	2.97632	ENSG00000134489	HRH4
ENSG00000134490	7.76023	12.2445	13.5312	19.6621	ENSG00000134490	TMEM241
ENSG00000134504	24.7243	27.065	30.7844	29.4591	ENSG00000134504	KCTD1
ENSG00000134508	0.993488	0.653921	1.24978	3.5844	ENSG00000134508	CABLES1
ENSG00000134516	0.847626	1.13192	1.13642	3.50664	ENSG00000134516	DOCK2
ENSG00000134531	797.973	183.652	44.4884	247.163	ENSG00000134531	EMP1
ENSG00000134532	0.958473	1.60773	1.58458	5.22923	ENSG00000134532	SOX5
ENSG00000134533	3.36465	9.07648	7.2436	14.0961	ENSG00000134533	RERG
ENSG00000134538	0	0	0.0655202	0.0275196	ENSG00000134538	SLCO1B1
ENSG00000134539	5.23528	11.4644	9.86459	18.693	ENSG00000134539	KLRD1
ENSG00000134545	3.00211	8.45993	9.76698	17.4513	ENSG00000134545	KLRC1
ENSG00000134548	0.162671	0.307131	1.55692	1.10569	ENSG00000134548	SPX
ENSG00000134551	0.301483	0.748608	0.79526	1.42681	ENSG00000134551	PRH2
ENSG00000134569	1.77871	6.64244	5.70667	7.62201	ENSG00000134569	LRP4
ENSG00000134571	0.152814	0.178547	0.143819	0.236621	ENSG00000134571	MYBPC3
ENSG00000134574	11.0819	25.9754	14.8079	11.4075	ENSG00000134574	DDB2
ENSG00000134575	15.6581	18.3115	17.5184	10.8483	ENSG00000134575	ACP2
ENSG00000134588	0.413453	2.29086	1.37069	4.02712	ENSG00000134588	USP26
ENSG00000134590	38.4338	22.3485	20.699	28.3541	ENSG00000134590	RTL8C
ENSG00000134594	0.320926	0.436356	1.12896	1.55658	ENSG00000134594	RAB33A

ENSG00000134595	0	0	0.023606	0.0298745	ENSG00000134595	SOX3
ENSG00000134597	11.8147	19.8641	17.5672	17.357	ENSG00000134597	RBMX2
ENSG00000134602	18.1749	17.999	13.353	7.19687	ENSG00000134602	STK26
ENSG00000134612	0	1.93489	0.0266228	8.15561	ENSG00000134612	FOLH1B
ENSG00000134627	0.102374	0.494377	0.406799	1.52738	ENSG00000134627	PIWIL4
ENSG00000134640	0.0979188	0.701691	0.232993	0.931289	ENSG00000134640	MTNR1B
ENSG00000134644	48.0566	60.9248	72.0955	79.222	ENSG00000134644	PUM1
ENSG00000134668	5.46714	11.3393	9.68111	21.1187	ENSG00000134668	SPOCD1
ENSG00000134684	36.1877	73.6061	109.569	67.6852	ENSG00000134684	YARS
ENSG00000134686	80.3913	74.8699	49.4446	85.9284	ENSG00000134686	PHC2
ENSG00000134690	2.44709	10.3102	1.98642	4.82634	ENSG00000134690	CDCA8
ENSG00000134697	50.1226	47.9157	44.9361	49.1945	ENSG00000134697	GNL2
ENSG00000134698	4.28777	7.02216	9.29764	10.1439	ENSG00000134698	AGO4
ENSG00000134709	11.4555	16.7404	16.5595	7.08652	ENSG00000134709	HOOK1
ENSG00000134716	3.2438	6.42896	3.71132	2.01277	ENSG00000134716	CYP2J2
ENSG00000134717	22.3164	32.3943	35.2349	21.6744	ENSG00000134717	BTF3L4
ENSG00000134744	27.0047	47.6152	45.6054	50.0975	ENSG00000134744	ZCCHC11
ENSG00000134748	6.54244	9.41718	9.18392	6.06566	ENSG00000134748	PRPF38A
ENSG00000134755	181.355	64.5523	102.927	45.2163	ENSG00000134755	DSC2
ENSG00000134757	609.646	261.696	487.97	133.96	ENSG00000134757	DSG3
ENSG00000134758	6.34263	11.1266	11.7792	9.57445	ENSG00000134758	RNF138
ENSG00000134759	50.2378	69.0702	79.0274	70.0037	ENSG00000134759	ELP2
ENSG00000134760	21.2246	2.50381	19.0896	2.08878	ENSG00000134760	DSG1
ENSG00000134762	208.758	219.769	297.963	73.6739	ENSG00000134762	DSC3
ENSG00000134765	3.30786	0.895286	9.2124	1.11155	ENSG00000134765	DSC1
ENSG00000134769	3.28261	10.8669	9.80651	16.3029	ENSG00000134769	DTNA
ENSG00000134775	1.95561	6.70284	6.22987	8.4201	ENSG00000134775	FHOD3
ENSG00000134779	29.6304	40.3094	34.264	35.7701	ENSG00000134779	TPGS2
ENSG00000134780	0.203893	0.162643	0.226258	0.357301	ENSG00000134780	DAGLA
ENSG00000134802	10.7506	42.95	10.1922	22.9857	ENSG00000134802	SLC43A3
ENSG00000134809	10.5514	10.1436	13.3125	5.97599	ENSG00000134809	TIMM10
ENSG00000134812	1.23862	1.43451	1.94761	1.23209	ENSG00000134812	GIF
ENSG00000134815	9.27602	10.2231	13.0097	9.61118	ENSG00000134815	DHX34
ENSG00000134817	0.0331133	0.0579949	0.092012	0.0661809	ENSG00000134817	APLNR
ENSG00000134824	131.937	209.765	30.8542	172.955	ENSG00000134824	FADS2
ENSG00000134825	51.2381	62.7091	38.2743	26.4468	ENSG00000134825	TMEM258
ENSG00000134827	30.715	0.429343	3.54178	1.51773	ENSG00000134827	TCN1
ENSG00000134830	1.32164	2.25906	2.5958	3.89696	ENSG00000134830	C5AR2
ENSG00000134851	79.7686	115.109	106.971	117.963	ENSG00000134851	TMEM165
ENSG00000134852	17.8658	17.2064	12.4304	19.5353	ENSG00000134852	CLOCK
ENSG00000134853	3.27481	3.78891	5.32225	59.1467	ENSG00000134853	PDGFRA
ENSG00000134864	4.29835	11.1779	8.17823	2.75405	ENSG00000134864	GGACT
ENSG00000134871	35.878	93.8165	71.6736	202.688	ENSG00000134871	COL4A2
ENSG00000134873	0.531209	1.02086	0.271955	0.606937	ENSG00000134873	CLDN10
ENSG00000134874	1.40906	1.81315	12.7167	20.8122	ENSG00000134874	DZIP1
ENSG00000134882	39.6577	44.776	38.9077	28.9674	ENSG00000134882	UBAC2
ENSG00000134884	57.2096	110.06	103.253	85.8809	ENSG00000134884	ARGLU1
ENSG00000134897	24.206	29.7325	24.2335	35.5715	ENSG00000134897	BIVM
ENSG00000134899	37.6839	39.1851	35.4981	37.9233	ENSG00000134899	ERCC5
ENSG00000134900	23.7977	46.8235	31.1888	40.8193	ENSG00000134900	TPP2
ENSG00000134901	4.482	13.4627	7.27921	9.87149	ENSG00000134901	KDELC1
ENSG00000134905	46.9907	59.8023	72.5997	62.5381	ENSG00000134905	CARS2
ENSG00000134909	30.9451	24.7894	21.4734	19.0921	ENSG00000134909	ARHGAP32
ENSG00000134910	111.27	188.545	116.274	119.351	ENSG00000134910	STT3A

ENSG00000134917	1.18165	1.92541	2.1823	5.29997	ENSG00000134917	ADAMTS8
ENSG00000134940	0.254983	0.831296	0.317243	0.681503	ENSG00000134940	ACRV1
ENSG00000134954	30.9341	57.3819	50.1558	88.9278	ENSG00000134954	ETS1
ENSG00000134955	24.1774	23.6147	13.2161	7.23844	ENSG00000134955	SLC37A2
ENSG00000134962	0.638743	1.1951	1.58883	1.63319	ENSG00000134962	KLB
ENSG00000134970	75.1174	72.5722	34.4811	35.6495	ENSG00000134970	TMED7
ENSG00000134982	20.0344	27.2018	20.7164	28.611	ENSG00000134982	APC
ENSG00000134986	5.27786	12.0967	17.1497	59.4747	ENSG00000134986	NREP
ENSG00000134987	19.7559	23.6001	30.8553	22.6439	ENSG00000134987	WDR36
ENSG00000134996	33.4763	19.6051	19.7313	14.616	ENSG00000134996	OSTF1
ENSG00000135002	8.1954	6.73722	10.2429	7.55192	ENSG00000135002	RFK
ENSG00000135018	45.7323	41.4322	38.7176	38.474	ENSG00000135018	UBQLN1
ENSG00000135040	13.88	19.3324	21.7831	16.0566	ENSG00000135040	NAA35
ENSG00000135045	2.97989	3.62146	3.70815	3.31603	ENSG00000135045	C9orf40
ENSG00000135046	1410.62	466.248	220.12	211.007	ENSG00000135046	ANXA1
ENSG00000135047	58.5489	83.5685	41.9432	56.4	ENSG00000135047	CTSL
ENSG00000135048	33.9408	61.6411	38.9927	60.5816	ENSG00000135048	TMEM2
ENSG00000135049	6.52247	10.7309	12.8573	13.3039	ENSG00000135049	AGTPBP1
ENSG00000135052	12.4068	11.0338	18.1548	21.062	ENSG00000135052	GOLM1
ENSG00000135063	0.731464	1.17537	1.00299	0.423611	ENSG00000135063	FAM189A2
ENSG00000135069	7.25415	70.7485	123.769	22.041	ENSG00000135069	PSAT1
ENSG00000135070	12.46	15.0817	14.5661	12.3889	ENSG00000135070	ISCA1
ENSG00000135074	28.0415	40.6151	5.4322	58.8111	ENSG00000135074	ADAM19
ENSG00000135077	2.02616	2.5437	2.17859	2.70369	ENSG00000135077	HAVCR2
ENSG00000135083	2.18785	2.91515	5.53654	3.74839	ENSG00000135083	CCNJL
ENSG00000135090	18.0897	27.2825	30.1416	48.663	ENSG00000135090	TAOK3
ENSG00000135093	9.82759	10.2595	11.5671	10.6266	ENSG00000135093	USP30
ENSG00000135094	1.64208	4.31614	4.48634	4.72943	ENSG00000135094	SDS
ENSG00000135097	1.03023	0.813093	1.12771	1.70246	ENSG00000135097	MSI1
ENSG00000135100	0.559586	1.00978	1.51923	1.6991	ENSG00000135100	HNF1A
ENSG00000135108	14.4972	17.4161	15.5481	11.5747	ENSG00000135108	FBXO21
ENSG00000135111	13.5245	20.5695	3.81444	21.0051	ENSG00000135111	TBX3
ENSG00000135114	1.93667	4.20687	3.7271	2.08179	ENSG00000135114	OASL
ENSG00000135116	4.95762	12.5777	14.4133	18.0315	ENSG00000135116	HRK
ENSG00000135119	4.58736	8.3544	8.83191	10.0545	ENSG00000135119	RNFT2
ENSG00000135124	9.09251	20.8922	21.1638	29.5504	ENSG00000135124	P2RX4
ENSG00000135127	8.46801	20.1353	20.1322	15.5581	ENSG00000135127	BICDL1
ENSG00000135144	0.318376	0.231494	0.311848	0.532328	ENSG00000135144	DTX1
ENSG00000135148	18.3465	19.2696	19.8915	17.1677	ENSG00000135148	TRAFD1
ENSG00000135164	65.1836	133.293	92.5966	120.218	ENSG00000135164	DMTF1
ENSG00000135175	0	0	0	0	ENSG00000135175	OCM2
ENSG00000135185	17.9644	30.0319	17.7395	21.8062	ENSG00000135185	TMEM243
ENSG00000135205	3.14124	9.33576	20.4137	6.58872	ENSG00000135205	CCDC146
ENSG00000135211	11.4176	11.0309	5.09362	3.86276	ENSG00000135211	TMEM60
ENSG00000135213	13.1343	20.5666	24.1012	28.7497	ENSG00000135213	POM121C
ENSG00000135218	0.513389	1.38059	7.98843	2.07997	ENSG00000135218	CD36
ENSG00000135220	0.0180495	0	0.0314606	0.019942	ENSG00000135220	UGT2A3
ENSG00000135222	0.0572402	0	0	0	ENSG00000135222	CSN2
ENSG00000135226	0	0	0	0	ENSG00000135226	UGT2B28
ENSG00000135241	15.6113	16.6173	13.6042	14.1242	ENSG00000135241	PNPLA8
ENSG00000135245	7.52265	8.57622	14.4572	10.7609	ENSG00000135245	HILPDA
ENSG00000135248	0.0733643	0.143877	0.241181	0.221365	ENSG00000135248	FAM71F1
ENSG00000135249	12.9076	20.5962	22.7546	28.5549	ENSG00000135249	RINT1
ENSG00000135250	32.2527	41.5414	40.0633	43.3905	ENSG00000135250	SRPK2

ENSG00000135269	88.8012	118.403	86.6254	65.9954	ENSG00000135269	TES
ENSG00000135272	12.5128	8.00368	7.32425	11.7796	ENSG00000135272	MDFIC
ENSG00000135297	19.8117	40.0129	27.618	28.2896	ENSG00000135297	MTO1
ENSG00000135298	0.150566	0.463221	0.445929	0.840608	ENSG00000135298	ADGRB3
ENSG00000135299	20.5144	38.1619	26.2001	28.9031	ENSG00000135299	ANKRD6
ENSG00000135312	0.524935	0.794638	0.620356	9.11471	ENSG00000135312	HTR1B
ENSG00000135314	4.86786	8.32764	9.37875	12.9438	ENSG00000135314	KHDC1
ENSG00000135315	3.86714	6.4571	4.20704	9.57361	ENSG00000135315	CEP162
ENSG00000135316	48.7896	42.9675	51.4231	42.944	ENSG00000135316	SYNCRIP
ENSG00000135317	68.2474	96.1784	60.7557	61.1038	ENSG00000135317	SNX14
ENSG00000135318	142.329	213.793	27.8977	129.631	ENSG00000135318	NT5E
ENSG00000135324	1.33308	2.28873	2.37694	3.47761	ENSG00000135324	MRAP2
ENSG00000135333	0.159169	0.277306	0.215753	0.403902	ENSG00000135333	EPHA7
ENSG00000135334	17.945	21.008	24.3924	15.5222	ENSG00000135334	AKIRIN2
ENSG00000135336	14.2031	19.7038	15.3468	14.6841	ENSG00000135336	ORC3
ENSG00000135338	2.32591	2.14478	2.92692	2.4631	ENSG00000135338	LCA5
ENSG00000135341	19.2352	21.8009	22.2818	17.3846	ENSG00000135341	MAP3K7
ENSG00000135346	0.47106	0	0	0	ENSG00000135346	CGA
ENSG00000135355	0.0347558	0.0669708	0.181618	0.0761869	ENSG00000135355	GJA10
ENSG00000135362	25.0221	14.1266	8.07548	27.6178	ENSG00000135362	PRR5L
ENSG00000135363	1.37129	0.327191	0.296709	1.03576	ENSG00000135363	LMO2
ENSG00000135365	14.9224	27.2441	30.4488	38.9844	ENSG00000135365	PHF21A
ENSG00000135372	20.5754	26.6546	38.2047	28.2741	ENSG00000135372	NAT10
ENSG00000135373	168.723	118.172	53.9574	50.0594	ENSG00000135373	EHF
ENSG00000135374	0.734019	1.21161	1.27043	1.54025	ENSG00000135374	ELF5
ENSG00000135378	14.3461	10.8863	17.7252	6.00784	ENSG00000135378	PRRG4
ENSG00000135387	97.354	97.8298	78.1081	87.6749	ENSG00000135387	CAPRIN1
ENSG00000135390	102.09	83.5972	53.5111	52.3382	ENSG00000135390	ATP5G2
ENSG00000135392	17.4259	22.0136	19.6966	18.8876	ENSG00000135392	DNAJC14
ENSG00000135404	431.319	379.365	172.191	217.3	ENSG00000135404	CD63
ENSG00000135406	0.0843602	0.317319	0.396712	0.297919	ENSG00000135406	PRPH
ENSG00000135407	14.827	18.2549	17.3378	23.2748	ENSG00000135407	AVIL
ENSG00000135409	0.117292	0.0249654	0.146516	0.126757	ENSG00000135409	AMHR2
ENSG00000135413	0	0	0	0	ENSG00000135413	LACRT
ENSG00000135414	3.24868	2.4132	2.10734	4.11737	ENSG00000135414	GDF11
ENSG00000135423	3.36557	3.96349	6.19707	2.30972	ENSG00000135423	GLS2
ENSG00000135424	1.34468	1.71596	1.68978	3.06072	ENSG00000135424	ITGA7
ENSG00000135426	1.13407	2.57986	1.91069	3.17741	ENSG00000135426	TESPA1
ENSG00000135436	0.914542	1.73981	1.70418	1.99538	ENSG00000135436	FAM186B
ENSG00000135437	2.15514	3.39612	3.31613	6.28114	ENSG00000135437	RDH5
ENSG00000135439	0.52884	1.24794	0.563792	0.324764	ENSG00000135439	AGAP2
ENSG00000135441	25.3836	24.3779	8.41193	11.6419	ENSG00000135441	BLOC1S1
ENSG00000135443	0	0	0.0420985	0	ENSG00000135443	KRT85
ENSG00000135446	26.0636	30.0989	43.2353	32.8721	ENSG00000135446	CDK4
ENSG00000135447	1.20502	3.43522	5.60087	3.2566	ENSG00000135447	PPP1R1A
ENSG00000135451	8.02932	28.7682	8.20781	17.6305	ENSG00000135451	TROAP
ENSG00000135452	33.2944	27.4682	21.7214	21.1493	ENSG00000135452	TSPAN31
ENSG00000135454	0.788911	1.37233	0.947298	4.70709	ENSG00000135454	B4GALNT1
ENSG00000135457	7.9329	11.5689	10.7393	12.266	ENSG00000135457	TFCP2
ENSG00000135469	3.62064	7.07138	4.93492	8.64703	ENSG00000135469	COQ10A
ENSG00000135472	0.188638	0.60547	0.727356	1.20207	ENSG00000135472	FAIM2
ENSG00000135473	22.469	56.2947	40.9929	28.0262	ENSG00000135473	PAN2
ENSG00000135476	2.18347	13.1957	1.96154	6.46491	ENSG00000135476	ESPL1
ENSG00000135477	1.2277	0.919744	0.603614	0.57773	ENSG00000135477	KRT87P

ENSG00000135480	698.179	490.604	247.481	167.182	ENSG00000135480	KRT7
ENSG00000135482	2.48568	3.66798	3.62712	2.03225	ENSG00000135482	ZC3H10
ENSG00000135486	139.629	190.456	178.998	220.364	ENSG00000135486	HNRNPA1
ENSG00000135502	0.126462	0.526681	0.475094	2.16699	ENSG00000135502	SLC26A10
ENSG00000135503	15.1745	16.9448	16.0956	11.8119	ENSG00000135503	ACVR1B
ENSG00000135506	95.4134	102.881	78.6872	72.1825	ENSG00000135506	OS9
ENSG00000135517	0.365082	1.61495	1.24893	0.919598	ENSG00000135517	MIP
ENSG00000135519	0.535963	1.3373	1.15149	0.720698	ENSG00000135519	KCNH3
ENSG00000135521	8.78297	10.9372	13.8194	9.99144	ENSG00000135521	LTV1
ENSG00000135525	16.5512	10.783	10.0988	5.82823	ENSG00000135525	MAP7
ENSG00000135535	86.0312	99.163	71.2596	56.2506	ENSG00000135535	CD164
ENSG00000135537	7.72299	12.0553	7.67135	12.6369	ENSG00000135537	AFG1L
ENSG00000135540	22.0616	48.7549	37.9755	17.035	ENSG00000135540	NHSL1
ENSG00000135541	10.7829	14.1232	11.6388	13.8881	ENSG00000135541	AHI1
ENSG00000135547	0.0450746	0.108624	0.161838	0.373602	ENSG00000135547	HEY2
ENSG00000135549	14.1679	13.6051	6.22006	11.1339	ENSG00000135549	PKIB
ENSG00000135569	0	0	0.0914227	0	ENSG00000135569	TAAR5
ENSG00000135577	0.0434315	0.167303	0.0756119	0.189977	ENSG00000135577	NMBR
ENSG00000135587	8.61556	10.9327	9.0909	6.31793	ENSG00000135587	SMPD2
ENSG00000135596	19.4149	25.805	26.0005	29.222	ENSG00000135596	MICAL1
ENSG00000135597	46.2454	53.4961	35.6118	49.2391	ENSG00000135597	REPS1
ENSG00000135604	0.264265	0.19808	0.35837	0.289896	ENSG00000135604	STX11
ENSG00000135605	1.29191	0.831543	1.36396	1.06092	ENSG00000135605	TEC
ENSG00000135617	8.53338	5.84583	5.71308	3.80779	ENSG00000135617	PRADC1
ENSG00000135622	8.70422	10.2679	5.17689	7.33481	ENSG00000135622	SEMA4F
ENSG00000135624	108.465	105.228	86.8191	68.574	ENSG00000135624	CCT7
ENSG00000135625	0.023442	0.0677936	0.0205144	0.0523008	ENSG00000135625	EGR4
ENSG00000135631	29.2667	22.8445	25.4143	27.8683	ENSG00000135631	RAB11FIP5
ENSG00000135632	26.7803	24.3494	20.9114	20.3905	ENSG00000135632	SMYD5
ENSG00000135636	1.21214	0.610136	1.57623	7.52925	ENSG00000135636	DYSF
ENSG00000135637	12.1353	11.6206	10.2296	12.8561	ENSG00000135637	CCDC142
ENSG00000135638	0.102276	0.270908	0.458151	0.372383	ENSG00000135638	EMX1
ENSG00000135643	1.38107	1.67094	1.28993	1.61893	ENSG00000135643	KCNMB4
ENSG00000135655	60.2759	67.9035	63.445	56.5136	ENSG00000135655	USP15
ENSG00000135677	43.5917	50.489	40.7824	33.75	ENSG00000135677	GNS
ENSG00000135678	14.7731	20.6878	14.273	30.2802	ENSG00000135678	CPM
ENSG00000135679	138.542	73.0138	99.4195	86.0808	ENSG00000135679	MDM2
ENSG00000135686	41.6366	38.054	28.3383	23.9204	ENSG00000135686	KLHL36
ENSG00000135697	0.0413173	0.0632167	0.126483	0.138506	ENSG00000135697	BCO1
ENSG00000135698	36.6404	46.2778	45.0402	40.2077	ENSG00000135698	MPHOSPH6
ENSG00000135702	1.07728	1.83945	1.81532	3.51291	ENSG00000135702	CHST5
ENSG00000135709	7.82328	7.46869	6.39251	7.09575	ENSG00000135709	KIAA0513
ENSG00000135720	62.9464	52.1579	62.4838	61.0668	ENSG00000135720	DYNC1LI2
ENSG00000135722	7.13787	13.7578	9.43528	8.82868	ENSG00000135722	FBXL8
ENSG00000135723	15.5607	36.4662	17.4844	39.5854	ENSG00000135723	FHOD1
ENSG00000135736	770.493	100.857	60.0178	121.379	ENSG00000135736	CCDC102A
ENSG00000135740	1.73648	3.21369	2.12572	4.41272	ENSG00000135740	SLC9A5
ENSG00000135744	0.0243331	0.140735	0.0848221	0.133616	ENSG00000135744	AGT
ENSG00000135747	9.93781	21.5646	19.6603	32.1335	ENSG00000135747	ZNF670
ENSG00000135749	24.1235	58.6164	68.1611	63.472	ENSG00000135749	PCNX2
ENSG00000135750	19.4671	24.3055	17.471	16.3304	ENSG00000135750	KCNK1
ENSG00000135763	5.17426	6.3001	8.65116	5.6174	ENSG00000135763	URB2
ENSG00000135766	10.8095	7.89727	10.2586	9.22513	ENSG00000135766	EGLN1
ENSG00000135773	0.147666	0	0.127832	0.157981	ENSG00000135773	CAPN9

ENSG00000135775	14.2207	13.7136	15.0591	9.96558	ENSG00000135775	COG2
ENSG00000135776	14.9916	17.7386	13.6312	18.3601	ENSG00000135776	ABCB10
ENSG00000135778	17.1431	10.6149	14.1024	10.5186	ENSG00000135778	NTPCR
ENSG00000135801	12.4105	16.5995	14.4452	10.1277	ENSG00000135801	TAF5L
ENSG00000135821	167.464	155.59	50.3239	97.7676	ENSG00000135821	GLUL
ENSG00000135823	17.9926	22.4056	21.9498	18.728	ENSG00000135823	STX6
ENSG00000135824	0.374864	0.285165	0.779249	1.10454	ENSG00000135824	RGS8
ENSG00000135828	6.91482	8.08702	6.19081	10.3092	ENSG00000135828	RNASEL
ENSG00000135829	82.8053	87.9318	71.1639	85.2444	ENSG00000135829	DHX9
ENSG00000135835	1.36208	4.72854	3.41287	5.14236	ENSG00000135835	KIAA1614
ENSG00000135837	25.7982	33.9485	25.7145	30.9313	ENSG00000135837	CEP350
ENSG00000135838	2.60472	4.25142	8.98264	6.03854	ENSG00000135838	NPL
ENSG00000135842	10.0438	36.4971	27.2117	23.882	ENSG00000135842	FAM129A
ENSG00000135845	14.9302	17.8596	13.139	8.24622	ENSG00000135845	PIGC
ENSG00000135847	22.3128	33.6381	37.9036	28.2592	ENSG00000135847	ACBD6
ENSG00000135862	115.849	166.531	105.123	174.883	ENSG00000135862	LAMC1
ENSG00000135870	12.6812	9.82724	15.1189	16.4965	ENSG00000135870	RC3H1
ENSG00000135898	0.285867	0.526014	0.306756	0.647067	ENSG00000135898	GPR55
ENSG00000135899	9.97092	15.3522	18.9715	17.3172	ENSG00000135899	SP110
ENSG00000135900	11.8736	9.43279	8.5448	8.17066	ENSG00000135900	MRPL44
ENSG00000135902	0.492717	1.00312	1.43122	1.35024	ENSG00000135902	CHRND
ENSG00000135903	0.334392	0.611761	0.600103	5.07285	ENSG00000135903	PAX3
ENSG00000135905	1.39447	3.34375	1.78743	17.7608	ENSG00000135905	DOCK10
ENSG00000135912	7.96664	21.7508	15.6265	16.608	ENSG00000135912	TTLL4
ENSG00000135913	11.4047	16.0458	13.4759	20.7745	ENSG00000135913	USP37
ENSG00000135914	0.685127	1.80307	1.54973	2.81388	ENSG00000135914	HTR2B
ENSG00000135916	14.4623	20.1172	14.1036	30.924	ENSG00000135916	ITM2C
ENSG00000135917	4.4463	6.45422	7.35816	14.6602	ENSG00000135917	SLC19A3
ENSG00000135919	543.914	419.111	95.4409	235.672	ENSG00000135919	SERPINE2
ENSG00000135924	43.286	22.0651	36.2485	21.6557	ENSG00000135924	DNAJB2
ENSG00000135925	1.38785	13.1171	20.0657	8.48033	ENSG00000135925	WNT10A
ENSG00000135926	1044.93	410.812	166.33	152.13	ENSG00000135926	TMBIM1
ENSG00000135929	0.536587	0.649873	0.67105	3.21866	ENSG00000135929	CYP27A1
ENSG00000135930	35.8398	32.0957	29.3746	42.0299	ENSG00000135930	EIF4E2
ENSG00000135931	11.7909	13.5081	14.3681	29.5615	ENSG00000135931	ARMC9
ENSG00000135932	123.143	98.7676	56.2565	97.9425	ENSG00000135932	CAB39
ENSG00000135940	83.2509	84.3718	57.4581	43.9136	ENSG00000135940	COX5B
ENSG00000135945	40.125	77.4843	48.5994	50.3144	ENSG00000135945	REV1
ENSG00000135951	4.45561	9.84176	10.0379	9.14787	ENSG00000135951	TSGA10
ENSG00000135953	11.383	8.91774	7.49101	6.54949	ENSG00000135953	MFSD9
ENSG00000135956	26.1912	18.7802	19.3551	12.6947	ENSG00000135956	TMEM127
ENSG00000135960	0.897549	0.160372	0.463015	0.253496	ENSG00000135960	EDAR
ENSG00000135966	8.55076	7.51506	8.18921	5.84854	ENSG00000135966	TGFBRAP1
ENSG00000135968	18.4265	25.6563	28.109	55.2053	ENSG00000135968	GCC2
ENSG00000135972	9.91	14.6313	14.3275	9.60021	ENSG00000135972	MRPS9
ENSG00000135973	0.0662688	0.223481	0.317464	0.399492	ENSG00000135973	GPR45
ENSG00000135974	10.0274	8.21894	9.23447	6.7289	ENSG00000135974	C2orf49
ENSG00000135976	15.15	32.2281	30.0117	51.0155	ENSG00000135976	ANKRD36
ENSG00000135999	6.91823	9.94712	9.50632	9.1071	ENSG00000135999	EPC2
ENSG00000136002	72.3676	63.876	88.4642	48.1738	ENSG00000136002	ARHGEF4
ENSG00000136003	30.3224	31.5894	29.3158	20.0462	ENSG00000136003	ISCU
ENSG00000136010	2.53964	14.7966	45.6532	22.9608	ENSG00000136010	ALDH1L2
ENSG00000136011	1.04678	1.79378	1.55178	2.39151	ENSG00000136011	STAB2
ENSG00000136014	0.643199	1.04046	1.20188	1.07418	ENSG00000136014	USP44

ENSG00000136021	36.4093	32.2547	39.0581	25.1915	ENSG00000136021	SCYL2
ENSG00000136026	62.78	135.876	101.563	105.337	ENSG00000136026	CKAP4
ENSG00000136040	1.17951	2.67826	2.78841	4.80632	ENSG00000136040	PLXNC1
ENSG00000136044	23.3532	54.6512	37.4097	85.18	ENSG00000136044	APPL2
ENSG00000136045	32.0023	24.4317	28.4944	23.667	ENSG00000136045	PWP1
ENSG00000136048	23.4375	44.7751	44.5079	48.8495	ENSG00000136048	DRAM1
ENSG00000136051	46.5082	54.7549	50.4478	69.626	ENSG00000136051	WASHC4
ENSG00000136052	3.53497	3.87348	4.35472	12.331	ENSG00000136052	SLC41A2
ENSG00000136059	14.2816	3.51403	6.02081	4.0807	ENSG00000136059	VILL
ENSG00000136068	641.452	540.725	258.024	443.885	ENSG00000136068	FLNB
ENSG00000136098	6.12148	13.8387	9.57922	11.6933	ENSG00000136098	NEK3
ENSG00000136099	0	0.131137	0.0706471	0.148855	ENSG00000136099	PCDH8
ENSG00000136100	18.3373	35.3936	42.2247	39.0755	ENSG00000136100	VPS36
ENSG00000136104	7.27974	14.8512	19.5972	11.9295	ENSG00000136104	RNASEH2B
ENSG00000136108	6.13832	21.2317	10.8598	12.1185	ENSG00000136108	CKAP2
ENSG00000136110	0.207427	0.119867	0.180894	0.363087	ENSG00000136110	CNMD
ENSG00000136111	6.07039	8.59817	8.5266	9.18757	ENSG00000136111	TBC1D4
ENSG00000136114	3.9146	8.1982	25.4505	4.2293	ENSG00000136114	THSD1
ENSG00000136122	3.53717	8.37167	2.99216	3.11374	ENSG00000136122	BORA
ENSG00000136141	4.76995	9.97728	8.51592	11.739	ENSG00000136141	LRCH1
ENSG00000136143	25.4496	21.1976	21.1538	19.8324	ENSG00000136143	SUCLA2
ENSG00000136144	15.8058	17.1447	19.5134	19.455	ENSG00000136144	RCBTB1
ENSG00000136146	17.5443	21.1336	19.378	27.0733	ENSG00000136146	MED4
ENSG00000136147	21.0443	36.8959	22.8929	42.0005	ENSG00000136147	PHF11
ENSG00000136149	0.152405	0	0	0.169333	ENSG00000136149	RPL13AP25
ENSG00000136152	27.1535	46.9518	36.8958	41.6828	ENSG00000136152	COG3
ENSG00000136153	144.84	32.8646	22.3788	79.6304	ENSG00000136153	LMO7
ENSG00000136155	246.28	14.9206	12.1929	14.6545	ENSG00000136155	SCEL
ENSG00000136156	224.283	303.508	282.902	135.923	ENSG00000136156	ITM2B
ENSG00000136158	9.25567	11.5871	4.26263	12.2706	ENSG00000136158	SPRY2
ENSG00000136159	7.48731	11.6969	7.68666	7.32572	ENSG00000136159	NUDT15
ENSG00000136160	1.22034	0.766837	0.739734	2.52427	ENSG00000136160	EDNRB
ENSG00000136161	1.52023	3.04678	5.77053	2.12533	ENSG00000136161	RCBTB2
ENSG00000136167	0.885204	14.3759	21.4921	9.26807	ENSG00000136167	LCP1
ENSG00000136169	10.3777	18.4871	17.9456	24.6104	ENSG00000136169	SETDB2
ENSG00000136193	24.7043	28.7081	30.1239	30.0678	ENSG00000136193	SCRN1
ENSG00000136197	2.41716	3.12269	2.09337	0.909417	ENSG00000136197	C7orf25
ENSG00000136205	2.59161	5.0156	11.2823	66.5406	ENSG00000136205	TNS3
ENSG00000136206	0.874011	1.92341	2.58893	4.08986	ENSG00000136206	SPDYE1
ENSG00000136213	4.70171	2.94907	3.60736	3.48291	ENSG00000136213	CHST12
ENSG00000136231	25.9565	58.1955	47.2843	53.0014	ENSG00000136231	IGF2BP3
ENSG00000136235	51.1909	20.9375	69.7795	39.1592	ENSG00000136235	GPNMB
ENSG00000136237	12.7122	16.6588	5.72348	8.29972	ENSG00000136237	RAPGEF5
ENSG00000136238	93.7369	67.8538	76.5709	69.4102	ENSG00000136238	RAC1
ENSG00000136240	74.0082	82.6041	43.309	53.0433	ENSG00000136240	KDELR2
ENSG00000136243	26.3916	24.295	40.1358	25.5781	ENSG00000136243	NUPL2
ENSG00000136244	0.669937	0.678252	0.675075	34.0477	ENSG00000136244	IL6
ENSG00000136247	31.2352	33.4151	26.5209	25.685	ENSG00000136247	ZDHHC4
ENSG00000136250	0.898654	1.92773	1.60586	3.08448	ENSG00000136250	AOAH
ENSG00000136261	18.5036	22.1378	28.3587	15.6613	ENSG00000136261	BZW2
ENSG00000136267	3.24144	7.72723	7.10683	15.8332	ENSG00000136267	DGKB
ENSG00000136270	58.8282	64.1544	71.1979	39.2356	ENSG00000136270	TBRG4
ENSG00000136271	38.724	40.6598	43.488	28.2776	ENSG00000136271	DDX56
ENSG00000136273	14.3208	17.4111	18.1103	16.6244	ENSG00000136273	HUS1

ENSG00000136274	0.871283	1.53438	0.513334	2.15508	ENSG00000136274	NACAD
ENSG00000136275	0.611904	2.4327	2.66549	6.72217	ENSG00000136275	C7orf69
ENSG00000136279	59.0088	36.2177	37.7597	35.1905	ENSG00000136279	DBNL
ENSG00000136280	16.6914	29.8423	24.7957	28.6876	ENSG00000136280	CCM2
ENSG00000136286	1.02815	1.66746	1.45253	2.67886	ENSG00000136286	MYO1G
ENSG00000136295	25.9527	27.9173	28.3085	46.1441	ENSG00000136295	TTYH3
ENSG00000136297	0.143077	0.0919275	0.0273563	0.0261855	ENSG00000136297	MMD2
ENSG00000136305	0.206576	0.344224	0.508286	0.418522	ENSG00000136305	CIDEB
ENSG00000136319	6.86545	9.78796	8.53839	11.0358	ENSG00000136319	TTC5
ENSG00000136327	0	0.045351	0	0.103041	ENSG00000136327	NKX2-8
ENSG00000136352	1.13671	0.774339	3.3983	11.0429	ENSG00000136352	NKX2-1
ENSG00000136367	0.474403	0.69334	0.852466	0.993815	ENSG00000136367	ZFHX2
ENSG00000136371	5.10834	12.2218	12.498	14.6028	ENSG00000136371	MTHFS
ENSG00000136378	0.972779	1.59821	2.85943	9.06895	ENSG00000136378	ADAMTS7
ENSG00000136379	9.69783	14.3255	8.23262	8.37614	ENSG00000136379	ABHD17C
ENSG00000136381	18.9817	22.0751	24.0844	31.6762	ENSG00000136381	IREB2
ENSG00000136383	0.473759	0.668236	0.303885	0.311116	ENSG00000136383	ALPK3
ENSG00000136404	4.50073	6.85362	7.35736	7.1013	ENSG00000136404	TM6SF1
ENSG00000136425	3.7721	1.47152	2.57202	3.02765	ENSG00000136425	CIB2
ENSG00000136436	47.6459	70.8005	78.6856	96.0175	ENSG00000136436	CALCOCO2
ENSG00000136444	10.148	27.8828	18.2303	18.3732	ENSG00000136444	RSAD1
ENSG00000136448	63.2961	61.0623	45.1702	52.2303	ENSG00000136448	NMT1
ENSG00000136449	20.5599	38.7686	26.5458	58.5177	ENSG00000136449	MYCBPAP
ENSG00000136450	77.5348	84.8036	77.076	65.0484	ENSG00000136450	SRSF1
ENSG00000136451	12.37	21.1101	12.9812	10.1378	ENSG00000136451	VEZF1
ENSG00000136457	2.2972	2.94157	3.46475	2.68151	ENSG00000136457	CHAD
ENSG00000136463	8.41975	6.56015	6.77254	4.59265	ENSG00000136463	TACO1
ENSG00000136478	17.8315	13.8003	10.3096	9.71797	ENSG00000136478	TEX2
ENSG00000136485	15.9717	20.0587	16.8525	16.2795	ENSG00000136485	DCAF7
ENSG00000136487	0.262229	0.168002	0.227656	0.115723	ENSG00000136487	GH2
ENSG00000136488	0.0363646	0.259614	0.123758	0.541373	ENSG00000136488	CSH1
ENSG00000136490	2.36055	5.97152	5.03156	11.6402	ENSG00000136490	LIMD2
ENSG00000136492	10.2928	25.246	17.0705	28.0054	ENSG00000136492	BRIP1
ENSG00000136504	16.0124	28.15	18.7889	22.031	ENSG00000136504	KAT7
ENSG00000136514	0.70679	0.46586	0.291539	0.692511	ENSG00000136514	RTP4
ENSG00000136518	29.9442	31.9844	26.9109	23.1154	ENSG00000136518	ACTL6A
ENSG00000136521	31.7372	32.6419	23.6986	25.4945	ENSG00000136521	NDUFB5
ENSG00000136522	18.3748	14.8772	17.956	10.9287	ENSG00000136522	MRPL47
ENSG00000136527	54.6382	100.489	56.1693	71.4798	ENSG00000136527	TRA2B
ENSG00000136531	0.160797	0.659771	1.49959	1.25145	ENSG00000136531	SCN2A
ENSG00000136535	0.19379	0.371424	0.414695	0.639676	ENSG00000136535	TBR1
ENSG00000136536	78.0462	62.2817	60.9644	52.0491	ENSG00000136536	MARCH7
ENSG00000136541	0.753131	1.71588	1.04901	2.69373	ENSG00000136541	ERMN
ENSG00000136542	70.1116	43.3701	17.9074	10.339	ENSG00000136542	GALNT5
ENSG00000136546	2.21391	2.51177	4.57114	8.2127	ENSG00000136546	SCN7A
ENSG00000136560	47.8249	71.0021	61.1182	58.9756	ENSG00000136560	TANK
ENSG00000136573	0.83735	1.39686	1.22688	1.52695	ENSG00000136573	BLK
ENSG00000136574	0.274415	0.258559	0.184441	0.172702	ENSG00000136574	GATA4
ENSG00000136603	37.4048	16.7466	27.0682	32.2988	ENSG00000136603	SKIL
ENSG00000136628	51.8361	81.325	77.1142	49.0102	ENSG00000136628	EPRS
ENSG00000136630	0.114754	0.494386	0.456266	6.09226	ENSG00000136630	HLX
ENSG00000136631	9.37887	13.8834	14.7904	17.8758	ENSG00000136631	VPS45
ENSG00000136634	0.670898	1.4587	0.80948	2.01082	ENSG00000136634	IL10
ENSG00000136636	14.2994	26.6332	22.397	33.5057	ENSG00000136636	KCTD3

ENSG00000136643	9.68839	10.324	10.5617	11.7602	ENSG00000136643	RPS6KC1
ENSG00000136653	2.06631	1.39322	0.629516	0.961976	ENSG00000136653	RASSF5
ENSG00000136682	15.0953	24.6677	31.3018	24.7744	ENSG00000136682	CBWD2
ENSG00000136688	2.62736	1.5901	6.09637	1.86827	ENSG00000136688	IL36G
ENSG00000136689	237.503	29.0408	21.2473	27.4302	ENSG00000136689	IL1RN
ENSG00000136694	0.213674	0.95893	0.495107	1.08356	ENSG00000136694	IL36A
ENSG00000136695	9.48011	4.99947	8.0048	9.4872	ENSG00000136695	IL36RN
ENSG00000136696	0.290694	0.0973168	0.0505638	0.0551847	ENSG00000136696	IL36B
ENSG00000136697	1.33514	0.808682	2.21179	2.17463	ENSG00000136697	IL1F10
ENSG00000136698	0	0	0	0.0637927	ENSG00000136698	CFC1
ENSG00000136699	23.1893	30.7783	24.6854	23.0059	ENSG00000136699	SMPD4
ENSG00000136709	22.3512	24.9654	22.292	19.0595	ENSG00000136709	WDR33
ENSG00000136710	8.53534	4.37079	5.66741	3.04945	ENSG00000136710	CCDC115
ENSG00000136715	9.10642	7.99301	5.28051	6.27249	ENSG00000136715	SAP130
ENSG00000136717	3.34241	8.84987	6.76321	14.2014	ENSG00000136717	BIN1
ENSG00000136718	28.1093	28.0544	32.3372	21.7497	ENSG00000136718	IMP4
ENSG00000136720	20.1954	18.2771	14.7734	10.3615	ENSG00000136720	HS6ST1
ENSG00000136731	41.3194	65.0398	49.0817	43.5623	ENSG00000136731	UGGT1
ENSG00000136732	0.451409	0.275856	0.772411	7.25247	ENSG00000136732	GYPC
ENSG00000136738	13.7702	15.3835	15.3122	12.7722	ENSG00000136738	STAM
ENSG00000136750	0.208425	0.191665	0.331977	0.461333	ENSG00000136750	GAD2
ENSG00000136754	56.9638	38.0097	40.0106	25.0079	ENSG00000136754	ABI1
ENSG00000136758	66.2577	59.0554	60.8565	44.4888	ENSG00000136758	YME1L1
ENSG00000136770	13.8359	20.379	25.193	15.1832	ENSG00000136770	DNAJC1
ENSG00000136783	14.8789	11.2442	12.6888	6.73218	ENSG00000136783	NIPSNAP3A
ENSG00000136802	134.109	144.942	58.4788	49.4819	ENSG00000136802	LRRC8A
ENSG00000136807	26.6536	26.4457	26.7694	20.7782	ENSG00000136807	CDK9
ENSG00000136810	161.206	147.321	91.9892	68.4818	ENSG00000136810	TXN
ENSG00000136811	16.3947	34.6823	19.0796	26.7868	ENSG00000136811	ODF2
ENSG00000136813	62.6904	78.2462	71.7976	59.9885	ENSG00000136813	KIAA0368
ENSG00000136816	18.377	17.3746	11.8851	10.336	ENSG00000136816	TOR1B
ENSG00000136819	28.8973	29.6471	35.7387	48.0826	ENSG00000136819	C9orf78
ENSG00000136824	7.18538	20.2803	6.96324	11.3527	ENSG00000136824	SMC2
ENSG00000136826	29.644	23.2653	27.5971	5.33757	ENSG00000136826	KLF4
ENSG00000136827	30.6242	27.4176	27.1151	19.3232	ENSG00000136827	TOR1A
ENSG00000136828	3.87397	5.36207	3.53969	7.11649	ENSG00000136828	RALGPS1
ENSG00000136830	341.79	161.071	85.2127	155.617	ENSG00000136830	FAM129B
ENSG00000136834	0.414105	0.529715	0.514002	0.651196	ENSG00000136834	OR1J1
ENSG00000136839	0	0	0	0	ENSG00000136839	OR13C9
ENSG00000136840	3.78527	12.2629	8.03685	5.67613	ENSG00000136840	ST6GALNAC4
ENSG00000136842	0.158466	0.0938338	0.270185	0.281869	ENSG00000136842	TMOD1
ENSG00000136848	25.3548	24.7745	27.0096	20.5612	ENSG00000136848	DAB2IP
ENSG00000136854	6.70578	12.3575	9.79153	16.0301	ENSG00000136854	STXBP1
ENSG00000136856	13.9886	22.5857	16.2295	16.0127	ENSG00000136856	SLC2A8
ENSG00000136859	0.32207	0.248403	0.374296	6.96662	ENSG00000136859	ANGPTL2
ENSG00000136861	16.5382	27.4384	19.6413	25.1742	ENSG00000136861	CDK5RAP2
ENSG00000136866	0.44382	1.37148	1.47579	1.81664	ENSG00000136866	ZFP37
ENSG00000136867	76.7354	37.3756	40.3973	13.8394	ENSG00000136867	SLC31A2
ENSG00000136868	22.0958	37.2742	36.3444	32.7461	ENSG00000136868	SLC31A1
ENSG00000136869	1.09556	2.21887	2.21451	4.00373	ENSG00000136869	TLR4
ENSG00000136870	6.47654	6.33411	6.32884	5.5319	ENSG00000136870	ZNF189
ENSG00000136872	0.0679007	0.609342	0.0789058	0.174064	ENSG00000136872	ALDOB
ENSG00000136874	13.7516	19.3252	20.8753	21.5188	ENSG00000136874	STX17
ENSG00000136875	12.8144	10.9879	14.5865	8.67288	ENSG00000136875	PRPF4

ENSG00000136877	39.2804	49.011	46.6324	31.93	ENSG00000136877	FPGS
ENSG00000136878	5.55475	7.27876	11.5263	11.9081	ENSG00000136878	USP20
ENSG00000136881	0.804182	1.81057	1.79367	2.82583	ENSG00000136881	BAAT
ENSG00000136883	3.39218	5.67595	5.60746	6.23128	ENSG00000136883	KIF12
ENSG00000136888	89.101	39.3075	53.8619	35.5306	ENSG00000136888	ATP6V1G1
ENSG00000136891	18.7228	23.6428	20.6862	27.7776	ENSG00000136891	TEX10
ENSG00000136895	4.01135	6.07592	6.97773	6.31542	ENSG00000136895	GARNL3
ENSG00000136897	6.49959	6.5469	7.83284	3.98628	ENSG00000136897	MRPL50
ENSG00000136908	10.5371	15.7494	13.327	9.79514	ENSG00000136908	DPM2
ENSG00000136918	0.569872	0.779107	1.11585	0.985799	ENSG00000136918	WDR38
ENSG00000136925	8.23413	8.93006	15.8188	11.1919	ENSG00000136925	TSTD2
ENSG00000136928	0.693142	0.714153	0.615831	1.98448	ENSG00000136928	GABBR2
ENSG00000136929	0.165582	0.310822	0.15976	0.314456	ENSG00000136929	HEMGN
ENSG00000136930	76.4197	65.9909	52.2988	52.1816	ENSG00000136930	PSMB7
ENSG00000136931	66.8425	66.523	156.163	836.558	ENSG00000136931	NR5A1
ENSG00000136932	8.05035	5.25453	6.29025	3.2743	ENSG00000136932	TRMO
ENSG00000136933	8.17255	10.9849	13.5265	12.6906	ENSG00000136933	RABEPK
ENSG00000136935	8.21966	8.42504	7.84797	8.77936	ENSG00000136935	GOLGA1
ENSG00000136936	6.9684	8.04191	8.43068	8.54278	ENSG00000136936	XPA
ENSG00000136937	15.8917	24.9917	19.2111	25.8269	ENSG00000136937	NCBP1
ENSG00000136938	10.427	22.4117	22.2561	30.2049	ENSG00000136938	ANP32B
ENSG00000136939	0	0.0321361	0	0.363477	ENSG00000136939	OR1L4
ENSG00000136940	10.7747	8.79475	11.055	14.9427	ENSG00000136940	PDCL
ENSG00000136942	784.535	559.464	505.706	284.849	ENSG00000136942	RPL35
ENSG00000136943	905.248	68.1914	35.3925	106.198	ENSG00000136943	CTSV
ENSG00000136944	0.729941	0.501366	3.23803	1.51563	ENSG00000136944	LMX1B
ENSG00000136950	27.8883	30.9109	23.9835	16.3018	ENSG00000136950	ARPC5L
ENSG00000136960	0.268503	0.599725	0.325521	7.303	ENSG00000136960	ENPP2
ENSG00000136982	1.41692	2.14027	0.766876	1.65965	ENSG00000136982	DSCC1
ENSG00000136986	53.998	62.3605	32.3297	25.8709	ENSG00000136986	DERL1
ENSG00000136997	97.8523	79.4411	106.905	55.5232	ENSG00000136997	MYC
ENSG00000136999	1.56799	0.404383	0.153074	2.85525	ENSG00000136999	NOV
ENSG00000137033	4.74414	15.4227	12.2381	16.7376	ENSG00000137033	IL33
ENSG00000137038	17.2925	19.9985	20.7617	15.4228	ENSG00000137038	DMAC1
ENSG00000137040	11.5999	9.2932	10.7153	7.36132	ENSG00000137040	RANBP6
ENSG00000137054	9.8592	12.8085	11.5282	11.5747	ENSG00000137054	POLR1E
ENSG00000137055	16.293	20.1297	16.9137	19.2816	ENSG00000137055	PLAA
ENSG00000137070	4.93269	8.6588	10.4724	11.069	ENSG00000137070	IL11RA
ENSG00000137073	19.962	23.5173	27.3013	33.5963	ENSG00000137073	UBAP2
ENSG00000137074	24.2659	36.8451	41.7628	27.9507	ENSG00000137074	APTX
ENSG00000137075	8.98096	7.67467	6.59197	8.61486	ENSG00000137075	RNF38
ENSG00000137076	55.9263	99.4652	67.3149	161.877	ENSG00000137076	TLN1
ENSG00000137077	0.224743	0.452727	0.597055	1.14033	ENSG00000137077	CCL21
ENSG00000137078	0.0710365	0.139856	0.126408	0.211563	ENSG00000137078	SIT1
ENSG00000137080	0.0600233	0	0.0521969	0.265542	ENSG00000137080	IFNA21
ENSG00000137090	0.585214	1.02518	1.51157	2.07658	ENSG00000137090	DMRT1
ENSG00000137094	6.76867	8.67616	8.28214	10.0615	ENSG00000137094	DNAJB5
ENSG00000137098	0.659266	0.664212	0.663557	1.12113	ENSG00000137098	SPAG8
ENSG00000137100	22.6826	18.4143	13.245	11.8286	ENSG00000137100	DCTN3
ENSG00000137101	0.793175	1.80579	2.52272	1.82609	ENSG00000137101	CD72
ENSG00000137103	2.4955	4.98825	4.69099	6.69042	ENSG00000137103	TMEM8B
ENSG00000137106	59.8492	46.269	36.9873	33.5205	ENSG00000137106	GRHPR
ENSG00000137124	5.47568	7.59983	7.61174	8.87953	ENSG00000137124	ALDH1B1
ENSG00000137133	8.86962	11.2166	7.37235	4.26274	ENSG00000137133	HINT2

ENSG00000137135	2.37968	7.31405	3.78838	4.44679	ENSG00000137135	ARHGEF39
ENSG00000137142	0.0555972	0.161088	0.0966975	0.12125	ENSG00000137142	IGFBPL1
ENSG00000137145	22.1168	36.0204	23.0761	22.5527	ENSG00000137145	DENND4C
ENSG00000137154	603.28	547.456	471.971	301.843	ENSG00000137154	RPS6
ENSG00000137161	11.7268	20.8374	8.76369	10.708	ENSG00000137161	CNPY3
ENSG00000137166	4.03587	4.6704	5.11506	4.97864	ENSG00000137166	FOXP4
ENSG00000137168	12.6726	8.09142	7.09496	4.71307	ENSG00000137168	PPIL1
ENSG00000137171	12.8708	27.3307	23.4524	33.0731	ENSG00000137171	KLC4
ENSG00000137177	86.6678	61.6867	60.8417	80.9855	ENSG00000137177	KIF13A
ENSG00000137185	5.83626	8.3245	9.52181	8.26972	ENSG00000137185	ZSCAN9
ENSG00000137193	64.6374	25.3989	26.2876	16.5901	ENSG00000137193	PIM1
ENSG00000137197	0	0.108641	0	0	ENSG00000137197	CDSN
ENSG00000137198	2.01296	2.28175	2.13995	4.92536	ENSG00000137198	GMPR
ENSG00000137200	21.685	34.0122	25.992	23.4043	ENSG00000137200	CMTR1
ENSG00000137203	36.2311	50.5087	65.2751	42.6027	ENSG00000137203	TFAP2A
ENSG00000137204	0.0747103	0.159669	0.258918	0.145683	ENSG00000137204	SLC22A7
ENSG00000137207	71.8301	67.4241	48.9487	32.8362	ENSG00000137207	YIPF3
ENSG00000137210	39.0873	50.3006	44.906	61.0568	ENSG00000137210	TMEM14B
ENSG00000137216	65.2934	63.2298	50.3603	30.1954	ENSG00000137216	TMEM63B
ENSG00000137218	3.2754	5.30612	4.20289	5.4541	ENSG00000137218	FRS3
ENSG00000137221	14.4016	28.7121	24.8809	19.2931	ENSG00000137221	TJAP1
ENSG00000137225	0.291214	0.960565	0.854019	0.737785	ENSG00000137225	CAPN11
ENSG00000137251	0	0.350096	0.169047	0.178307	ENSG00000137251	TINAG
ENSG00000137252	0.0618425	0.148984	0.161618	0.101725	ENSG00000137252	HCRTR2
ENSG00000137259	9.81376	24.4724	4.93001	7.81806	ENSG00000137259	HIST1H2AB
ENSG00000137261	0.245765	0.3158	0.398898	0.505419	ENSG00000137261	KIAA0319
ENSG00000137265	0.544376	0.468879	0.53642	0.672128	ENSG00000137265	IRF4
ENSG00000137266	10.1526	11.4823	39.4437	9.71306	ENSG00000137266	SLC22A23
ENSG00000137267	38.2764	14.8809	20.1753	16.2911	ENSG00000137267	TUBB2A
ENSG00000137269	16.0723	18.6461	13.2011	12.0741	ENSG00000137269	LRRC1
ENSG00000137270	0.334563	1.00034	0.710632	1.28058	ENSG00000137270	GCM1
ENSG00000137273	14.4694	4.05803	5.30946	29.4228	ENSG00000137273	FOXF2
ENSG00000137274	12.0311	19.3941	16.1331	16.9018	ENSG00000137274	BPHL
ENSG00000137275	8.53119	7.36548	10.4767	9.6271	ENSG00000137275	RIPK1
ENSG00000137285	1.45929	0.0917207	0.116606	0.229622	ENSG00000137285	TUBB2B
ENSG00000137288	34.6568	43.8678	31.2957	25.3106	ENSG00000137288	UQCC2
ENSG00000137309	125.424	143.844	30.8758	88.2606	ENSG00000137309	HMGA1
ENSG00000137310	2.47772	9.16524	0.437574	2.46262	ENSG00000137310	TCF19
ENSG00000137312	1.28296	2.78707	0.96359	3.22941	ENSG00000137312	FLOT1
ENSG00000137313	1.82591	0.98202	3.03185	0.727691	ENSG00000137313	TRIM26
ENSG00000137321	0.000636314	0	0.000200736	2.08E-06	ENSG00000137321	RANP1
ENSG00000137331	69.3318	0	0	0	ENSG00000137331	IER3
ENSG00000137332	16.0798	10.5294	19.3023	30.6249	ENSG00000137332	DDR1
ENSG00000137337	0.44099	0.690666	0.460788	0.460338	ENSG00000137337	MDC1
ENSG00000137338	2.42844	2.52019	3.56815	2.5613	ENSG00000137338	PGBD1
ENSG00000137343	0.378914	0.763133	0.686203	0.442347	ENSG00000137343	ATAT1
ENSG00000137345	0.777593	0.983953	1.81207	2.41946	ENSG00000137345	MOG
ENSG00000137364	14.8438	8.24187	7.06145	9.46824	ENSG00000137364	TPMT
ENSG00000137384	0.208044	0.749081	0.160154	0.231175	ENSG00000137384	TRIM15
ENSG00000137392	0	0	0	0	ENSG00000137392	CLPS
ENSG00000137393	22.3882	14.262	20.8009	9.47845	ENSG00000137393	RNF144B
ENSG00000137394	0.23677	0.25603	0.238475	0.299427	ENSG00000137394	TRIM10
ENSG00000137397	0.37616	0.29168	0.333678	0.561387	ENSG00000137397	TRIM31
ENSG00000137403	2.13744	11.6444	4.5817	3.01734	ENSG00000137403	HLA-F

ENSG00000137404	1.98587	4.95101	0.827239	2.09252	ENSG00000137404	NRM
ENSG00000137409	85.9292	64.987	48.3839	47.3388	ENSG00000137409	MTCH1
ENSG00000137411	3.07241	1.13555	1.45912	2.74232	ENSG00000137411	VARS2
ENSG00000137413	12.0789	22.0648	18.8566	22.2816	ENSG00000137413	TAF8
ENSG00000137414	8.48718	7.56358	6.81009	5.46146	ENSG00000137414	FAM8A1
ENSG00000137434	1.28125	3.0162	2.5804	1.91978	ENSG00000137434	C6orf52
ENSG00000137440	956.565	1631.51	109.708	302.235	ENSG00000137440	FGFBP1
ENSG00000137441	0	0.172535	0.622956	0.191672	ENSG00000137441	FGFBP2
ENSG00000137449	15.5868	13.9567	13.4858	22.726	ENSG00000137449	CPEB2
ENSG00000137460	3.18018	3.61555	4.1325	3.95727	ENSG00000137460	FHDC1
ENSG00000137462	1.80244	3.67648	5.37091	2.34876	ENSG00000137462	TLR2
ENSG00000137463	0.30792	0.216186	0.376388	0.529018	ENSG00000137463	MGARP
ENSG00000137473	0.130345	0.125049	0.0305972	0.208645	ENSG00000137473	TTC29
ENSG00000137474	0.601676	0.661183	0.811951	0.832111	ENSG00000137474	MYO7A
ENSG00000137478	4.67868	9.71756	9.47178	14.9633	ENSG00000137478	FCHSD2
ENSG00000137486	2.85988	3.54989	3.79744	12.4137	ENSG00000137486	ARRB1
ENSG00000137491	2.81607	5.75283	4.01103	6.78459	ENSG00000137491	SLCO2B1
ENSG00000137492	14.7195	17.1883	24.0584	15.8812	ENSG00000137492	THAP12
ENSG00000137494	5.9997	9.51834	9.94991	11.824	ENSG00000137494	ANKRD42
ENSG00000137496	2.02241	4.90002	6.02898	5.04238	ENSG00000137496	IL18BP
ENSG00000137497	62.2655	100.474	90.5193	106.495	ENSG00000137497	NUMA1
ENSG00000137500	58.3777	101.557	92.1982	150.987	ENSG00000137500	CCDC90B
ENSG00000137501	21.768	4.6457	7.26946	25.2052	ENSG00000137501	SYTL2
ENSG00000137502	2.67718	5.05885	6.48954	7.28697	ENSG00000137502	RAB30
ENSG00000137504	18.7725	26.0447	22.4087	23.9664	ENSG00000137504	CREBZF
ENSG00000137507	0.254921	0.733866	0.130003	1.23201	ENSG00000137507	LRRC32
ENSG00000137509	18.059	38.4654	36.7936	31.2936	ENSG00000137509	PRCP
ENSG00000137513	8.74101	12.5339	14.643	8.44125	ENSG00000137513	NARS2
ENSG00000137522	18.987	21.0288	22.278	19.603	ENSG00000137522	RNF121
ENSG00000137547	24.7317	16.9324	15.9629	12.3869	ENSG00000137547	MRPL15
ENSG00000137558	0.260554	1.34789	0.40108	0.472918	ENSG00000137558	PI15
ENSG00000137561	0.60045	2.22042	1.1757	2.15186	ENSG00000137561	TTPA
ENSG00000137563	12.9286	51.5536	15.1006	19.6698	ENSG00000137563	GGH
ENSG00000137571	0.543026	0.970421	0.978456	1.66	ENSG00000137571	SLCO5A1
ENSG00000137573	15.7967	28.6766	28.2578	36.6711	ENSG00000137573	SULF1
ENSG00000137574	9.58626	12.1614	11.9996	10.0852	ENSG00000137574	TGS1
ENSG00000137575	30.9926	34.0406	20.3613	41.6295	ENSG00000137575	SDCBP
ENSG00000137601	5.37141	9.71039	9.85656	13.2154	ENSG00000137601	NEK1
ENSG00000137628	21.0061	65.2802	37.2345	44.58	ENSG00000137628	DDX60
ENSG00000137634	0.135836	0.226172	0.236618	0.655841	ENSG00000137634	NXPE4
ENSG00000137642	37.8979	106.453	83.4042	60.2761	ENSG00000137642	SORL1
ENSG00000137648	26.9293	11.2844	6.4381	12.3938	ENSG00000137648	TMPRSS4
ENSG00000137656	4.03833	6.73088	3.42885	4.59241	ENSG00000137656	BUD13
ENSG00000137672	1.50273	2.92125	2.6471	6.05601	ENSG00000137672	TRPC6
ENSG00000137673	4.40341	6.05845	6.51024	10.1919	ENSG00000137673	MMP7
ENSG00000137674	5.78067	12.4702	9.49283	12.2471	ENSG00000137674	MMP20
ENSG00000137675	0.0599594	0	0	0.032448	ENSG00000137675	MMP27
ENSG00000137691	1.13091	2.46814	3.16508	3.05322	ENSG00000137691	C11orf70
ENSG00000137692	24.4947	32.3263	36.7505	21.8408	ENSG00000137692	DCUN1D5
ENSG00000137693	52.0963	61.7371	59.2376	59.6862	ENSG00000137693	YAP1
ENSG00000137699	235.009	97.9699	199.352	47.5094	ENSG00000137699	TRIM29
ENSG00000137700	1.12589	3.99783	1.38614	0.379839	ENSG00000137700	SLC37A4
ENSG00000137707	0.312251	0.347914	0.526296	0.459689	ENSG00000137707	BTG4
ENSG00000137709	2.53483	4.93508	4.31257	2.29223	ENSG00000137709	POU2F3

ENSG00000137710	54.3584	55.2807	34.6672	45.8601	ENSG00000137710	RDX
ENSG00000137713	14.9888	22.2606	10.9162	14.2988	ENSG00000137713	PPP2R1B
ENSG00000137714	5.99303	6.46345	6.20261	6.26971	ENSG00000137714	FDX1
ENSG00000137720	4.79857	2.97443	3.09637	4.0071	ENSG00000137720	C11orf1
ENSG00000137726	0.716169	3.25256	3.44552	6.69929	ENSG00000137726	FXYD6
ENSG00000137727	0.149503	0.207377	0.175244	0.351896	ENSG00000137727	ARHGAP20
ENSG00000137731	0.112729	0.352785	0.352618	1.03361	ENSG00000137731	FXYD2
ENSG00000137745	0.130213	0.219386	0.135032	0.384115	ENSG00000137745	MMP13
ENSG00000137747	9.77775	3.80859	5.13397	5.11306	ENSG00000137747	TMPRSS13
ENSG00000137752	11.66	17.1839	26.6466	6.02656	ENSG00000137752	CASP1
ENSG00000137757	0.0728264	0.54175	1.03708	0.812747	ENSG00000137757	CASP5
ENSG00000137760	4.57779	4.96167	4.92272	3.42394	ENSG00000137760	ALKBH8
ENSG00000137764	5.97167	12.7291	13.4863	17.0966	ENSG00000137764	MAP2K5
ENSG00000137766	0.045528	0.391095	0.26696	0.878259	ENSG00000137766	UNC13C
ENSG00000137767	77.6403	70.3473	27.8486	27.0843	ENSG00000137767	SQOR
ENSG00000137770	17.8225	29.2892	23.6593	28.9416	ENSG00000137770	CTDSPL2
ENSG00000137776	46.3012	68.1658	70.3638	60.7166	ENSG00000137776	SLTM
ENSG00000137801	1402.64	1853.73	811.399	2666.1	ENSG00000137801	THBS1
ENSG00000137802	50.5791	97.0432	63.1865	72.4884	ENSG00000137802	MAPKBP1
ENSG00000137804	15.9199	65.276	10.1307	23.0566	ENSG00000137804	NUSAP1
ENSG00000137806	12.267	8.24878	6.61598	6.19974	ENSG00000137806	NDUFAF1
ENSG00000137807	10.5968	42.185	10.1175	22.9948	ENSG00000137807	KIF23
ENSG00000137809	0.305555	0.590814	0.967378	16.3069	ENSG00000137809	ITGA11
ENSG00000137812	3.50304	23.6982	3.15274	11.1973	ENSG00000137812	KNL1
ENSG00000137814	15.2272	12.8779	12.9097	11.6513	ENSG00000137814	HAUS2
ENSG00000137815	13.764	15.5952	16.319	18.137	ENSG00000137815	RTF1
ENSG00000137817	28.1821	40.0717	48.6904	37.2886	ENSG00000137817	PARP6
ENSG00000137818	193.923	117.526	214.862	141.031	ENSG00000137818	RPLP1
ENSG00000137819	1.38945	2.22354	3.59891	3.8983	ENSG00000137819	PAQR5
ENSG00000137821	8.53645	21.5561	24.6648	22.5868	ENSG00000137821	LRRC49
ENSG00000137822	16.7558	22.6556	22.9212	25.3297	ENSG00000137822	TUBGCP4
ENSG00000137824	17.4515	15.9851	15.0297	14.0011	ENSG00000137824	RMDN3
ENSG00000137825	0.30754	0.791957	0.451425	0.449685	ENSG00000137825	ITPKA
ENSG00000137831	17.0298	39.0062	22.5505	61.3851	ENSG00000137831	UACA
ENSG00000137834	1.07728	1.67998	0.977692	3.56321	ENSG00000137834	SMAD6
ENSG00000137841	0.647852	1.78158	1.52062	2.05364	ENSG00000137841	PLCB2
ENSG00000137842	17.4819	29.2238	18.1273	21.6194	ENSG00000137842	TMEM62
ENSG00000137843	8.96227	25.9552	18.5141	17.6979	ENSG00000137843	PAK6
ENSG00000137845	81.3067	112.943	75.7274	89.2058	ENSG00000137845	ADAM10
ENSG00000137857	85.3383	109.393	126.163	111.392	ENSG00000137857	DUOX1
ENSG00000137860	1.20833	2.24354	2.75379	3.7959	ENSG00000137860	SLC28A2
ENSG00000137868	8.4692	6.56621	4.49027	12.93	ENSG00000137868	STRA6
ENSG00000137869	0.98808	2.26245	2.36752	3.57879	ENSG00000137869	CYP19A1
ENSG00000137871	27.2159	52.8633	49.0176	77.0928	ENSG00000137871	ZNF280D
ENSG00000137872	5.86637	9.56541	10.5227	12.5366	ENSG00000137872	SEMA6D
ENSG00000137875	0.285719	0.229248	0.851589	0.0523991	ENSG00000137875	BCL2L10
ENSG00000137876	30.6976	44.8169	39.2404	24.7424	ENSG00000137876	RSL24D1
ENSG00000137877	4.41817	4.47677	4.19691	2.09508	ENSG00000137877	SPTBN5
ENSG00000137878	5.76855	5.41211	2.63541	2.51591	ENSG00000137878	GCOM1
ENSG00000137880	10.3877	7.77129	4.73507	2.70344	ENSG00000137880	GCHFR
ENSG00000137936	55.2766	77.3049	38.362	79.3631	ENSG00000137936	BCAR3
ENSG00000137941	5.04284	9.53143	6.24431	15.8989	ENSG00000137941	TTLL7
ENSG00000137942	11.7608	7.47244	9.16608	9.47981	ENSG00000137942	FNBP1L
ENSG00000137944	14.5174	15.9976	9.5032	8.97195	ENSG00000137944	KYAT3

ENSG00000137947	22.1027	11.524	10.5134	10.8354	ENSG00000137947	GTF2B
ENSG00000137948	5.45886	8.86193	6.95983	15.9218	ENSG00000137948	BRDT
ENSG00000137955	80.1578	107.778	112.272	75.1646	ENSG00000137955	RABGGTB
ENSG00000137959	5.00223	24.2328	30.069	32.221	ENSG00000137959	IFI44L
ENSG00000137960	0.411726	0.45454	0.392099	0.74472	ENSG00000137960	GIPC2
ENSG00000137962	58.9022	45.2596	32.5879	88.0682	ENSG00000137962	ARHGAP29
ENSG00000137965	21.0298	57.934	42.4263	53.8346	ENSG00000137965	IFI44
ENSG00000137968	5.46871	0.805267	11.811	1.24863	ENSG00000137968	SLC44A5
ENSG00000137970	1.4392	0	1.82822	0.753472	ENSG00000137970	RPL7P9
ENSG00000137975	67.1853	156.121	238.247	100.656	ENSG00000137975	CLCA2
ENSG00000137976	0.160388	0.154382	0.18604	0.175	ENSG00000137976	DNASE2B
ENSG00000137992	5.15697	7.6359	7.33683	6.36127	ENSG00000137992	DBT
ENSG00000137996	29.4223	34.415	27.121	25.2887	ENSG00000137996	RTCA
ENSG00000138002	13.0275	18.3032	12.5726	23.9203	ENSG00000138002	IFT172
ENSG00000138018	41.4733	46.2757	35.2388	19.1707	ENSG00000138018	SELENOI
ENSG00000138028	3.58321	6.72348	6.49079	3.23854	ENSG00000138028	CGREF1
ENSG00000138029	42.2078	57.9016	63.3378	32.6119	ENSG00000138029	HADHB
ENSG00000138030	0.131655	0.829281	0.232885	0.148776	ENSG00000138030	KHK
ENSG00000138031	26.1427	62.4346	36.127	43.1808	ENSG00000138031	ADCY3
ENSG00000138032	15.0573	16.2711	16.4282	17.4161	ENSG00000138032	PPM1B
ENSG00000138035	25.7643	34.4714	36.3706	38.5399	ENSG00000138035	PNPT1
ENSG00000138036	12.0632	19.4025	17.1648	18.2515	ENSG00000138036	DYNC2LI1
ENSG00000138039	2.22563	2.80542	2.89843	5.65292	ENSG00000138039	LHCGR
ENSG00000138041	16.3679	18.3534	22.7512	17.9761	ENSG00000138041	SMEK2
ENSG00000138050	8.27196	19.5503	15.4479	13.9003	ENSG00000138050	THUMPD2
ENSG00000138061	7.33847	2.84235	9.8442	5.81799	ENSG00000138061	CYP1B1
ENSG00000138068	0.0933638	0.448575	0.364605	0.100976	ENSG00000138068	SULT6B1
ENSG00000138069	73.1172	43.9592	48.7705	59.153	ENSG00000138069	RAB1A
ENSG00000138071	46.5421	35.6606	46.1035	61.8527	ENSG00000138071	ACTR2
ENSG00000138073	20.7428	18.7764	17.6267	13.762	ENSG00000138073	PREB
ENSG00000138074	17.4824	27.5494	26.17	14.1217	ENSG00000138074	SLC5A6
ENSG00000138075	0.254877	0.333576	0.388988	0.964108	ENSG00000138075	ABCG5
ENSG00000138078	22.1842	33.8228	28.6272	31.5907	ENSG00000138078	PREPL
ENSG00000138079	2.0082	5.83525	4.81539	6.5046	ENSG00000138079	SLC3A1
ENSG00000138080	0.653577	1.06237	1.06563	55.514	ENSG00000138080	EMILIN1
ENSG00000138081	25.2228	38.6533	33.7333	49.4337	ENSG00000138081	FBXO11
ENSG00000138083	0.498821	0.636963	0.493781	1.33262	ENSG00000138083	SIX3
ENSG00000138085	53.6636	71.086	46.0411	29.1272	ENSG00000138085	ATRAID
ENSG00000138092	4.17981	10.3066	4.69672	8.26586	ENSG00000138092	CENPO
ENSG00000138095	46.7948	62.7035	69.8577	56.513	ENSG00000138095	LRPPRC
ENSG00000138100	0.213528	0.738248	0.959583	1.26547	ENSG00000138100	TRIM54
ENSG00000138101	9.91443	23.9648	14.6221	23.2967	ENSG00000138101	DTNB
ENSG00000138107	70.8896	54.0816	45.4885	44.8581	ENSG00000138107	ACTR1A
ENSG00000138109	1.2886	2.81276	2.08768	6.90082	ENSG00000138109	CYP2C9
ENSG00000138111	7.63476	19.0326	11.2193	26.0742	ENSG00000138111	MFSD13A
ENSG00000138115	0.077804	0.140032	0.296757	0.159206	ENSG00000138115	CYP2C8
ENSG00000138119	95.7254	102.451	107.572	137.839	ENSG00000138119	MYOF
ENSG00000138131	0.593828	1.18825	0.78958	11.7271	ENSG00000138131	LOXL4
ENSG00000138134	2.24342	7.0882	2.04673	7.93073	ENSG00000138134	STAMBPL1
ENSG00000138135	0.0429039	0.0410033	0.185583	1.62985	ENSG00000138135	CH25H
ENSG00000138136	0.264914	0.433731	1.13016	0.938048	ENSG00000138136	LBX1
ENSG00000138138	52.9536	55.7931	47.7062	24.5091	ENSG00000138138	ATAD1
ENSG00000138152	0.727829	1.64664	0.870962	3.30563	ENSG00000138152	BTBD16
ENSG00000138160	3.26042	16.8305	2.30381	7.32756	ENSG00000138160	KIF11

ENSG00000138161	1.28712	1.20343	1.43946	0.833295	ENSG00000138161	CUZD1
ENSG00000138162	18.3041	30.3878	43.7947	41.6018	ENSG00000138162	TACC2
ENSG00000138166	35.5092	33.165	10.4047	33.2392	ENSG00000138166	DUSP5
ENSG00000138172	2.91221	5.1201	3.92769	4.10692	ENSG00000138172	CALHM2
ENSG00000138175	0.823475	2.2005	1.6361	1.92301	ENSG00000138175	ARL3
ENSG00000138180	5.35946	26.9287	2.77231	8.91019	ENSG00000138180	CEP55
ENSG00000138182	5.93864	25.752	5.07045	12.814	ENSG00000138182	KIF20B
ENSG00000138185	9.60502	18.7558	18.0459	31.4836	ENSG00000138185	ENTPD1
ENSG00000138190	6.2236	3.13655	2.91213	4.64154	ENSG00000138190	EXOC6
ENSG00000138193	5.02264	10.7492	10.7471	21.2115	ENSG00000138193	PLCE1
ENSG00000138207	0.158533	0	0.0496756	0.124533	ENSG00000138207	RBP4
ENSG00000138231	10.6152	8.66973	8.09962	11.886	ENSG00000138231	DBR1
ENSG00000138246	21.089	38.8846	28.2652	41.1313	ENSG00000138246	DNAJC13
ENSG00000138271	62.4134	42.7541	48.4477	8.62023	ENSG00000138271	GPR87
ENSG00000138279	63.8894	64.7011	57.2126	37.5863	ENSG00000138279	ANXA7
ENSG00000138286	8.3976	16.5825	14.4758	12.222	ENSG00000138286	FAM149B1
ENSG00000138293	40.5095	21.2091	21.6568	16.0782	ENSG00000138293	NCOA4
ENSG00000138294	3.66718	3.60987	4.02814	7.2244	ENSG00000138294	MSMB
ENSG00000138297	30.4784	23.8199	28.123	23.9398	ENSG00000138297	TIMM23
ENSG00000138303	17.2345	26.7031	25.6699	27.762	ENSG00000138303	ASCC1
ENSG00000138308	0.214293	0.0515666	0.0466059	0	ENSG00000138308	PLA2G12B
ENSG00000138311	12.7263	11.4034	9.51854	15.4643	ENSG00000138311	ZNF365
ENSG00000138315	0.117582	0.0453391	0.0409896	0.132636	ENSG00000138315	OIT3
ENSG00000138316	6.67284	0.699806	0.656883	8.20167	ENSG00000138316	ADAMTS14
ENSG00000138326	870.269	687.472	576.959	402.757	ENSG00000138326	RPS24
ENSG00000138336	0.374905	0.263526	0.436481	2.02811	ENSG00000138336	TET1
ENSG00000138346	6.10807	15.0546	10.6344	14.2042	ENSG00000138346	DNA2
ENSG00000138347	0.597949	0.838436	1.14807	2.89294	ENSG00000138347	MYPN
ENSG00000138356	1.53453	7.81795	5.10167	6.33815	ENSG00000138356	AOX1
ENSG00000138363	16.6064	31.5509	31.5445	44.7139	ENSG00000138363	ATIC
ENSG00000138375	10.3152	20.055	19.9876	30.1534	ENSG00000138375	SMARCAL1
ENSG00000138376	5.68173	14.0542	2.49566	4.97011	ENSG00000138376	BARD1
ENSG00000138378	0.75661	2.69802	6.19769	5.46957	ENSG00000138378	STAT4
ENSG00000138379	0.155832	0.320219	0.44245	0.408389	ENSG00000138379	MSTN
ENSG00000138380	5.32159	14.6121	19.1966	21.898	ENSG00000138380	CARF
ENSG00000138381	12.3215	9.91703	10.8202	8.22516	ENSG00000138381	ASNSD1
ENSG00000138382	36.5159	33.5653	28.6695	18.4729	ENSG00000138382	METTL5
ENSG00000138385	47.0647	52.3957	54.225	51.526	ENSG00000138385	SSB
ENSG00000138386	14.5216	25.3876	40.3239	29.4234	ENSG00000138386	NAB1
ENSG00000138395	0.534046	1.0331	1.51423	4.57033	ENSG00000138395	CDK15
ENSG00000138398	25.0385	23.0808	24.2759	24.2265	ENSG00000138398	PPIG
ENSG00000138399	12.9164	23.193	22.2758	20.5189	ENSG00000138399	FASTKD1
ENSG00000138400	2.09822	5.06914	3.95425	4.8086	ENSG00000138400	MDH1B
ENSG00000138411	1.46896	0.907141	1.84407	10.7363	ENSG00000138411	HECW2
ENSG00000138413	77.5026	54.9043	27.9466	42.6144	ENSG00000138413	IDH1
ENSG00000138430	52.4966	49.2703	54.5438	37.6269	ENSG00000138430	OLA1
ENSG00000138433	9.84991	16.0686	18.4274	24.3148	ENSG00000138433	CIR1
ENSG00000138434	114.111	94.2718	72.278	87.836	ENSG00000138434	SSFA2
ENSG00000138435	0.0398897	0.082376	0.138921	0.125044	ENSG00000138435	CHRNA1
ENSG00000138439	1.34626	2.21781	2.41738	2.63745	ENSG00000138439	FAM117B
ENSG00000138442	22.3246	30.4071	31.6454	16.5696	ENSG00000138442	WDR12
ENSG00000138443	10.6191	19.39	16.1866	26.1281	ENSG00000138443	ABI2
ENSG00000138448	64.861	122.803	227.239	90.0817	ENSG00000138448	ITGAV
ENSG00000138449	0.347578	0.121174	0.219887	0.583912	ENSG00000138449	SLC40A1

ENSG00000138459	17.0403	22.4748	15.9124	12.6977	ENSG00000138459	SLC35A5
ENSG00000138463	22.7264	20.8804	21.1087	8.95665	ENSG00000138463	DIRC2
ENSG00000138468	23.1272	44.0014	42.9648	78.3852	ENSG00000138468	SENP7
ENSG00000138472	0	0	0	0.118011	ENSG00000138472	GUCA1C
ENSG00000138483	0	0	0.0398011	0.199927	ENSG00000138483	CCDC54
ENSG00000138495	22.9451	20.1291	16.7651	24.7799	ENSG00000138495	COX17
ENSG00000138496	13.7858	17.2319	12.2304	20.2624	ENSG00000138496	PARP9
ENSG00000138587	3.97646	3.84392	5.47701	8.26497	ENSG00000138587	MNS1
ENSG00000138592	27.4978	33.1418	36.4574	39.2529	ENSG00000138592	USP8
ENSG00000138593	49.8378	83.1348	73.8392	128.37	ENSG00000138593	SECISBP2L
ENSG00000138594	190.574	112.44	79.9416	108.289	ENSG00000138594	TMOD3
ENSG00000138600	66.0345	55.2119	36.6058	32.4031	ENSG00000138600	SPPL2A
ENSG00000138604	16.5507	18.6448	12.0884	14.1497	ENSG00000138604	GLCE
ENSG00000138606	14.7197	6.50815	7.60944	9.27289	ENSG00000138606	SHF
ENSG00000138613	8.90507	8.64065	7.38174	6.98398	ENSG00000138613	APH1B
ENSG00000138614	18.7783	23.5148	21.0581	14.3878	ENSG00000138614	INTS14
ENSG00000138615	0.181131	0.326183	0.115841	0.425538	ENSG00000138615	CILP
ENSG00000138617	2.71298	4.15648	3.56228	4.13194	ENSG00000138617	PARP16
ENSG00000138621	6.64875	13.2031	10.6781	15.2287	ENSG00000138621	PPCDC
ENSG00000138622	2.897	1.11697	0.930861	1.88963	ENSG00000138622	HCN4
ENSG00000138623	49.4718	25.5385	4.5272	56.2944	ENSG00000138623	SEMA7A
ENSG00000138629	11.5977	10.671	8.73263	6.11795	ENSG00000138629	UBL7
ENSG00000138639	2.7502	5.86635	4.88919	34.022	ENSG00000138639	ARHGAP24
ENSG00000138640	9.28347	13.4482	13.2164	22.5219	ENSG00000138640	FAM13A
ENSG00000138641	50.0187	40.8948	21.3374	39.8173	ENSG00000138641	HERC3
ENSG00000138642	12.6514	20.0591	16.3521	14.5426	ENSG00000138642	HERC6
ENSG00000138646	1.60639	4.32526	5.14458	4.80808	ENSG00000138646	HERC5
ENSG00000138650	0.99763	1.44828	1.17626	3.99545	ENSG00000138650	PCDH10
ENSG00000138653	0.0808862	0.271807	0.322203	0.269383	ENSG00000138653	NDST4
ENSG00000138658	4.89127	11.957	6.67843	16.2402	ENSG00000138658	ZGRF1
ENSG00000138660	12.8139	13.3983	12.7504	8.55902	ENSG00000138660	AP1AR
ENSG00000138663	18.3576	17.5789	14.9136	13.7033	ENSG00000138663	COPS4
ENSG00000138668	24.0229	44.3249	39.2818	56.8675	ENSG00000138668	HNRNPD
ENSG00000138669	1.68336	2.45976	1.61088	1.38476	ENSG00000138669	PRKG2
ENSG00000138670	10.6271	12.8679	9.83019	18.63	ENSG00000138670	RASGEF1B
ENSG00000138674	141.137	153.892	146.276	210.842	ENSG00000138674	SEC31A
ENSG00000138675	3.03048	3.80805	2.79867	10.2718	ENSG00000138675	FGF5
ENSG00000138678	38.812	7.70162	1.65181	3.10702	ENSG00000138678	GPAT3
ENSG00000138684	0	0	0	0	ENSG00000138684	IL21
ENSG00000138685	1.32602	1.53449	2.33852	15.9821	ENSG00000138685	FGF2
ENSG00000138686	12.4404	19.4666	14.264	9.56528	ENSG00000138686	BBS7
ENSG00000138688	35.6356	57.7183	43.746	44.8549	ENSG00000138688	KIAA1109
ENSG00000138696	0.847736	0.427482	1.57922	1.17119	ENSG00000138696	BMPR1B
ENSG00000138698	41.9641	57.172	34.2255	38.7554	ENSG00000138698	RAP1GDS1
ENSG00000138709	14.0454	15.655	12.5932	12.6984	ENSG00000138709	LARP1B
ENSG00000138722	0.206087	0.157592	0.170648	0.243802	ENSG00000138722	MMRN1
ENSG00000138735	9.52504	20.0391	12.0572	21.3377	ENSG00000138735	PDE5A
ENSG00000138738	14.8328	39.611	36.9358	65.1912	ENSG00000138738	PRDM5
ENSG00000138741	0.491186	0.789472	0.622478	1.5573	ENSG00000138741	TRPC3
ENSG00000138744	14.6519	12.946	10.4103	14.171	ENSG00000138744	NAAA
ENSG00000138750	23.8331	38.1048	32.0653	37.2524	ENSG00000138750	NUP54
ENSG00000138755	0	0.0193776	0.140154	0.154653	ENSG00000138755	CXCL9
ENSG00000138756	22.8312	20.869	27.5896	30.0047	ENSG00000138756	BMP2K
ENSG00000138757	53.1733	48.0795	41.9091	45.866	ENSG00000138757	G3BP2

ENSG00000138758	28.5918	39.8692	40.8249	150.047	ENSG00000138758	SEPT11
ENSG00000138759	17.3488	27.9431	30.8131	20.2817	ENSG00000138759	FRAS1
ENSG00000138760	46.1692	77.7437	72.2852	52.6765	ENSG00000138760	SCARB2
ENSG00000138764	51.554	45.7757	25.3796	40.2135	ENSG00000138764	CCNG2
ENSG00000138767	7.75093	11.3593	11.417	9.83241	ENSG00000138767	CNOT6L
ENSG00000138768	118.561	112.208	86.44	97.5705	ENSG00000138768	USO1
ENSG00000138769	0.378038	1.11547	0.784041	0.701139	ENSG00000138769	CDKL2
ENSG00000138771	14.7546	10.5964	5.05458	13.5327	ENSG00000138771	SHROOM3
ENSG00000138772	400.562	229.29	129.868	105.567	ENSG00000138772	ANXA3
ENSG00000138777	51.6557	65.6601	45.8191	42.619	ENSG00000138777	PPA2
ENSG00000138778	6.50926	28.5298	3.06436	12.588	ENSG00000138778	CENPE
ENSG00000138780	7.92117	16.1657	8.65006	10.2504	ENSG00000138780	GSTCD
ENSG00000138785	5.3333	12.3643	15.6686	12.5281	ENSG00000138785	INTS12
ENSG00000138792	1.2039	1.77144	2.00053	2.1261	ENSG00000138792	ENPEP
ENSG00000138794	14.2713	11.6546	9.5803	11.8859	ENSG00000138794	CASP6
ENSG00000138795	2.17933	2.33331	1.75763	6.60951	ENSG00000138795	LEF1
ENSG00000138796	6.09748	11.129	12.2842	6.26264	ENSG00000138796	HADH
ENSG00000138798	2.66841	0.990413	1.09269	0.64047	ENSG00000138798	EGF
ENSG00000138801	31.5514	34.7083	33.1557	36.9519	ENSG00000138801	PAPSS1
ENSG00000138802	16.9272	16.9644	13.7743	15.4406	ENSG00000138802	SEC24B
ENSG00000138813	2.31978	3.10786	2.43975	4.157	ENSG00000138813	C4orf17
ENSG00000138814	43.2686	35.2981	38.1694	37.2458	ENSG00000138814	PPP3CA
ENSG00000138821	20.2574	8.81414	6.79855	14.6067	ENSG00000138821	SLC39A8
ENSG00000138823	0.606911	3.57491	0.939484	3.81616	ENSG00000138823	MTTP
ENSG00000138829	29.2958	111.303	50.3611	208.612	ENSG00000138829	FBN2
ENSG00000138834	74.56	44.4621	77.189	69.0564	ENSG00000138834	MAPK8IP3
ENSG00000138835	12.1407	35.1957	28.5845	30.1066	ENSG00000138835	RGS3
ENSG00000138867	23.8634	18.2214	17.3444	13.7163	ENSG00000138867	GUCD1
ENSG00000138892	0.10999	0.149374	0.0776625	0.0954847	ENSG00000138892	TTLL8
ENSG00000138942	14.1779	9.71379	17.2693	10.3836	ENSG00000138942	RNF185
ENSG00000138944	0.311118	0.547975	0.601001	0.590058	ENSG00000138944	KIAA1644
ENSG00000138964	1.84142	2.21181	2.84894	3.04872	ENSG00000138964	PARVG
ENSG00000139044	37.9517	8.00255	16.5089	10.2382	ENSG00000139044	B4GALNT3
ENSG00000139053	0	0	0.0766565	0	ENSG00000139053	PDE6H
ENSG00000139055	0.507938	0.860212	0.71154	0.708147	ENSG00000139055	ERP27
ENSG00000139083	4.5998	7.35936	11.0321	11.7706	ENSG00000139083	ETV6
ENSG00000139112	11.268	9.39585	15.3895	8.11803	ENSG00000139112	GABARAPL1
ENSG00000139116	25.7994	28.1546	28.2458	23.577	ENSG00000139116	KIF21A
ENSG00000139117	8.27116	23.3956	11.6635	16.9129	ENSG00000139117	CPNE8
ENSG00000139131	16.1705	18.9397	15.4083	11.2562	ENSG00000139131	YARS2
ENSG00000139132	24.3877	28.0011	17.1304	20.9976	ENSG00000139132	FGD4
ENSG00000139133	8.36463	16.7873	10.0789	7.71619	ENSG00000139133	ALG10
ENSG00000139144	1.12846	8.61773	8.5298	5.63614	ENSG00000139144	PIK3C2G
ENSG00000139146	34.2157	38.8919	44.4219	26.2237	ENSG00000139146	FAM60A
ENSG00000139151	2.51978	2.54088	3.48779	4.96967	ENSG00000139151	PLCZ1
ENSG00000139154	16.5077	30.1131	30.0245	37.4358	ENSG00000139154	AEBP2
ENSG00000139155	1.71074	2.86398	2.94514	6.0407	ENSG00000139155	SLCO1C1
ENSG00000139160	1.78167	4.43205	3.88745	5.53537	ENSG00000139160	ETFBKMT
ENSG00000139163	40.6293	35.7471	32.3041	41.7435	ENSG00000139163	ETNK1
ENSG00000139168	35.012	29.2199	25.1981	24.9957	ENSG00000139168	ZCRB1
ENSG00000139173	29.1453	17.913	11.5273	10.0175	ENSG00000139173	TMEM117
ENSG00000139174	6.85069	5.0039	7.1854	4.50431	ENSG00000139174	PRICKLE1
ENSG00000139178	19.5561	28.2489	53.7512	25.6283	ENSG00000139178	C1RL
ENSG00000139180	41.2354	63.0253	37.6519	32.799	ENSG00000139180	NDUFA9

ENSG00000139182	17.6463	26.4242	39.7425	26.243	ENSG00000139182	CLSTN3
ENSG00000139187	1.16151	2.15286	1.65554	3.98561	ENSG00000139187	KLRG1
ENSG00000139190	2.15168	3.05047	2.17552	3.89748	ENSG00000139190	VAMP1
ENSG00000139192	4.66677	10.6208	8.67949	5.77883	ENSG00000139192	TAPBPL
ENSG00000139193	1.05478	3.79327	3.64312	2.31935	ENSG00000139193	CD27
ENSG00000139194	6.25966	11.509	16.4038	18.4204	ENSG00000139194	RBP5
ENSG00000139197	9.82534	11.6127	16.9547	10.4331	ENSG00000139197	PEX5
ENSG00000139200	0.388643	0.691526	1.26914	1.28958	ENSG00000139200	PIANP
ENSG00000139209	1.04801	2.08752	2.18275	3.78016	ENSG00000139209	SLC38A4
ENSG00000139211	23.0861	36.9449	88.8304	24.2661	ENSG00000139211	AMIGO2
ENSG00000139218	73.3026	114.049	115.04	147.695	ENSG00000139218	SCAF11
ENSG00000139219	0.386523	0.594545	0.215039	1.04339	ENSG00000139219	COL2A1
ENSG00000139220	0.299072	1.50313	0.649693	2.38008	ENSG00000139220	PPFIA2
ENSG00000139223	0	0.20754	0	0.229641	ENSG00000139223	ANP32D
ENSG00000139233	16.8534	11.8688	14.3799	14.6412	ENSG00000139233	LLPH
ENSG00000139239	0.364151	0.523881	0.889984	1.05064	ENSG00000139239	RPL14P1
ENSG00000139263	17.9485	54.4113	49.9465	23.6368	ENSG00000139263	LRIG3
ENSG00000139266	9.95383	15.8507	15.829	15.1581	ENSG00000139266	MARCH9
ENSG00000139269	0.410005	1.55368	3.20305	1.56681	ENSG00000139269	INHBE
ENSG00000139278	9.414	7.34015	6.66392	9.82574	ENSG00000139278	GLIPR1
ENSG00000139287	9.85216	17.9728	18.4394	30.407	ENSG00000139287	TPH2
ENSG00000139289	78.4017	78.9209	82.4612	62.8563	ENSG00000139289	PHLDA1
ENSG00000139291	15.3324	15.2074	9.66267	10.1588	ENSG00000139291	TMEM19
ENSG00000139292	0.0933795	0.190637	0.505608	0.0384906	ENSG00000139292	LGR5
ENSG00000139304	0.505645	2.52598	1.28717	5.63198	ENSG00000139304	PTPRQ
ENSG00000139318	121.582	142.046	47.9541	76.6898	ENSG00000139318	DUSP6
ENSG00000139323	13.0667	23.7098	18.4425	24.5338	ENSG00000139323	POC1B
ENSG00000139324	40.4795	48.5427	35.1575	28.1891	ENSG00000139324	TMTC3
ENSG00000139329	2.43755	0.0703864	0.668019	72.2176	ENSG00000139329	LUM
ENSG00000139330	0	0.049995	0.0679503	0.116061	ENSG00000139330	KERA
ENSG00000139343	10.4645	14.3406	14.4149	14.5728	ENSG00000139343	SNRPF
ENSG00000139344	14.8471	23.5385	27.862	43.4254	ENSG00000139344	AMDHD1
ENSG00000139350	11.7732	23.1484	20.0784	15.1434	ENSG00000139350	NEDD1
ENSG00000139351	0.585806	1.32034	1.52982	2.83641	ENSG00000139351	SYCP3
ENSG00000139352	0.340274	0.230237	0.498962	0.744539	ENSG00000139352	ASCL1
ENSG00000139354	3.53158	19.7124	2.73041	7.67127	ENSG00000139354	GAS2L3
ENSG00000139364	1.19249	3.30267	3.04499	30.3693	ENSG00000139364	TMEM132B
ENSG00000139370	28.4498	37.2628	30.2647	24.2209	ENSG00000139370	SLC15A4
ENSG00000139372	26.0709	24.5437	30.2686	29.8032	ENSG00000139372	TDG
ENSG00000139405	6.09292	3.64525	5.67952	4.84759	ENSG00000139405	RITA1
ENSG00000139410	1.14353	2.15904	3.77199	1.62582	ENSG00000139410	SDSL
ENSG00000139428	26.4388	34.8952	22.8048	29.6609	ENSG00000139428	MMAB
ENSG00000139433	213.594	42.4979	44.6748	40.6616	ENSG00000139433	GLTP
ENSG00000139436	21.4368	29.7419	25.0658	31.9688	ENSG00000139436	GIT2
ENSG00000139437	15.7067	14.3056	15.1729	16.2771	ENSG00000139437	TCHP
ENSG00000139438	0.744531	0.0831957	0.103505	0.440209	ENSG00000139438	FAM222A
ENSG00000139445	0.111653	0.210957	0.0985758	0.175975	ENSG00000139445	FOXN4
ENSG00000139496	41.179	44.5987	45.0299	37.5811	ENSG00000139496	NUP58
ENSG00000139505	16.9334	16.4803	12.5324	10.1751	ENSG00000139505	MTMR6
ENSG00000139508	7.94216	4.61022	2.6362	6.61377	ENSG00000139508	SLC46A3
ENSG00000139514	44.0317	80.7735	78.6187	41.1958	ENSG00000139514	SLC7A1
ENSG00000139515	0.310099	0.371131	0.272591	1.51372	ENSG00000139515	PDX1
ENSG00000139517	9.44498	8.82508	9.74384	6.28737	ENSG00000139517	LNX2
ENSG00000139531	15.8847	20.3577	16.5779	23.5572	ENSG00000139531	SUOX

ENSG00000139537	2.59297	3.13157	3.48412	4.15115	ENSG00000139537	CCDC65
ENSG00000139540	1.80157	2.23143	2.19653	3.19729	ENSG00000139540	SLC39A5
ENSG00000139546	18.5462	21.0921	21.4765	13.2043	ENSG00000139546	TARBP2
ENSG00000139547	2.46806	6.24315	6.33077	9.86788	ENSG00000139547	RDH16
ENSG00000139549	0.0291974	0.14069	0.0508745	0.352335	ENSG00000139549	DHH
ENSG00000139567	1.04915	4.23146	3.51191	11.5798	ENSG00000139567	ACVRL1
ENSG00000139572	0.0387856	0	0.101314	0.169831	ENSG00000139572	GPR84
ENSG00000139574	0.151742	0	0	0	ENSG00000139574	NPFF
ENSG00000139579	11.1973	10.7085	10.0808	9.37934	ENSG00000139579	NABP2
ENSG00000139597	2.18032	3.5481	5.08205	4.12445	ENSG00000139597	N4BP2L1
ENSG00000139610	0.132628	0.190202	0	0	ENSG00000139610	CELA1
ENSG00000139613	21.4363	39.1898	31.8874	46.6271	ENSG00000139613	SMARCC2
ENSG00000139618	5.52536	19.197	10.0637	15.239	ENSG00000139618	BRCA2
ENSG00000139620	28.0442	29.0427	24.4848	19.3336	ENSG00000139620	KANSL2
ENSG00000139624	45.2159	95.7478	68.2061	124.124	ENSG00000139624	CERS5
ENSG00000139625	6.28021	25.3742	34.279	33.9307	ENSG00000139625	MAP3K12
ENSG00000139626	8.2207	7.48254	9.04919	3.18382	ENSG00000139626	ITGB7
ENSG00000139629	49.2207	48.4703	60.7403	48.7825	ENSG00000139629	GALNT6
ENSG00000139631	18.1461	31.0758	37.3868	45.1297	ENSG00000139631	CSAD
ENSG00000139636	38.1824	45.9387	45.3643	39.5892	ENSG00000139636	LMBR1L
ENSG00000139637	16.0515	18.6694	13.6685	14.649	ENSG00000139637	C12orf10
ENSG00000139641	91.4869	132.826	89.2096	66.6378	ENSG00000139641	ESYT1
ENSG00000139644	469.915	496.692	297.604	168.598	ENSG00000139644	TMBIM6
ENSG00000139645	19.5355	13.2135	19.4695	18.1695	ENSG00000139645	ANKRD52
ENSG00000139648	0.0246348	0.0237455	0	0	ENSG00000139648	KRT71
ENSG00000139651	10.1851	12.7244	15.8345	9.47601	ENSG00000139651	ZNF740
ENSG00000139656	0.0783088	0.150563	0.13603	0	ENSG00000139656	SMIM2
ENSG00000139668	23.531	37.8576	35.1269	44.1419	ENSG00000139668	WDFY2
ENSG00000139675	2.49421	4.60655	5.69536	3.99576	ENSG00000139675	HNRNPA1L2
ENSG00000139679	13.1085	24.1787	18.4339	20.8629	ENSG00000139679	LPAR6
ENSG00000139684	31.4994	44.0446	28.425	26.4142	ENSG00000139684	ESD
ENSG00000139687	11.7819	18.8533	15.7787	16.4594	ENSG00000139687	RB1
ENSG00000139697	18.0918	16.5364	12.9386	17.5627	ENSG00000139697	SBNO1
ENSG00000139714	0.466241	0.88347	0.892285	0.969875	ENSG00000139714	MORN3
ENSG00000139718	4.88036	5.1569	7.0601	6.68306	ENSG00000139718	SETD1B
ENSG00000139719	9.94731	8.52192	9.11691	10.4392	ENSG00000139719	VPS33A
ENSG00000139722	47.895	36.3402	30.5718	33.358	ENSG00000139722	VPS37B
ENSG00000139725	7.35036	11.2201	10.1233	9.66603	ENSG00000139725	RHOF
ENSG00000139726	26.8014	25.0322	27.952	28.713	ENSG00000139726	DENR
ENSG00000139734	2.19512	12.9371	2.28116	11.0756	ENSG00000139734	DIAPH3
ENSG00000139737	0.512659	0.564698	0.309258	0.541979	ENSG00000139737	SLAIN1
ENSG00000139746	21.4596	33.2386	31.1035	32.1488	ENSG00000139746	RBM26
ENSG00000139767	0.171393	0.699768	1.19759	1.73859	ENSG00000139767	SRRM4
ENSG00000139780	0.111766	0.161351	0.145825	0.121882	ENSG00000139780	METTL21C
ENSG00000139793	21.5272	15.5468	19.3081	14.8013	ENSG00000139793	MBNL2
ENSG00000139797	0.50473	0.786436	1.34287	3.13794	ENSG00000139797	RNF113B
ENSG00000139800	0.373638	0.621299	0.508884	0.978175	ENSG00000139800	ZIC5
ENSG00000139826	6.1605	5.19539	6.08428	4.3716	ENSG00000139826	ABHD13
ENSG00000139832	0.423435	1.97158	1.60525	0.676713	ENSG00000139832	RAB20
ENSG00000139835	6.49642	8.27051	8.06061	4.61087	ENSG00000139835	GRTP1
ENSG00000139842	31.7752	36.6573	39.4244	32.5325	ENSG00000139842	CUL4A
ENSG00000139865	11.06	25.2462	20.5965	37.2594	ENSG00000139865	TTC6
ENSG00000139874	0.101681	0.12102	0.0657014	0.649826	ENSG00000139874	SSTR1
ENSG00000139880	3.58422	6.61945	4.60254	4.66808	ENSG00000139880	CDH24

ENSG00000139890	0.309278	0.817671	0.544958	0.225856	ENSG00000139890	REM2
ENSG00000139899	2.40016	3.3849	2.24558	2.57046	ENSG00000139899	CBLN3
ENSG00000139908	2.48573	6.06765	6.17914	5.24894	ENSG00000139908	TSSK4
ENSG00000139910	0.771687	2.53761	1.2449	7.52004	ENSG00000139910	NOVA1
ENSG00000139914	0.162	0.0778583	0.284188	0.175657	ENSG00000139914	FITM1
ENSG00000139915	0.383446	1.5117	1.3201	1.64588	ENSG00000139915	MDGA2
ENSG00000139921	33.9901	40.5181	23.1126	16.8198	ENSG00000139921	TMX1
ENSG00000139926	129.442	145.069	165.31	291.275	ENSG00000139926	FRMD6
ENSG00000139946	0.30109	0.221161	0.452755	6.84274	ENSG00000139946	PELI2
ENSG00000139970	0.130122	0.297102	0.234399	0.397438	ENSG00000139970	RTN1
ENSG00000139971	12.9134	18.501	17.4823	22.8054	ENSG00000139971	C14orf37
ENSG00000139973	0.228297	0.151611	0.0425603	0.279791	ENSG00000139973	SYT16
ENSG00000139974	31.3286	81.9555	75.5146	206.709	ENSG00000139974	SLC38A6
ENSG00000139977	8.7198	7.88345	10.6791	5.9384	ENSG00000139977	NAA30
ENSG00000139985	0.560463	0.660719	0.656198	0.563266	ENSG00000139985	ADAM21
ENSG00000139988	0.988367	4.69802	4.31932	0.581817	ENSG00000139988	RDH12
ENSG00000139990	20.0345	18.2163	20.6906	19.4814	ENSG00000139990	DCAF5
ENSG00000139998	2.14825	2.38093	2.63955	3.75192	ENSG00000139998	RAB15
ENSG00000140006	7.6429	10.0652	9.26586	8.33583	ENSG00000140006	WDR89
ENSG00000140009	2.38998	5.62696	4.67404	7.34226	ENSG00000140009	ESR2
ENSG00000140015	0.433532	0.360532	0.525819	0.516522	ENSG00000140015	KCNH5
ENSG00000140022	93.5116	88.3087	152.073	83.1483	ENSG00000140022	STON2
ENSG00000140025	7.76214	19.9223	14.7337	31.8182	ENSG00000140025	EFCAB11
ENSG00000140030	0.0637825	0.0618961	0	0.700405	ENSG00000140030	GPR65
ENSG00000140043	6.46896	15.3363	14.1418	20.8202	ENSG00000140043	PTGR2
ENSG00000140044	3.7818	27.1607	19.1671	17.5565	ENSG00000140044	JDP2
ENSG00000140057	4.88496	10.9413	10.6433	20.9183	ENSG00000140057	AK7
ENSG00000140067	0.304051	0.292359	0.180979	0.114242	ENSG00000140067	FAM181A
ENSG00000140090	0.308567	0.850804	0.783828	0.751963	ENSG00000140090	SLC24A4
ENSG00000140092	2.32959	3.07562	3.94026	27.9523	ENSG00000140092	FBLN5
ENSG00000140093	3.02319	8.83985	8.61836	10.2081	ENSG00000140093	SERPINA10
ENSG00000140104	10.477	11.8771	19.3761	10.8547	ENSG00000140104	C14orf79
ENSG00000140105	46.4598	77.7307	93.4909	40.2194	ENSG00000140105	WARS
ENSG00000140107	0.0745059	0.0949897	0.0648793	0	ENSG00000140107	SLC25A47
ENSG00000140153	19.2597	22.1751	22.631	36.8831	ENSG00000140153	WDR20
ENSG00000140157	57.1811	44.2948	28.8604	22.3429	ENSG00000140157	NIPA2
ENSG00000140181	23.5716	32.369	36.4129	51.7086	ENSG00000140181	HERC2P2
ENSG00000140199	21.7011	15.7306	10.0694	12.3896	ENSG00000140199	SLC12A6
ENSG00000140254	66.6114	35.7187	41.1428	15.1323	ENSG00000140254	DUOXA1
ENSG00000140259	14.8888	7.97307	9.82089	8.04239	ENSG00000140259	MFAP1
ENSG00000140262	48.7767	75.9878	62.0826	88.8499	ENSG00000140262	TCF12
ENSG00000140263	10.9911	14.6125	11.1148	9.10101	ENSG00000140263	SORD
ENSG00000140264	193.972	163.868	128.304	154.249	ENSG00000140264	SERF2
ENSG00000140265	16.6764	22.8473	28.4654	14.7782	ENSG00000140265	ZSCAN29
ENSG00000140274	1.18242	0.757662	1.9423	1.4397	ENSG00000140274	DUOXA2
ENSG00000140279	1.0635	1.38018	2.07579	1.47854	ENSG00000140279	DUOX2
ENSG00000140280	3.28707	2.43028	1.75644	1.27863	ENSG00000140280	LYSMD2
ENSG00000140284	2.41746	0.519351	0.314928	0.335625	ENSG00000140284	SLC27A2
ENSG00000140285	0.648426	1.15162	1.07693	12.2285	ENSG00000140285	FGF7
ENSG00000140287	0.283569	0.0392878	0.116386	0.0845502	ENSG00000140287	HDC
ENSG00000140297	6.86613	2.80297	2.44993	2.64199	ENSG00000140297	GCNT3
ENSG00000140299	50.9141	51.2571	51.4394	44.6628	ENSG00000140299	BNIP2
ENSG00000140307	46.6596	29.5191	26.4172	25.985	ENSG00000140307	GTF2A2
ENSG00000140319	58.285	28.548	35.7076	43.006	ENSG00000140319	SRP14

ENSG00000140320	10.4635	8.08452	8.82781	8.56603	ENSG00000140320	BAHD1
ENSG00000140323	1.08653	2.18784	6.2312	0.462459	ENSG00000140323	DISP2
ENSG00000140326	8.72215	9.53635	6.8141	8.97712	ENSG00000140326	CDAN1
ENSG00000140332	21.2778	27.6085	32.5557	28.0117	ENSG00000140332	TLE3
ENSG00000140350	31.1461	36.3312	39.9247	33.8038	ENSG00000140350	ANP32A
ENSG00000140365	33.1621	36.534	28.7408	34.189	ENSG00000140365	COMMD4
ENSG00000140367	17.6964	16.3017	18.4823	16.8662	ENSG00000140367	UBE2Q2
ENSG00000140368	2.84322	9.92794	11.2047	9.61783	ENSG00000140368	PSTPIP1
ENSG00000140374	60.6452	62.1181	51.3207	41.7017	ENSG00000140374	ETFA
ENSG00000140379	0.569918	0.634738	0.161235	0.970954	ENSG00000140379	BCL2A1
ENSG00000140382	14.9786	18.3516	19.9721	18.8214	ENSG00000140382	HMG20A
ENSG00000140386	7.27463	15.9848	12.6769	23.9244	ENSG00000140386	SCAPER
ENSG00000140391	92.4251	81.4253	57.5228	38.1178	ENSG00000140391	TSPAN3
ENSG00000140395	28.8479	28.8553	35.9013	22.753	ENSG00000140395	WDR61
ENSG00000140396	12.9195	14.9599	21.9772	17.2082	ENSG00000140396	NCOA2
ENSG00000140398	24.1083	29.1788	27.9346	23.5219	ENSG00000140398	NEIL1
ENSG00000140400	128.622	133.764	156.341	106.64	ENSG00000140400	MAN2C1
ENSG00000140403	8.45133	5.32194	7.46856	5.81423	ENSG00000140403	DNAJA4
ENSG00000140406	9.7575	12.4309	8.57025	8.10287	ENSG00000140406	TLNRD1
ENSG00000140416	135.237	66.2938	173.264	348.967	ENSG00000140416	TPM1
ENSG00000140443	50.5021	67.717	69.9114	90.7266	ENSG00000140443	IGF1R
ENSG00000140450	40.1193	25.4392	110.036	33.6367	ENSG00000140450	ARRDC4
ENSG00000140451	6.10349	37.77	7.72736	21.6599	ENSG00000140451	PIF1
ENSG00000140455	18.2236	36.8126	40.3439	35.0559	ENSG00000140455	USP3
ENSG00000140459	3.47366	4.26756	2.826	5.09695	ENSG00000140459	CYP11A1
ENSG00000140463	7.26543	16.4559	14.7542	13.5813	ENSG00000140463	BBS4
ENSG00000140464	24.6219	36.7141	29.317	45.8218	ENSG00000140464	PML
ENSG00000140465	35.07	4.07925	4.58797	6.13987	ENSG00000140465	CYP1A1
ENSG00000140470	3.08842	1.25585	1.11363	1.54529	ENSG00000140470	ADAMTS17
ENSG00000140471	14.9728	19.7398	21.8335	18.0937	ENSG00000140471	LINS1
ENSG00000140474	16.4604	15.4549	14.9902	10.2107	ENSG00000140474	ULK3
ENSG00000140478	0	0	0	0	ENSG00000140478	GOLGA6D
ENSG00000140479	12.6412	21.9525	21.9318	35.8203	ENSG00000140479	PCSK6
ENSG00000140481	0.508123	0.122469	0.109824	0.175478	ENSG00000140481	CCDC33
ENSG00000140488	0.594316	0.495753	0.79771	4.23299	ENSG00000140488	CELF6
ENSG00000140497	47.3423	32.2086	23.994	17.8664	ENSG00000140497	SCAMP2
ENSG00000140505	1.49176	2.92241	2.85802	5.81463	ENSG00000140505	CYP1A2
ENSG00000140506	0.842204	1.1957	0.614351	0.971404	ENSG00000140506	LMAN1L
ENSG00000140511	4.62198	8.50344	6.74391	10.1442	ENSG00000140511	HAPLN3
ENSG00000140519	297.331	29.8063	36.5894	35.8855	ENSG00000140519	RHCG
ENSG00000140521	50.3586	64.9813	54.3522	47.7296	ENSG00000140521	POLG
ENSG00000140522	3.80274	4.62089	4.31963	2.79538	ENSG00000140522	RLBP1
ENSG00000140525	11.5844	32.4056	7.8496	20.6771	ENSG00000140525	FANCI
ENSG00000140526	32.3259	35.7484	15.4521	25.9285	ENSG00000140526	ABHD2
ENSG00000140527	1.897	4.89021	3.24444	8.0138	ENSG00000140527	WDR93
ENSG00000140534	2.39378	8.93244	3.96042	8.83487	ENSG00000140534	TICRR
ENSG00000140538	0.53446	2.09164	1.06872	4.41713	ENSG00000140538	NTRK3
ENSG00000140543	5.60306	5.60163	4.20301	3.40841	ENSG00000140543	DET1
ENSG00000140545	74.6752	62.0268	111.057	117.852	ENSG00000140545	MFGE8
ENSG00000140548	19.2884	17.8882	15.2802	19.736	ENSG00000140548	ZNF710
ENSG00000140553	27.7543	31.6507	29.7959	33.0157	ENSG00000140553	UNC45A
ENSG00000140557	0.168267	0.393757	0.389256	2.69028	ENSG00000140557	ST8SIA2
ENSG00000140563	10.2192	25.7942	15.4553	12.2093	ENSG00000140563	MCTP2
ENSG00000140564	103.183	81.6439	37.6641	44.8996	ENSG00000140564	FURIN

ENSG00000140575	191.143	274.26	171.781	184.143	ENSG00000140575	IQGAP1
ENSG00000140577	8.42977	12.152	14.9357	24.5982	ENSG00000140577	CRTC3
ENSG00000140598	24.4861	35.4648	24.7139	33.1156	ENSG00000140598	EFL1
ENSG00000140600	1.23023	0.613081	1.01398	8.70125	ENSG00000140600	SH3GL3
ENSG00000140612	79.2338	94.4924	62.0842	56.2205	ENSG00000140612	SEC11A
ENSG00000140623	0.558519	0.586337	0.412974	0.496085	ENSG00000140623	SEPT12
ENSG00000140632	26.4457	31.0451	33.6005	34.4174	ENSG00000140632	GLYR1
ENSG00000140650	37.2068	36.5766	44.6678	48.1558	ENSG00000140650	PMM2
ENSG00000140675	0.874999	1.44989	1.59746	1.67641	ENSG00000140675	SLC5A2
ENSG00000140678	3.01234	3.95512	3.50736	4.82118	ENSG00000140678	ITGAX
ENSG00000140682	4.38252	9.31377	9.80663	15.6447	ENSG00000140682	TGFB1I1
ENSG00000140688	29.7072	36.4899	32.3082	23.6565	ENSG00000140688	C16orf58
ENSG00000140691	9.00013	11.508	20.6405	13.2097	ENSG00000140691	ARMC5
ENSG00000140694	23.3622	37.3824	36.2466	36.3296	ENSG00000140694	PARN
ENSG00000140718	12.4954	17.59	18.9418	23.5203	ENSG00000140718	FTO
ENSG00000140740	87.5081	84.2601	75.0374	66.734	ENSG00000140740	UQCRC2
ENSG00000140743	9.0572	11.5704	10.4829	16.1574	ENSG00000140743	CDR2
ENSG00000140749	2.40256	4.7208	4.10672	7.77913	ENSG00000140749	IGSF6
ENSG00000140750	26.7346	36.0619	49.8368	104.454	ENSG00000140750	ARHGAP17
ENSG00000140795	6.24262	14.2421	14.0401	29.5843	ENSG00000140795	MYLK3
ENSG00000140798	0.186678	0.779368	0.469389	1.79538	ENSG00000140798	ABCC12
ENSG00000140807	0.651388	0.552826	0.266024	0.957117	ENSG00000140807	NKD1
ENSG00000140829	20.124	25.8526	28.4398	23.9668	ENSG00000140829	DHX38
ENSG00000140830	5.82841	6.45093	7.75092	4.64596	ENSG00000140830	TXNL4B
ENSG00000140832	10.8439	13.2073	15.4724	8.83701	ENSG00000140832	MARVELD3
ENSG00000140835	0.0460511	0.215246	0.269367	0.0988431	ENSG00000140835	CHST4
ENSG00000140836	5.57291	7.1036	6.75416	24.7907	ENSG00000140836	ZFHX3
ENSG00000140839	0.911422	0.43537	1.13246	0.643778	ENSG00000140839	CLEC18B
ENSG00000140848	7.61443	11.3778	6.12629	10.5953	ENSG00000140848	CPNE2
ENSG00000140853	6.44195	15.8376	7.8226	22.1682	ENSG00000140853	NLRC5
ENSG00000140854	8.57805	9.48245	8.82907	5.12085	ENSG00000140854	KATNB1
ENSG00000140859	59.2785	89.1668	89.6197	131.927	ENSG00000140859	KIFC3
ENSG00000140873	0.105684	1.18063	0.864335	0.811566	ENSG00000140873	ADAMTS18
ENSG00000140876	2.74245	5.61344	2.67358	3.13603	ENSG00000140876	NUDT7
ENSG00000140905	10.7558	6.99071	7.46107	8.26482	ENSG00000140905	GCSH
ENSG00000140931	10.8766	11.3839	12.6911	10.655	ENSG00000140931	CMTM3
ENSG00000140932	0	0.33584	0.167208	0.227299	ENSG00000140932	CMTM2
ENSG00000140937	9.36426	38.4863	38.7855	117.619	ENSG00000140937	CDH11
ENSG00000140939	20.4994	37.3243	33.2787	46.931	ENSG00000140939	NOL3
ENSG00000140941	19.6862	19.0539	28.956	19.124	ENSG00000140941	MAP1LC3B
ENSG00000140943	32.1038	40.098	54.8715	46.1435	ENSG00000140943	MBTPS1
ENSG00000140945	60.4827	181.541	121.057	96.3196	ENSG00000140945	CDH13
ENSG00000140948	4.58736	6.46048	6.79559	6.9336	ENSG00000140948	ZCCHC14
ENSG00000140950	57.082	102.149	90.4885	72.4634	ENSG00000140950	TLDC1
ENSG00000140955	1.88864	4.18091	4.22474	1.41853	ENSG00000140955	ADAD2
ENSG00000140961	4.98482	7.61734	5.95523	5.00855	ENSG00000140961	OSGIN1
ENSG00000140968	0.0729339	0.375816	0.290637	0.60576	ENSG00000140968	IRF8
ENSG00000140983	62.9846	89.5319	94.5238	53.9194	ENSG00000140983	RHOT2
ENSG00000140986	3.35227	5.76043	5.27726	9.36683	ENSG00000140986	RPL3L
ENSG00000140987	7.94002	7.97016	12.9744	5.34564	ENSG00000140987	ZSCAN32
ENSG00000140988	464.266	679.982	474.331	366.975	ENSG00000140988	RPS2
ENSG00000140990	48.9259	39.0044	32.448	23.7382	ENSG00000140990	NDUFB10
ENSG00000140992	23.9635	19.6436	33.0517	26.5393	ENSG00000140992	PDPK1
ENSG00000140993	3.96544	7.15225	8.32969	6.18073	ENSG00000140993	TIGD7

ENSG00000140995	43.0779	43.5636	47.9549	37.3934	ENSG00000140995	DEF8
ENSG00000141002	101.898	118.132	136.242	121.508	ENSG00000141002	TCF25
ENSG00000141012	18.0141	27.4954	33.501	22.2921	ENSG00000141012	GALNS
ENSG00000141013	10.8991	13.8031	18.333	14.6341	ENSG00000141013	GAS8
ENSG00000141026	6.68582	7.59806	7.12898	5.89492	ENSG00000141026	MED9
ENSG00000141027	50.6159	95.1259	94.5366	126.639	ENSG00000141027	NCOR1
ENSG00000141028	0	0.604868	1.00459	1.08474	ENSG00000141028	CDRT15P1
ENSG00000141030	27.2515	29.1897	28.2445	23.3709	ENSG00000141030	COPS3
ENSG00000141034	8.40053	10.1924	9.51301	10.1216	ENSG00000141034	GID4
ENSG00000141040	6.85646	7.59301	7.37347	6.05838	ENSG00000141040	ZNF287
ENSG00000141052	0.252136	0.230155	0.321839	1.8138	ENSG00000141052	MYOCD
ENSG00000141068	6.50937	5.98647	7.44953	12.8806	ENSG00000141068	KSR1
ENSG00000141076	15.0926	31.5127	31.9511	44.5273	ENSG00000141076	UTP4
ENSG00000141084	5.60552	6.0268	8.05451	6.61919	ENSG00000141084	RANBP10
ENSG00000141086	0.295611	0.367334	0.311452	0.162357	ENSG00000141086	CTRL
ENSG00000141096	0.0279087	0	0	0.0306256	ENSG00000141096	DPEP3
ENSG00000141098	28.5329	18.0784	23.5812	23.7298	ENSG00000141098	GFOD2
ENSG00000141101	8.41709	11.2052	12.1504	9.53318	ENSG00000141101	NOB1
ENSG00000141127	23.945	37.0846	31.5818	25.9889	ENSG00000141127	PRPSAP2
ENSG00000141140	34.5239	88.9441	77.2673	59.1446	ENSG00000141140	MYO19
ENSG00000141141	18.6543	17.9819	18.1922	18.2382	ENSG00000141141	DDX52
ENSG00000141150	6.76921	21.0509	21.2527	41.4554	ENSG00000141150	RASL10B
ENSG00000141161	0.233205	0.43613	0.556074	0.643367	ENSG00000141161	UNC45B
ENSG00000141179	6.65496	6.83017	4.70459	5.53365	ENSG00000141179	PCTP
ENSG00000141194	0	0	0	0	ENSG00000141194	OR4D1
ENSG00000141198	32.2406	53.421	53.1105	33.4527	ENSG00000141198	TOM1L1
ENSG00000141200	0	0.0919275	0.0207771	0	ENSG00000141200	KIF2B
ENSG00000141219	4.29498	5.07552	5.67457	3.85758	ENSG00000141219	C17orf80
ENSG00000141232	43.2706	24.3799	17.4608	19.4283	ENSG00000141232	TOB1
ENSG00000141252	24.4788	24.7104	35.9038	40.4728	ENSG00000141252	VPS53
ENSG00000141255	0	0.141838	0.0819151	0.340804	ENSG00000141255	SPATA22
ENSG00000141258	23.6023	26.9703	33.9101	26.5377	ENSG00000141258	SGSM2
ENSG00000141279	90.938	92.3108	82.1928	110.904	ENSG00000141279	NPEPPS
ENSG00000141293	0.716419	2.09446	0.818794	1.59474	ENSG00000141293	SKAP1
ENSG00000141294	1.07229	2.11833	1.47705	1.86239	ENSG00000141294	LRRC46
ENSG00000141295	26.6886	24.0858	18.0154	16.3111	ENSG00000141295	SCRN2
ENSG00000141298	19.0864	26.3418	21.3532	38.3834	ENSG00000141298	SSH2
ENSG00000141314	0.0973338	0.208848	0.275044	0.612855	ENSG00000141314	RHBDL3
ENSG00000141316	1.03648	0.679934	1.35328	0.861064	ENSG00000141316	SPACA3
ENSG00000141337	3.44938	5.30755	6.10137	10.7123	ENSG00000141337	ARSG
ENSG00000141338	3.2799	6.46426	5.39932	10.8037	ENSG00000141338	ABCA8
ENSG00000141349	19.139	28.0823	21.9995	15.7833	ENSG00000141349	G6PC3
ENSG00000141367	188.137	191.407	152.496	202.608	ENSG00000141367	CLTC
ENSG00000141371	0	0	0	0.827104	ENSG00000141371	C17orf64
ENSG00000141376	32.6062	59.245	61.1078	85.8494	ENSG00000141376	BCAS3
ENSG00000141378	14.6652	10.8214	12.1375	11.0635	ENSG00000141378	PTRH2
ENSG00000141380	56.3659	79.5253	66.8482	75.8833	ENSG00000141380	SS18
ENSG00000141384	3.36129	5.52672	5.09783	4.74921	ENSG00000141384	TAF4B
ENSG00000141385	25.4367	32.0361	35.6725	21.4862	ENSG00000141385	AFG3L2
ENSG00000141391	4.34704	9.16367	10.5288	10.6669	ENSG00000141391	PRELID3A
ENSG00000141401	10.9633	25.4813	54.6391	21.4413	ENSG00000141401	IMPA2
ENSG00000141404	9.69454	10.027	11.0758	5.82787	ENSG00000141404	GNAL
ENSG00000141424	88.9797	64.8341	85.2293	32.0678	ENSG00000141424	SLC39A6
ENSG00000141425	37.1964	36.6428	36.3772	36.6279	ENSG00000141425	RPRD1A

ENSG00000141428	12.2707	12.2637	14.6855	8.02587	ENSG00000141428	C18orf21
ENSG00000141429	231.209	129.184	106.048	118.439	ENSG00000141429	GALNT1
ENSG00000141431	0.453665	0.951191	1.05662	2.31688	ENSG00000141431	ASXL3
ENSG00000141433	0.0976558	0.204264	0.186354	0.296221	ENSG00000141433	ADCYAP1
ENSG00000141434	1.51239	2.7159	2.72977	6.4369	ENSG00000141434	MEP1B
ENSG00000141437	0	0.0948749	0.12734	0.163496	ENSG00000141437	SLC25A52
ENSG00000141441	6.26002	3.90956	5.28786	6.13414	ENSG00000141441	GAREM1
ENSG00000141446	30.0008	43.7986	48.3588	66.1564	ENSG00000141446	ESCO1
ENSG00000141447	29.7821	31.0491	26.9401	31.5096	ENSG00000141447	OSBPL1A
ENSG00000141448	0.328018	0.421529	1.36308	0.126582	ENSG00000141448	GATA6
ENSG00000141449	3.45484	4.63526	2.52424	5.11946	ENSG00000141449	GREB1L
ENSG00000141452	24.2252	26.9617	20.558	24.0839	ENSG00000141452	C18orf8
ENSG00000141456	16.5017	22.0888	21.3752	22.8801	ENSG00000141456	PELP1
ENSG00000141458	100.674	178.592	104.769	155.968	ENSG00000141458	NPC1
ENSG00000141469	1.17347	2.60158	1.93246	3.50352	ENSG00000141469	SLC14A1
ENSG00000141480	6.40612	11.1537	10.8296	16.4937	ENSG00000141480	ARRB2
ENSG00000141485	3.07721	2.47551	3.51913	6.14482	ENSG00000141485	SLC13A5
ENSG00000141497	0.944512	1.23924	1.23536	1.24883	ENSG00000141497	ZMYND15
ENSG00000141499	3.92321	7.13896	5.18525	3.61639	ENSG00000141499	WRAP53
ENSG00000141503	68.9095	107.911	113.986	62.7771	ENSG00000141503	MINK1
ENSG00000141504	18.3746	16.1817	23.6476	16.0931	ENSG00000141504	SAT2
ENSG00000141505	1.50784	3.22429	4.39943	6.74774	ENSG00000141505	ASGR1
ENSG00000141506	0.513451	0.664008	0.767541	2.02528	ENSG00000141506	PIK3R5
ENSG00000141510	10.4522	19.4839	29.2188	23.8522	ENSG00000141510	TP53
ENSG00000141519	3.34257	6.89848	10.4736	11.1202	ENSG00000141519	CCDC40
ENSG00000141522	161.085	144.53	117.544	123.629	ENSG00000141522	ARHGDIA
ENSG00000141524	63.4799	71.5775	62.4421	46.9547	ENSG00000141524	TMC6
ENSG00000141526	63.4964	157.032	57.7163	100.924	ENSG00000141526	SLC16A3
ENSG00000141527	7.69857	8.98079	9.20216	14.0359	ENSG00000141527	CARD14
ENSG00000141540	1.49721	2.74135	4.27212	2.95726	ENSG00000141540	TTYH2
ENSG00000141542	7.91897	5.39357	10.1165	11.0603	ENSG00000141542	RAB40B
ENSG00000141543	34.9997	31.2213	27.8785	20.036	ENSG00000141543	EIF4A3
ENSG00000141551	34.4222	61.3692	56.1143	89.7912	ENSG00000141551	CSNK1D
ENSG00000141552	40.8186	43.7242	21.7779	26.4554	ENSG00000141552	ANAPC11
ENSG00000141556	29.4464	67.8193	44.81	56.4262	ENSG00000141556	TBCD
ENSG00000141560	10.8661	11.3731	11.2576	9.89078	ENSG00000141560	FN3KRP
ENSG00000141562	20.5632	19.8855	20.5568	26.9846	ENSG00000141562	NARF
ENSG00000141564	18.4481	25.5	30.1907	30.074	ENSG00000141564	RPTOR
ENSG00000141568	30.9601	31.5775	44.4834	31.3084	ENSG00000141568	FOXK2
ENSG00000141569	13.3555	15.7037	17.3961	21.3458	ENSG00000141569	TRIM65
ENSG00000141570	1.72239	0.923682	1.12912	0.819366	ENSG00000141570	CBX8
ENSG00000141574	0.596092	3.89981	0.481828	2.93429	ENSG00000141574	SECTM1
ENSG00000141576	0.996338	2.32168	2.09457	5.9254	ENSG00000141576	RNF157
ENSG00000141577	6.68215	9.29775	8.82564	6.85226	ENSG00000141577	CEP131
ENSG00000141579	9.1224	5.51306	11.9142	3.95366	ENSG00000141579	ZNF750
ENSG00000141580	42.8176	29.2308	34.8179	29.1824	ENSG00000141580	WDR45B
ENSG00000141582	15.6823	25.0856	68.6182	6.39121	ENSG00000141582	CBX4
ENSG00000141622	1.31525	2.4106	3.07844	4.4893	ENSG00000141622	RNF165
ENSG00000141627	20.9748	39.2035	30.9473	43.071	ENSG00000141627	DYM
ENSG00000141639	0.044376	0.0780537	0.0681454	0.154546	ENSG00000141639	MAPK4
ENSG00000141642	4.83404	7.38109	7.83819	6.97155	ENSG00000141642	ELAC1
ENSG00000141644	84.5732	94.9068	104.568	48.7893	ENSG00000141644	MBD1
ENSG00000141646	36.0787	52.7743	48.2372	50.9372	ENSG00000141646	SMAD4
ENSG00000141655	1.28453	1.90372	1.50913	2.34341	ENSG00000141655	TNFRSF11A

ENSG00000141664	5.66934	10.9557	11.1514	8.72614	ENSG00000141664	ZCCHC2
ENSG00000141665	12.3156	32.9121	32.4149	62.2944	ENSG00000141665	FBXO15
ENSG00000141668	0.835568	3.53394	2.67464	3.65124	ENSG00000141668	CBLN2
ENSG00000141682	11.9242	14.9634	13.4415	9.06682	ENSG00000141682	PMAIP1
ENSG00000141696	9.88786	13.4782	12.6293	19.757	ENSG00000141696	P3H4
ENSG00000141698	11.7949	13.6639	12.6527	15.3044	ENSG00000141698	NT5C3B
ENSG00000141699	48.8679	49.5433	42.5548	25.1517	ENSG00000141699	RETREG3
ENSG00000141720	17.0735	17.6931	17.4367	16.0226	ENSG00000141720	PIP4K2B
ENSG00000141736	47.6034	63.6073	55.9188	36.7296	ENSG00000141736	ERBB2
ENSG00000141738	40.7226	29.8978	8.95032	11.7932	ENSG00000141738	GRB7
ENSG00000141741	23.8377	12.433	10.0207	9.2392	ENSG00000141741	MIEN1
ENSG00000141744	0	0.15079	0.340587	0.170175	ENSG00000141744	PNMT
ENSG00000141748	0.908691	1.3225	0.75585	2.57068	ENSG00000141748	ARL5C
ENSG00000141750	0.729236	1.37275	1.09791	2.44422	ENSG00000141750	STAC2
ENSG00000141753	5.04657	16.4153	9.16212	33.5833	ENSG00000141753	IGFBP4
ENSG00000141756	3.65833	17.0302	21.1554	76.1413	ENSG00000141756	FKBP10
ENSG00000141759	45.8931	38.9669	38.3	37.6051	ENSG00000141759	TXNL4A
ENSG00000141837	1.43085	1.35823	1.96574	4.98661	ENSG00000141837	CACNA1A
ENSG00000141854	1.61016	1.23762	0.799309	0.497214	ENSG00000141854	MISP3
ENSG00000141858	14.1522	11.4438	8.31967	11.2261	ENSG00000141858	SAMD1
ENSG00000141867	22.4707	32.4523	43.7995	44.1467	ENSG00000141867	BRD4
ENSG00000141873	30.2241	31.2087	28.1298	24.1169	ENSG00000141873	SLC39A3
ENSG00000141905	14.3503	27.2167	23.8998	29.4204	ENSG00000141905	NFIC
ENSG00000141933	4.29599	4.63013	5.29972	6.44482	ENSG00000141933	TPGS1
ENSG00000141934	17.7467	28.5356	13.34	5.25701	ENSG00000141934	PLPP2
ENSG00000141946	0.281111	1.0299	0.786849	1.50053	ENSG00000141946	ZIM3
ENSG00000141956	4.56457	6.43749	4.91681	6.39563	ENSG00000141956	PRDM15
ENSG00000141959	46.5976	57.6116	51.4793	35.8332	ENSG00000141959	PFKL
ENSG00000141965	14.4252	8.55522	12.2801	5.83493	ENSG00000141965	FEM1A
ENSG00000141968	3.79878	6.76374	6.80259	10.8977	ENSG00000141968	VAV1
ENSG00000141971	19.5841	22.2961	15.8951	20.0379	ENSG00000141971	MVB12A
ENSG00000141977	0	0	0	0	ENSG00000141977	CIB3
ENSG00000141979	0.165099	0.218034	0.194117	2.85E-09	ENSG00000141979	CTD-3222D19.2
ENSG00000141985	63.4487	40.9406	53.8822	50.3585	ENSG00000141985	SH3GL1
ENSG00000141994	16.2353	17.3946	31.5131	17.208	ENSG00000141994	DUS3L
ENSG00000142002	61.0092	80.1501	51.8475	74.9875	ENSG00000142002	DPP9
ENSG00000142025	0.459625	0.428689	0.469558	0.202455	ENSG00000142025	DMRTC2
ENSG00000142039	8.79926	8.01617	10.3163	10.7436	ENSG00000142039	CCDC97
ENSG00000142046	8.96766	11.7847	10.6296	10.6634	ENSG00000142046	TMEM91
ENSG00000142065	2.59417	4.37711	3.37773	6.64139	ENSG00000142065	ZFP14
ENSG00000142082	5.31491	9.96754	11.4536	10.2433	ENSG00000142082	SIRT3
ENSG00000142089	69.4838	212.467	126.859	139.896	ENSG00000142089	IFITM3
ENSG00000142102	15.6346	16.9624	12.3392	28.269	ENSG00000142102	PGGHG
ENSG00000142149	0.600233	2.32639	2.60323	2.77772	ENSG00000142149	HUNK
ENSG00000142156	3.09989	8.29595	33.519	1506.77	ENSG00000142156	COL6A1
ENSG00000142163	0	0	0	0	ENSG00000142163	OR1E3
ENSG00000142166	7.75476	7.85455	10.1433	9.50326	ENSG00000142166	IFNAR1
ENSG00000142168	44.7869	54.5368	33.923	40.7545	ENSG00000142168	SOD1
ENSG00000142173	1.18371	3.05192	38.2949	2095.89	ENSG00000142173	COL6A2
ENSG00000142178	55.143	25.1701	37.0321	38.333	ENSG00000142178	SIK1
ENSG00000142182	0	0.339445	0.415258	0.125776	ENSG00000142182	DNMT3L
ENSG00000142185	0.971245	0.513794	0.902456	0.662213	ENSG00000142185	TRPM2
ENSG00000142186	27.7669	26.6472	24.4063	25.7442	ENSG00000142186	SCYL1
ENSG00000142188	15.5369	21.0292	6.1952	12.2347	ENSG00000142188	TMEM50B

ENSG00000142192	513.481	477.801	697.304	579.469	ENSG00000142192	APP
ENSG00000142197	9.64452	10.3291	10.5201	11.776	ENSG00000142197	DOPEY2
ENSG00000142207	15.2177	26.7478	27.0153	22.9309	ENSG00000142207	URB1
ENSG00000142208	40.1739	54.7945	47.4689	44.4717	ENSG00000142208	AKT1
ENSG00000142224	0.522	2.25231	1.58512	2.93391	ENSG00000142224	IL19
ENSG00000142227	55.4924	124.33	24.6789	50.6322	ENSG00000142227	EMP3
ENSG00000142230	24.2759	27.3441	21.124	24.5739	ENSG00000142230	SAE1
ENSG00000142233	0.286142	0.80279	1.22283	0.722997	ENSG00000142233	NTN5
ENSG00000142235	4.16885	3.91073	2.68475	3.88159	ENSG00000142235	LMTK3
ENSG00000142252	15.3516	16.2375	17.0745	16.4346	ENSG00000142252	GEMIN7
ENSG00000142273	58.017	44.806	42.6924	21.9785	ENSG00000142273	CBLC
ENSG00000142279	11.5109	10.5714	9.91132	10.2606	ENSG00000142279	WTIP
ENSG00000142303	0.280392	0.536517	0.422555	0.982542	ENSG00000142303	ADAMTS10
ENSG00000142319	0	0.0631369	0.114113	0.142914	ENSG00000142319	SLC6A3
ENSG00000142327	11.2909	12.4375	7.52062	10.754	ENSG00000142327	RNPEPL1
ENSG00000142330	23.7176	30.5845	32.7784	25.6276	ENSG00000142330	CAPN10
ENSG00000142347	10.273	24.4092	19.0177	41.3262	ENSG00000142347	MYO1F
ENSG00000142405	1.74737	3.73496	3.07929	6.37982	ENSG00000142405	NLRP12
ENSG00000142408	2.15403	5.30055	4.43555	8.45284	ENSG00000142408	CACNG8
ENSG00000142409	9.16958	12.4396	13.9089	10.2571	ENSG00000142409	ZNF787
ENSG00000142444	20.6949	20.1795	25.9571	21.1669	ENSG00000142444	TIMM29
ENSG00000142449	0.644953	1.0369	0.634894	2.40683	ENSG00000142449	FBN3
ENSG00000142453	27.2347	29.4411	30.2446	29.8264	ENSG00000142453	CARM1
ENSG00000142459	12.3814	14.6092	18.4001	11.6411	ENSG00000142459	EVI5L
ENSG00000142484	0	0	0	0	ENSG00000142484	TM4SF5
ENSG00000142494	2.33576	6.39505	5.6454	9.92362	ENSG00000142494	SLC47A1
ENSG00000142507	74.1229	37.6152	43.4758	33.1648	ENSG00000142507	PSMB6
ENSG00000142511	0.181123	0.416752	0.197454	0.221859	ENSG00000142511	GPR32
ENSG00000142512	3.78365	9.2322	6.85268	14.0949	ENSG00000142512	SIGLEC10
ENSG00000142513	1.14228	1.43483	1.51248	1.06457	ENSG00000142513	ACP4
ENSG00000142515	0.382333	0.506526	0.341089	0.657214	ENSG00000142515	KLK3
ENSG00000142528	7.77276	9.92077	7.67398	5.14706	ENSG00000142528	ZNF473
ENSG00000142530	1.16253	0.329755	0.680165	0.402832	ENSG00000142530	FAM71E1
ENSG00000142534	658.826	493.245	368.53	254.927	ENSG00000142534	RPS11
ENSG00000142538	0.19539	0	0.323278	0	ENSG00000142538	PTH2
ENSG00000142539	0	0	0	0	ENSG00000142539	CTD-2545M3.6
ENSG00000142541	854.349	617.027	631.524	366.488	ENSG00000142541	RPL13A
ENSG00000142544	4.3309	4.36747	4.52726	3.21944	ENSG00000142544	CTU1
ENSG00000142546	33.7141	22.1362	18.8799	21.1482	ENSG00000142546	NOSIP
ENSG00000142549	0.817082	0.920562	0.840429	1.62379	ENSG00000142549	IGLON5
ENSG00000142552	0.736992	0.75097	1.06209	46.4388	ENSG00000142552	RCN3
ENSG00000142556	8.30841	9.25097	10.4627	10.6366	ENSG00000142556	ZNF614
ENSG00000142583	2.62011	4.69533	3.97829	6.6313	ENSG00000142583	SLC2A5
ENSG00000142599	19.0511	31.5939	28.3682	48.3601	ENSG00000142599	RERE
ENSG00000142606	0.466301	0	0.239942	0.183128	ENSG00000142606	MMEL1
ENSG00000142609	8.0552	12.4095	9.70709	22.8502	ENSG00000142609	CFAP74
ENSG00000142611	2.68792	3.17557	3.10292	9.46706	ENSG00000142611	PRDM16
ENSG00000142615	3.01876	5.08648	6.7339	7.83337	ENSG00000142615	CELA2A
ENSG00000142619	1.68416	6.6154	0.781143	1.96644	ENSG00000142619	PADI3
ENSG00000142621	5.26643	5.18311	4.6881	5.31271	ENSG00000142621	FHAD1
ENSG00000142623	23.0605	1.06055	1.65327	3.59709	ENSG00000142623	PADI1
ENSG00000142627	184.218	145.467	61.9699	66.6292	ENSG00000142627	EPHA2
ENSG00000142632	1.85518	8.97348	5.83678	3.48634	ENSG00000142632	ARHGEF19
ENSG00000142634	31.347	33.6761	15.0698	17.2664	ENSG00000142634	EFHD2

ENSG00000142655	17.8444	20.1121	20.8988	9.60505	ENSG00000142655	PEX14
ENSG00000142657	49.2551	28.3114	20.1377	46.7887	ENSG00000142657	PGD
ENSG00000142661	9.19659	9.88825	7.92527	14.8553	ENSG00000142661	MYOM3
ENSG00000142669	82.2399	66.0518	49.3971	42.3745	ENSG00000142669	SH3BGRL3
ENSG00000142675	30.7439	29.4801	27.5272	15.4518	ENSG00000142675	CNKSR1
ENSG00000142676	633.885	470.649	380.865	255.32	ENSG00000142676	RPL11
ENSG00000142677	2.31943	5.18595	3.75982	2.04563	ENSG00000142677	IL22RA1
ENSG00000142684	3.65209	3.83288	4.90218	2.5707	ENSG00000142684	ZNF593
ENSG00000142686	11.1511	14.3657	15.2064	28.6668	ENSG00000142686	C1orf216
ENSG00000142687	27.007	35.2247	41.9554	29.2571	ENSG00000142687	KIAA0319L
ENSG00000142694	22.2302	16.4619	18.1311	26.5559	ENSG00000142694	EVA1B
ENSG00000142698	0.0791714	0.25822	0.419826	0.472967	ENSG00000142698	C1orf94
ENSG00000142700	0.0580565	0.0842857	0.0850437	0.0857315	ENSG00000142700	DMRTA2
ENSG00000142731	5.33134	22.2443	4.54115	9.03507	ENSG00000142731	PLK4
ENSG00000142733	37.2293	36.9164	22.5767	25.7242	ENSG00000142733	MAP3K6
ENSG00000142748	0.54862	0.773072	0.375781	0.950824	ENSG00000142748	FCN3
ENSG00000142751	20.775	15.4814	19.5501	13.9753	ENSG00000142751	GPN2
ENSG00000142765	41.0746	84.9118	77.8981	26.5339	ENSG00000142765	SYTL1
ENSG00000142784	9.93427	7.58603	7.89811	7.71098	ENSG00000142784	WDTC1
ENSG00000142789	0	0	0	0	ENSG00000142789	CELA3A
ENSG00000142794	11.4584	16.2855	15.3418	25.4206	ENSG00000142794	NBPF3
ENSG00000142798	103.691	170.764	233.601	260.53	ENSG00000142798	HSPG2
ENSG00000142856	13.6566	41.6114	32.1545	39.0241	ENSG00000142856	ITGB3BP
ENSG00000142864	89.2251	76.5762	107.701	81.8123	ENSG00000142864	SERBP1
ENSG00000142867	16.7047	17.2694	11.8572	12.887	ENSG00000142867	BCL10
ENSG00000142871	33.2492	40.8491	18.28	253.796	ENSG00000142871	CYR61
ENSG00000142875	3.86651	5.65083	6.60872	6.73745	ENSG00000142875	PRKACB
ENSG00000142892	15.2604	25.3502	15.2502	11.526	ENSG00000142892	PIGK
ENSG00000142910	356.742	234.71	85.6822	71.2545	ENSG00000142910	TINAGL1
ENSG00000142920	3.05277	8.35722	4.26148	5.55155	ENSG00000142920	AZIN2
ENSG00000142937	655.36	536.695	524.753	337.808	ENSG00000142937	RPS8
ENSG00000142945	3.15372	29.4298	2.99111	9.09193	ENSG00000142945	KIF2C
ENSG00000142949	116.847	173.307	216.621	121.354	ENSG00000142949	PTPRF
ENSG00000142959	0.522401	0.832019	1.22877	0.822296	ENSG00000142959	BEST4
ENSG00000142961	5.94489	9.33621	6.07878	5.10745	ENSG00000142961	MOB3C
ENSG00000142973	2.55367	5.58159	6.55138	8.52051	ENSG00000142973	CYP4B1
ENSG00000143001	1.27296	2.92975	1.03422	2.22263	ENSG00000143001	TMEM61
ENSG00000143006	0.0594043	0.515177	0.181055	0.976126	ENSG00000143006	DMRTB1
ENSG00000143013	17.5673	30.6068	34.8385	20.361	ENSG00000143013	LMO4
ENSG00000143028	0.0748923	0.173232	0.143574	0.346791	ENSG00000143028	SYPL2
ENSG00000143032	0	0.110324	0.0747467	0.0944718	ENSG00000143032	BARHL2
ENSG00000143033	12.0982	21.1651	22.1753	22.1573	ENSG00000143033	MTF2
ENSG00000143036	6.30767	3.98933	1.48782	2.94476	ENSG00000143036	SLC44A3
ENSG00000143061	29.9119	47.5217	47.786	24.4374	ENSG00000143061	IGSF3
ENSG00000143067	2.57206	4.46212	3.54931	5.51191	ENSG00000143067	ZNF697
ENSG00000143079	24.2294	19.3082	17.2105	21.8543	ENSG00000143079	CTTNBP2NL
ENSG00000143093	31.444	35.7187	47.4163	35.1577	ENSG00000143093	STRIP1
ENSG00000143105	0	0	0	0	ENSG00000143105	KCNA10
ENSG00000143106	59.6174	43.2107	35.6195	33.4501	ENSG00000143106	PSMA5
ENSG00000143107	0.137639	0.0517058	0.0712631	0.179848	ENSG00000143107	FNDC7
ENSG00000143110	0.469887	0.732944	0.99798	1.02182	ENSG00000143110	C1orf162
ENSG00000143119	0.327716	0.0742771	0	0.40893	ENSG00000143119	CD53
ENSG00000143125	0	0	0.114954	0	ENSG00000143125	PROK1
ENSG00000143126	30.6868	33.0179	41.6635	17.9764	ENSG00000143126	CELSR2

ENSG00000143127	1.12177	2.68004	2.39223	3.13624	ENSG00000143127	ITGA10
ENSG00000143140	9.69326	0.660731	1.58388	2.87727	ENSG00000143140	GJA5
ENSG00000143147	18.1185	25.6541	21.3126	27.4213	ENSG00000143147	GPR161
ENSG00000143149	17.4496	24.902	19.4582	17.0247	ENSG00000143149	ALDH9A1
ENSG00000143153	38.0568	29.5779	21.3851	23.4367	ENSG00000143153	ATP1B1
ENSG00000143155	22.039	21.8799	24.239	18.7156	ENSG00000143155	TIPRL
ENSG00000143156	13.6378	22.189	23.6597	38.4471	ENSG00000143156	NME7
ENSG00000143157	17.1962	22.9093	26.2309	19.6038	ENSG00000143157	POGK
ENSG00000143158	11.1331	13.7112	8.26898	7.82077	ENSG00000143158	MPC2
ENSG00000143162	43.5149	19.5734	23.941	9.491	ENSG00000143162	CREG1
ENSG00000143164	25.9779	30.1997	29.2315	40.4659	ENSG00000143164	DCAF6
ENSG00000143167	0.195345	0.27385	0.273738	0.215104	ENSG00000143167	GPA33
ENSG00000143171	0	0.0532987	0	0	ENSG00000143171	RXRG
ENSG00000143178	1.1515	1.71352	2.22581	3.24678	ENSG00000143178	TBX19
ENSG00000143179	24.4432	23.5953	28.8859	41.3791	ENSG00000143179	UCK2
ENSG00000143183	67.6663	54.5809	37.8561	23.5022	ENSG00000143183	TMCO1
ENSG00000143184	0.129456	0	0.112963	0.0625734	ENSG00000143184	XCL1
ENSG00000143185	0.131022	0.245221	0.329849	0.503355	ENSG00000143185	XCL2
ENSG00000143190	9.50022	16.5335	13.6797	18.1394	ENSG00000143190	POU2F1
ENSG00000143194	0.737959	1.33517	1.1091	2.09867	ENSG00000143194	MAEL
ENSG00000143195	0.11488	0.27724	0.194565	0.434918	ENSG00000143195	ILDR2
ENSG00000143196	0	0.0309195	0	2.86709	ENSG00000143196	DPT
ENSG00000143198	73.2013	130.364	59.8748	93.061	ENSG00000143198	MGST3
ENSG00000143199	0.0850584	0.400474	0.395143	0.531323	ENSG00000143199	ADCY10
ENSG00000143207	24.086	36.8259	25.9478	36.5135	ENSG00000143207	RFWD2
ENSG00000143217	47.861	8.71189	20.1899	7.0082	ENSG00000143217	NECTIN4
ENSG00000143222	20.6396	20.6702	19.0667	20.598	ENSG00000143222	UFC1
ENSG00000143224	10.3146	16.8999	15.3936	11.1146	ENSG00000143224	PPOX
ENSG00000143226	2.07598	3.33924	3.66895	1.96204	ENSG00000143226	FCGR2A
ENSG00000143228	5.4795	29.2799	4.04917	13.3425	ENSG00000143228	NUF2
ENSG00000143248	2.87554	4.60692	6.09643	2.76593	ENSG00000143248	RGS5
ENSG00000143252	22.5713	10.442	12.4971	15.6901	ENSG00000143252	SDHC
ENSG00000143256	19.1296	16.7138	21.9941	13.4511	ENSG00000143256	PFDN2
ENSG00000143257	2.00859	2.67893	2.79375	3.22846	ENSG00000143257	NR1I3
ENSG00000143258	8.58393	11.1501	10.3474	9.79977	ENSG00000143258	USP21
ENSG00000143278	0.237481	0.569775	0.308726	0.519607	ENSG00000143278	F13B
ENSG00000143294	15.0761	18.6555	24.1883	18.7972	ENSG00000143294	PRCC
ENSG00000143297	4.1048	9.87175	11.4757	19.6664	ENSG00000143297	FCRL5
ENSG00000143303	12.1606	30.9356	24.6177	18.0466	ENSG00000143303	RRNAD1
ENSG00000143314	33.526	37.8592	39.4121	26.187	ENSG00000143314	MRPL24
ENSG00000143315	4.96286	4.94229	5.23561	4.04663	ENSG00000143315	PIGM
ENSG00000143318	0.499352	1.87771	0.810745	2.46789	ENSG00000143318	CASQ1
ENSG00000143319	14.682	14.43	20.0179	15.8452	ENSG00000143319	ISG20L2
ENSG00000143320	59.8726	31.1385	53.7924	20.2455	ENSG00000143320	CRABP2
ENSG00000143321	113.128	120.525	119.631	69.6241	ENSG00000143321	HDGF
ENSG00000143322	68.0985	18.8266	18.4222	40.2135	ENSG00000143322	ABL2
ENSG00000143324	20.9165	40.8866	34.7211	113.065	ENSG00000143324	XPR1
ENSG00000143333	0.720509	0.450268	0.893124	0.429833	ENSG00000143333	RGS16
ENSG00000143337	52.6354	40.6226	26.0895	26.2481	ENSG00000143337	TOR1AIP1
ENSG00000143340	0.301841	0.805693	0.53814	1.40506	ENSG00000143340	FAM163A
ENSG00000143341	0.196336	2.12824	3.13051	3.79783	ENSG00000143341	HMCN1
ENSG00000143344	0.364633	0.774813	1.31307	2.37815	ENSG00000143344	RGL1
ENSG00000143353	17.145	25.6594	22.9279	18.0233	ENSG00000143353	LYPLAL1
ENSG00000143355	1.67409	3.39274	2.85524	4.36888	ENSG00000143355	LHX9

ENSG00000143363	5.16828	4.60355	4.82812	3.14421	ENSG00000143363	PRUNE1
ENSG00000143365	1.66303	2.26627	1.35469	3.72052	ENSG00000143365	RORC
ENSG00000143367	50.3738	20.4112	30.3622	22.5003	ENSG00000143367	TUFT1
ENSG00000143368	9.84457	6.18921	7.51618	6.34517	ENSG00000143368	SF3B4
ENSG00000143369	365.309	71.0581	20.2207	52.5812	ENSG00000143369	ECM1
ENSG00000143373	12.5162	12.5788	12.1315	8.22699	ENSG00000143373	ZNF687
ENSG00000143374	23.6423	34.3034	30.031	34.3027	ENSG00000143374	TARS2
ENSG00000143375	18.4465	8.26364	7.10366	6.021	ENSG00000143375	CGN
ENSG00000143376	7.77878	8.00782	8.07486	10.4565	ENSG00000143376	SNX27
ENSG00000143379	20.9302	35.2272	40.7807	30.3452	ENSG00000143379	SETDB1
ENSG00000143382	27.3427	18.7825	18.323	8.76686	ENSG00000143382	ADAMTSL4
ENSG00000143384	118.296	161.586	106.439	112.32	ENSG00000143384	MCL1
ENSG00000143387	5.86871	18.6708	9.71509	51.6306	ENSG00000143387	CTSK
ENSG00000143390	19.599	18.453	26.3881	17.3495	ENSG00000143390	RFX5
ENSG00000143393	14.3819	18.6864	22.8766	18.1542	ENSG00000143393	PI4KB
ENSG00000143398	60.8002	65.6807	82.9138	94.0004	ENSG00000143398	PIP5K1A
ENSG00000143401	7.68933	12.1626	7.50165	11.3566	ENSG00000143401	ANP32E
ENSG00000143409	15.7576	7.73376	7.26309	6.85159	ENSG00000143409	MINDY1
ENSG00000143412	4.97399	1.87842	1.16608	1.46763	ENSG00000143412	ANXA9
ENSG00000143416	2.74711	3.40687	2.47264	6.89181	ENSG00000143416	SELENBP1
ENSG00000143418	92.7346	108.181	49.5016	41.145	ENSG00000143418	CERS2
ENSG00000143420	47.8688	61.7029	54.5937	49.2736	ENSG00000143420	ENSA
ENSG00000143429	48.3518	36.7989	72.7432	94.7725	ENSG00000143429	AC116050.1
ENSG00000143434	1.30116	1.72606	2.76878	2.3735	ENSG00000143434	SEMA6C
ENSG00000143436	30.8807	33.2764	31.5677	20.3792	ENSG00000143436	MRPL9
ENSG00000143437	18.3285	25.5292	23.7458	41.9063	ENSG00000143437	ARNT
ENSG00000143442	42.7988	68.3686	65.1773	111.359	ENSG00000143442	POGZ
ENSG00000143443	4.31695	7.60635	8.09111	8.5186	ENSG00000143443	C1orf56
ENSG00000143450	2.41924	2.94925	3.81911	3.80793	ENSG00000143450	OAZ3
ENSG00000143452	0	0.0310156	0	0.0705756	ENSG00000143452	HORMAD1
ENSG00000143457	11.3055	10.6254	8.4227	8.1515	ENSG00000143457	GOLPH3L
ENSG00000143458	7.23248	8.68051	9.61163	11.8115	ENSG00000143458	GABPB2
ENSG00000143466	1.66404	1.54191	6.32448	5.82837	ENSG00000143466	IKBKE
ENSG00000143469	1.55629	1.33766	0.945368	1.08224	ENSG00000143469	SYT14
ENSG00000143473	0.0535299	0.0516169	0.0784581	0.796276	ENSG00000143473	KCNH1
ENSG00000143476	1.991	10.2707	1.01055	5.59354	ENSG00000143476	DTL
ENSG00000143479	2.51423	4.11444	4.24146	4.29501	ENSG00000143479	DYRK3
ENSG00000143486	2.69903	3.35454	3.72664	5.12555	ENSG00000143486	EIF2D
ENSG00000143493	6.54697	12.6873	11.4588	9.84326	ENSG00000143493	INTS7
ENSG00000143494	5.38478	12.9624	11.998	22.6821	ENSG00000143494	VASH2
ENSG00000143498	7.02816	10.7447	6.17804	8.3353	ENSG00000143498	TAF1A
ENSG00000143499	13.8056	20.2741	15.5866	14.4609	ENSG00000143499	SMYD2
ENSG00000143502	2.12693	2.38923	0.806473	0.604209	ENSG00000143502	SUSD4
ENSG00000143507	31.6408	14.2342	9.66883	16.5995	ENSG00000143507	DUSP10
ENSG00000143512	0.461114	0.5992	0.503974	0.917123	ENSG00000143512	HHIPL2
ENSG00000143514	19.7586	16.5568	11.382	21.0406	ENSG00000143514	TP53BP2
ENSG00000143515	10.7643	23.6884	23.4498	23.9819	ENSG00000143515	ATP8B2
ENSG00000143520	0.207703	0.165498	1.12818	0.383557	ENSG00000143520	FLG2
ENSG00000143536	6.99656	0.0573729	0.311195	1.66523	ENSG00000143536	CRNN
ENSG00000143537	162.606	233.083	193.052	69.6509	ENSG00000143537	ADAM15
ENSG00000143543	51.4811	37.7283	26.4689	17.7122	ENSG00000143543	JTB
ENSG00000143545	11.9723	13.9537	15.0308	34.9359	ENSG00000143545	RAB13
ENSG00000143546	175.2	100.05	458.527	130.019	ENSG00000143546	S100A8
ENSG00000143549	202.533	138.271	91.9757	123.328	ENSG00000143549	TPM3

ENSG00000143552	0.475606	0.674103	0.744846	0.567017	ENSG00000143552	NUP210L
ENSG00000143553	12.5506	11.1607	8.50228	7.3775	ENSG00000143553	SNAPIN
ENSG00000143554	0.936828	5.65572	1.66553	2.70066	ENSG00000143554	SLC27A3
ENSG00000143556	36.2315	3.2545	45.6335	40.0355	ENSG00000143556	S100A7
ENSG00000143569	53.5182	61.4471	62.7908	75.8169	ENSG00000143569	UBAP2L
ENSG00000143570	40.6531	56.6539	31.9771	19.758	ENSG00000143570	SLC39A1
ENSG00000143575	34.5179	40.4516	52.6129	17.0913	ENSG00000143575	HAX1
ENSG00000143578	5.74901	12.2939	10.5427	9.83858	ENSG00000143578	CREB3L4
ENSG00000143590	27.6328	7.38626	9.40758	5.79468	ENSG00000143590	EFNA3
ENSG00000143595	0.190761	0.197338	1.12106	0.197555	ENSG00000143595	AQP10
ENSG00000143603	0.284928	0.539012	0.52339	0.94581	ENSG00000143603	KCNN3
ENSG00000143612	60.09	63.9287	58.3651	36.3451	ENSG00000143612	C1orf43
ENSG00000143614	1.8829	2.51489	3.91181	3.89848	ENSG00000143614	GATAD2B
ENSG00000143621	64.1798	51.0004	36.6129	36.647	ENSG00000143621	ILF2
ENSG00000143622	21.9595	14.6762	15.5786	13.4403	ENSG00000143622	RIT1
ENSG00000143624	11.5059	20.2922	18.3733	20.2426	ENSG00000143624	INTS3
ENSG00000143627	0.0616161	0.0862252	0.160192	0.0772759	ENSG00000143627	PKLR
ENSG00000143630	0.966423	0.82364	0.64468	0.938463	ENSG00000143630	HCN3
ENSG00000143631	4.1737	0.434102	7.56523	3.84361	ENSG00000143631	FLG
ENSG00000143632	0.116957	0.099513	0.135837	0	ENSG00000143632	ACTA1
ENSG00000143633	11.4867	13.2495	16.1409	14.2872	ENSG00000143633	C1orf131
ENSG00000143641	43.3997	63.6069	51.4858	43.0112	ENSG00000143641	GALNT2
ENSG00000143643	8.4866	12.0329	10.5622	9.67991	ENSG00000143643	TTC13
ENSG00000143653	4.16545	3.28583	1.85176	2.91806	ENSG00000143653	SCCPDH
ENSG00000143669	19.5255	29.7985	21.8412	33.248	ENSG00000143669	LYST
ENSG00000143674	3.20971	5.42987	3.91909	2.98205	ENSG00000143674	MAP3K21
ENSG00000143702	33.243	62.1219	45.0749	121.734	ENSG00000143702	CEP170
ENSG00000143727	43.4394	39.1625	42.2132	25.6429	ENSG00000143727	ACP1
ENSG00000143740	14.453	14.7111	14.8204	9.89558	ENSG00000143740	SNAP47
ENSG00000143742	77.1193	65.8419	56.6869	55.732	ENSG00000143742	SRP9
ENSG00000143748	24.5118	43.2562	45.3808	57.0329	ENSG00000143748	NVL
ENSG00000143751	11.2487	9.00649	13.0212	11.7925	ENSG00000143751	SDE2
ENSG00000143753	56.3945	73.8072	62.316	55.151	ENSG00000143753	DEGS1
ENSG00000143756	23.5801	19.3032	22.7865	15.6749	ENSG00000143756	FBXO28
ENSG00000143761	94.1085	59.6426	71.3707	88.1788	ENSG00000143761	ARF1
ENSG00000143768	0	0.187999	0.0850261	0.318849	ENSG00000143768	LEFTY2
ENSG00000143771	56.9237	69.8385	40.8397	16.8453	ENSG00000143771	CNIH4
ENSG00000143772	4.55294	7.27856	4.28049	7.49471	ENSG00000143772	ITPKB
ENSG00000143774	233.372	181.295	140.471	92.0213	ENSG00000143774	GUK1
ENSG00000143776	13.2641	21.8763	26.7502	28.9627	ENSG00000143776	CDC42BPA
ENSG00000143786	9.7041	17.6531	17.3019	33.3225	ENSG00000143786	CNIH3
ENSG00000143793	10.2902	8.14701	10.4107	7.27366	ENSG00000143793	C1orf35
ENSG00000143797	168.195	166.029	42.9241	80.7778	ENSG00000143797	MBOAT2
ENSG00000143799	14.9087	34.1664	20.4504	28.8329	ENSG00000143799	PARP1
ENSG00000143801	16.8505	14.3365	10.7145	8.77566	ENSG00000143801	PSEN2
ENSG00000143811	18.4269	41.8587	31.0244	22.4364	ENSG00000143811	PYCR2
ENSG00000143815	27.3166	42.0894	18.5548	25.5236	ENSG00000143815	LBR
ENSG00000143816	5.84888	5.51028	0.70915	1.89317	ENSG00000143816	WNT9A
ENSG00000143819	4.43478	5.83275	4.85782	5.72416	ENSG00000143819	EPHX1
ENSG00000143839	0.201463	0.0385401	0.0350802	0.0440926	ENSG00000143839	REN
ENSG00000143842	9.83927	17.5188	10.7183	12.585	ENSG00000143842	SOX13
ENSG00000143845	9.61846	12.5324	9.93064	5.03143	ENSG00000143845	ETNK2
ENSG00000143847	5.26345	2.49039	3.61219	11.5706	ENSG00000143847	PPFIA4
ENSG00000143850	7.01327	3.08637	2.91915	3.29799	ENSG00000143850	PLEKHA6

ENSG00000143851	3.08992	5.40741	4.46715	9.16401	ENSG00000143851	PTPN7
ENSG00000143858	0.489127	0.847464	0.787925	0.897392	ENSG00000143858	SYT2
ENSG00000143862	17.7691	12.4051	13.815	8.42519	ENSG00000143862	ARL8A
ENSG00000143867	0.354876	0.802164	1.21311	2.71117	ENSG00000143867	OSR1
ENSG00000143869	0.328172	0.768731	0.774134	1.2791	ENSG00000143869	GDF7
ENSG00000143870	209.249	370.395	124.132	167.065	ENSG00000143870	PDIA6
ENSG00000143878	27.2689	10.4257	18.8523	46.3475	ENSG00000143878	RHOB
ENSG00000143882	8.45415	4.35102	5.49375	7.2334	ENSG00000143882	ATP6V1C2
ENSG00000143889	22.0058	27.4186	29.2886	25.453	ENSG00000143889	HNRNPLL
ENSG00000143891	1.56321	2.51145	1.98291	3.94367	ENSG00000143891	GALM
ENSG00000143919	10.9838	21.6055	18.7503	18.6549	ENSG00000143919	CAMKMT
ENSG00000143921	0.165599	0.159658	0.108347	0.185205	ENSG00000143921	ABCG8
ENSG00000143924	15.3718	23.6306	17.3824	20.2357	ENSG00000143924	EML4
ENSG00000143933	242.954	194.704	113.158	234.364	ENSG00000143933	CALM2
ENSG00000143942	3.34756	2.57422	2.87855	1.07428	ENSG00000143942	CHAC2
ENSG00000143947	442.5	353.382	350.397	177.468	ENSG00000143947	RPS27A
ENSG00000143951	15.5773	37.9096	35.2394	72.9165	ENSG00000143951	WDPCP
ENSG00000143952	13.8794	17.2332	15.2288	14.3292	ENSG00000143952	VPS54
ENSG00000143954	0.213311	0.14325	0.0647209	0.647107	ENSG00000143954	REG3G
ENSG00000143970	8.98186	12.1998	13.4207	14.0391	ENSG00000143970	ASXL2
ENSG00000143971	8.16884	10.904	8.13659	7.84606	ENSG00000143971	ETAA1
ENSG00000143977	42.8958	44.5172	32.4995	23.7088	ENSG00000143977	SNRPG
ENSG00000143994	1.75534	1.4098	2.93878	1.82088	ENSG00000143994	ABHD1
ENSG00000143995	16.8568	18.8907	8.66459	24.3787	ENSG00000143995	MEIS1
ENSG00000144010	0.131127	0.176373	0.153065	0.25901	ENSG00000144010	TRIM43B
ENSG00000144015	0.128846	0	0	0	ENSG00000144015	TRIM43
ENSG00000144021	27.6128	24.2489	24.7268	19.1763	ENSG00000144021	CIAO1
ENSG00000144026	11.0168	9.69307	12.3586	12.946	ENSG00000144026	ZNF514
ENSG00000144028	29.796	39.1764	43.0473	56.2628	ENSG00000144028	SNRNP200
ENSG00000144029	31.4432	36.3221	28.2341	37.9535	ENSG00000144029	MRPS5
ENSG00000144031	1.44614	1.23374	1.39403	1.5094	ENSG00000144031	ANKRD53
ENSG00000144034	14.4992	18.287	18.6565	17.679	ENSG00000144034	TPRKB
ENSG00000144035	0	0	0.171802	0	ENSG00000144035	NAT8
ENSG00000144036	18.3782	29.4779	30.729	28.88	ENSG00000144036	EXOC6B
ENSG00000144040	12.695	23.575	23.3646	36.7023	ENSG00000144040	SFXN5
ENSG00000144043	10.1529	9.91141	8.97219	4.26757	ENSG00000144043	TEX261
ENSG00000144045	11.3657	6.64537	13.5222	11.4066	ENSG00000144045	DQX1
ENSG00000144048	32.4036	25.46	28.8841	28.8247	ENSG00000144048	DUSP11
ENSG00000144057	0.258085	0.547453	0.604449	1.70999	ENSG00000144057	ST6GAL2
ENSG00000144061	3.46157	5.12352	4.55672	5.82695	ENSG00000144061	NPHP1
ENSG00000144063	185.055	77.2531	22.5957	36.1328	ENSG00000144063	MALL
ENSG00000144115	13.3097	12.0938	15.751	9.57661	ENSG00000144115	THNSL2
ENSG00000144118	23.6961	14.8907	14.4576	14.9221	ENSG00000144118	RALB
ENSG00000144119	0.0275382	0.215113	0.0479881	1.08797	ENSG00000144119	C1QL2
ENSG00000144120	5.74588	6.96612	7.58074	5.00688	ENSG00000144120	TMEM177
ENSG00000144130	2.57373	6.68716	5.64736	12.8731	ENSG00000144130	NT5DC4
ENSG00000144134	8.7044	14.9505	16.6916	14.2612	ENSG00000144134	RABL2A
ENSG00000144136	172.611	228.639	82.9332	240.093	ENSG00000144136	SLC20A1
ENSG00000144140	0	0	0	0	ENSG00000144140	RP11-143M1.7
ENSG00000144152	0.848154	1.67045	2.32897	17.5649	ENSG00000144152	FBLN7
ENSG00000144158	0	0	0	0	ENSG00000144158	RP11-395L14.17
ENSG00000144161	12.209	11.4715	19.6516	18.5721	ENSG00000144161	ZC3H8
ENSG00000144182	5.9386	15.024	15.5027	24.6145	ENSG00000144182	LIPT1
ENSG00000144188	0.537719	0.384353	0.471484	0.333694	ENSG00000144188	TRIM43CP

ENSG00000144191	0.093992	0.151639	0.551194	0.652536	ENSG00000144191	CNGA3
ENSG00000144199	7.37087	14.2464	13.275	8.75	ENSG00000144199	FAHD2B
ENSG00000144214	1.23335	1.01312	1.2858	1.72914	ENSG00000144214	LYG1
ENSG00000144218	3.03781	5.84328	7.16352	19.497	ENSG00000144218	AFF3
ENSG00000144224	29.7149	40.6564	39.537	44.9278	ENSG00000144224	UBXN4
ENSG00000144227	0.125765	0.27004	0.202255	0.571789	ENSG00000144227	NXPH2
ENSG00000144228	7.40501	9.15252	11.338	9.15843	ENSG00000144228	SPOPL
ENSG00000144229	0.157603	1.23131	0.318463	0.453906	ENSG00000144229	THSD7B
ENSG00000144230	0.0545429	0.22328	0.112123	1.86715	ENSG00000144230	GPR17
ENSG00000144231	7.50381	9.63967	11.3226	10.223	ENSG00000144231	POLR2D
ENSG00000144233	14.0848	13.2873	21.4357	9.78998	ENSG00000144233	AMMECR1L
ENSG00000144278	1.78837	2.66941	3.47541	4.16158	ENSG00000144278	GALNT13
ENSG00000144283	24.2105	55.7757	45.1988	37.7774	ENSG00000144283	PKP4
ENSG00000144285	1.35703	3.26178	4.21378	3.79056	ENSG00000144285	SCN1A
ENSG00000144290	3.82294	10.5558	11.4298	17.707	ENSG00000144290	SLC4A10
ENSG00000144306	18.9107	19.9042	25.4115	29.4717	ENSG00000144306	SCRN3
ENSG00000144320	30.8825	30.282	17.4113	21.8639	ENSG00000144320	LNPK
ENSG00000144331	0.720686	1.94842	1.31004	3.55238	ENSG00000144331	ZNF385B
ENSG00000144339	0.118318	1.12759	0.703202	4.64919	ENSG00000144339	TMEFF2
ENSG00000144354	2.84311	11.706	2.78633	5.33859	ENSG00000144354	CDCA7
ENSG00000144355	1.344	4.66327	0.744342	0.95188	ENSG00000144355	DLX1
ENSG00000144357	11.7987	16.4304	19.1926	27.3689	ENSG00000144357	UBR3
ENSG00000144362	3.76004	4.86139	7.62509	2.52201	ENSG00000144362	PHOSPHO2
ENSG00000144366	18.2924	12.9194	6.83288	9.5545	ENSG00000144366	GULP1
ENSG00000144369	2.67572	2.34107	3.33689	1.97129	ENSG00000144369	FAM171B
ENSG00000144381	111.673	165.576	192.514	116.563	ENSG00000144381	HSPD1
ENSG00000144395	4.04628	14.5765	5.68926	11.2435	ENSG00000144395	CCDC150
ENSG00000144401	15.8196	29.8725	26.8252	43.0773	ENSG00000144401	METTL21A
ENSG00000144406	16.3293	42.0604	38.0064	65.4628	ENSG00000144406	UNC80
ENSG00000144407	2.93322	7.25385	3.42773	5.80469	ENSG00000144407	PTH2R
ENSG00000144410	0.247179	0.285564	0.30112	0.0539878	ENSG00000144410	CPO
ENSG00000144426	32.1301	44.7912	34.9024	44.9106	ENSG00000144426	NBEAL1
ENSG00000144445	5.32287	10.5076	10.7275	13.8371	ENSG00000144445	KANSL1L
ENSG00000144451	16.1129	14.1569	12.5893	16.8745	ENSG00000144451	SPAG16
ENSG00000144452	41.2417	15.6483	37.0735	10.2511	ENSG00000144452	ABCA12
ENSG00000144455	33.2426	34.5996	20.9179	24.4118	ENSG00000144455	SUMF1
ENSG00000144460	0.205042	0.322597	0.52792	0.80404	ENSG00000144460	NYAP2
ENSG00000144468	21.865	51.2107	44.1295	31.057	ENSG00000144468	RHBDD1
ENSG00000144476	4.41197	1.22534	20.5399	4.45868	ENSG00000144476	ACKR3
ENSG00000144481	3.17605	5.71863	4.7047	11.25	ENSG00000144481	TRPM8
ENSG00000144485	2.01928	2.95599	1.84841	1.65111	ENSG00000144485	HES6
ENSG00000144488	0.788706	1.33647	0.634494	0.704569	ENSG00000144488	ESPNL
ENSG00000144504	3.28366	10.5545	15.2281	12.79	ENSG00000144504	ANKMY1
ENSG00000144524	20.0874	29.0089	31.7377	34.902	ENSG00000144524	COPS7B
ENSG00000144535	17.1583	23.6234	21.0309	20.9656	ENSG00000144535	DIS3L2
ENSG00000144550	0.121679	0.469893	0.104816	0.262508	ENSG00000144550	CPNE9
ENSG00000144554	10.8592	34.3546	14.1675	26.6836	ENSG00000144554	FANCD2
ENSG00000144559	5.08841	10.5369	10.7664	11.9229	ENSG00000144559	TAMM41
ENSG00000144560	35.4536	54.4929	56.8362	67.8984	ENSG00000144560	VGLL4
ENSG00000144566	30.1643	28.7363	35.5843	28.9205	ENSG00000144566	RAB5A
ENSG00000144567	35.6942	38.8239	34.6531	16.3119	ENSG00000144567	RETREG2
ENSG00000144579	32.8928	44.6227	37.4282	29.8692	ENSG00000144579	CTDSP1
ENSG00000144580	30.7545	40.6803	38.2965	36.7797	ENSG00000144580	CNOT9
ENSG00000144583	1.74921	1.92897	0.478666	2.43004	ENSG00000144583	MARCH4

ENSG00000144589	19.7812	27.7946	25.7983	17.3574	ENSG00000144589	STK11IP
ENSG00000144591	18.8056	22.7246	12.876	14.7533	ENSG00000144591	GMPPA
ENSG00000144597	12.6518	7.25758	11.8672	7.03367	ENSG00000144597	EAF1
ENSG00000144619	0.705419	1.73442	1.43774	3.00022	ENSG00000144619	CNTN4
ENSG00000144635	17.7385	26.0739	20.6841	19.0369	ENSG00000144635	DYNC1LI1
ENSG00000144642	6.62784	11.7724	21.2418	30.5628	ENSG00000144642	RBMS3
ENSG00000144644	3.7194	10.7952	9.41555	15.7298	ENSG00000144644	GADL1
ENSG00000144645	42.6161	73.934	45.4399	56.4417	ENSG00000144645	OSBPL10
ENSG00000144647	7.27763	5.49392	2.88329	2.74026	ENSG00000144647	POMGNT2
ENSG00000144648	3.16894	5.87504	4.80491	8.53973	ENSG00000144648	ACKR2
ENSG00000144649	0.486703	2.03771	3.10872	0.501095	ENSG00000144649	FAM198A
ENSG00000144655	7.63491	5.50432	2.61223	3.85367	ENSG00000144655	CSRNP1
ENSG00000144659	7.07943	9.00696	10.367	5.29289	ENSG00000144659	SLC25A38
ENSG00000144668	0.187841	0.664071	0.367173	0.476544	ENSG00000144668	ITGA9
ENSG00000144671	0.587734	0.335806	1.01451	1.29719	ENSG00000144671	SLC22A14
ENSG00000144674	60.6109	54.8128	55.2166	59.939	ENSG00000144674	GOLGA4
ENSG00000144677	21.7156	28.5132	25.9757	24.1851	ENSG00000144677	CTDSPL
ENSG00000144681	0.37704	1.82801	0.988976	0.569228	ENSG00000144681	STAC
ENSG00000144711	6.29275	7.25372	12.0612	10.3886	ENSG00000144711	IQSEC1
ENSG00000144712	0.933337	1.12992	1.70118	1.54907	ENSG00000144712	CAND2
ENSG00000144713	644.576	511.122	433.343	245.567	ENSG00000144713	RPL32
ENSG00000144724	17.2155	27.081	23.758	36.1258	ENSG00000144724	PTPRG
ENSG00000144730	2.23406	2.38652	1.98593	3.11235	ENSG00000144730	IL17RD
ENSG00000144736	9.13492	23.7373	19.6086	34.2679	ENSG00000144736	SHQ1
ENSG00000144741	6.89054	5.97651	6.66339	4.24912	ENSG00000144741	SLC25A26
ENSG00000144744	33.2421	38.7909	31.3258	31.7382	ENSG00000144744	UBA3
ENSG00000144746	75.3017	58.6626	39.7597	31.3923	ENSG00000144746	ARL6IP5
ENSG00000144747	32.057	28.0386	30.0823	38.0272	ENSG00000144747	TMF1
ENSG00000144749	3.57818	21.6815	12.2085	15.7085	ENSG00000144749	LRIG1
ENSG00000144771	0.132817	0.0439954	0.119298	0.242362	ENSG00000144771	LRTM1
ENSG00000144785	10.0475	7.06469	2.70477	3.55878	ENSG00000144785	RP11-977G19.10
ENSG00000144791	7.10628	13.3536	11.4147	24.4154	ENSG00000144791	LIMD1
ENSG00000144792	0.61239	1.682	1.97941	3.2384	ENSG00000144792	ZNF660
ENSG00000144802	78.8858	78.0497	88.0043	90.1695	ENSG00000144802	NFKBIZ
ENSG00000144810	33.9261	61.534	50.4618	119.084	ENSG00000144810	COL8A1
ENSG00000144815	5.21927	7.52463	10.2803	10.9135	ENSG00000144815	NXPE3
ENSG00000144820	0.39029	0.547375	53.3694	0.566044	ENSG00000144820	ADGRG7
ENSG00000144821	0.541479	2.40629	0.347508	1.98453	ENSG00000144821	MYH15
ENSG00000144824	189.115	154.383	133.635	96.9098	ENSG00000144824	PHLDB2
ENSG00000144827	6.5789	12.4155	7.1945	11.4159	ENSG00000144827	ABHD10
ENSG00000144834	4.18262	8.44244	1.50371	5.56803	ENSG00000144834	TAGLN3
ENSG00000144837	0.160182	0.196075	0.326373	0.297189	ENSG00000144837	PLA1A
ENSG00000144840	8.37704	7.31539	9.52918	9.92531	ENSG00000144840	RABL3
ENSG00000144843	0.48261	0.610467	0.700597	0.59068	ENSG00000144843	ADPRH
ENSG00000144847	1.88599	3.57926	3.35413	6.289	ENSG00000144847	IGSF11
ENSG00000144848	18.6152	19.7923	21.6425	19.4134	ENSG00000144848	ATG3
ENSG00000144852	0.193115	0.169018	0.143492	0.267187	ENSG00000144852	NR1I2
ENSG00000144857	2.84262	5.44057	6.59706	9.70712	ENSG00000144857	BOC
ENSG00000144867	41.2878	26.1321	30.6465	12.6039	ENSG00000144867	SRPRB
ENSG00000144868	0.742775	1.26181	1.14925	1.97335	ENSG00000144868	TMEM108
ENSG00000144891	0.112324	0.304721	0.401841	2.46088	ENSG00000144891	AGTR1
ENSG00000144893	4.52067	10.1667	6.73948	6.85698	ENSG00000144893	MED12L
ENSG00000144895	52.2447	64.8372	49.035	42.8876	ENSG00000144895	EIF2A
ENSG00000144908	4.53976	13.9756	8.97317	15.4734	ENSG00000144908	ALDH1L1

ENSG00000144909	5.05255	4.05853	5.79835	4.30986	ENSG00000144909	OSBPL11
ENSG00000144935	8.10287	14.7236	9.51583	13.2361	ENSG00000144935	TRPC1
ENSG00000144959	12.1618	24.9321	6.33305	8.71376	ENSG00000144959	NCEH1
ENSG00000144962	0.0799397	0.0785131	0.116092	0.116995	ENSG00000144962	SPATA16
ENSG00000145002	0.104724	0.708518	0.378508	0	ENSG00000145002	FAM86B2
ENSG00000145012	35.5483	48.143	48.3951	81.6974	ENSG00000145012	LPP
ENSG00000145014	17.1839	20.2073	19.0153	21.4741	ENSG00000145014	TMEM44
ENSG00000145016	24.9637	17.5978	18.9538	23.593	ENSG00000145016	RUBCN
ENSG00000145020	2.82536	11.2082	14.3005	9.13298	ENSG00000145020	AMT
ENSG00000145022	7.52514	5.04561	6.79291	6.48823	ENSG00000145022	TCTA
ENSG00000145029	6.10217	10.9706	13.2251	10.8335	ENSG00000145029	NICN1
ENSG00000145040	13.3232	26.0194	21.8782	23.0216	ENSG00000145040	UCN2
ENSG00000145041	4.01902	5.01565	4.14584	5.83929	ENSG00000145041	DCAF1
ENSG00000145050	42.7462	61.0704	21.1734	20.422	ENSG00000145050	MANF
ENSG00000145075	1.93124	6.03651	10.0395	10.1118	ENSG00000145075	CCDC39
ENSG00000145087	0.174283	0.621745	0.28	0.671444	ENSG00000145087	STXBP5L
ENSG00000145088	1.43364	0.700445	1.17322	1.57404	ENSG00000145088	EAF2
ENSG00000145103	2.12394	0.808825	0.741608	1.29648	ENSG00000145103	ILDR1
ENSG00000145107	22.5539	5.12465	3.4007	14.509	ENSG00000145107	TM4SF19
ENSG00000145113	0.646078	0.371226	0.793052	0.982764	ENSG00000145113	MUC4
ENSG00000145147	4.15569	14.5882	2.84496	34.5932	ENSG00000145147	SLIT2
ENSG00000145191	27.9259	32.1367	37.8095	25.5614	ENSG00000145191	EIF2B5
ENSG00000145192	0.147062	0.109452	0.157178	0.476357	ENSG00000145192	AHSG
ENSG00000145194	3.45064	3.53135	4.80041	2.87204	ENSG00000145194	ECE2
ENSG00000145198	0.116399	0.509287	0.570799	0.121518	ENSG00000145198	VWA5B2
ENSG00000145214	19.3638	19.4433	26.9542	11.8172	ENSG00000145214	DGKQ
ENSG00000145216	40.8222	40.6135	36.2628	35.2944	ENSG00000145216	FIP1L1
ENSG00000145217	12.0429	7.85103	15.6225	5.39783	ENSG00000145217	SLC26A1
ENSG00000145220	10.6857	11.6651	11.567	8.94069	ENSG00000145220	LYAR
ENSG00000145241	9.57283	17.7081	12.1005	16.242	ENSG00000145241	CENPC
ENSG00000145242	0.21057	0.405512	0.28463	0.730341	ENSG00000145242	EPHA5
ENSG00000145244	2.0549	4.90919	4.77445	7.85939	ENSG00000145244	CORIN
ENSG00000145246	45.6914	67.8689	70.6885	40.4384	ENSG00000145246	ATP10D
ENSG00000145247	69.6999	91.6428	46.9349	30.4721	ENSG00000145247	OCIAD2
ENSG00000145248	0.0636259	0.0919639	0.0831347	0.279035	ENSG00000145248	SLC10A4
ENSG00000145283	37.6537	9.3798	8.07346	14.5774	ENSG00000145283	SLC10A6
ENSG00000145284	87.3989	52.0444	51.8409	70.1592	ENSG00000145284	SCD5
ENSG00000145287	4.93475	12.3897	8.4057	15.8895	ENSG00000145287	PLAC8
ENSG00000145293	17.9351	13.9475	14.1991	11.1118	ENSG00000145293	ENOPH1
ENSG00000145309	0.037796	0.036409	0.197469	0.0413837	ENSG00000145309	CABS1
ENSG00000145321	0.0397064	0.0844262	0.152538	0.0351578	ENSG00000145321	GC
ENSG00000145331	4.42227	3.52699	5.34559	5.751	ENSG00000145331	TRMT10A
ENSG00000145332	3.63139	4.9852	4.24764	5.50109	ENSG00000145332	KLHL8
ENSG00000145335	9.40417	16.0983	14.9849	10.3696	ENSG00000145335	SNCA
ENSG00000145337	13.8111	14.423	13.6472	8.62545	ENSG00000145337	PYURF
ENSG00000145348	29.6213	77.1306	68.0082	89.413	ENSG00000145348	TBCK
ENSG00000145349	25.4	16.324	17.5227	20.4228	ENSG00000145349	CAMK2D
ENSG00000145354	16.831	20.3357	10.657	14.0802	ENSG00000145354	CISD2
ENSG00000145358	0.277275	0.523444	0.570196	0.468026	ENSG00000145358	DDIT4L
ENSG00000145362	2.60894	4.29564	10.6788	6.00812	ENSG00000145362	ANK2
ENSG00000145365	2.45131	3.68839	2.73966	2.12091	ENSG00000145365	TIFA
ENSG00000145375	6.03126	10.7333	5.2918	10.9124	ENSG00000145375	SPATA5
ENSG00000145384	1.33941	2.71868	2.70954	4.46532	ENSG00000145384	FABP2
ENSG00000145386	5.23677	26.2328	3.12751	7.02804	ENSG00000145386	CCNA2

ENSG00000145388	12.9704	12.3029	12.8273	9.92648	ENSG00000145388	METTL14
ENSG00000145390	52.7829	41.5438	36.6722	48.562	ENSG00000145390	USP53
ENSG00000145391	22.2886	15.269	20.8439	23.9874	ENSG00000145391	SETD7
ENSG00000145414	8.23185	9.93143	13.9925	13.3841	ENSG00000145414	NAF1
ENSG00000145416	2.4974	5.87338	5.75202	7.18846	ENSG00000145416	MARCH1
ENSG00000145423	0.0277	0	0	0.364775	ENSG00000145423	SFRP2
ENSG00000145425	519.458	369.381	357.217	230.728	ENSG00000145425	RPS3A
ENSG00000145428	1.49355	4.10934	3.64536	5.3911	ENSG00000145428	RNF175
ENSG00000145431	29.0783	35.2335	35.3127	47.0622	ENSG00000145431	PDGFC
ENSG00000145439	14.8646	25.4755	24.4042	27.0242	ENSG00000145439	CBR4
ENSG00000145451	0.362415	0.634847	0.654736	0.969278	ENSG00000145451	GLRA3
ENSG00000145476	1.92229	8.66054	7.5072	10.3037	ENSG00000145476	CYP4V2
ENSG00000145491	0.268897	0.353205	0.159626	0.406523	ENSG00000145491	ROPN1L
ENSG00000145494	18.1525	21.0953	16.5983	13.0431	ENSG00000145494	NDUFS6
ENSG00000145495	62.7701	101.776	70.2082	60.8059	ENSG00000145495	MARCH6
ENSG00000145506	0.3792	0.0563774	0.412277	2.92058	ENSG00000145506	NKD2
ENSG00000145526	4.51524	11.4529	9.53392	19.4983	ENSG00000145526	CDH18
ENSG00000145536	1.05634	1.72756	1.80385	4.24001	ENSG00000145536	ADAMTS16
ENSG00000145545	10.7739	12.712	22.868	8.1055	ENSG00000145545	SRD5A1
ENSG00000145555	38.1434	52.7059	39.74	74.8407	ENSG00000145555	MYO10
ENSG00000145569	2.8872	5.63512	3.01339	5.5679	ENSG00000145569	FAM105A
ENSG00000145592	647.648	519.295	454.449	267.286	ENSG00000145592	RPL37
ENSG00000145604	9.34274	15.3444	7.78767	11.6464	ENSG00000145604	SKP2
ENSG00000145623	40.6998	62.654	54.3404	35.9575	ENSG00000145623	OSMR
ENSG00000145626	1.08828	1.56452	1.87551	2.74053	ENSG00000145626	UGT3A1
ENSG00000145632	305.179	134.789	115.594	73.6224	ENSG00000145632	PLK2
ENSG00000145642	0.599186	1.1739	1.69653	0.884985	ENSG00000145642	FAM159B
ENSG00000145649	0	0	0	0	ENSG00000145649	GZMA
ENSG00000145675	12.9442	36.0255	31.8598	28.3625	ENSG00000145675	PIK3R1
ENSG00000145681	0.144534	0.241632	0.340508	1.26304	ENSG00000145681	HAPLN1
ENSG00000145685	42.8576	28.4446	27.4606	32.2195	ENSG00000145685	LHFPL2
ENSG00000145687	28.1454	71.9822	71.5707	107.98	ENSG00000145687	SSBP2
ENSG00000145692	1.40579	3.24774	5.39805	6.43819	ENSG00000145692	BHMT
ENSG00000145700	0.252867	0.206269	0.314182	0.213971	ENSG00000145700	ANKRD31
ENSG00000145703	0.698529	1.86049	2.57372	6.48288	ENSG00000145703	IQGAP2
ENSG00000145708	0.13168	0.273388	0.445653	1.18678	ENSG00000145708	CRHBP
ENSG00000145715	100.991	30.1903	26.3538	42.3375	ENSG00000145715	RASA1
ENSG00000145721	0.304238	0.978609	0.572426	1.17989	ENSG00000145721	LIX1
ENSG00000145723	2.67156	4.96934	3.79857	3.37823	ENSG00000145723	GIN1
ENSG00000145725	11.7544	14.2905	16.4871	19.86	ENSG00000145725	PPIP5K2
ENSG00000145730	68.6653	87.6468	83.3295	77.6132	ENSG00000145730	PAM
ENSG00000145734	8.12416	10.1393	9.81113	12.1967	ENSG00000145734	BDP1
ENSG00000145736	9.77651	11.1031	10.1157	16.5639	ENSG00000145736	GTF2H2
ENSG00000145740	35.1468	42.0273	30.3718	32.5127	ENSG00000145740	SLC30A5
ENSG00000145741	200.56	146.032	128.016	93.2417	ENSG00000145741	BTF3
ENSG00000145743	8.98935	12.3612	11.1818	9.2951	ENSG00000145743	FBXL17
ENSG00000145757	0.442999	0.174957	0.367677	0.501186	ENSG00000145757	SPATA9
ENSG00000145777	0.138215	0.43507	1.30499	0.253059	ENSG00000145777	TSLP
ENSG00000145779	12.1528	19.9007	14.8798	16.7358	ENSG00000145779	TNFAIP8
ENSG00000145780	5.2737	4.5602	4.29513	5.56008	ENSG00000145780	FEM1C
ENSG00000145781	13.4941	13.4032	13.3208	10.2891	ENSG00000145781	COMMD10
ENSG00000145782	21.3517	29.536	24.3387	25.6064	ENSG00000145782	ATG12
ENSG00000145794	0.848459	0.569263	0.416353	7.04663	ENSG00000145794	MEGF10
ENSG00000145808	0.341753	0.190281	0.407874	0.30817	ENSG00000145808	ADAMTS19

ENSG00000145817	51.2975	39.7375	24.5441	21.1166	ENSG00000145817	YIPF5
ENSG00000145819	9.57314	18.5995	64.2321	14.2235	ENSG00000145819	ARHGAP26
ENSG00000145824	0.400589	0.420441	21.301	0.53378	ENSG00000145824	CXCL14
ENSG00000145826	3.4046	10.0235	7.52281	19.9541	ENSG00000145826	LECT2
ENSG00000145832	0.275234	0.489751	1.27301	1.76132	ENSG00000145832	SLC25A48
ENSG00000145833	20.5508	29.7214	26.4977	38.68	ENSG00000145833	DDX46
ENSG00000145835	0	0	0	0	ENSG00000145835	CDKN2AIPNLP2
ENSG00000145839	0	0	0	0	ENSG00000145839	IL9
ENSG00000145850	0.210758	0.354766	0.852345	0.886961	ENSG00000145850	TIMD4
ENSG00000145860	75.9283	53.514	46.3191	28.4233	ENSG00000145860	RNF145
ENSG00000145861	0.501496	0.683307	0.763854	1.73935	ENSG00000145861	C1QTNF2
ENSG00000145863	1.00644	2.12809	2.65153	3.41812	ENSG00000145863	GABRA6
ENSG00000145864	0.250319	0.32048	0.259739	0.684386	ENSG00000145864	GABRB2
ENSG00000145868	42.8772	52.5872	47.546	52.6867	ENSG00000145868	FBXO38
ENSG00000145879	8.31155	1.56172	0.959799	6.64247	ENSG00000145879	SPINK7
ENSG00000145882	5.31397	9.17557	7.68633	5.16882	ENSG00000145882	PCYOX1L
ENSG00000145888	0.256435	1.01425	0.90026	1.3595	ENSG00000145888	GLRA1
ENSG00000145901	91.8657	54.7368	58.7108	75.8185	ENSG00000145901	TNIP1
ENSG00000145907	101.981	101.219	82.8291	81.3409	ENSG00000145907	G3BP1
ENSG00000145908	5.36986	9.29652	6.85258	4.49181	ENSG00000145908	ZNF300
ENSG00000145911	2.15738	2.97151	2.29167	1.26428	ENSG00000145911	N4BP3
ENSG00000145912	32.774	35.825	33.2497	25.1243	ENSG00000145912	NHP2
ENSG00000145916	14.8954	18.2885	19.2181	20.8202	ENSG00000145916	RMND5B
ENSG00000145919	20.807	28.372	33.2777	17.7805	ENSG00000145919	BOD1
ENSG00000145920	1.18433	3.47271	3.4512	4.75239	ENSG00000145920	CPLX2
ENSG00000145934	65.9764	179.411	330.027	115.443	ENSG00000145934	TENM2
ENSG00000145936	2.91544	5.68363	5.09897	9.42076	ENSG00000145936	KCNMB1
ENSG00000145945	1.48361	1.21933	1.2207	1.16235	ENSG00000145945	FAM50B
ENSG00000145949	0.284497	0.650058	0.749549	0.695971	ENSG00000145949	MYLK4
ENSG00000145965	5.53666	14.4089	12.036	19.3262	ENSG00000145965	C6ORF50
ENSG00000145975	3.76271	4.93782	3.47131	6.7565	ENSG00000145975	FAM217A
ENSG00000145979	11.5281	15.9903	21.0778	21.8562	ENSG00000145979	TBC1D7
ENSG00000145982	8.90564	13.1201	11.3642	12.1147	ENSG00000145982	FARS2
ENSG00000145990	7.13528	4.255	10.1114	5.99123	ENSG00000145990	GFOD1
ENSG00000145996	8.81462	10.9696	8.26036	9.35014	ENSG00000145996	CDKAL1
ENSG00000146001	0.0448865	0.00841702	0.0559991	0.0871754	ENSG00000146001	PCDHB18P
ENSG00000146005	0.0944229	0.0512728	0.030848	0.182095	ENSG00000146005	PSD2
ENSG00000146006	1.52087	2.75328	3.42988	4.34917	ENSG00000146006	LRRTM2
ENSG00000146007	28.8046	15.8072	18.4492	12.954	ENSG00000146007	ZMAT2
ENSG00000146013	0.0309594	0.159585	0.024045	0.151467	ENSG00000146013	GFRA3
ENSG00000146021	4.37429	10.3618	9.99619	9.62946	ENSG00000146021	KLHL3
ENSG00000146038	0.397255	0.49817	0.41245	0.742117	ENSG00000146038	DCDC2
ENSG00000146039	0.103283	0.106709	0.290491	0.347123	ENSG00000146039	SLC17A4
ENSG00000146047	0	0	0	0	ENSG00000146047	HIST1H2BA
ENSG00000146049	0.0526953	0.0833467	0.0747829	0.0968017	ENSG00000146049	KAAG1
ENSG00000146054	13.524	21.1678	11.9401	8.82691	ENSG00000146054	TRIM7
ENSG00000146063	9.62727	15.2776	15.0604	14.1572	ENSG00000146063	TRIM41
ENSG00000146066	20.2794	19.1419	16.2738	15.5588	ENSG00000146066	HIGD2A
ENSG00000146067	36.251	71.4675	65.0855	57.3293	ENSG00000146067	FAM193B
ENSG00000146070	9.62335	4.27868	1.20571	3.20838	ENSG00000146070	PLA2G7
ENSG00000146072	58.0149	114.142	71.2232	43.072	ENSG00000146072	TNFRSF21
ENSG00000146083	19.5904	17.0852	24.8952	15.2389	ENSG00000146083	RNF44
ENSG00000146085	6.67694	9.83797	5.42622	7.84884	ENSG00000146085	MUT

ENSG00000146090	0.432586	2.1138	1.87564	1.04552	ENSG00000146090	RASGEF1C
ENSG00000146094	2.35159	3.26216	7.58347	3.30512	ENSG00000146094	DOK3
ENSG00000146109	4.2123	2.95422	3.10517	2.43695	ENSG00000146109	ABT1
ENSG00000146112	9.90866	12.4966	9.60299	9.331	ENSG00000146112	PPP1R18
ENSG00000146122	0.750312	2.16223	0.486816	9.33023	ENSG00000146122	DAAM2
ENSG00000146143	12.7097	21.9625	10.9085	28.7646	ENSG00000146143	PRIM2
ENSG00000146147	3.67807	2.9284	2.79965	4.4718	ENSG00000146147	MLIP
ENSG00000146151	0.227727	0.419145	0.478397	0.573436	ENSG00000146151	HMGCLL1
ENSG00000146166	1.63701	1.36954	1.77462	1.75102	ENSG00000146166	LGSN
ENSG00000146192	3.82538	6.69647	6.2949	10.0402	ENSG00000146192	FGD2
ENSG00000146197	0.571546	1.24766	1.12846	3.14519	ENSG00000146197	SCUBE3
ENSG00000146205	0.867048	1.22789	0.999133	1.96467	ENSG00000146205	ANO7
ENSG00000146215	0.25423	1.29311	0.362931	0.857906	ENSG00000146215	CRIP3
ENSG00000146216	0.205931	0.185592	0.213191	0.224514	ENSG00000146216	TTBK1
ENSG00000146221	0.208768	0.278265	0.527247	0.94251	ENSG00000146221	TCTE1
ENSG00000146223	67.6558	63.9942	73.5351	67.435	ENSG00000146223	RPL7L1
ENSG00000146232	4.62725	5.20072	4.91166	3.66773	ENSG00000146232	NFKBIE
ENSG00000146233	0.334376	2.14216	4.45405	0.508933	ENSG00000146233	CYP39A1
ENSG00000146242	40.3234	125.193	107.769	46.9087	ENSG00000146242	TPBG
ENSG00000146243	3.66801	7.44621	9.73406	10.9885	ENSG00000146243	IRAK1BP1
ENSG00000146247	10.6594	15.5966	14.5216	14.2278	ENSG00000146247	PHIP
ENSG00000146250	0.33395	0.419808	0.399252	0.505485	ENSG00000146250	PRSS35
ENSG00000146263	9.39987	24.6907	15.3917	28.2383	ENSG00000146263	MMS22L
ENSG00000146267	1.25284	1.21206	1.33436	1.37909	ENSG00000146267	FAXC
ENSG00000146276	0.0389872	0.175486	0.156085	0.210935	ENSG00000146276	GABRR1
ENSG00000146278	22.0545	16.8086	33.6104	23.8593	ENSG00000146278	PNRC1
ENSG00000146281	4.73076	4.68484	3.65472	4.56629	ENSG00000146281	PM20D2
ENSG00000146282	22.7348	23.8096	27.8445	26.9614	ENSG00000146282	RARS2
ENSG00000146285	0.671834	1.8834	1.4744	2.82657	ENSG00000146285	SCML4
ENSG00000146350	18.8348	38.3349	37.1073	76.9562	ENSG00000146350	TBC1D32
ENSG00000146352	0.113481	0.307392	0.131893	0.281981	ENSG00000146352	CLVS2
ENSG00000146360	0	0	0.0617221	0.0388034	ENSG00000146360	GPR6
ENSG00000146373	71.5124	47.9168	50.3141	50.7912	ENSG00000146373	RNF217
ENSG00000146374	0.229458	0.415215	0.394682	2.59776	ENSG00000146374	RSPO3
ENSG00000146376	16.3945	33.0172	7.13777	32.8763	ENSG00000146376	ARHGAP18
ENSG00000146378	0.208059	0.211539	0.762029	0.621685	ENSG00000146378	TAAR2
ENSG00000146383	0.177198	0.341028	0.102735	0.261002	ENSG00000146383	TAAR6
ENSG00000146385	0	0.2297	0	0.195073	ENSG00000146385	TAAR8
ENSG00000146386	44.084	24.4472	13.6845	17.3786	ENSG00000146386	ABRACL
ENSG00000146399	0.0603025	0	0	0.262783	ENSG00000146399	TAAR1
ENSG00000146409	11.7889	16.139	13.3291	7.40934	ENSG00000146409	SLC18B1
ENSG00000146410	0.882799	3.27205	1.54255	2.00818	ENSG00000146410	MTFR2
ENSG00000146411	4.02924	2.08209	1.96746	0.625688	ENSG00000146411	SLC2A12
ENSG00000146414	9.30195	15.9037	15.3327	20.0793	ENSG00000146414	SHPRH
ENSG00000146416	57.4436	84.1038	52.0568	35.8806	ENSG00000146416	AIG1
ENSG00000146425	35.5156	23.9263	26.3531	23.0855	ENSG00000146425	DYNLT1
ENSG00000146426	12.8075	26.4706	18.0408	35.7223	ENSG00000146426	TIAM2
ENSG00000146433	24.8816	35.0779	26.4881	21.7609	ENSG00000146433	TMEM181
ENSG00000146453	0.58013	0.628242	0.716829	0.900867	ENSG00000146453	PNLDC1
ENSG00000146457	30.8662	40.3081	48.5967	54.0269	ENSG00000146457	WTAP
ENSG00000146463	22.6989	32.15	36.43	41.6332	ENSG00000146463	ZMYM4
ENSG00000146469	0	0	0.165552	0	ENSG00000146469	VIP
ENSG00000146476	13.5907	12.2457	6.16618	6.96372	ENSG00000146476	ARMT1
ENSG00000146477	4.39101	2.26299	12.0177	4.65733	ENSG00000146477	SLC22A3

ENSG00000146521	0.979471	1.95616	1.75887	2.64247	ENSG00000146521	LINC01558
ENSG00000146530	1.40792	3.58795	3.92112	0.933117	ENSG00000146530	VWDE
ENSG00000146535	7.89693	10.94	14.0166	21.6355	ENSG00000146535	GNA12
ENSG00000146540	28.7387	30.3323	26.6388	14.2844	ENSG00000146540	C7orf50
ENSG00000146555	0.216751	0.714714	1.76704	3.3477	ENSG00000146555	SDK1
ENSG00000146556	11.8419	12.4731	11.6699	11.1228	ENSG00000146556	WASH2P
ENSG00000146574	28.731	39.3344	47.8414	44.2267	ENSG00000146574	CCZ1B
ENSG00000146576	9.41182	10.7884	14.2152	11.7277	ENSG00000146576	C7orf26
ENSG00000146587	7.4243	9.10119	12.6561	11.3142	ENSG00000146587	RBAK
ENSG00000146592	1.19562	19.2024	25.5286	17.8321	ENSG00000146592	CREB5
ENSG00000146618	0	0	0	0	ENSG00000146618	FERD3L
ENSG00000146648	143.906	232.396	279.373	124.577	ENSG00000146648	EGFR
ENSG00000146670	2.59277	10.8259	1.65149	4.5588	ENSG00000146670	CDCA5
ENSG00000146674	34.945	1.01504	2.28955	41.3199	ENSG00000146674	IGFBP3
ENSG00000146676	7.21767	7.37809	10.988	9.56024	ENSG00000146676	PURB
ENSG00000146677	1.5049	3.90468	2.81936	4.12599	ENSG00000146677	AC004453.1
ENSG00000146678	0.148635	0.28559	0.227702	0.201042	ENSG00000146678	IGFBP1
ENSG00000146700	0.487388	0.635761	2.68984	0.955719	ENSG00000146700	SSC4D
ENSG00000146701	22.8288	25.6887	21.8568	19.9699	ENSG00000146701	MDH2
ENSG00000146707	7.27622	11.9688	9.92225	13.0917	ENSG00000146707	POMZP3
ENSG00000146722	0.294268	0.215491	0.956374	0.643708	ENSG00000146722	AC211486.1
ENSG00000146729	18.2515	28.3669	27.7779	29.9706	ENSG00000146729	NIPSNAP2
ENSG00000146731	81.5006	86.7351	96.2517	63.0676	ENSG00000146731	CCT6A
ENSG00000146733	18.7918	33.7986	41.8474	19.0133	ENSG00000146733	PSPH
ENSG00000146755	0.0149215	0.0177657	0.0279366	0	ENSG00000146755	TRIM50
ENSG00000146757	5.76198	7.85431	4.3604	4.80527	ENSG00000146757	ZNF92
ENSG00000146776	6.38108	9.99935	8.20221	7.53857	ENSG00000146776	ATXN7L1
ENSG00000146802	15.9043	24.7844	23.1839	14.7539	ENSG00000146802	TMEM168
ENSG00000146809	0.122199	0.199033	0.332352	0.471966	ENSG00000146809	ASB15
ENSG00000146826	15.7034	14.9295	17.8864	11.6707	ENSG00000146826	C7orf43
ENSG00000146828	23.3813	26.6213	29.511	24.6007	ENSG00000146828	SLC12A9
ENSG00000146830	16.7516	22.2793	19.9833	18.6145	ENSG00000146830	GIGYF1
ENSG00000146833	14.9439	14.7233	18.5836	18.526	ENSG00000146833	TRIM4
ENSG00000146834	10.709	16.4897	18.6189	11.7125	ENSG00000146834	MEPCE
ENSG00000146839	0.0127098	0.0541909	0.0114868	0.0763723	ENSG00000146839	ZAN
ENSG00000146842	21.379	37.7131	31.9325	34.1457	ENSG00000146842	TMEM209
ENSG00000146856	1.96538	5.34747	2.6864	5.40537	ENSG00000146856	AGBL3
ENSG00000146857	0	0.359397	0.21653	0.0677962	ENSG00000146857	STRA8
ENSG00000146858	5.91117	6.38944	7.51853	10.3053	ENSG00000146858	ZC3HAV1L
ENSG00000146859	24.5159	55.7261	50.0636	83.257	ENSG00000146859	TMEM140
ENSG00000146872	25.5017	40.9437	43.9131	51.1423	ENSG00000146872	TLK2
ENSG00000146904	44.5005	85.7282	40.8139	41.0006	ENSG00000146904	EPHA1
ENSG00000146909	11.5394	18.9372	20.675	22.9592	ENSG00000146909	NOM1
ENSG00000146910	2.11666	2.96892	3.09078	6.10203	ENSG00000146910	CNPY1
ENSG00000146918	3.85971	18.6572	4.79632	12.5544	ENSG00000146918	NCAPG2
ENSG00000146926	0.177755	0.512377	0.417905	0.490508	ENSG00000146926	ASB10
ENSG00000146938	0.207165	0.568346	0.286672	0.64513	ENSG00000146938	NLGN4X
ENSG00000146950	4.30413	6.37833	4.15104	7.64102	ENSG00000146950	SHROOM2
ENSG00000146955	0.0783088	0	0	0.0849613	ENSG00000146955	RAB19
ENSG00000146963	31.6607	50.74	62.2346	53.3539	ENSG00000146963	LUC7L2
ENSG00000146966	1.26028	2.61342	2.00948	11.457	ENSG00000146966	DENND2A
ENSG00000147003	0.914245	0.775057	0.57323	0.120156	ENSG00000147003	TMEM27
ENSG00000147010	20.8406	16.2757	10.4871	16.5804	ENSG00000147010	SH3KBP1
ENSG00000147027	0.15979	2.34238	0.5939	5.83529	ENSG00000147027	TMEM47

ENSG00000147036	0.387593	0.480455	0.263677	0.531088	ENSG00000147036	LANCL3
ENSG00000147041	0.477621	0.187115	0.0398265	0.477864	ENSG00000147041	SYTL5
ENSG00000147044	20.3721	27.1913	32.6261	17.9031	ENSG00000147044	CASK
ENSG00000147050	30.2346	24.7931	26.0336	35.5613	ENSG00000147050	KDM6A
ENSG00000147059	0.588913	1.2661	1.2281	1.82962	ENSG00000147059	SPIN2A
ENSG00000147065	190.094	226.699	71.4397	190.913	ENSG00000147065	MSN
ENSG00000147081	0.0340276	0.0311992	0.0582165	0.0532281	ENSG00000147081	AKAP4
ENSG00000147082	0.0602201	0.153425	0.264517	0.114834	ENSG00000147082	CCNB3
ENSG00000147099	7.24052	9.78437	8.7016	11.2435	ENSG00000147099	HDAC8
ENSG00000147100	18.0215	18.6096	5.70569	7.41002	ENSG00000147100	SLC16A2
ENSG00000147113	1.94817	4.76286	4.34457	7.05713	ENSG00000147113	CXorf36
ENSG00000147117	0.779752	1.7361	1.2827	3.49857	ENSG00000147117	ZNF157
ENSG00000147118	0.765516	1.46781	1.7399	1.67938	ENSG00000147118	ZNF182
ENSG00000147119	1.22174	2.06605	0.998006	2.40734	ENSG00000147119	CHST7
ENSG00000147121	7.98073	13.9039	12.6046	12.2446	ENSG00000147121	KRBOX4
ENSG00000147123	19.2887	8.73425	5.36901	6.15278	ENSG00000147123	NDUFB11
ENSG00000147124	4.06183	4.22089	4.14091	4.64336	ENSG00000147124	ZNF41
ENSG00000147127	1.19595	1.08298	1.02482	0.868505	ENSG00000147127	RAB41
ENSG00000147130	7.9181	10.5191	9.34731	10.6504	ENSG00000147130	ZMYM3
ENSG00000147133	14.1504	30.5511	28.5676	38.2043	ENSG00000147133	TAF1
ENSG00000147138	0.0944587	0.0909494	0.0822051	0.103207	ENSG00000147138	GPR174
ENSG00000147140	104.623	99.0197	129.588	97.2954	ENSG00000147140	NONO
ENSG00000147144	12.7028	6.37126	12.4517	8.94285	ENSG00000147144	CCDC120
ENSG00000147145	0.504819	0.856902	0.874919	4.65881	ENSG00000147145	LPAR4
ENSG00000147155	86.7328	97.7141	13.3466	24.2009	ENSG00000147155	EBP
ENSG00000147160	0.232165	0.595163	0.301891	0.938576	ENSG00000147160	AWAT2
ENSG00000147162	55.8093	103.505	145.248	78.2945	ENSG00000147162	OGT
ENSG00000147164	19.7195	14.4814	17.2707	12.8392	ENSG00000147164	SNX12
ENSG00000147166	0.962269	2.82486	3.4215	3.31327	ENSG00000147166	ITGB1BP2
ENSG00000147168	0.754024	1.80374	2.70645	4.42684	ENSG00000147168	IL2RG
ENSG00000147174	0.73792	2.36774	1.97941	2.08956	ENSG00000147174	GCNA
ENSG00000147180	1.85944	2.53873	6.56435	2.57429	ENSG00000147180	ZNF711
ENSG00000147183	0.0365956	0.141019	0.159343	0.16032	ENSG00000147183	CPXCR1
ENSG00000147202	5.89723	13.2874	9.47668	14.8948	ENSG00000147202	DIAPH2
ENSG00000147206	0.452695	0.238112	0.129822	0.331625	ENSG00000147206	NXF3
ENSG00000147223	0.414057	0.079592	0.0445854	0.361223	ENSG00000147223	RIPPLY1
ENSG00000147224	9.02387	7.77051	4.60644	5.81306	ENSG00000147224	PRPS1
ENSG00000147231	2.36643	7.41882	3.10376	4.51419	ENSG00000147231	CXorf57
ENSG00000147234	0.428429	0.709654	0.659764	1.0766	ENSG00000147234	FRMPD3
ENSG00000147246	0.0288577	0.100819	0.0858465	0.162255	ENSG00000147246	HTR2C
ENSG00000147251	1.00274	5.32374	3.35084	5.6922	ENSG00000147251	DOCK11
ENSG00000147255	0.490666	1.70786	1.69633	2.32906	ENSG00000147255	IGSF1
ENSG00000147256	0	0.0874423	0.0592827	0.0997926	ENSG00000147256	ARHGAP36
ENSG00000147257	0.101024	0.161478	0.310701	0.30972	ENSG00000147257	GPC3
ENSG00000147262	0	0	0	0	ENSG00000147262	GPR119
ENSG00000147274	61.8187	93.1727	84.451	54.1177	ENSG00000147274	RBMX
ENSG00000147316	12.9059	19.2895	19.8559	19.2316	ENSG00000147316	MCPH1
ENSG00000147324	6.82743	7.39129	6.77803	5.58289	ENSG00000147324	MFHAS1
ENSG00000147364	12.6945	17.5626	24.1986	20.8064	ENSG00000147364	FBXO25
ENSG00000147378	0.11411	0.0547246	0.0494585	0.55797	ENSG00000147378	FATE1
ENSG00000147380	0	0	0	0	ENSG00000147380	OPN1MW
ENSG00000147381	0.0687751	0.225911	0.144277	0.0779439	ENSG00000147381	MAGEA4
ENSG00000147382	7.44475	10.2837	7.35806	12.4248	ENSG00000147382	FAM58A
ENSG00000147383	13.0684	6.64504	3.71131	5.32819	ENSG00000147383	NSDHL

ENSG00000147394	75.1165	26.4508	17.5909	12.9591	ENSG00000147394	ZNF185
ENSG00000147400	6.95576	5.7747	3.64917	4.12646	ENSG00000147400	CETN2
ENSG00000147402	0.0872403	0.0480817	0.0753371	0.0690827	ENSG00000147402	GABRQ
ENSG00000147403	142.844	106.556	68.4335	51.1297	ENSG00000147403	RPL10
ENSG00000147408	2.47132	2.37503	2.85375	5.97239	ENSG00000147408	CSGALNACT1
ENSG00000147416	27.4328	25.2882	25.8083	23.7951	ENSG00000147416	ATP6V1B2
ENSG00000147419	15.7828	18.3152	16.9373	14.6173	ENSG00000147419	CCDC25
ENSG00000147421	22.9025	42.9986	33.6136	34.7697	ENSG00000147421	HMBOX1
ENSG00000147432	0	0	0.134357	0.82874	ENSG00000147432	CHRNB3
ENSG00000147434	0.140127	0.493801	0.242711	0.716093	ENSG00000147434	CHRNA6
ENSG00000147437	3.44974	6.39385	5.21809	4.43673	ENSG00000147437	GNRH1
ENSG00000147439	25.2432	27.9223	32.3102	24.6003	ENSG00000147439	BIN3
ENSG00000147443	0.262193	0.372245	0.156672	0.485963	ENSG00000147443	DOK2
ENSG00000147454	17.5689	32.2037	26.0215	35.8608	ENSG00000147454	SLC25A37
ENSG00000147457	15.0855	15.6559	14.2066	14.8464	ENSG00000147457	CHMP7
ENSG00000147459	59.4281	94.63	58.85	115.776	ENSG00000147459	DOCK5
ENSG00000147465	0.431449	0.744422	0.528547	0.780174	ENSG00000147465	STAR
ENSG00000147471	9.65214	9.66542	8.72539	7.91221	ENSG00000147471	PLPBP
ENSG00000147475	22.0881	39.9676	32.0106	16.7673	ENSG00000147475	ERLIN2
ENSG00000147481	2.2068	4.41934	3.30562	10.9511	ENSG00000147481	SNTG1
ENSG00000147485	0.441903	0.268566	0.389766	0.713336	ENSG00000147485	PXDNL
ENSG00000147488	3.33552	3.87355	4.53135	9.56557	ENSG00000147488	ST18
ENSG00000147509	28.0984	18.5577	12.2494	21.4431	ENSG00000147509	RGS20
ENSG00000147526	30.2105	39.2838	33.3298	44.7779	ENSG00000147526	TACC1
ENSG00000147533	24.1042	12.1975	15.0634	12.3068	ENSG00000147533	GOLGA7
ENSG00000147535	26.7083	40.561	28.3503	33.5231	ENSG00000147535	PLPP5
ENSG00000147536	4.85001	13.2698	10.0715	13.5319	ENSG00000147536	GINS4
ENSG00000147548	22.7062	41.8673	31.99	35.6927	ENSG00000147548	NSD3
ENSG00000147570	0.437675	1.20063	1.10475	1.58101	ENSG00000147570	DNAJC5B
ENSG00000147571	0	0.108672	0.0327212	0.205729	ENSG00000147571	CRH
ENSG00000147573	0.0735333	0.141429	0.128402	0.300671	ENSG00000147573	TRIM55
ENSG00000147576	2.05344	5.6887	4.13747	4.73597	ENSG00000147576	ADHFE1
ENSG00000147586	44.1876	69.8651	51.4824	74.5763	ENSG00000147586	MRPS28
ENSG00000147588	0.499716	1.01272	0.89131	1.48641	ENSG00000147588	PMP2
ENSG00000147592	9.08258	7.80577	7.23664	4.73986	ENSG00000147592	LACTB2
ENSG00000147596	0.392284	1.09273	1.13086	1.48205	ENSG00000147596	PRDM14
ENSG00000147601	11.2216	22.119	18.1881	27.4881	ENSG00000147601	TERF1
ENSG00000147604	527.061	438.032	290.606	211.531	ENSG00000147604	RPL7
ENSG00000147606	0.300418	1.00653	1.19229	1.00102	ENSG00000147606	SLC26A7
ENSG00000147613	0	0.0429753	0	0	ENSG00000147613	PSKH2
ENSG00000147614	2.1096	4.07689	3.55611	6.80278	ENSG00000147614	ATP6V0D2
ENSG00000147642	2.25911	11.1464	16.1292	4.61743	ENSG00000147642	SYBU
ENSG00000147647	0.592145	0.714484	0.726691	2.43769	ENSG00000147647	DPYS
ENSG00000147649	101.685	97.5657	71.4791	49.2483	ENSG00000147649	MTDH
ENSG00000147650	14.225	19.8882	23.9392	24.0727	ENSG00000147650	LRP12
ENSG00000147654	9.97911	14.3756	12.1079	10.0305	ENSG00000147654	EBAG9
ENSG00000147655	0.512899	0.869612	0.380026	1.57775	ENSG00000147655	RSPO2
ENSG00000147669	20.3546	16.3636	18.5577	16.3317	ENSG00000147669	POLR2K
ENSG00000147676	66.3466	26.0194	25.7211	6.9073	ENSG00000147676	MAL2
ENSG00000147677	64.8418	58.0348	55.4833	43.3055	ENSG00000147677	EIF3H
ENSG00000147679	8.56739	10.2819	11.8173	9.58662	ENSG00000147679	UTP23
ENSG00000147684	68.05	98.2853	72.2131	54.8775	ENSG00000147684	NDUFB9
ENSG00000147687	18.0388	21.207	20.8073	17.2933	ENSG00000147687	TATDN1
ENSG00000147689	3691.76	6254.68	7090.1	1732.39	ENSG00000147689	FAM83A

ENSG00000147697	15.1726	27.4784	21.779	22.7847	ENSG00000147697	GSDMC
ENSG00000147724	3.80927	11.3884	9.68949	15.1602	ENSG00000147724	FAM135B
ENSG00000147789	20.2235	30.7838	43.603	61.1412	ENSG00000147789	ZNF7
ENSG00000147799	4.8251	4.03337	5.19386	4.1252	ENSG00000147799	ARHGAP39
ENSG00000147804	3.13517	6.0836	5.15625	3.37636	ENSG00000147804	SLC39A4
ENSG00000147813	38.031	65.5101	34.5386	33.1769	ENSG00000147813	NAPRT
ENSG00000147852	12.5259	16.6779	17.7568	7.35982	ENSG00000147852	VLDLR
ENSG00000147853	15.5973	18.0037	19.2624	16.9871	ENSG00000147853	AK3
ENSG00000147854	41.6773	71.4099	31.4996	74.344	ENSG00000147854	UHRF2
ENSG00000147862	9.67513	25.2942	34.8587	17.9359	ENSG00000147862	NFIB
ENSG00000147869	0.0983094	0.0473239	0	0.161052	ENSG00000147869	CER1
ENSG00000147872	6.76974	14.8245	29.0724	21.9041	ENSG00000147872	PLIN2
ENSG00000147873	0	0.0921942	0	0	ENSG00000147873	IFNA5
ENSG00000147874	8.94053	16.4764	13.0737	13.307	ENSG00000147874	HAUS6
ENSG00000147883	22.6217	9.14379	49.3585	13.3024	ENSG00000147883	CDKN2B
ENSG00000147885	0	0	0	0.0950243	ENSG00000147885	IFNA16
ENSG00000147889	18.6424	15.4138	36.7491	15.6554	ENSG00000147889	CDKN2A
ENSG00000147894	5.00366	10.3278	6.26733	5.67945	ENSG00000147894	C9orf72
ENSG00000147896	17.5224	10.405	2.9924	21.4563	ENSG00000147896	IFNK
ENSG00000147905	10.4292	18.6203	18.3285	21.8296	ENSG00000147905	ZCCHC7
ENSG00000147912	6.12679	3.23545	5.39994	5.96675	ENSG00000147912	FBXO10
ENSG00000147926	0	0	0	0	ENSG00000147926	SPATA31A3
ENSG00000147955	66.4349	61.4656	46.153	31.5274	ENSG00000147955	SIGMAR1
ENSG00000147996	31.0467	64.4862	80.1948	49.4242	ENSG00000147996	CBWD5
ENSG00000148019	14.2008	21.1188	22.5078	14.4304	ENSG00000148019	CEP78
ENSG00000148053	0.192245	0.634198	0.534648	0.738313	ENSG00000148053	NTRK2
ENSG00000148057	2.39724	3.94547	5.1028	4.00611	ENSG00000148057	IDNK
ENSG00000148082	0.142382	0.545323	0.640878	0.743419	ENSG00000148082	SHC3
ENSG00000148090	17.0891	27.625	30.25	35.0288	ENSG00000148090	AUH
ENSG00000148110	54.0343	51.6332	37.7551	29.3535	ENSG00000148110	MFSD14B
ENSG00000148120	35.4665	72.7874	94.8639	81.7581	ENSG00000148120	C9orf3
ENSG00000148123	0.0560037	0.355095	0.174217	0.0826123	ENSG00000148123	PLPPR1
ENSG00000148136	0	0	0	0	ENSG00000148136	OR13C4
ENSG00000148143	8.0722	24.4428	23.1977	18.956	ENSG00000148143	ZNF462
ENSG00000148153	10.0158	15.3606	13.0151	15.395	ENSG00000148153	INIP
ENSG00000148154	84.3572	74.4828	27.5488	94.5944	ENSG00000148154	UGCG
ENSG00000148156	0	0.113143	0.163662	0.0773536	ENSG00000148156	ACTL7B
ENSG00000148158	5.81356	6.69558	4.84354	5.46848	ENSG00000148158	SNX30
ENSG00000148175	31.5339	47.2076	86.5162	30.0362	ENSG00000148175	STOM
ENSG00000148180	326.767	139.296	102.122	167.524	ENSG00000148180	GSN
ENSG00000148187	15.2106	18.4843	24.1478	13.5443	ENSG00000148187	MRRF
ENSG00000148200	2.33563	1.39704	2.26001	1.8254	ENSG00000148200	NR6A1
ENSG00000148204	3.30467	1.68005	1.06544	2.15878	ENSG00000148204	CRB2
ENSG00000148215	0	0	0.0486084	0.121882	ENSG00000148215	OR5C1
ENSG00000148218	6.55728	9.73909	9.49149	13.1974	ENSG00000148218	ALAD
ENSG00000148219	40.1191	90.6382	85.526	214.632	ENSG00000148219	ASTN2
ENSG00000148225	2.44671	4.70627	4.33752	6.14192	ENSG00000148225	WDR31
ENSG00000148229	14.0436	14.2978	13.4118	8.26126	ENSG00000148229	POLE3
ENSG00000148248	80.5575	94.1371	36.7113	35.287	ENSG00000148248	SURF4
ENSG00000148288	2.14925	4.72954	2.96213	6.04257	ENSG00000148288	GBGT1
ENSG00000148290	6.14564	7.11074	5.3643	5.0752	ENSG00000148290	SURF1
ENSG00000148291	6.18864	8.15228	3.12185	3.08808	ENSG00000148291	SURF2
ENSG00000148296	2.42135	2.18689	4.63696	3.21431	ENSG00000148296	SURF6
ENSG00000148297	8.47304	10.5725	10.1255	8.15434	ENSG00000148297	MED22

ENSG00000148300	5.47602	7.13599	3.50324	3.5358	ENSG00000148300	REXO4
ENSG00000148303	298.863	267.165	158.144	158.139	ENSG00000148303	RPL7A
ENSG00000148308	23.9273	29.5979	28.0362	21.9159	ENSG00000148308	GTF3C5
ENSG00000148331	15.158	10.6689	13.5081	8.78006	ENSG00000148331	ASB6
ENSG00000148334	26.8393	21.9601	21.1483	10.7141	ENSG00000148334	PTGES2
ENSG00000148335	16.4771	17.5611	14.9208	14.7586	ENSG00000148335	NTMT1
ENSG00000148337	28.2104	23.5096	36.6051	30.9329	ENSG00000148337	CIZ1
ENSG00000148339	13.3737	8.61952	7.03779	5.76385	ENSG00000148339	SLC25A25
ENSG00000148341	73.5952	48.6703	48.0082	31.2756	ENSG00000148341	SH3GLB2
ENSG00000148343	20.458	31.4079	28.3689	19.9358	ENSG00000148343	MIGA2
ENSG00000148344	47.7657	10.4623	3.67168	7.51665	ENSG00000148344	PTGES
ENSG00000148346	784.438	26.9487	81.8817	56.3646	ENSG00000148346	LCN2
ENSG00000148356	15.7578	15.0934	18.8002	14.7281	ENSG00000148356	LRSAM1
ENSG00000148357	0.364722	0.157515	0.232265	0.397507	ENSG00000148357	HMCN2
ENSG00000148358	12.7083	12.0488	11.5203	13.8327	ENSG00000148358	GPR107
ENSG00000148362	17.4558	31.3286	18.378	14.5885	ENSG00000148362	PAXX
ENSG00000148377	0.328392	0.169706	0.166408	0.291104	ENSG00000148377	IDI2
ENSG00000148384	8.64463	9.66502	8.75216	7.06344	ENSG00000148384	INPP5E
ENSG00000148386	2.09997	2.57029	2.34463	6.5456	ENSG00000148386	LCN9
ENSG00000148396	24.4723	32.9551	41.9297	41.2566	ENSG00000148396	SEC16A
ENSG00000148399	22.8621	28.6786	42.9817	21.4787	ENSG00000148399	DPH7
ENSG00000148400	59.9905	105.624	228.43	43.6833	ENSG00000148400	NOTCH1
ENSG00000148408	11.363	13.5695	10.9971	24.2175	ENSG00000148408	CACNA1B
ENSG00000148411	10.3275	7.87945	9.44729	11.3207	ENSG00000148411	NACC2
ENSG00000148426	30.1467	22.7244	18.752	16.6915	ENSG00000148426	PROSER2
ENSG00000148429	15.0524	7.73107	8.14799	9.80787	ENSG00000148429	USP6NL
ENSG00000148444	24.4768	22.6684	18.1984	14.4825	ENSG00000148444	COMMD3
ENSG00000148450	7.29424	10.5266	8.88788	12.7922	ENSG00000148450	MSRB2
ENSG00000148459	5.53816	8.51244	8.21136	7.37012	ENSG00000148459	PDSS1
ENSG00000148468	10.0313	5.93709	7.93473	7.91945	ENSG00000148468	FAM171A1
ENSG00000148481	14.1698	20.3093	20.9519	20.2646	ENSG00000148481	MINDY3
ENSG00000148482	0.0306942	0	0.0259626	0.0326888	ENSG00000148482	SLC39A12
ENSG00000148483	0.393264	0.899832	0.341663	1.95057	ENSG00000148483	TMEM236
ENSG00000148484	32.0919	26.4127	21.4446	23.1932	ENSG00000148484	RSU1
ENSG00000148488	1.24965	2.25724	1.6345	3.51704	ENSG00000148488	ST8SIA6
ENSG00000148498	46.6479	37.9343	29.0916	23.926	ENSG00000148498	PARD3
ENSG00000148513	3.33616	12.6029	6.7356	18.1464	ENSG00000148513	ANKRD30A
ENSG00000148516	1.90349	5.3837	4.14242	53.2112	ENSG00000148516	ZEB1
ENSG00000148541	2.74904	16.3851	6.89901	12.9163	ENSG00000148541	FAM13C
ENSG00000148572	19.8763	14.2537	25.555	9.36995	ENSG00000148572	NRBF2
ENSG00000148584	0.202	0.417622	0.573586	0.579349	ENSG00000148584	A1CF
ENSG00000148600	0.847658	3.84877	12.3336	4.06149	ENSG00000148600	CDHR1
ENSG00000148602	0.200595	0.169187	0.262212	0.41311	ENSG00000148602	LRIT1
ENSG00000148604	6.74778	13.2982	12.5499	23.62	ENSG00000148604	RGR
ENSG00000148606	9.04246	13.7371	12.9371	17.3071	ENSG00000148606	POLR3A
ENSG00000148634	57.1944	86.2882	66.4594	100.26	ENSG00000148634	HERC4
ENSG00000148655	26.1323	75.1185	64.9249	125.924	ENSG00000148655	LRMDA
ENSG00000148660	20.2111	15.1085	14.1843	17.202	ENSG00000148660	CAMK2G
ENSG00000148671	238.552	93.0525	16.4234	35.9222	ENSG00000148671	ADIRF
ENSG00000148672	45.9562	80.1571	39.776	43.826	ENSG00000148672	GLUD1
ENSG00000148677	0.0599713	0.117999	0.17982	0.654554	ENSG00000148677	ANKRD1
ENSG00000148680	8.4105	22.666	9.5881	4.41037	ENSG00000148680	HTR7
ENSG00000148688	18.0072	21.1691	16.7807	17.6351	ENSG00000148688	RPP30
ENSG00000148690	10.4271	22.8393	21.5217	20.9496	ENSG00000148690	FRA10AC1

ENSG00000148700	30.7751	33.9688	19.2068	34.5575	ENSG00000148700	ADD3
ENSG00000148702	0	0	0	0	ENSG00000148702	HABP2
ENSG00000148704	0.329167	0.528867	0.650644	0.797026	ENSG00000148704	VAX1
ENSG00000148719	24.2192	18.6129	17.8006	12.5221	ENSG00000148719	DNAJB12
ENSG00000148730	9.69018	6.63464	5.44481	8.70673	ENSG00000148730	EIF4EBP2
ENSG00000148734	1.1526	2.81074	2.68934	4.24087	ENSG00000148734	NPFFR1
ENSG00000148735	1.7271	3.24864	4.20529	4.94112	ENSG00000148735	PLEKHS1
ENSG00000148737	4.87646	7.28121	10.1883	13.0534	ENSG00000148737	TCF7L2
ENSG00000148773	5.57765	39.3023	4.16867	22.8341	ENSG00000148773	MKI67
ENSG00000148795	0.928705	2.34593	2.10794	3.10718	ENSG00000148795	CYP17A1
ENSG00000148798	0.337691	0.219335	0.176651	0.241464	ENSG00000148798	INA
ENSG00000148803	20.5623	22.5458	21.4466	17.9972	ENSG00000148803	FUOM
ENSG00000148814	5.97863	11.0391	12.8787	11.9893	ENSG00000148814	LRRC27
ENSG00000148824	10.3155	20.4751	22.1828	18.6665	ENSG00000148824	MTG1
ENSG00000148826	0.172674	0.0553909	0	0.125488	ENSG00000148826	NKX6-2
ENSG00000148828	0	0	0	0	ENSG00000148828	CT476828.1
ENSG00000148832	4.1124	4.48058	3.1182	5.2855	ENSG00000148832	PAOX
ENSG00000148834	64.5104	47.3383	28.7118	40.8641	ENSG00000148834	GSTO1
ENSG00000148835	1.91417	3.24143	1.60576	1.62081	ENSG00000148835	TAF5
ENSG00000148840	17.1949	18.3455	25.1735	21.5485	ENSG00000148840	PPRC1
ENSG00000148841	13.2687	28.9279	36.0229	20.1989	ENSG00000148841	ITPRIP
ENSG00000148842	1.82797	4.16043	2.92388	3.39711	ENSG00000148842	CNNM2
ENSG00000148843	35.6503	45.7622	64.4988	34.3984	ENSG00000148843	PDCD11
ENSG00000148848	0.364234	0.420662	0.867308	9.58767	ENSG00000148848	ADAM12
ENSG00000148908	13.252	21.7156	10.6358	15.3881	ENSG00000148908	RGS10
ENSG00000148925	46.0214	45.2166	38.3074	37.6955	ENSG00000148925	BTBD10
ENSG00000148926	77.315	39.2089	50.5277	89.787	ENSG00000148926	ADM
ENSG00000148935	0.405849	0.510488	1.17284	1.65845	ENSG00000148935	GAS2
ENSG00000148942	1.22373	2.53426	1.70815	3.23004	ENSG00000148942	SLC5A12
ENSG00000148943	19.5692	14.2309	18.2773	13.1933	ENSG00000148943	LIN7C
ENSG00000148948	0.43681	1.27643	1.35225	2.95885	ENSG00000148948	LRRC4C
ENSG00000148950	27.687	57.4679	46.7684	44.4955	ENSG00000148950	IMMP1L
ENSG00000148965	0.187077	0.268264	0.652843	0.0995634	ENSG00000148965	SAA4
ENSG00000148985	17.8247	17.4528	19.4495	14.7565	ENSG00000148985	PGAP2
ENSG00000149016	9.63786	10.6833	11.4402	12.8018	ENSG00000149016	TUT1
ENSG00000149021	0	0	0.158466	0	ENSG00000149021	SCGB1A1
ENSG00000149043	48.6785	12.07	18.6034	7.29393	ENSG00000149043	SYT8
ENSG00000149050	1.6366	3.24497	2.97431	1.94821	ENSG00000149050	ZNF214
ENSG00000149054	3.61763	9.42739	6.63289	9.50908	ENSG00000149054	ZNF215
ENSG00000149084	109.316	109.079	67.1796	73.8085	ENSG00000149084	HSD17B12
ENSG00000149089	7.41072	8.76375	6.42742	6.30864	ENSG00000149089	APIP
ENSG00000149090	0.602624	4.86888	15.8416	7.06301	ENSG00000149090	PAMR1
ENSG00000149091	34.55	39.5628	37.0271	27.5996	ENSG00000149091	DGKZ
ENSG00000149100	126.723	124.914	117.452	63.9016	ENSG00000149100	EIF3M
ENSG00000149115	87.2066	91.0743	182.729	109.865	ENSG00000149115	TNKS1BP1
ENSG00000149124	0.262336	0.285344	0.902058	0.404612	ENSG00000149124	GLYAT
ENSG00000149131	18.8454	5.97279	7.66668	10.9213	ENSG00000149131	SERPING1
ENSG00000149133	0.198196	0.190613	0.229651	0.574993	ENSG00000149133	OR5F1
ENSG00000149136	94.1746	100.036	173.841	1201.47	ENSG00000149136	SSRP1
ENSG00000149150	0.729244	3.64414	3.77145	5.288	ENSG00000149150	SLC43A1
ENSG00000149177	5.21717	3.81957	3.72401	10.9744	ENSG00000149177	PTPRJ
ENSG00000149179	29.7343	56.29	55.4461	85.8325	ENSG00000149179	C11orf49
ENSG00000149182	58.195	59.7641	54.4578	44.8173	ENSG00000149182	ARFGAP2
ENSG00000149187	61.0298	77.7123	79.4653	92.6262	ENSG00000149187	CELF1

ENSG00000149196	14.951	19.5332	18.6982	16.6127	ENSG00000149196	HIKESHI
ENSG00000149201	0.862383	1.73494	1.71972	2.93472	ENSG00000149201	CCDC81
ENSG00000149212	7.57586	10.2223	27.7775	9.5819	ENSG00000149212	SESN3
ENSG00000149218	32.9709	18.5281	17.9815	9.23128	ENSG00000149218	ENDOD1
ENSG00000149231	19.5669	27.2317	16.3908	31.1372	ENSG00000149231	CCDC82
ENSG00000149243	1.13966	1.59935	2.54427	2.65145	ENSG00000149243	KLHL35
ENSG00000149256	30.4392	49.7766	21.4773	51.7912	ENSG00000149256	TENM4
ENSG00000149257	69.0494	126.63	158.228	164.147	ENSG00000149257	SERPINH1
ENSG00000149260	1.6769	2.55042	1.80274	4.30688	ENSG00000149260	CAPN5
ENSG00000149262	12.5941	21.5423	18.335	20.7858	ENSG00000149262	INTS4
ENSG00000149269	38.9481	83.0112	53.4161	84.3102	ENSG00000149269	PAK1
ENSG00000149273	430.134	459.34	367.173	247.354	ENSG00000149273	RPS3
ENSG00000149289	5.45362	8.14661	9.36774	8.43497	ENSG00000149289	ZC3H12C
ENSG00000149292	9.82809	18.5491	20.6267	10.0908	ENSG00000149292	TTC12
ENSG00000149294	0.195373	0.651946	0.927461	1.9239	ENSG00000149294	NCAM1
ENSG00000149295	0.59068	1.08027	0.735229	0.595222	ENSG00000149295	DRD2
ENSG00000149300	1.62572	0.621015	0.407007	0.446628	ENSG00000149300	C11orf52
ENSG00000149305	0.581654	1.49562	1.77513	3.21219	ENSG00000149305	HTR3B
ENSG00000149308	11.2066	23.9847	16.8152	21.8621	ENSG00000149308	NPAT
ENSG00000149311	26.2487	63.9311	49.7043	82.3983	ENSG00000149311	ATM
ENSG00000149313	20.4414	19.127	22.6443	10.0677	ENSG00000149313	AASDHPPT
ENSG00000149328	6.43384	1.78476	2.33978	0.87659	ENSG00000149328	GLB1L2
ENSG00000149346	5.01045	8.38594	8.97886	7.73124	ENSG00000149346	SLX4IP
ENSG00000149357	35.774	28.78	29.5698	20.2825	ENSG00000149357	LAMTOR1
ENSG00000149380	8.08973	16.2348	20.3787	34.6563	ENSG00000149380	P4HA3
ENSG00000149403	0.414318	1.52364	2.47556	1.56844	ENSG00000149403	GRIK4
ENSG00000149418	126.993	101.314	62.2434	33.5356	ENSG00000149418	ST14
ENSG00000149428	87.1268	192.487	96.6299	79.1483	ENSG00000149428	HYOU1
ENSG00000149435	0	0	0	0.142043	ENSG00000149435	GGTLC1
ENSG00000149443	0	0	0.124345	0.153739	ENSG00000149443	C20orf78
ENSG00000149451	0.505499	1.19357	1.22156	19.1289	ENSG00000149451	ADAM33
ENSG00000149452	0.47746	0.756558	0.563083	0.75315	ENSG00000149452	SLC22A8
ENSG00000149474	7.63533	7.22156	9.31815	4.3826	ENSG00000149474	KAT14
ENSG00000149476	14.531	26.0377	35.5437	22.368	ENSG00000149476	TKFC
ENSG00000149480	57.7816	74.2748	74.5032	43.1394	ENSG00000149480	MTA2
ENSG00000149483	24.6326	40.3274	55.351	40.8404	ENSG00000149483	TMEM138
ENSG00000149485	23.8955	49.8493	16.5891	64.4891	ENSG00000149485	FADS1
ENSG00000149488	2.3898	4.05566	3.38086	6.04225	ENSG00000149488	TMC2
ENSG00000149489	0.242455	2.57152	0.964516	1.31093	ENSG00000149489	ROM1
ENSG00000149499	17.3421	23.7274	25.5421	25.7585	ENSG00000149499	EML3
ENSG00000149503	13.8299	34.8827	11.277	21.0196	ENSG00000149503	INCENP
ENSG00000149506	0.329838	0.212126	0.573671	0.782906	ENSG00000149506	ZP1
ENSG00000149507	0.0352042	0	0	1.58567	ENSG00000149507	OOSP2
ENSG00000149516	1.01104	0.676962	0.721437	1.31331	ENSG00000149516	MS4A3
ENSG00000149527	106.088	222.889	225.254	98.4566	ENSG00000149527	PLCH2
ENSG00000149531	26.0369	47.3728	37.4707	41.5282	ENSG00000149531	FRG1BP
ENSG00000149532	23.0106	24.5165	32.7458	23.2045	ENSG00000149532	CPSF7
ENSG00000149534	0.0564427	0.226021	0.195173	0.402563	ENSG00000149534	MS4A2
ENSG00000149541	21.8742	29.9218	22.5401	22.1593	ENSG00000149541	B3GAT3
ENSG00000149547	77.2553	66.8086	55.0463	40.7184	ENSG00000149547	EI24
ENSG00000149548	2.36091	6.28801	2.73136	8.06151	ENSG00000149548	CCDC15
ENSG00000149554	12.9448	36.7524	24.9608	36.4335	ENSG00000149554	CHEK1
ENSG00000149557	25.1866	61.9525	51.4858	45.0994	ENSG00000149557	FEZ1
ENSG00000149564	0.87507	1.36924	1.67571	2.66578	ENSG00000149564	ESAM

ENSG00000149571	2.19733	2.20954	1.70949	4.59916	ENSG00000149571	KIRREL3
ENSG00000149573	90.3114	121.337	65.0936	27.006	ENSG00000149573	MPZL2
ENSG00000149575	0.394668	1.03548	1.02645	1.0953	ENSG00000149575	SCN2B
ENSG00000149577	16.3395	17.6214	23.1802	25.3113	ENSG00000149577	SIDT2
ENSG00000149582	9.01531	9.46988	10.1335	7.41134	ENSG00000149582	TMEM25
ENSG00000149591	20.0431	26.7237	74.4712	57.6433	ENSG00000149591	TAGLN
ENSG00000149596	1.32467	2.60332	4.20222	2.08828	ENSG00000149596	JPH2
ENSG00000149599	0.113107	0.501448	0.294247	0.376768	ENSG00000149599	DUSP15
ENSG00000149600	13.4975	10.8206	10.755	5.25279	ENSG00000149600	COMMD7
ENSG00000149609	0.562067	1.19368	1.52878	2.02961	ENSG00000149609	C20orf144
ENSG00000149633	0.787205	1.48858	1.16636	2.36783	ENSG00000149633	KIAA1755
ENSG00000149634	0.781418	1.16817	1.95987	2.06847	ENSG00000149634	SPATA25
ENSG00000149635	0.248268	0.398117	0.359911	0.664872	ENSG00000149635	OCSTAMP
ENSG00000149636	5.33115	7.08717	3.09203	7.5498	ENSG00000149636	DSN1
ENSG00000149639	10.9538	22.8274	11.9225	26.0687	ENSG00000149639	SOGA1
ENSG00000149646	0.688002	1.12255	1.10459	1.68958	ENSG00000149646	CNBD2
ENSG00000149651	0	0.140791	0	0.314228	ENSG00000149651	SPINT4
ENSG00000149654	0.459013	1.12086	1.09751	1.89255	ENSG00000149654	CDH22
ENSG00000149657	11.2137	13.8393	18.9222	12.6027	ENSG00000149657	LSM14B
ENSG00000149658	12.4361	11.7895	19.0685	11.6586	ENSG00000149658	YTHDF1
ENSG00000149679	2.69724	2.35739	2.80336	2.20115	ENSG00000149679	CABLES2
ENSG00000149716	21.1058	28.4437	39.7124	33.6426	ENSG00000149716	ORAOV1
ENSG00000149735	1.48259	1.34767	2.299	0.539091	ENSG00000149735	GPHA2
ENSG00000149742	0.17582	0.86714	0.813838	1.2063	ENSG00000149742	SLC22A9
ENSG00000149743	20.7766	19.4311	13.7188	8.72532	ENSG00000149743	TRPT1
ENSG00000149761	30.335	36.3425	33.8301	27.7835	ENSG00000149761	NUDT22
ENSG00000149781	4.02351	2.90192	5.24377	5.87887	ENSG00000149781	FERMT3
ENSG00000149782	29.985	37.2521	29.3196	25.5478	ENSG00000149782	PLCB3
ENSG00000149792	22.5956	10.5843	10.7681	9.38285	ENSG00000149792	MRPL49
ENSG00000149798	8.9394	8.46738	6.99418	9.08105	ENSG00000149798	CDC42EP2
ENSG00000149806	270.748	204.979	177.547	107.165	ENSG00000149806	FAU
ENSG00000149809	21.5908	6.29825	7.30927	5.09768	ENSG00000149809	TM7SF2
ENSG00000149823	51.7552	52.9434	51.8948	54.8269	ENSG00000149823	VPS51
ENSG00000149922	1.87971	3.24542	2.45773	3.94838	ENSG00000149922	TBX6
ENSG00000149923	52.9676	41.3946	45.1288	33.8137	ENSG00000149923	PPP4C
ENSG00000149925	640.646	545.132	253.838	341.308	ENSG00000149925	ALDOA
ENSG00000149926	1.502	3.46613	2.15825	4.62567	ENSG00000149926	FAM57B
ENSG00000149927	2.91942	5.51518	3.67691	8.47842	ENSG00000149927	DOC2A
ENSG00000149929	1.66929	3.98005	3.37961	2.60935	ENSG00000149929	HIRIP3
ENSG00000149930	20.7078	19.8442	21.1441	20.2111	ENSG00000149930	TAOK2
ENSG00000149932	39.3199	39.9961	27.6774	28.7275	ENSG00000149932	TMEM219
ENSG00000149948	54.83	143.738	27.6541	156.289	ENSG00000149948	HMGA2
ENSG00000149968	0.0140023	0.340584	0.614199	9.84528	ENSG00000149968	MMP3
ENSG00000149970	0.530663	0.7412	0.156145	0.424892	ENSG00000149970	CNKSR2
ENSG00000149972	0.338889	0.649004	0.485607	0.65422	ENSG00000149972	CNTN5
ENSG00000150045	0.382306	0.220558	0.199253	0.322004	ENSG00000150045	KLRF1
ENSG00000150048	1.94998	4.31927	3.79487	7.23644	ENSG00000150048	CLEC1A
ENSG00000150051	0.134177	0.546171	0.432971	9.45016	ENSG00000150051	MKX
ENSG00000150054	5.61166	7.25819	6.99341	2.9426	ENSG00000150054	MPP7
ENSG00000150076	0.893553	1.4695	1.29841	1.9014	ENSG00000150076	C10ORF68
ENSG00000150093	947.859	1272.8	576.152	842.631	ENSG00000150093	ITGB1
ENSG00000150165	0	6.98611	38.8071	1.16387	ENSG00000150165	ANXA8L1
ENSG00000150175	0	0	0	0	ENSG00000150175	FRMPD2B
ENSG00000150201	0	0.960548	1.32431	4.16401	ENSG00000150201	FXYD4

ENSG00000150244	0	0	0	0	ENSG00000150244	TRIM48
ENSG00000150261	0	0	0	0	ENSG00000150261	OR8K1
ENSG00000150269	0	0	0.116601	0	ENSG00000150269	OR5M9
ENSG00000150275	0.149351	0.281872	0.501989	0.541943	ENSG00000150275	PCDH15
ENSG00000150276	0	0	0	0	ENSG00000150276	PPIAP26
ENSG00000150281	1.26125	2.34234	2.21035	3.11959	ENSG00000150281	CTF1
ENSG00000150316	4.13514	1.17592	2.22813	0.353184	ENSG00000150316	CWC15
ENSG00000150337	0.541904	0.133385	0.252688	0.0983392	ENSG00000150337	FCGR1A
ENSG00000150347	5.32081	9.22937	7.59026	11.1515	ENSG00000150347	ARID5B
ENSG00000150361	0.0262224	0.025303	0.0228549	0.0863785	ENSG00000150361	KLHL1
ENSG00000150394	5.10077	10.4134	16.0612	28.2168	ENSG00000150394	CDH8
ENSG00000150401	10.4686	11.2728	17.8391	18.224	ENSG00000150401	DCUN1D2
ENSG00000150403	36.6301	44.6331	28.1197	31.2356	ENSG00000150403	TMCO3
ENSG00000150433	10.8845	13.5415	8.07616	9.5501	ENSG00000150433	TMEM218
ENSG00000150455	3.82043	6.53795	6.64564	7.12659	ENSG00000150455	TIRAP
ENSG00000150456	2.26621	4.13732	3.85448	3.74029	ENSG00000150456	EEF1AKMT1
ENSG00000150457	6.20257	5.90631	7.41573	12.7989	ENSG00000150457	LATS2
ENSG00000150459	69.8837	34.2699	33.367	31.5903	ENSG00000150459	SAP18
ENSG00000150471	1.89972	0.264887	0.593958	0.64017	ENSG00000150471	ADGRL3
ENSG00000150477	118.125	284.315	267.573	607.493	ENSG00000150477	KIAA1328
ENSG00000150510	0.560174	1.4351	2.55634	2.47489	ENSG00000150510	FAM124A
ENSG00000150526	2.18778	3.54797	2.86789	8.37263	ENSG00000150526	MIA2
ENSG00000150527	26.2305	44.3176	51.1806	29.5841	ENSG00000150527	CTAGE5
ENSG00000150540	7.73746	19.1592	19.4652	35.4285	ENSG00000150540	HNMT
ENSG00000150551	1.02062	0.832235	0.502564	1.95599	ENSG00000150551	LYPD1
ENSG00000150556	3.73004	4.07631	9.18926	7.617	ENSG00000150556	LYPD6B
ENSG00000150593	62.622	48.875	87.3328	48.8691	ENSG00000150593	PDCD4
ENSG00000150594	0.126167	0.230883	0.256794	0.232321	ENSG00000150594	ADRA2A
ENSG00000150625	2.57545	2.97088	4.01869	5.78976	ENSG00000150625	GPM6A
ENSG00000150627	1.08357	1.54359	2.40397	3.95273	ENSG00000150627	WDR17
ENSG00000150628	0.975428	2.79345	2.2342	4.11577	ENSG00000150628	SPATA4
ENSG00000150630	8.70102	33.2566	9.18468	31.4121	ENSG00000150630	VEGFC
ENSG00000150636	2.22969	3.16288	3.9799	8.26057	ENSG00000150636	CCDC102B
ENSG00000150637	3.37091	5.37697	7.42664	8.50537	ENSG00000150637	CD226
ENSG00000150656	6.49192	19.1767	19.6464	32.1412	ENSG00000150656	CNDP1
ENSG00000150667	0.450895	3.4756	8.08403	6.57679	ENSG00000150667	FSIP1
ENSG00000150672	2.74347	3.55144	3.84914	4.9986	ENSG00000150672	DLG2
ENSG00000150676	0.914585	1.4475	1.20397	2.60623	ENSG00000150676	CCDC83
ENSG00000150681	1.80132	1.05318	0.81503	0.732252	ENSG00000150681	RGS18
ENSG00000150687	101.042	79.7205	78.0696	64.587	ENSG00000150687	PRSS23
ENSG00000150712	10.2411	14.5423	12.9665	12.1871	ENSG00000150712	MTMR12
ENSG00000150722	4.77008	7.82202	6.58888	8.19692	ENSG00000150722	PPP1R1C
ENSG00000150732	0	0	0	0	ENSG00000150732	RP11-134C1.1
ENSG00000150750	0	0	0	0	ENSG00000150750	C11orf53
ENSG00000150753	150.879	167.075	103.537	103.855	ENSG00000150753	CCT5
ENSG00000150756	4.91861	6.25451	4.09848	7.48679	ENSG00000150756	FAM173B
ENSG00000150760	18.7771	33.5093	35.3334	38.4398	ENSG00000150760	DOCK1
ENSG00000150764	3.24384	2.56922	4.67667	2.66913	ENSG00000150764	DIXDC1
ENSG00000150768	13.01	11.3768	8.03905	12.0537	ENSG00000150768	DLAT
ENSG00000150773	1.31691	1.14937	1.16131	1.73239	ENSG00000150773	PIH1D2
ENSG00000150776	5.69504	7.00381	9.18764	8.24352	ENSG00000150776	C11orf57
ENSG00000150779	21.4601	11.991	17.622	7.85877	ENSG00000150779	TIMM8B
ENSG00000150782	144.472	19.1495	13.1964	20.414	ENSG00000150782	IL18
ENSG00000150783	0.105084	0.397328	0.513825	0.448078	ENSG00000150783	TEX12

ENSG00000150787	32.1701	27.0011	27.7131	26.4052	ENSG00000150787	PTS
ENSG00000150867	10.1939	15.3061	7.99985	17.0883	ENSG00000150867	PIP4K2A
ENSG00000150873	1.40584	2.4321	2.43524	4.42514	ENSG00000150873	C2orf50
ENSG00000150893	0.0563742	0.140062	0.270786	0.17948	ENSG00000150893	FREM2
ENSG00000150907	12.2259	7.39716	12.097	4.90979	ENSG00000150907	FOXO1
ENSG00000150938	56.6742	49.786	41.2562	76.3929	ENSG00000150938	CRIM1
ENSG00000150961	28.7627	38.8985	27.3595	62.5531	ENSG00000150961	SEC24D
ENSG00000150967	17.1382	22.744	17.679	25.2547	ENSG00000150967	ABCB9
ENSG00000150977	2.33298	3.62137	3.68603	2.79202	ENSG00000150977	RILPL2
ENSG00000150990	14.734	14.4438	16.5866	16.8823	ENSG00000150990	DHX37
ENSG00000150991	1257.45	839.718	504.943	427.966	ENSG00000150991	UBC
ENSG00000150995	2.37909	5.2744	4.69745	9.95922	ENSG00000150995	ITPR1
ENSG00000151005	0	0.0760095	0.12026	0.0866674	ENSG00000151005	TKTL2
ENSG00000151006	1.12763	1.81303	2.18548	2.82908	ENSG00000151006	PRSS53
ENSG00000151012	6.04913	58.053	99.2783	11.1429	ENSG00000151012	SLC7A11
ENSG00000151014	17.6061	6.0211	10.8794	11.7361	ENSG00000151014	NOCT
ENSG00000151023	0.406232	0.410362	0.351802	0.497666	ENSG00000151023	ENKUR
ENSG00000151025	0.211779	0.21015	0.0398242	0.423574	ENSG00000151025	GPR158
ENSG00000151033	0.0800003	0.0769011	0.14247	0.0867638	ENSG00000151033	LYZL2
ENSG00000151062	1.75224	2.50494	1.34056	3.76222	ENSG00000151062	CACNA2D4
ENSG00000151065	4.46691	7.70611	9.70381	5.51863	ENSG00000151065	DCP1B
ENSG00000151067	0.321215	0.97195	1.03993	8.86194	ENSG00000151067	CACNA1C
ENSG00000151079	0.038198	0.0613337	0.0998717	0.280271	ENSG00000151079	KCNA6
ENSG00000151090	5.42869	3.6953	3.34381	3.58087	ENSG00000151090	THRB
ENSG00000151092	14.6425	26.1903	20.0586	21.7148	ENSG00000151092	NGLY1
ENSG00000151093	8.16281	9.09543	9.65315	3.89383	ENSG00000151093	OXSM
ENSG00000151116	25.3627	23.4309	23.1861	35.3178	ENSG00000151116	UEVLD
ENSG00000151117	24.9439	2.957	5.6568	4.95301	ENSG00000151117	TMEM86A
ENSG00000151131	9.85459	13.28	15.3992	15.5547	ENSG00000151131	C12orf45
ENSG00000151135	12.2813	19.1272	13.2824	33.751	ENSG00000151135	TMEM263
ENSG00000151136	11.3191	12.6401	6.08935	6.39829	ENSG00000151136	BTBD11
ENSG00000151148	18.0351	19.0229	26.4071	21.6328	ENSG00000151148	UBE3B
ENSG00000151150	25.6064	30.1881	25.4362	19.8419	ENSG00000151150	ANK3
ENSG00000151151	3.84811	2.939	3.01958	2.91164	ENSG00000151151	IPMK
ENSG00000151164	3.48716	7.70592	8.14341	9.0551	ENSG00000151164	RAD9B
ENSG00000151176	12.2866	18.6409	17.1473	20.5514	ENSG00000151176	PLBD2
ENSG00000151208	25.4166	38.8608	32.067	38.006	ENSG00000151208	DLG5
ENSG00000151224	0.493714	0.949067	0.42871	0.802772	ENSG00000151224	MAT1A
ENSG00000151229	3.70647	6.67572	4.05981	7.49537	ENSG00000151229	SLC2A13
ENSG00000151233	5.66636	6.31076	5.54342	5.17924	ENSG00000151233	GXYLT1
ENSG00000151239	84.3292	49.2344	41.8032	28.2168	ENSG00000151239	TWF1
ENSG00000151240	5.4915	7.53872	6.02589	17.3646	ENSG00000151240	DIP2C
ENSG00000151247	72.1918	67.0263	60.795	88.0302	ENSG00000151247	EIF4E
ENSG00000151276	9.06362	15.3668	14.4744	13.4056	ENSG00000151276	MAGI1
ENSG00000151287	5.64641	6.68886	3.50371	5.21642	ENSG00000151287	TEX30
ENSG00000151292	14.29	21.7465	23.8668	21.5408	ENSG00000151292	CSNK1G3
ENSG00000151304	10.1078	9.86535	11.3015	11.2529	ENSG00000151304	SRFBP1
ENSG00000151320	2.86957	5.13929	12.1366	7.79404	ENSG00000151320	AKAP6
ENSG00000151322	1.75571	6.09814	5.69688	8.11764	ENSG00000151322	NPAS3
ENSG00000151327	51.9208	54.1097	49.7611	67.9702	ENSG00000151327	FAM177A1
ENSG00000151332	9.64802	10.1219	10.1264	12.3137	ENSG00000151332	MBIP
ENSG00000151338	41.3592	96.3213	85.6189	185.473	ENSG00000151338	MIPOL1
ENSG00000151348	87.3325	151.27	113.415	106.967	ENSG00000151348	EXT2
ENSG00000151353	16.5857	16.95	9.60085	7.50646	ENSG00000151353	TMEM18

ENSG00000151360	0.474815	0.05971	0.105731	0.232945	ENSG00000151360	ALLC
ENSG00000151364	1.22026	3.69163	1.92031	1.84086	ENSG00000151364	KCTD14
ENSG00000151365	0.268012	0.370493	0.418334	0.303136	ENSG00000151365	THRSP
ENSG00000151366	129.387	84.3378	40.7263	36.5536	ENSG00000151366	NDUFC2
ENSG00000151376	7.05406	6.15111	3.14532	8.24687	ENSG00000151376	ME3
ENSG00000151379	0	0.222836	0	0	ENSG00000151379	MSGN1
ENSG00000151388	0.141818	0.598348	0.583448	33.2208	ENSG00000151388	ADAMTS12
ENSG00000151413	24.2541	40.9878	36.8059	51.9318	ENSG00000151413	NUBPL
ENSG00000151414	41.5732	28.8453	20.5791	36.053	ENSG00000151414	NEK7
ENSG00000151418	0.110633	0.531127	0.0770968	0.432101	ENSG00000151418	ATP6V1G3
ENSG00000151422	46.1326	86.1231	77.7576	119.429	ENSG00000151422	FER
ENSG00000151445	8.61145	9.06464	10.1289	7.8006	ENSG00000151445	VIPAS39
ENSG00000151458	8.09971	11.2572	16.8016	15.3869	ENSG00000151458	ANKRD50
ENSG00000151461	10.6467	10.6981	11.8592	11.1387	ENSG00000151461	UPF2
ENSG00000151465	32.1059	31.5641	26.6494	22.2208	ENSG00000151465	CDC123
ENSG00000151466	5.45142	17.1786	10.5637	14.4686	ENSG00000151466	SCLT1
ENSG00000151468	0.0515091	0.105818	0.394794	0.133351	ENSG00000151468	CCDC3
ENSG00000151470	6.5236	8.60875	6.5068	6.86793	ENSG00000151470	C4orf33
ENSG00000151474	4.5958	17.2139	10.604	35.205	ENSG00000151474	FRMD4A
ENSG00000151475	0.0928746	0.119329	0.0809052	0.0678974	ENSG00000151475	SLC25A31
ENSG00000151490	0.64135	2.1041	1.12952	2.06143	ENSG00000151490	PTPRO
ENSG00000151491	4.07094	14.2351	12.1528	37.5451	ENSG00000151491	EPS8
ENSG00000151498	19.5085	18.3791	23.0118	15.6999	ENSG00000151498	ACAD8
ENSG00000151500	15.4314	21.055	16.5234	11.0778	ENSG00000151500	THYN1
ENSG00000151502	25.5433	30.7484	30.9148	32.2813	ENSG00000151502	VPS26B
ENSG00000151503	9.10274	25.479	14.1222	17.2904	ENSG00000151503	NCAPD3
ENSG00000151532	24.6261	36.715	34.8635	42.6177	ENSG00000151532	VTI1A
ENSG00000151552	3.1807	4.98828	7.28796	8.28345	ENSG00000151552	QDPR
ENSG00000151553	10.1688	11.6574	8.55851	11.2978	ENSG00000151553	FAM160B1
ENSG00000151572	29.7634	46.9789	6.26887	27.0509	ENSG00000151572	ANO4
ENSG00000151575	17.9479	32.5757	33.8162	50.3485	ENSG00000151575	TEX9
ENSG00000151576	17.0571	28.8594	31.7202	28.125	ENSG00000151576	QTRT2
ENSG00000151577	0	0.107429	0.163528	0.203246	ENSG00000151577	DRD3
ENSG00000151611	1.6351	3.07477	3.27834	4.24851	ENSG00000151611	MMAA
ENSG00000151612	7.27035	12.3726	11.4596	15.5444	ENSG00000151612	ZNF827
ENSG00000151615	0.0180384	0.16064	0.0659227	0.186861	ENSG00000151615	POU4F2
ENSG00000151617	1.78668	4.81183	4.99924	9.7959	ENSG00000151617	EDNRA
ENSG00000151623	1.27699	0.609318	0.62902	0.883212	ENSG00000151623	NR3C2
ENSG00000151631	0	0.303096	0.109576	0.331184	ENSG00000151631	AKR1C6P
ENSG00000151632	8.15967	8.32934	17.0844	6.32825	ENSG00000151632	AKR1C2
ENSG00000151640	0.343527	1.53015	9.67584	1.93256	ENSG00000151640	DPYSL4
ENSG00000151650	0.689126	1.62396	1.30042	2.65486	ENSG00000151650	VENTX
ENSG00000151651	72.3019	294.682	34.8121	72.4634	ENSG00000151651	ADAM8
ENSG00000151655	0.188057	0.379172	0.462076	0.150518	ENSG00000151655	ITIH2
ENSG00000151657	6.99504	10.4676	11.7458	12.8412	ENSG00000151657	KIN
ENSG00000151665	18.2737	29.9045	15.7557	18.0537	ENSG00000151665	PIGF
ENSG00000151687	2.12901	3.40401	4.42678	5.14163	ENSG00000151687	ANKAR
ENSG00000151689	7.48796	9.89758	12.6624	9.28532	ENSG00000151689	INPP1
ENSG00000151690	20.1426	20.4514	19.2809	13.7404	ENSG00000151690	MFSD6
ENSG00000151692	0.899826	2.22794	3.32859	8.92171	ENSG00000151692	RNF144A
ENSG00000151693	41.8714	40.8511	20.7018	47.5321	ENSG00000151693	ASAP2
ENSG00000151694	25.9883	40.8431	45.4196	23.334	ENSG00000151694	ADAM17
ENSG00000151702	1.21943	4.23429	5.18304	6.602	ENSG00000151702	FLI1
ENSG00000151704	0.557174	0.17847	0.426566	0.705184	ENSG00000151704	KCNJ1

ENSG00000151715	63.3967	18.9219	16.4005	17.1795	ENSG00000151715	TMEM45B
ENSG00000151718	14.5615	20.6118	14.9464	23.8944	ENSG00000151718	WWC2
ENSG00000151725	11.6319	14.5041	5.24394	11.6003	ENSG00000151725	CENPU
ENSG00000151726	102.493	23.5024	17.3465	20.015	ENSG00000151726	ACSL1
ENSG00000151729	11.0271	4.71528	3.20835	2.65431	ENSG00000151729	SLC25A4
ENSG00000151743	19.5711	32.4703	31.3405	48.0068	ENSG00000151743	AMN1
ENSG00000151746	8.04989	8.17805	8.49579	16.8361	ENSG00000151746	BICD1
ENSG00000151748	20.1372	13.8747	15.2739	13.4307	ENSG00000151748	SAV1
ENSG00000151773	17.4535	43.4258	40.6748	74.1538	ENSG00000151773	CCDC122
ENSG00000151778	0.737388	1.15264	0.393442	0.211117	ENSG00000151778	SERP2
ENSG00000151779	20.1003	32.709	24.9574	29.0303	ENSG00000151779	NBAS
ENSG00000151789	1.09274	2.92393	2.55555	5.94171	ENSG00000151789	ZNF385D
ENSG00000151790	0.354038	0.77446	0.59702	1.85683	ENSG00000151790	TDO2
ENSG00000151806	12.1264	15.2764	16.5836	13.4965	ENSG00000151806	GUF1
ENSG00000151812	3.18838	5.37621	5.61921	5.44841	ENSG00000151812	SLC35F4
ENSG00000151834	1.16627	1.48896	1.18812	2.6499	ENSG00000151834	GABRA2
ENSG00000151835	11.7761	18.8885	9.80757	34.9354	ENSG00000151835	SACS
ENSG00000151838	0	0.214813	0.115085	0.144678	ENSG00000151838	CCDC175
ENSG00000151846	0.0357073	0.172757	0.17405	0.425454	ENSG00000151846	PABPC3
ENSG00000151849	4.45156	15.2662	3.99123	12.2949	ENSG00000151849	CENPJ
ENSG00000151876	3.97215	9.44911	8.88476	7.11663	ENSG00000151876	FBXO4
ENSG00000151881	9.79001	15.5184	17.723	10.9041	ENSG00000151881	TMEM267
ENSG00000151882	3.67354	6.26887	7.27483	11.9415	ENSG00000151882	CCL28
ENSG00000151883	23.9745	54.9196	52.6028	40.8877	ENSG00000151883	PARP8
ENSG00000151892	0.225971	0.523946	0.437571	2.81707	ENSG00000151892	GFRA1
ENSG00000151893	27.3324	36.9981	31.3085	34.2855	ENSG00000151893	CACUL1
ENSG00000151914	148.077	465.177	542.698	330.646	ENSG00000151914	DST
ENSG00000151917	2.8843	6.64201	7.35598	12.962	ENSG00000151917	BEND6
ENSG00000151923	43.2901	72.4783	52.9908	79.5627	ENSG00000151923	TIAL1
ENSG00000151929	37.03	28.8223	21.898	27.38	ENSG00000151929	BAG3
ENSG00000151948	0.091752	0.0964455	0.0871928	0.182863	ENSG00000151948	GLT1D1
ENSG00000151952	0.148496	0.239325	0.333866	0.825045	ENSG00000151952	TMEM132D
ENSG00000151962	0.760232	0.270034	0.404891	0.586616	ENSG00000151962	RBM46
ENSG00000151963	0	0	0	0	ENSG00000151963	RP11-775A3.1
ENSG00000151967	3.77071	7.22821	5.239	11.0079	ENSG00000151967	SCHIP1
ENSG00000152022	1.64364	4.09437	2.68297	5.72183	ENSG00000152022	LIX1L
ENSG00000152034	0.182771	0.534217	0.384053	0.793278	ENSG00000152034	MCHR2
ENSG00000152042	4.55493	7.7869	9.6612	8.99635	ENSG00000152042	NBPF11
ENSG00000152049	21.9307	52.8421	52.9776	119.983	ENSG00000152049	KCNE4
ENSG00000152056	36.4752	15.2272	11.3642	11.2048	ENSG00000152056	AP1S3
ENSG00000152061	21.8586	43.9083	37.0715	47.4165	ENSG00000152061	RABGAP1L
ENSG00000152076	1.36847	3.73124	3.49013	4.65765	ENSG00000152076	CCDC74B
ENSG00000152078	0.345924	0.421485	0.311496	0.542232	ENSG00000152078	TMEM56
ENSG00000152082	87.9838	93.8063	58.2526	49.0171	ENSG00000152082	MZT2B
ENSG00000152086	0	0.10749	0.0397424	0	ENSG00000152086	TUBA3E
ENSG00000152092	0.886303	1.99279	2.08323	3.08906	ENSG00000152092	ASTN1
ENSG00000152093	0	0	0	0	ENSG00000152093	CFC1B
ENSG00000152102	27.464	23.3055	29.2664	24.1159	ENSG00000152102	FAM168B
ENSG00000152104	33.3045	42.9844	79.5724	56.2368	ENSG00000152104	PTPN14
ENSG00000152117	11.4136	15.7673	12.3812	14.9967	ENSG00000152117	AC073869.1
ENSG00000152127	31.0443	38.6116	26.4526	24.9589	ENSG00000152127	MGAT5
ENSG00000152128	0.352635	1.07043	0.84054	1.31455	ENSG00000152128	TMEM163
ENSG00000152133	3.976	6.69903	4.74021	9.8268	ENSG00000152133	GPATCH11
ENSG00000152137	13.0198	1.67376	1.59333	4.37918	ENSG00000152137	HSPB8

ENSG00000152147	8.44784	7.86959	8.32319	9.65922	ENSG00000152147	GEMIN6
ENSG00000152154	0.437247	1.05086	1.89717	3.10262	ENSG00000152154	TMEM178A
ENSG00000152192	0.261337	1.15239	0.582284	1.55043	ENSG00000152192	POU4F1
ENSG00000152193	6.03497	8.756	8.55482	5.78648	ENSG00000152193	RNF219
ENSG00000152207	0.286497	0.607088	0.397449	0.51262	ENSG00000152207	CYSLTR2
ENSG00000152208	0.0952638	0.553946	0.101769	0.831057	ENSG00000152208	GRID2
ENSG00000152213	0.880015	2.18602	1.40817	1.78728	ENSG00000152213	ARL11
ENSG00000152214	0.0556431	0.749746	0.145203	0.364095	ENSG00000152214	RIT2
ENSG00000152217	13.0809	7.27024	3.67693	13.1779	ENSG00000152217	SETBP1
ENSG00000152219	9.87959	18.3817	16.9163	15.6153	ENSG00000152219	ARL14EP
ENSG00000152223	21.4289	24.7108	17.783	39.7127	ENSG00000152223	EPG5
ENSG00000152229	13.2157	14.2589	9.57677	12.1746	ENSG00000152229	PSTPIP2
ENSG00000152234	173.497	162.429	113.218	102.36	ENSG00000152234	ATP5A1
ENSG00000152240	12.6692	24.966	15.9165	21.8748	ENSG00000152240	HAUS1
ENSG00000152242	19.4795	14.6346	13.6968	12.9613	ENSG00000152242	C18orf25
ENSG00000152253	6.7559	16.9892	12.6993	22.0199	ENSG00000152253	SPC25
ENSG00000152254	0.172329	0.181488	0.279031	0.453639	ENSG00000152254	G6PC2
ENSG00000152256	9.81656	12.4617	14.0151	13.532	ENSG00000152256	PDK1
ENSG00000152266	0	0.234998	0.140901	0.0879635	ENSG00000152266	PTH
ENSG00000152270	0.624617	1.52522	1.26264	2.20742	ENSG00000152270	PDE3B
ENSG00000152284	12.0027	21.9295	22.3448	34.7448	ENSG00000152284	TCF7L1
ENSG00000152291	34.7788	33.4929	31.0496	32.9441	ENSG00000152291	TGOLN2
ENSG00000152292	2.75963	10.1344	3.61891	8.25955	ENSG00000152292	SH2D6
ENSG00000152315	0	0.0848666	0.0382684	0.121036	ENSG00000152315	KCNK13
ENSG00000152332	24.4549	21.0465	15.9704	18.0394	ENSG00000152332	UHMK1
ENSG00000152348	8.56535	16.1256	14.6599	17.9545	ENSG00000152348	ATG10
ENSG00000152359	5.70828	13.9905	13.1151	10.0725	ENSG00000152359	POC5
ENSG00000152377	2.21724	1.85824	5.85178	7.19768	ENSG00000152377	SPOCK1
ENSG00000152380	15.0718	34.6893	34.2762	49.0251	ENSG00000152380	FAM151B
ENSG00000152382	5.14263	5.13696	4.48264	4.9139	ENSG00000152382	TADA1
ENSG00000152402	0.109222	0.268179	0.457752	4.73192	ENSG00000152402	GUCY1A2
ENSG00000152404	5.1439	10.6561	7.05404	9.196	ENSG00000152404	CWF19L2
ENSG00000152409	3.30001	4.8833	7.41561	5.05126	ENSG00000152409	JMY
ENSG00000152413	8.00147	9.2181	11.2976	9.24419	ENSG00000152413	HOMER1
ENSG00000152422	4.17578	7.05316	4.46901	4.62579	ENSG00000152422	XRCC4
ENSG00000152430	0.0201884	0.436624	0.431075	0.814437	ENSG00000152430	BOLL
ENSG00000152433	2.45673	3.24331	5.31508	4.34952	ENSG00000152433	ZNF547
ENSG00000152439	10.7955	21.4649	28.4951	12.306	ENSG00000152439	ZNF773
ENSG00000152443	13.2359	13.1135	14.5298	20.3904	ENSG00000152443	ZNF776
ENSG00000152454	3.86586	4.49714	6.07613	2.79632	ENSG00000152454	ZNF256
ENSG00000152455	5.06188	7.4185	6.06378	8.074	ENSG00000152455	SUV39H2
ENSG00000152457	11.7321	24.3055	19.0529	21.3508	ENSG00000152457	DCLRE1C
ENSG00000152463	3.66952	4.54709	3.8213	7.17869	ENSG00000152463	OLAH
ENSG00000152464	9.77455	8.35664	12.5754	10.0392	ENSG00000152464	RPP38
ENSG00000152465	13.197	13.1784	13.1328	16.8266	ENSG00000152465	NMT2
ENSG00000152467	0.460065	0.689435	0.755169	0.922783	ENSG00000152467	ZSCAN1
ENSG00000152475	1.23012	1.48635	2.23947	0.727234	ENSG00000152475	ZNF837
ENSG00000152484	7.56078	6.68359	7.32672	8.63108	ENSG00000152484	USP12
ENSG00000152492	29.0651	34.5785	34.3848	31.9378	ENSG00000152492	CCDC50
ENSG00000152495	0.562225	1.22295	1.02244	2.06602	ENSG00000152495	CAMK4
ENSG00000152503	2.15716	3.51305	2.83643	2.86251	ENSG00000152503	TRIM36
ENSG00000152518	50.6735	37.7521	43.3759	63.2213	ENSG00000152518	ZFP36L2
ENSG00000152520	10.5814	16.7096	15.9512	17.7792	ENSG00000152520	PAN3
ENSG00000152527	1.92879	3.27484	3.23931	6.84549	ENSG00000152527	PLEKHH2

ENSG00000152556	32.7176	54.693	48.107	67.5136	ENSG00000152556	PFKM
ENSG00000152558	108.314	141.252	74.4433	44.8616	ENSG00000152558	TMEM123
ENSG00000152578	0.879107	1.21332	1.36836	3.04133	ENSG00000152578	GRIA4
ENSG00000152580	2.66402	5.0965	3.54514	7.73888	ENSG00000152580	IGSF10
ENSG00000152582	2.46363	4.35232	5.5287	5.57796	ENSG00000152582	SPEF2
ENSG00000152583	1.09139	3.53522	3.1818	3.9795	ENSG00000152583	SPARCL1
ENSG00000152591	0	0.0121358	0.0556637	0.0692738	ENSG00000152591	DSPP
ENSG00000152592	0.0209593	0.223062	0.18269	0.138213	ENSG00000152592	DMP1
ENSG00000152595	0	0.109474	0.0920706	0.0623178	ENSG00000152595	MEPE
ENSG00000152601	38.3723	57.6785	58.1495	48.115	ENSG00000152601	MBNL1
ENSG00000152611	0	0	0	0.139544	ENSG00000152611	CAPSL
ENSG00000152620	10.0481	14.6175	13.9477	21.8207	ENSG00000152620	NADK2
ENSG00000152642	4.15679	4.38846	4.05428	6.18726	ENSG00000152642	GPD1L
ENSG00000152661	76.1002	75.7971	98.2835	39.9035	ENSG00000152661	GJA1
ENSG00000152669	1.40406	2.80467	1.18492	1.78067	ENSG00000152669	CCNO
ENSG00000152670	0.356385	1.3456	0.369375	1.37241	ENSG00000152670	DDX4
ENSG00000152672	0	0.0134924	0.024395	0.0123049	ENSG00000152672	CLEC4F
ENSG00000152683	18.3017	20.5187	19.8934	12.3934	ENSG00000152683	SLC30A6
ENSG00000152684	8.5961	9.46921	8.4437	7.55759	ENSG00000152684	PELO
ENSG00000152689	13.7802	32.8494	26.9127	62.5635	ENSG00000152689	RASGRP3
ENSG00000152700	48.9249	54.5103	51.6963	60.5845	ENSG00000152700	SAR1B
ENSG00000152705	0.306653	0.312132	0.240351	0.288035	ENSG00000152705	CATSPER3
ENSG00000152726	6.40218	5.19297	9.36113	7.17862	ENSG00000152726	FAM21B
ENSG00000152749	8.98275	11.3354	5.00646	6.92434	ENSG00000152749	GPR180
ENSG00000152760	0	0.129914	0.152811	1.07549	ENSG00000152760	TCTEX1D1
ENSG00000152763	9.14053	16.2252	18.9786	21.8008	ENSG00000152763	WDR78
ENSG00000152766	17.5106	7.91758	5.23016	6.65485	ENSG00000152766	ANKRD22
ENSG00000152767	23.0382	39.1706	36.4092	73.6791	ENSG00000152767	FARP1
ENSG00000152778	9.60787	10.2038	10.8828	9.57004	ENSG00000152778	IFIT5
ENSG00000152779	1.16157	0.538847	1.03822	1.65086	ENSG00000152779	SLC16A12
ENSG00000152782	3.573	6.01276	4.69706	7.2159	ENSG00000152782	PANK1
ENSG00000152784	4.72744	18.9293	4.56889	13.2111	ENSG00000152784	PRDM8
ENSG00000152785	0.250699	0.519047	0.430201	0.887106	ENSG00000152785	BMP3
ENSG00000152795	115.059	178.785	151.644	121.176	ENSG00000152795	HNRNPDL
ENSG00000152804	0.26724	0.246734	0.279313	0.318574	ENSG00000152804	HHEX
ENSG00000152818	24.7612	59.0258	32.7522	64.7946	ENSG00000152818	UTRN
ENSG00000152822	0.313143	1.10608	0.380455	1.35994	ENSG00000152822	GRM1
ENSG00000152894	107.987	169.666	129.049	114.807	ENSG00000152894	PTPRK
ENSG00000152904	13.507	8.74525	12.4451	10.7775	ENSG00000152904	GGPS1
ENSG00000152910	0.757198	0.803454	8.04988	1.3526	ENSG00000152910	CNTNAP4
ENSG00000152926	6.76463	7.45388	7.05739	9.28657	ENSG00000152926	ZNF117
ENSG00000152932	0.581227	0.662867	0.11114	0.482669	ENSG00000152932	RAB3C
ENSG00000152936	1.68355	3.23107	2.9507	6.05399	ENSG00000152936	LMNTD1
ENSG00000152939	2.29458	12.812	3.20919	4.60445	ENSG00000152939	MARVELD2
ENSG00000152942	3.29915	7.85709	5.01645	8.08965	ENSG00000152942	RAD17
ENSG00000152944	20.9005	23.2189	20.8308	21.5305	ENSG00000152944	MED21
ENSG00000152952	17.2383	19.585	36.2474	116.779	ENSG00000152952	PLOD2
ENSG00000152953	1.42279	5.90273	1.01653	4.40975	ENSG00000152953	STK32B
ENSG00000152954	0.472093	0.739977	1.60247	2.69524	ENSG00000152954	NRSN1
ENSG00000152969	0.157535	0.245668	0.141791	0.322183	ENSG00000152969	JAKMIP1
ENSG00000152977	3.24108	4.1319	6.11029	12.4585	ENSG00000152977	ZIC1
ENSG00000152990	38.5725	75.6707	45.4706	51.3228	ENSG00000152990	ADGRA3
ENSG00000153002	0.783754	2.16213	2.21001	4.02319	ENSG00000153002	CPB1
ENSG00000153006	25.1287	19.1145	21.6911	21.7503	ENSG00000153006	SREK1IP1

ENSG00000153012	0.0579063	0.0957662	0.0793762	0.277535	ENSG00000153012	LGI2
ENSG00000153015	7.4169	9.7146	9.8346	13.752	ENSG00000153015	CWC27
ENSG00000153029	21.1083	28.9394	27.5863	12.9351	ENSG00000153029	MR1
ENSG00000153037	30.2202	27.1873	38.2179	21.6908	ENSG00000153037	SRP19
ENSG00000153044	4.88113	14.511	5.18605	7.27625	ENSG00000153044	CENPH
ENSG00000153046	21.0229	16.6373	20.4087	15.523	ENSG00000153046	CDYL
ENSG00000153048	45.8755	52.1181	35.0445	38.6133	ENSG00000153048	CARHSP1
ENSG00000153060	0.0357134	0.139428	0.159376	1.04707	ENSG00000153060	TEKT5
ENSG00000153064	1.3235	1.73223	1.66774	1.95627	ENSG00000153064	BANK1
ENSG00000153066	24.0112	25.7282	18.2763	16.9898	ENSG00000153066	TXNDC11
ENSG00000153071	4.13513	10.2875	8.30449	95.7938	ENSG00000153071	DAB2
ENSG00000153086	0.438896	0.627794	0.23687	0.723738	ENSG00000153086	ACMSD
ENSG00000153093	1.70875	3.3994	2.95557	3.74726	ENSG00000153093	ACOXL
ENSG00000153094	5.90173	9.87115	11.61	11.8917	ENSG00000153094	BCL2L11
ENSG00000153107	26.3938	47.0211	37.0855	31.0345	ENSG00000153107	ANAPC1
ENSG00000153113	632.282	223.163	174.68	175.657	ENSG00000153113	CAST
ENSG00000153130	32.1864	25.8031	33.0667	19.1959	ENSG00000153130	SCOC
ENSG00000153132	0.126179	0.49131	1.67655	0.394881	ENSG00000153132	CLGN
ENSG00000153140	13.3424	16.3355	11.3061	12.4842	ENSG00000153140	CETN3
ENSG00000153147	26.5738	25.4929	23.9149	25.0605	ENSG00000153147	SMARCA5
ENSG00000153157	0.725144	2.50702	9.22908	3.24222	ENSG00000153157	SYCP2L
ENSG00000153162	13.3058	1.98454	0.717375	3.3537	ENSG00000153162	BMP6
ENSG00000153165	0.275477	0.172578	0.168849	0.212958	ENSG00000153165	RGPD3
ENSG00000153179	6.25473	5.83746	5.31969	8.64823	ENSG00000153179	RASSF3
ENSG00000153187	88.4169	89.2487	107.887	119.855	ENSG00000153187	HNRNPU
ENSG00000153201	42.7814	44.1962	44.537	40.7625	ENSG00000153201	RANBP2
ENSG00000153207	40.3629	49.5505	44.6399	47.4665	ENSG00000153207	AHCTF1
ENSG00000153208	0.134358	0.8135	0.712965	1.76103	ENSG00000153208	MERTK
ENSG00000153214	46.1089	43.5719	36.1541	23.0457	ENSG00000153214	TMEM87B
ENSG00000153230	0	0	0	0	ENSG00000153230	OR14K1
ENSG00000153233	0.980317	0.260088	0.337057	0.39848	ENSG00000153233	PTPRR
ENSG00000153234	1.03042	0.820893	0.642036	0.857696	ENSG00000153234	NR4A2
ENSG00000153237	1.96702	6.47622	5.03423	9.04666	ENSG00000153237	CCDC148
ENSG00000153246	10.6731	14.9671	27.5368	17.4569	ENSG00000153246	PLA2R1
ENSG00000153250	49.9576	44.3364	44.8576	74.2083	ENSG00000153250	RBMS1
ENSG00000153253	0.154304	1.13697	0.611575	1.19953	ENSG00000153253	SCN3A
ENSG00000153266	0.362897	0.3996	0.203615	0.519319	ENSG00000153266	FEZF2
ENSG00000153283	1.28507	4.38523	4.39287	7.09702	ENSG00000153283	CD96
ENSG00000153291	3.48699	10.9013	12.3923	9.63075	ENSG00000153291	SLC25A27
ENSG00000153292	58.9338	45.8823	8.2354	18.331	ENSG00000153292	ADGRF1
ENSG00000153294	26.4775	5.56068	15.9681	3.30102	ENSG00000153294	ADGRF4
ENSG00000153303	0.480732	0.419884	0.552651	2.59769	ENSG00000153303	FRMD1
ENSG00000153310	51.5974	50.0666	40.4158	48.7696	ENSG00000153310	FAM49B
ENSG00000153317	23.6301	44.3603	33.5246	84.7618	ENSG00000153317	ASAP1
ENSG00000153339	34.0353	46.1495	38.1651	52.6567	ENSG00000153339	TRAPPC8
ENSG00000153347	0.03704	0.685294	0.875299	1.3769	ENSG00000153347	FAM81B
ENSG00000153391	103.997	166.679	119.662	198.051	ENSG00000153391	INO80C
ENSG00000153395	38.5707	34.7695	18.953	27.8309	ENSG00000153395	LPCAT1
ENSG00000153404	0.352614	0.769977	0.692738	1.74172	ENSG00000153404	PLEKHG4B
ENSG00000153406	41.5654	36.1939	37.7805	38.7831	ENSG00000153406	NMRAL1
ENSG00000153443	9.61426	9.04813	12.4573	7.66301	ENSG00000153443	UBALD1
ENSG00000153446	1.20756	2.23302	1.73222	3.48356	ENSG00000153446	C16orf89
ENSG00000153485	5.75123	6.37623	4.8596	3.12244	ENSG00000153485	TMEM251
ENSG00000153487	2.29934	2.07068	2.56623	2.04147	ENSG00000153487	ING1

ENSG00000153495	0.188767	0.272071	0.409611	0.452014	ENSG00000153495	TEX29
ENSG00000153498	0.684689	1.99801	1.44068	2.64703	ENSG00000153498	SPACA7
ENSG00000153531	1.31064	0.923719	1.71666	0.765024	ENSG00000153531	ADPRHL1
ENSG00000153551	56.2233	38.8108	10.0959	14.1444	ENSG00000153551	CMTM7
ENSG00000153558	29.3016	34.2511	30.6491	34.3059	ENSG00000153558	FBXL2
ENSG00000153560	18.2683	31.5599	35.306	35.7872	ENSG00000153560	UBP1
ENSG00000153561	29.3108	17.2947	14.9451	11.9203	ENSG00000153561	RMND5A
ENSG00000153563	0.287917	0.56848	0.471312	1.14758	ENSG00000153563	CD8A
ENSG00000153574	2.43181	3.26024	2.72923	3.63051	ENSG00000153574	RPIA
ENSG00000153575	10.7155	15.3734	14.975	14.2289	ENSG00000153575	TUBGCP5
ENSG00000153666	1.01078	2.92784	3.01077	1.49655	ENSG00000153666	GOLGA8I
ENSG00000153684	0.222769	0.417009	0.350738	0.371893	ENSG00000153684	GOLGA8F
ENSG00000153707	0.0786643	1.2362	1.01149	2.74244	ENSG00000153707	PTPRD
ENSG00000153714	19.0098	8.31098	21.9634	5.58245	ENSG00000153714	LURAP1L
ENSG00000153721	1.57768	3.0526	3.36681	5.95046	ENSG00000153721	CNKSR3
ENSG00000153767	5.58291	4.82246	7.05164	4.68874	ENSG00000153767	GTF2E1
ENSG00000153774	30.3079	35.5812	29.8914	44.2853	ENSG00000153774	CFDP1
ENSG00000153779	0	0	0	0	ENSG00000153779	TGIF2LX
ENSG00000153786	44.7649	46.4098	41.8287	38.6552	ENSG00000153786	ZDHHC7
ENSG00000153789	0.728076	2.76954	2.44355	4.46409	ENSG00000153789	FAM92B
ENSG00000153790	0.43724	0.754065	1.19797	0.726773	ENSG00000153790	C7orf31
ENSG00000153802	29.0981	20.316	1.01665	7.92741	ENSG00000153802	TMPRSS11D
ENSG00000153814	3.20149	5.37017	5.03558	12.8106	ENSG00000153814	JAZF1
ENSG00000153815	23.452	27.2977	30.6034	27.3344	ENSG00000153815	CMIP
ENSG00000153820	0.0312167	0.0903485	0.0612704	0.0516159	ENSG00000153820	SPHKAP
ENSG00000153822	1.07626	5.54014	4.42582	2.95244	ENSG00000153822	KCNJ16
ENSG00000153823	1.12115	3.67307	5.74572	7.9348	ENSG00000153823	PID1
ENSG00000153827	101.795	115.67	112.858	125.608	ENSG00000153827	TRIP12
ENSG00000153832	3.33865	5.38771	6.40823	8.51873	ENSG00000153832	FBXO36
ENSG00000153879	10.3777	20.3993	23.2374	8.34026	ENSG00000153879	CEBPG
ENSG00000153885	10.4765	33.6613	39.4173	17.1693	ENSG00000153885	KCTD15
ENSG00000153896	3.1953	3.72906	4.51228	4.54093	ENSG00000153896	ZNF599
ENSG00000153898	2.41037	5.44633	3.18267	4.05681	ENSG00000153898	MCOLN2
ENSG00000153902	1.04164	1.64762	2.12824	2.78935	ENSG00000153902	LGI4
ENSG00000153904	6.12588	15.0891	12.3214	59.1501	ENSG00000153904	DDAH1
ENSG00000153914	28.0247	42.5984	48.879	48.8064	ENSG00000153914	SREK1
ENSG00000153922	27.3175	42.811	40.0241	44.5647	ENSG00000153922	CHD1
ENSG00000153923	0.395674	0.158246	0.279295	0.263159	ENSG00000153923	CLCA3P
ENSG00000153930	0.895084	0.197036	0.682007	0.419984	ENSG00000153930	ANKFN1
ENSG00000153933	12.4823	22.8498	20.6014	27.3114	ENSG00000153933	DGKE
ENSG00000153936	12.1104	18.0494	17.7057	13.6231	ENSG00000153936	HS2ST1
ENSG00000153944	22.3522	44.8589	34.4798	62.9271	ENSG00000153944	MSI2
ENSG00000153956	2.17412	3.00322	4.59484	9.58501	ENSG00000153956	CACNA2D1
ENSG00000153975	12.8883	14.2643	15.6795	10.6285	ENSG00000153975	ZUFSP
ENSG00000153976	2.6375	0.506429	1.16913	7.59371	ENSG00000153976	HS3ST3A1
ENSG00000153982	6.07541	6.34273	9.79073	6.8289	ENSG00000153982	GDPD1
ENSG00000153989	10.2158	8.76331	8.89181	10.5172	ENSG00000153989	NUS1
ENSG00000153993	0.963436	4.28998	2.26989	3.09734	ENSG00000153993	SEMA3D
ENSG00000154001	17.4518	19.978	19.676	18.2984	ENSG00000154001	PPP2R5E
ENSG00000154007	0.0547615	0.263536	0	0.0597329	ENSG00000154007	ASB17
ENSG00000154016	0.0359629	0.777974	0.643293	0.464358	ENSG00000154016	GRAP
ENSG00000154025	0.270441	0.551816	0.482018	0.94877	ENSG00000154025	SLC5A10
ENSG00000154027	2.9741	8.92003	6.60234	41.4562	ENSG00000154027	AK5
ENSG00000154035	2.73411	1.87823	2.79789	2.78864	ENSG00000154035	C17ORF103

ENSG00000154040	9.51132	13.0621	8.6466	19.7216	ENSG00000154040	CABYR
ENSG00000154059	15.6811	15.075	15.2016	8.39164	ENSG00000154059	IMPACT
ENSG00000154065	7.43802	12.5545	7.31369	7.84001	ENSG00000154065	ANKRD29
ENSG00000154079	11.8718	16.8774	14.8627	15.8099	ENSG00000154079	SDHAF4
ENSG00000154080	0.222588	0.336748	0.120703	0.243054	ENSG00000154080	CHST9
ENSG00000154096	1.29567	2.39611	6.33186	50.5851	ENSG00000154096	THY1
ENSG00000154099	1.60359	2.4554	2.00273	3.95304	ENSG00000154099	DNAAF1
ENSG00000154102	31.3906	63.8628	42.2466	32.3618	ENSG00000154102	C16orf74
ENSG00000154114	6.81661	9.31761	12.6356	10.6222	ENSG00000154114	TBCEL
ENSG00000154118	0.250417	0.440367	0.410035	1.06437	ENSG00000154118	JPH3
ENSG00000154122	5.06763	14.232	14.1846	13.1241	ENSG00000154122	ANKH
ENSG00000154124	15.253	21.7901	16.7434	14.737	ENSG00000154124	OTULIN
ENSG00000154127	15.9442	21.1122	6.11848	23.0425	ENSG00000154127	UBASH3B
ENSG00000154133	1.48842	4.15342	4.52438	6.45595	ENSG00000154133	ROBO4
ENSG00000154134	7.4058	20.7108	42.0902	19.9625	ENSG00000154134	ROBO3
ENSG00000154143	0.0344098	0.0331526	0.059938	0.0754091	ENSG00000154143	PANX3
ENSG00000154144	20.5327	26.9763	32.0539	18.3166	ENSG00000154144	TBRG1
ENSG00000154146	0.135753	1.95222	0.238499	1.15017	ENSG00000154146	NRGN
ENSG00000154153	1.18315	2.41378	3.3376	2.58289	ENSG00000154153	RETREG1
ENSG00000154162	0.358553	2.77835	1.54392	6.17108	ENSG00000154162	CDH12
ENSG00000154165	0	0.14157	0.0426522	0.160601	ENSG00000154165	GPR15
ENSG00000154174	22.5893	22.3225	22.7618	18.0814	ENSG00000154174	TOMM70
ENSG00000154175	22.3697	55.5114	58.4225	351.356	ENSG00000154175	ABI3BP
ENSG00000154188	1.01541	1.5636	1.20824	10.1089	ENSG00000154188	ANGPT1
ENSG00000154198	0	0	0.101179	0	ENSG00000154198	CYP4Z2P
ENSG00000154217	32.9663	29.4321	9.61353	31.4842	ENSG00000154217	PITPNC1
ENSG00000154222	36.4197	42.4064	47.2925	23.4989	ENSG00000154222	CC2D1B
ENSG00000154227	33.8082	35.8273	40.1945	9.6607	ENSG00000154227	CERS3
ENSG00000154229	7.03349	11.0863	9.52451	29.4026	ENSG00000154229	PRKCA
ENSG00000154237	8.10559	17.2448	13.5236	24.7349	ENSG00000154237	LRRK1
ENSG00000154240	9.17131	23.7549	22.2646	34.4745	ENSG00000154240	CEP112
ENSG00000154252	0.0857142	0.168511	0.0377737	0.187488	ENSG00000154252	GAL3ST2
ENSG00000154258	4.43407	10.4416	10.8184	16.4534	ENSG00000154258	ABCA9
ENSG00000154262	1.47991	3.82159	3.27544	7.79468	ENSG00000154262	ABCA6
ENSG00000154263	1.11136	3.34458	2.8259	2.10901	ENSG00000154263	ABCA10
ENSG00000154265	21.4527	36.5511	28.8833	38.5322	ENSG00000154265	ABCA5
ENSG00000154269	1.51214	2.50422	1.98036	4.93469	ENSG00000154269	ENPP3
ENSG00000154274	3.9403	5.13228	4.74593	10.0205	ENSG00000154274	C4orf19
ENSG00000154277	1.11958	2.29102	4.90647	9.94989	ENSG00000154277	UCHL1
ENSG00000154305	51.3765	98.4114	83.468	103.31	ENSG00000154305	MIA3
ENSG00000154309	2.48277	4.44106	6.2542	8.97671	ENSG00000154309	DISP1
ENSG00000154310	2.88438	3.47342	2.05963	6.04581	ENSG00000154310	TNIK
ENSG00000154316	0.194371	0.0933894	0.393821	0.364905	ENSG00000154316	TDH
ENSG00000154319	1.11622	7.49655	12.9061	8.34601	ENSG00000154319	FAM167A
ENSG00000154328	3.4979	5.04988	7.58942	5.59622	ENSG00000154328	NEIL2
ENSG00000154330	2.90886	4.5597	4.43284	7.03992	ENSG00000154330	PGM5
ENSG00000154342	0.112236	0.126257	0.186844	0.0205693	ENSG00000154342	WNT3A
ENSG00000154358	10.3235	32.8336	34.9739	22.3324	ENSG00000154358	OBSCN
ENSG00000154359	7.71196	17.0268	7.46669	8.05493	ENSG00000154359	LONRF1
ENSG00000154370	22.2402	22.8624	28.8141	16.6971	ENSG00000154370	TRIM11
ENSG00000154380	24.5941	28.9121	77.8607	21.5523	ENSG00000154380	ENAH
ENSG00000154415	0.0829185	0.155717	0.0552703	0.221209	ENSG00000154415	PPP1R3A
ENSG00000154429	3.84943	6.44171	4.85952	6.04565	ENSG00000154429	CCSAP
ENSG00000154438	0.745775	1.26326	1.35623	1.96051	ENSG00000154438	ASZ1

ENSG00000154447	12.2196	13.4061	13.2938	11.6712	ENSG00000154447	SH3RF1
ENSG00000154451	0.827879	1.80498	1.46428	3.45732	ENSG00000154451	GBP5
ENSG00000154473	53.9831	73.9066	47.0551	38.7117	ENSG00000154473	BUB3
ENSG00000154478	0.144303	0.16684	0.12494	0.260775	ENSG00000154478	GPR26
ENSG00000154479	0.748262	1.22403	1.57473	1.85496	ENSG00000154479	CCDC173
ENSG00000154485	0.442294	0.227277	0.283227	0.356144	ENSG00000154485	MMP21
ENSG00000154493	0.444448	0.865409	0.470861	1.23131	ENSG00000154493	C10orf90
ENSG00000154511	10.4114	7.56162	5.49253	5.45354	ENSG00000154511	FAM69A
ENSG00000154518	89.4522	58.8569	48.1899	43.297	ENSG00000154518	ATP5G3
ENSG00000154529	12.0836	22.1414	15.2841	28.8091	ENSG00000154529	CNTNAP3B
ENSG00000154537	0	0	0	0	ENSG00000154537	FAM27C
ENSG00000154545	0.426395	1.04204	1.0666	4.95676	ENSG00000154545	MAGED4
ENSG00000154548	0.370775	1.12545	1.69219	2.72958	ENSG00000154548	SRSF12
ENSG00000154553	0.493401	1.41992	1.05892	2.79088	ENSG00000154553	PDLIM3
ENSG00000154556	1.91143	2.65065	3.58059	10.1936	ENSG00000154556	SORBS2
ENSG00000154582	54.662	48.9292	43.3631	50.0821	ENSG00000154582	ELOC
ENSG00000154589	1.73735	8.04185	1.00752	2.63196	ENSG00000154589	LY96
ENSG00000154608	0.132836	0.455187	0.373986	0.830249	ENSG00000154608	CEP170P1
ENSG00000154611	0.138905	0.314582	0.353259	0.761508	ENSG00000154611	PSMA8
ENSG00000154620	0.240549	0.695351	0.310691	0.037655	ENSG00000154620	TMSB4Y
ENSG00000154639	38.3591	24.6196	25.4302	10.7328	ENSG00000154639	CXADR
ENSG00000154640	24.7212	32.7331	27.5554	22.6779	ENSG00000154640	BTG3
ENSG00000154642	9.76798	9.02371	15.6215	6.19825	ENSG00000154642	C21orf91
ENSG00000154645	0.680368	0.973325	1.18002	1.61633	ENSG00000154645	CHODL
ENSG00000154646	0.217406	0.356572	0.343251	0.749556	ENSG00000154646	TMPRSS15
ENSG00000154654	0.489439	0.35847	0.369942	1.76624	ENSG00000154654	NCAM2
ENSG00000154655	2.63478	4.5486	7.20648	5.1561	ENSG00000154655	L3MBTL4
ENSG00000154678	1.94727	6.77889	0.777166	3.48042	ENSG00000154678	PDE1C
ENSG00000154710	31.1681	22.4743	32.1231	26.5084	ENSG00000154710	RABGEF1
ENSG00000154719	14.4158	14.626	13.3859	9.38064	ENSG00000154719	MRPL39
ENSG00000154721	4.89621	13.841	10.6956	22.5497	ENSG00000154721	JAM2
ENSG00000154723	19.0069	15.0468	18.7097	15.4279	ENSG00000154723	ATP5J
ENSG00000154727	6.30448	6.36859	6.74534	6.49265	ENSG00000154727	GABPA
ENSG00000154734	199.395	46.0297	9.44158	92.5646	ENSG00000154734	ADAMTS1
ENSG00000154736	0.0705375	0.119034	0.457734	2.67235	ENSG00000154736	ADAMTS5
ENSG00000154743	10.6648	31.867	27.9171	30.3593	ENSG00000154743	TSEN2
ENSG00000154760	1.69068	6.3384	2.46764	4.03144	ENSG00000154760	SLFN13
ENSG00000154764	35.6233	41.6706	9.88939	17.4356	ENSG00000154764	WNT7A
ENSG00000154767	16.0041	37.2779	30.7494	36.7524	ENSG00000154767	XPC
ENSG00000154768	0.181329	0.145398	0.449884	0.137648	ENSG00000154768	C17orf50
ENSG00000154781	12.675	11.3026	20.1194	10.898	ENSG00000154781	CCDC174
ENSG00000154783	1.08546	2.74675	2.67975	5.37415	ENSG00000154783	FGD5
ENSG00000154803	24.4412	20.735	29.6543	29.6135	ENSG00000154803	FLCN
ENSG00000154813	7.42066	5.10332	6.22626	5.3999	ENSG00000154813	DPH3
ENSG00000154814	6.72135	11.3532	11.8294	12.7383	ENSG00000154814	OXNAD1
ENSG00000154822	0.128372	0.566105	0.601418	3.06346	ENSG00000154822	PLCL2
ENSG00000154832	23.2254	28.251	26.865	21.267	ENSG00000154832	CXXC1
ENSG00000154839	1.86849	6.49837	2.68942	4.85877	ENSG00000154839	SKA1
ENSG00000154845	136.54	155.546	126.865	149.206	ENSG00000154845	PPP4R1
ENSG00000154856	21.5935	1.58406	7.64118	36.3525	ENSG00000154856	APCDD1
ENSG00000154864	5.64909	15.081	15.4452	28.923	ENSG00000154864	PIEZO2
ENSG00000154874	10.4376	27.3374	25.8261	44.5518	ENSG00000154874	CCDC144B
ENSG00000154889	34.0076	32.1641	37.5038	37.0734	ENSG00000154889	MPPE1
ENSG00000154898	1.79677	5.78045	4.00688	4.57024	ENSG00000154898	CCDC144CP

ENSG00000154914	6.82675	5.202	5.23732	9.23778	ENSG00000154914	USP43
ENSG00000154917	1.2209	1.05772	1.01688	1.30388	ENSG00000154917	RAB6B
ENSG00000154920	3.6028	7.52113	3.65332	5.94143	ENSG00000154920	EME1
ENSG00000154928	0.908329	1.81547	2.12432	3.97134	ENSG00000154928	EPHB1
ENSG00000154930	0.583081	2.56208	2.39457	4.08948	ENSG00000154930	ACSS1
ENSG00000154945	23.2993	23.7877	24.435	28.9691	ENSG00000154945	ANKRD40
ENSG00000154957	4.05236	9.29707	8.62777	8.13926	ENSG00000154957	ZNF18
ENSG00000154975	1.19785	2.85801	2.13763	3.23313	ENSG00000154975	CA10
ENSG00000154978	53.5459	48.3319	24.9635	37.9434	ENSG00000154978	VOPP1
ENSG00000154997	1.91702	5.03308	5.25243	7.05202	ENSG00000154997	SEPT14
ENSG00000155008	7.29494	4.47174	4.73579	4.23147	ENSG00000155008	APOOL
ENSG00000155011	0.271171	0.858863	0.408726	0.863999	ENSG00000155011	DKK2
ENSG00000155016	4.52614	4.85078	4.45414	5.62176	ENSG00000155016	CYP2U1
ENSG00000155026	1.99238	3.64809	3.88891	7.05751	ENSG00000155026	RSPH10B
ENSG00000155034	10.3878	10.5936	14.2327	15.6178	ENSG00000155034	FBXL18
ENSG00000155052	0.32984	0.496476	0.419603	0.694408	ENSG00000155052	CNTNAP5
ENSG00000155066	121.673	38.9549	42.1027	38.4644	ENSG00000155066	PROM2
ENSG00000155070	0	0	0.0952239	0.300587	ENSG00000155070	UNC93B2
ENSG00000155085	2.68367	3.62373	4.18912	6.10357	ENSG00000155085	AK9
ENSG00000155087	0	0	0.0528677	0	ENSG00000155087	ODF1
ENSG00000155090	29.0461	22.9468	43.4286	15.4161	ENSG00000155090	KLF10
ENSG00000155093	0.0686231	0.0220235	0.0764395	0.0578623	ENSG00000155093	PTPRN2
ENSG00000155096	62.6453	61.3738	76.0075	54.6161	ENSG00000155096	AZIN1
ENSG00000155097	30.0563	17.7635	15.0619	16.9717	ENSG00000155097	ATP6V1C1
ENSG00000155099	4.12693	8.47766	3.83642	4.6441	ENSG00000155099	TMEM55A
ENSG00000155100	9.81681	10.5371	12.5755	8.91901	ENSG00000155100	OTUD6B
ENSG00000155111	3.85746	3.61696	4.11849	6.0583	ENSG00000155111	CDK19
ENSG00000155115	12.697	9.4906	11.9573	9.06855	ENSG00000155115	GTF3C6
ENSG00000155130	32.7032	26.9555	43.3527	69.2111	ENSG00000155130	MARCKS
ENSG00000155158	6.4769	18.1827	18.5601	12.303	ENSG00000155158	TTC39B
ENSG00000155189	29.1257	33.0352	24.999	23.9122	ENSG00000155189	AGPAT5
ENSG00000155229	52.8547	67.7759	50.2612	57.0366	ENSG00000155229	MMS19
ENSG00000155249	0	0	0	0	ENSG00000155249	OR4K1
ENSG00000155252	22.9495	15.6658	18.4725	11.8639	ENSG00000155252	PI4K2A
ENSG00000155254	29.6752	32.5023	18.3706	18.0055	ENSG00000155254	MARVELD1
ENSG00000155256	31.5499	33.6125	38.4705	25.015	ENSG00000155256	ZFYVE27
ENSG00000155265	3.11696	1.50205	1.67031	2.81418	ENSG00000155265	GOLGA7B
ENSG00000155269	1.3902	4.29109	2.18868	3.50636	ENSG00000155269	GPR78
ENSG00000155275	20.6823	27.072	30.6964	16.3799	ENSG00000155275	TRMT44
ENSG00000155282	0	0.114519	0	0.272326	ENSG00000155282	RP11-195B21.3
ENSG00000155287	18.4016	46.6607	30.9126	19.5332	ENSG00000155287	SLC25A28
ENSG00000155304	22.7853	50.4465	35.4323	15.4468	ENSG00000155304	HSPA13
ENSG00000155307	0.798193	1.14121	1.0274	1.32571	ENSG00000155307	SAMSN1
ENSG00000155313	21.4077	41.5005	39.4517	31.7752	ENSG00000155313	USP25
ENSG00000155324	28.1266	33.8989	24.2915	37.986	ENSG00000155324	GRAMD2B
ENSG00000155329	16.7413	18.6145	13.2485	13.1336	ENSG00000155329	ZCCHC10
ENSG00000155330	6.05437	5.45993	5.37332	8.92828	ENSG00000155330	C16orf87
ENSG00000155363	37.9872	52.5827	40.7068	36.8393	ENSG00000155363	MOV10
ENSG00000155366	238.67	162.388	79.7737	79.2796	ENSG00000155366	RHOC
ENSG00000155367	6.52223	8.07077	4.66887	3.78589	ENSG00000155367	PPM1J
ENSG00000155368	93.6017	65.1721	34.6579	44.9909	ENSG00000155368	DBI
ENSG00000155380	94.4243	153.638	132.811	72.1542	ENSG00000155380	SLC16A1
ENSG00000155393	12.9473	11.8996	17.4539	16.9049	ENSG00000155393	HEATR3
ENSG00000155428	0	0.114076	0.420376	0.216958	ENSG00000155428	TRIM74

ENSG00000155438	32.1531	29.3105	44.5562	23.7935	ENSG00000155438	NIFK
ENSG00000155463	40.4601	42.3839	37.1626	26.3446	ENSG00000155463	OXA1L
ENSG00000155465	2.77556	6.36108	4.79885	12.6044	ENSG00000155465	SLC7A7
ENSG00000155495	0.0561249	0.108031	0.158604	0.0612014	ENSG00000155495	MAGEC1
ENSG00000155506	64.5932	94.3521	116.23	95.2698	ENSG00000155506	LARP1
ENSG00000155508	19.0489	19.5204	18.8239	21.5774	ENSG00000155508	CNOT8
ENSG00000155511	15.1656	33.9501	22.1749	40.3116	ENSG00000155511	GRIA1
ENSG00000155530	0.310805	0.234863	0.866685	0.398855	ENSG00000155530	LRGUK
ENSG00000155542	2.61578	3.29284	5.2878	2.98968	ENSG00000155542	SETD9
ENSG00000155545	17.6789	14.4744	14.8446	12.5531	ENSG00000155545	MIER3
ENSG00000155561	36.4978	51.4813	31.707	33.1853	ENSG00000155561	NUP205
ENSG00000155592	1.83518	2.33595	2.8319	1.9657	ENSG00000155592	ZKSCAN2
ENSG00000155621	14.9442	16.9549	23.686	25.9527	ENSG00000155621	C9orf85
ENSG00000155622	0	0	0	0	ENSG00000155622	XAGE2
ENSG00000155629	2.69919	3.10572	2.43283	3.8941	ENSG00000155629	PIK3AP1
ENSG00000155636	8.18045	9.52395	9.72456	10.389	ENSG00000155636	RBM45
ENSG00000155640	3.93354	4.66484	5.21653	5.32148	ENSG00000155640	C10orf12
ENSG00000155657	2.82807	5.81252	4.30079	7.74728	ENSG00000155657	TTN
ENSG00000155659	0.0513451	0.0988547	0.0893468	0.168147	ENSG00000155659	VSIG4
ENSG00000155660	176.481	343.421	80.2866	125.188	ENSG00000155660	PDIA4
ENSG00000155666	5.49087	3.91287	7.98995	7.73288	ENSG00000155666	KDM8
ENSG00000155714	0.639469	1.9802	2.29352	3.64107	ENSG00000155714	PDZD9
ENSG00000155719	1.3628	4.05921	4.14519	4.7064	ENSG00000155719	OTOA
ENSG00000155729	18.8313	30.328	26.02	38.6807	ENSG00000155729	KCTD18
ENSG00000155744	11.0608	11.5533	12.8027	19.6771	ENSG00000155744	FAM126B
ENSG00000155749	3.46436	6.95059	10.1106	8.60475	ENSG00000155749	ALS2CR12
ENSG00000155754	0.0800219	0.247552	0.357928	0.489854	ENSG00000155754	C2CD6
ENSG00000155755	31.8745	45.4576	34.7518	24.3062	ENSG00000155755	TMEM237
ENSG00000155760	5.84266	5.59012	3.18198	5.58244	ENSG00000155760	FZD7
ENSG00000155761	1.69787	4.77806	4.37142	5.72193	ENSG00000155761	SPAG17
ENSG00000155792	0.256995	0.121124	0.942249	0.0946162	ENSG00000155792	DEPTOR
ENSG00000155816	0.351018	1.07335	0.989909	3.66502	ENSG00000155816	FMN2
ENSG00000155827	11.705	16.575	17.5089	12.7816	ENSG00000155827	RNF20
ENSG00000155833	0.753017	1.79187	0.429323	1.51136	ENSG00000155833	CYLC2
ENSG00000155846	8.57617	21.1096	21.772	24.9612	ENSG00000155846	PPARGC1B
ENSG00000155849	2.01706	4.22437	4.27304	7.18773	ENSG00000155849	ELMO1
ENSG00000155850	6.83584	8.28733	7.86749	8.16203	ENSG00000155850	SLC26A2
ENSG00000155858	1.61368	2.46349	1.93638	2.08604	ENSG00000155858	LSM11
ENSG00000155868	7.01748	7.70704	7.6802	5.89456	ENSG00000155868	MED7
ENSG00000155875	0.13431	0.132348	0.29081	0.378022	ENSG00000155875	SAXO1
ENSG00000155876	16.2049	14.4937	12.9406	15.3047	ENSG00000155876	RRAGA
ENSG00000155886	0.231874	0.370312	0.886399	0.788713	ENSG00000155886	SLC24A2
ENSG00000155890	0.0435926	0.106345	0.0949883	0.0239509	ENSG00000155890	TRIM42
ENSG00000155893	5.48811	6.10322	6.21186	5.73673	ENSG00000155893	PXYLP1
ENSG00000155897	0.0359091	0.0865702	0.0391785	0.195925	ENSG00000155897	ADCY8
ENSG00000155903	18.4787	23.9643	9.9637	26.7723	ENSG00000155903	RASA2
ENSG00000155906	8.66484	12.3918	8.65758	10.1392	ENSG00000155906	RMND1
ENSG00000155918	33.1542	4.29981	5.71424	4.92152	ENSG00000155918	RAET1L
ENSG00000155926	1.5056	2.5764	2.17148	4.2477	ENSG00000155926	SLA
ENSG00000155957	64.9949	68.0144	37.5735	36.1812	ENSG00000155957	TMBIM4
ENSG00000155959	7.16746	8.59821	2.15571	4.18823	ENSG00000155959	VBP1
ENSG00000155961	0.0232902	0.172436	0.170452	0.222191	ENSG00000155961	RAB39B
ENSG00000155962	1.35541	1.70223	1.38133	3.23517	ENSG00000155962	CLIC2
ENSG00000155966	0.0727876	0.156562	0.352237	0.269915	ENSG00000155966	AFF2

ENSG00000155970	3.01576	9.88134	7.80907	14.8199	ENSG00000155970	MICU3
ENSG00000155974	7.19208	12.1251	16.3851	9.01546	ENSG00000155974	GRIP1
ENSG00000155975	39.03	31.4368	34.162	28.6674	ENSG00000155975	VPS37A
ENSG00000155980	0.587428	0.328861	0.429519	1.1209	ENSG00000155980	KIF5A
ENSG00000155984	6.47934	14.5074	9.76823	17.1847	ENSG00000155984	TMEM185A
ENSG00000156006	0	0.0429753	0	0.0975785	ENSG00000156006	NAT2
ENSG00000156009	0.13544	0.477178	0.27434	0.390848	ENSG00000156009	MAGEA8
ENSG00000156011	15.5154	24.5264	24.7334	44.6446	ENSG00000156011	PSD3
ENSG00000156017	8.92262	9.62143	9.34027	7.95125	ENSG00000156017	CARNMT1
ENSG00000156026	31.6302	25.7603	18.9169	22.8104	ENSG00000156026	MCU
ENSG00000156030	19.5676	45.738	44.2965	33.6711	ENSG00000156030	ELMSAN1
ENSG00000156042	1.06796	2.10861	3.19404	2.5082	ENSG00000156042	CFAP70
ENSG00000156049	0.112695	0.279646	0.335541	0.576786	ENSG00000156049	GNA14
ENSG00000156050	2.36612	2.86828	3.63829	4.44287	ENSG00000156050	FAM161B
ENSG00000156052	29.4202	21.7526	20.7895	21.2096	ENSG00000156052	GNAQ
ENSG00000156076	0.0499075	0.0242064	0.109907	0.544952	ENSG00000156076	WIF1
ENSG00000156096	2.45401	4.28649	2.41167	5.82596	ENSG00000156096	UGT2B4
ENSG00000156097	1.47549	2.65794	1.6429	3.75471	ENSG00000156097	GPR61
ENSG00000156103	0.115066	0.262302	0.611534	2.75065	ENSG00000156103	MMP16
ENSG00000156110	29.6035	49.4703	33.9957	35.4827	ENSG00000156110	ADK
ENSG00000156113	1.57872	6.95147	3.23748	9.65539	ENSG00000156113	KCNMA1
ENSG00000156127	0	0.122386	0	0.532618	ENSG00000156127	BATF
ENSG00000156136	6.03824	10.7691	5.67921	7.69469	ENSG00000156136	DCK
ENSG00000156140	0.183667	0.44534	0.609552	0.706681	ENSG00000156140	ADAMTS3
ENSG00000156150	2.468	3.29433	4.04986	2.37654	ENSG00000156150	ALX3
ENSG00000156162	21.2325	20.0078	13.351	12.6699	ENSG00000156162	DPY19L4
ENSG00000156170	15.3577	25.2877	26.4127	33.3326	ENSG00000156170	NDUFAF6
ENSG00000156171	85.2748	56.5069	38.1506	24.5146	ENSG00000156171	DRAM2
ENSG00000156172	1.22944	2.00598	1.80689	2.2335	ENSG00000156172	C8orf37
ENSG00000156194	6.38613	9.85504	14.5661	16.4064	ENSG00000156194	PPEF2
ENSG00000156206	0.605815	0.602959	0.13903	0.11586	ENSG00000156206	CFAP161
ENSG00000156218	40.1768	95.9966	85.7306	185.09	ENSG00000156218	ADAMTSL3
ENSG00000156219	2.85599	3.90179	3.98575	5.57859	ENSG00000156219	ART3
ENSG00000156222	0.405576	0.260387	0.572042	0.274058	ENSG00000156222	SLC28A1
ENSG00000156232	6.15405	5.13823	5.69743	6.3953	ENSG00000156232	WHAMM
ENSG00000156234	0.0497204	0.239336	0.387696	0.109784	ENSG00000156234	CXCL13
ENSG00000156239	4.48853	9.97193	9.80504	10.6584	ENSG00000156239	N6AMT1
ENSG00000156253	7.17565	7.86772	9.85313	5.29993	ENSG00000156253	RWDD2B
ENSG00000156256	20.4421	20.6921	18.5684	20.5289	ENSG00000156256	USP16
ENSG00000156261	94.6825	80.0687	62.4455	60.8341	ENSG00000156261	CCT8
ENSG00000156265	11.9043	20.3888	17.1378	26.5584	ENSG00000156265	MAP3K7CL
ENSG00000156269	1.00888	1.98509	2.11851	2.59513	ENSG00000156269	NAA11
ENSG00000156273	58.4655	73.631	65.1687	82.5522	ENSG00000156273	BACH1
ENSG00000156282	0.544549	0.0872132	0	0.19641	ENSG00000156282	CLDN17
ENSG00000156284	0.462576	0.253238	0.310094	0.49403	ENSG00000156284	CLDN8
ENSG00000156298	0.719336	2.27707	1.0993	2.42488	ENSG00000156298	TSPAN7
ENSG00000156299	23.1537	13.5769	10.1704	7.74534	ENSG00000156299	TIAM1
ENSG00000156304	8.08181	13.2111	12.5208	16.7983	ENSG00000156304	SCAF4
ENSG00000156313	4.46995	4.93745	7.07365	8.04202	ENSG00000156313	RPGR
ENSG00000156345	2.71946	2.77109	3.30503	1.18465	ENSG00000156345	CDK20
ENSG00000156374	5.30954	11.3519	7.85342	8.8981	ENSG00000156374	PCGF6
ENSG00000156381	14.1062	15.3037	11.3595	9.49558	ENSG00000156381	ANKRD9
ENSG00000156384	8.34706	7.30041	5.23814	6.5075	ENSG00000156384	SFR1
ENSG00000156395	0.239473	0.440945	0.0826059	0.38955	ENSG00000156395	SORCS3

ENSG00000156398	3.59669	9.39691	6.08664	9.87128	ENSG00000156398	SFXN2
ENSG00000156411	75.3928	52.5188	45.569	37.1006	ENSG00000156411	C14orf2
ENSG00000156413	3.13049	2.5027	2.90574	4.39964	ENSG00000156413	FUT6
ENSG00000156414	1.46152	0.822061	1.71284	1.53827	ENSG00000156414	TDRD9
ENSG00000156427	0.208503	0.340853	0.54501	0.776087	ENSG00000156427	FGF18
ENSG00000156453	124.837	25.5	14.7038	12.7631	ENSG00000156453	PCDH1
ENSG00000156463	15.2578	38.9857	49.2958	24.4334	ENSG00000156463	SH3RF2
ENSG00000156466	0.0738631	0.101123	0.0514989	1.05972	ENSG00000156466	GDF6
ENSG00000156467	79.3269	73.7017	50.3278	45.9499	ENSG00000156467	UQCRB
ENSG00000156469	11.3362	15.7295	14.3393	15.0717	ENSG00000156469	MTERF3
ENSG00000156471	94.2098	117.902	69.99	31.5585	ENSG00000156471	PTDSS1
ENSG00000156475	4.899	7.04948	8.6659	12.7138	ENSG00000156475	PPP2R2B
ENSG00000156482	573.5	492.237	401.439	214.758	ENSG00000156482	RPL30
ENSG00000156486	0.205043	0.609886	0.554249	0.710307	ENSG00000156486	KCNS2
ENSG00000156500	10.9318	23.7643	17.4815	35.8495	ENSG00000156500	FAM122C
ENSG00000156502	14.6755	19.7264	20.8898	17.2386	ENSG00000156502	SUPV3L1
ENSG00000156504	4.9697	7.68225	6.36979	11.776	ENSG00000156504	FAM122B
ENSG00000156508	2852.31	2176.34	2058.79	1541.77	ENSG00000156508	EEF1A1
ENSG00000156509	0.516771	1.52365	1.0243	2.13288	ENSG00000156509	FBXO43
ENSG00000156510	1.38834	2.90013	1.49982	2.13412	ENSG00000156510	HKDC1
ENSG00000156515	43.7103	46.5853	46.2755	46.9294	ENSG00000156515	HK1
ENSG00000156521	10.8985	16.4891	15.2479	8.26633	ENSG00000156521	TYSND1
ENSG00000156531	10.1977	14.7269	13.4276	15.013	ENSG00000156531	PHF6
ENSG00000156535	82.8235	78.7046	66.9112	79.8353	ENSG00000156535	CD109
ENSG00000156564	0.122876	0.065554	0.130828	0.372506	ENSG00000156564	LRFN2
ENSG00000156574	0.083529	0.219441	0.270079	0.302034	ENSG00000156574	NODAL
ENSG00000156575	0	0	0	0	ENSG00000156575	PRG3
ENSG00000156587	10.4607	19.4577	13.8578	14.0036	ENSG00000156587	UBE2L6
ENSG00000156599	60.2966	41.1279	44.1661	25.6752	ENSG00000156599	ZDHHC5
ENSG00000156603	8.44944	8.69259	10.5828	8.8885	ENSG00000156603	MED19
ENSG00000156639	17.5066	23.9037	33.5807	37.415	ENSG00000156639	ZFAND3
ENSG00000156642	147.846	179.86	81.9626	88.1743	ENSG00000156642	NPTN
ENSG00000156650	4.6237	5.92996	5.06152	5.65356	ENSG00000156650	KAT6B
ENSG00000156671	18.4424	23.0672	17.7267	15.5025	ENSG00000156671	SAMD8
ENSG00000156675	98.1346	11.8015	13.8698	17.394	ENSG00000156675	RAB11FIP1
ENSG00000156687	0.109597	0.353506	0.411542	0.636626	ENSG00000156687	UNC5D
ENSG00000156689	0	0.404866	0.531405	1.98027	ENSG00000156689	GLYATL2
ENSG00000156697	11.1881	10.5027	14.0783	11.9	ENSG00000156697	UTP14A
ENSG00000156709	8.74532	15.5506	10.5262	13.8369	ENSG00000156709	AIFM1
ENSG00000156711	13.063	15.3905	12.5188	8.25679	ENSG00000156711	MAPK13
ENSG00000156735	12.6694	10.7012	10.9513	7.67961	ENSG00000156735	BAG4
ENSG00000156738	0.393597	0.73691	0.199273	0.888068	ENSG00000156738	MS4A1
ENSG00000156750	0.151571	0.233609	1.15715	0.898925	ENSG00000156750	AQP7P3
ENSG00000156755	9.84118	3.87248	1.59369	1.55351	ENSG00000156755	IGKV1OR-2
ENSG00000156787	5.60945	14.3955	10.5143	12.822	ENSG00000156787	TBC1D31
ENSG00000156795	5.18224	9.398	9.2007	7.10848	ENSG00000156795	WDYHV1
ENSG00000156802	8.48083	24.8107	9.23721	21.6792	ENSG00000156802	ATAD2
ENSG00000156804	12.1485	5.89055	12.1139	11.6324	ENSG00000156804	FBXO32
ENSG00000156831	23.623	32.6148	31.2582	37.517	ENSG00000156831	NSMCE2
ENSG00000156853	3.27666	3.0625	3.22921	1.90458	ENSG00000156853	ZNF689
ENSG00000156858	14.2717	12.0627	17.6345	11.8397	ENSG00000156858	PRR14
ENSG00000156860	39.3415	30.3455	41.6808	22.3064	ENSG00000156860	FBRS
ENSG00000156869	13.2303	26.208	20.5458	19.072	ENSG00000156869	FRRS1
ENSG00000156873	24.5732	20.0759	27.3466	19.2608	ENSG00000156873	PHKG2

ENSG00000156875	41.7421	43.4261	21.9129	16.7698	ENSG00000156875	MFSD14A
ENSG00000156876	2.34052	4.794	2.33727	3.25783	ENSG00000156876	SASS6
ENSG00000156885	0	0.179752	0.164392	0.214476	ENSG00000156885	COX6A2
ENSG00000156886	0.91374	3.98027	4.1114	5.71954	ENSG00000156886	ITGAD
ENSG00000156920	0.128314	0.283218	0.277306	0.484413	ENSG00000156920	ADGRG4
ENSG00000156925	0.0691034	0.10591	0.195037	0.0905235	ENSG00000156925	ZIC3
ENSG00000156928	24.1963	23.2107	16.3151	16.2514	ENSG00000156928	MALSU1
ENSG00000156931	37.8327	58.9246	59.5093	70.0914	ENSG00000156931	VPS8
ENSG00000156958	25.4323	36.1559	33.3049	50.2986	ENSG00000156958	GALK2
ENSG00000156959	2.83013	1.41117	1.10075	2.16867	ENSG00000156959	LHFPL4
ENSG00000156966	1.57942	1.47522	1.88712	2.27418	ENSG00000156966	B3GNT7
ENSG00000156968	8.3352	18.5495	18.1503	25.2293	ENSG00000156968	MPV17L
ENSG00000156970	3.84446	25.0472	3.01869	19.0134	ENSG00000156970	BUB1B
ENSG00000156973	8.27825	9.51194	6.08828	5.91195	ENSG00000156973	PDE6D
ENSG00000156976	242.478	344.151	334.052	165.883	ENSG00000156976	EIF4A2
ENSG00000156983	11.0594	11.2638	13.5823	7.96717	ENSG00000156983	BRPF1
ENSG00000156990	23.4661	28.7667	25.4941	30.7153	ENSG00000156990	RPUSD3
ENSG00000157005	0	0	0	1.21776	ENSG00000157005	SST
ENSG00000157014	5.40425	6.53713	10.8537	8.76683	ENSG00000157014	TATDN2
ENSG00000157017	12.126	31.3176	27.7029	14.6984	ENSG00000157017	GHRL
ENSG00000157020	78.9072	51.9826	42.7128	60.9217	ENSG00000157020	SEC13
ENSG00000157021	0	0	0	0.263868	ENSG00000157021	FAM92A1P1
ENSG00000157036	7.22674	14.1907	13.62	16.6344	ENSG00000157036	EXOG
ENSG00000157045	23.0548	18.8439	14.6654	18.8864	ENSG00000157045	NTAN1
ENSG00000157060	0.347545	1.31223	1.92548	1.92749	ENSG00000157060	SHCBP1L
ENSG00000157064	3.87531	6.62453	2.82918	11.8202	ENSG00000157064	NMNAT2
ENSG00000157077	13.8277	24.3121	28.6507	15.1106	ENSG00000157077	ZFYVE9
ENSG00000157087	0.624939	1.14658	0.665576	0.952143	ENSG00000157087	ATP2B2
ENSG00000157093	0.324288	0.207644	0.187501	0.116569	ENSG00000157093	LYZL4
ENSG00000157103	0.518756	0.718489	0.414609	0.493219	ENSG00000157103	SLC6A1
ENSG00000157106	64.6668	136.975	135.375	150.206	ENSG00000157106	SMG1
ENSG00000157107	23.6399	13.1328	13.1509	19.6262	ENSG00000157107	FCHO2
ENSG00000157110	13.5824	26.4541	21.9814	51.3324	ENSG00000157110	RBPMS
ENSG00000157111	3.9137	5.18564	1.11947	2.95276	ENSG00000157111	TMEM171
ENSG00000157119	0.0219997	0	0	0	ENSG00000157119	KLHL40
ENSG00000157131	0.0472256	0	0.061737	0.0518728	ENSG00000157131	C8A
ENSG00000157150	0.13921	0.335303	0.0606205	0.228789	ENSG00000157150	TIMP4
ENSG00000157168	25.9648	50.3849	30.3285	68.2462	ENSG00000157168	NRG1
ENSG00000157181	23.9348	25.3079	18.4804	14.7901	ENSG00000157181	C1orf27
ENSG00000157184	6.29168	9.80379	8.12995	4.78653	ENSG00000157184	CPT2
ENSG00000157191	35.1528	23.3855	25.7851	21.7097	ENSG00000157191	NECAP2
ENSG00000157193	18.1531	44.9821	7.66001	25.4137	ENSG00000157193	LRP8
ENSG00000157211	0.0809256	0.175554	0.053316	0.608608	ENSG00000157211	CDCP2
ENSG00000157212	5.4811	8.41916	9.65143	11.8277	ENSG00000157212	PAXIP1
ENSG00000157214	7.34755	14.8707	7.58184	20.1149	ENSG00000157214	STEAP2
ENSG00000157216	9.17403	19.2377	20.2362	17.8362	ENSG00000157216	SSBP3
ENSG00000157219	0.0189229	0.0552393	0.0831129	0.146446	ENSG00000157219	HTR5A
ENSG00000157224	52.8008	62.3117	45.5092	44.4097	ENSG00000157224	CLDN12
ENSG00000157227	196.488	538.106	292.107	328.158	ENSG00000157227	MMP14
ENSG00000157240	1.87541	2.76374	2.81672	4.9751	ENSG00000157240	FZD1
ENSG00000157259	16.1817	27.3757	25.7419	29.8997	ENSG00000157259	GATAD1
ENSG00000157303	0.258872	0.255408	0.457206	0.191823	ENSG00000157303	SUSD3
ENSG00000157315	1.17888	2.34277	2.02676	2.54309	ENSG00000157315	TMED6
ENSG00000157322	0.850582	1.42325	2.2755	1.39705	ENSG00000157322	CLEC18A

ENSG00000157326	8.06429	11.1064	12.39	7.82882	ENSG00000157326	DHRS4
ENSG00000157330	7.1613	17.9081	16.783	29.1957	ENSG00000157330	C1orf158
ENSG00000157335	0.657676	0.63499	0.546671	0.869271	ENSG00000157335	CLEC18C
ENSG00000157343	1.60717	2.90797	3.29457	3.92495	ENSG00000157343	ARMC12
ENSG00000157349	13.8053	14.4767	16.9385	17.1498	ENSG00000157349	DDX19B
ENSG00000157350	3.97432	5.92415	6.2057	16.5477	ENSG00000157350	ST3GAL2
ENSG00000157353	12.3298	17.9088	16.8477	18.8117	ENSG00000157353	FUK
ENSG00000157358	0	0	0	0	ENSG00000157358	PRAMEF15
ENSG00000157368	0.632005	1.01112	1.3499	2.71874	ENSG00000157368	IL34
ENSG00000157379	42.9486	45.4669	29.2226	22.9931	ENSG00000157379	DHRS1
ENSG00000157388	2.03391	5.03313	5.64759	9.98085	ENSG00000157388	CACNA1D
ENSG00000157399	9.61632	17.9295	13.3033	28.7453	ENSG00000157399	ARSE
ENSG00000157404	0.280391	0.140286	0.1632	1.7171	ENSG00000157404	KIT
ENSG00000157423	2.36277	6.37342	4.03057	7.52805	ENSG00000157423	HYDIN
ENSG00000157426	6.45975	11.2547	10.7167	8.2566	ENSG00000157426	AASDH
ENSG00000157429	7.18785	15.6338	17.7498	29.4764	ENSG00000157429	ZNF19
ENSG00000157445	0.0622509	0.621284	0.773627	0.634073	ENSG00000157445	CACNA2D3
ENSG00000157450	16.4824	21.9586	19.7814	19.8062	ENSG00000157450	RNF111
ENSG00000157456	6.68073	30.0298	5.69964	9.0474	ENSG00000157456	CCNB2
ENSG00000157470	0.634794	1.15771	0.885218	1.10382	ENSG00000157470	FAM81A
ENSG00000157483	189.989	156.524	111.248	138.123	ENSG00000157483	MYO1E
ENSG00000157500	18.2039	20.3092	14.8301	17.172	ENSG00000157500	APPL1
ENSG00000157502	0.754834	0.144878	0.439448	0.451003	ENSG00000157502	MUM1L1
ENSG00000157510	10.1016	12.7382	8.07794	9.02104	ENSG00000157510	AFAP1L1
ENSG00000157514	30.1016	54.7175	31.6122	16.578	ENSG00000157514	TSC22D3
ENSG00000157538	22.2301	29.2908	26.5262	36.0138	ENSG00000157538	DSCR3
ENSG00000157540	43.6526	60.5511	52.7127	56.4004	ENSG00000157540	DYRK1A
ENSG00000157542	1.39916	2.7185	2.49605	5.38062	ENSG00000157542	KCNJ6
ENSG00000157551	18.9076	35.5472	8.08499	23.3764	ENSG00000157551	KCNJ15
ENSG00000157554	0.567993	0.897793	0.716551	1.22893	ENSG00000157554	ERG
ENSG00000157557	37.6737	46.0964	109.628	19.0335	ENSG00000157557	ETS2
ENSG00000157570	0.376565	0.784101	0.357916	1.56233	ENSG00000157570	TSPAN18
ENSG00000157578	2.43239	7.53156	7.49456	10.4907	ENSG00000157578	LCA5L
ENSG00000157593	54.7944	52.1228	26.7685	21.2302	ENSG00000157593	SLC35B2
ENSG00000157600	13.6979	16.1969	12.3908	9.30307	ENSG00000157600	TMEM164
ENSG00000157601	51.4571	119.632	68.2785	77.0796	ENSG00000157601	MX1
ENSG00000157613	3.10893	6.74448	6.9026	28.9412	ENSG00000157613	CREB3L1
ENSG00000157617	22.986	29.0711	16.8571	50.409	ENSG00000157617	C2CD2
ENSG00000157625	12.2209	10.805	11.3791	10.3667	ENSG00000157625	TAB3
ENSG00000157637	40.0708	54.7103	54.813	50.3044	ENSG00000157637	SLC38A10
ENSG00000157653	0.157931	0.55815	0.482136	0.210882	ENSG00000157653	C9orf43
ENSG00000157654	0.52371	1.64717	6.26059	12.0849	ENSG00000157654	PALM2-AKAP2
ENSG00000157657	3.23341	4.37109	5.54831	9.31799	ENSG00000157657	ZNF618
ENSG00000157680	0.434552	0.562669	0.610797	3.85501	ENSG00000157680	DGKI
ENSG00000157693	3.07174	7.19527	8.41804	6.66268	ENSG00000157693	TMEM268
ENSG00000157703	0.311375	0.417441	0.711807	0.996573	ENSG00000157703	SVOPL
ENSG00000157734	3.44491	4.54334	4.41352	4.97947	ENSG00000157734	SNX22
ENSG00000157741	5.79773	7.81639	8.88573	11.0991	ENSG00000157741	UBN2
ENSG00000157764	10.6512	13.3822	13.8854	14.4314	ENSG00000157764	BRAF
ENSG00000157765	0.393202	1.46524	1.90984	3.68225	ENSG00000157765	SLC34A2
ENSG00000157766	0.989705	1.18459	1.16913	2.29684	ENSG00000157766	ACAN
ENSG00000157778	26.8036	28.5381	24.3329	21.7928	ENSG00000157778	PSMG3
ENSG00000157782	1.78703	2.46934	2.70572	3.4092	ENSG00000157782	CABP1
ENSG00000157796	15.9046	34.1045	24.8971	39.029	ENSG00000157796	WDR19

ENSG00000157800	42.8803	54.6149	37.6459	61.9597	ENSG00000157800	SLC37A3
ENSG00000157823	20.1035	22.4111	26.9949	23.263	ENSG00000157823	AP3S2
ENSG00000157827	28.5448	47.9695	32.2072	38.771	ENSG00000157827	FMNL2
ENSG00000157828	0	0	0	0	ENSG00000157828	RPS4Y2
ENSG00000157833	0.733684	1.16385	1.2069	2.4601	ENSG00000157833	GAREM2
ENSG00000157837	25.0792	25.9798	29.0401	24.0378	ENSG00000157837	SPPL3
ENSG00000157851	0.359589	0.982417	0.752717	1.44887	ENSG00000157851	DPYSL5
ENSG00000157856	0.758719	0.497603	1.13585	0.141616	ENSG00000157856	DRC1
ENSG00000157869	12.7517	18.9044	11.6443	17.2478	ENSG00000157869	RAB28
ENSG00000157870	8.91647	8.04302	8.15726	6.91767	ENSG00000157870	FAM213B
ENSG00000157873	9.24784	16.9276	10.611	8.51157	ENSG00000157873	TNFRSF14
ENSG00000157881	23.6695	26.5944	21.272	21.5413	ENSG00000157881	PANK4
ENSG00000157884	0	0	0.417329	0	ENSG00000157884	CIB4
ENSG00000157890	5.39469	5.45616	6.93422	2.50301	ENSG00000157890	MEGF11
ENSG00000157895	11.1426	15.3585	17.7149	19.4051	ENSG00000157895	C12orf43
ENSG00000157911	15.3896	15.167	14.596	10.7114	ENSG00000157911	PEX10
ENSG00000157916	172.548	134.945	81.7934	64.2728	ENSG00000157916	RER1
ENSG00000157927	0.167478	0.306126	0.261889	1.69644	ENSG00000157927	RADIL
ENSG00000157933	14.6807	27.7213	36.4384	39.8083	ENSG00000157933	SKI
ENSG00000157950	0.288183	0.489732	0.132226	1.17928	ENSG00000157950	SSBX2B
ENSG00000157954	33.7829	23.2117	28.5934	29.0346	ENSG00000157954	WIPI2
ENSG00000157965	0.228319	0.0313706	0	0.216676	ENSG00000157965	SSX8
ENSG00000157978	11.3063	22.4674	21.4253	14.1878	ENSG00000157978	LDLRAP1
ENSG00000157985	8.61882	14.9547	17.2269	19.9592	ENSG00000157985	AGAP1
ENSG00000157992	11.7872	19.4808	7.38481	6.14645	ENSG00000157992	KRTCAP3
ENSG00000157999	0.567269	2.328	1.61005	2.63416	ENSG00000157999	ANKRD61
ENSG00000158006	10.8464	7.81186	11.4568	5.92976	ENSG00000158006	PAFAH2
ENSG00000158008	0.295404	0.382361	0.270307	1.2725	ENSG00000158008	EXTL1
ENSG00000158014	0.923225	1.18387	1.40159	2.10431	ENSG00000158014	SLC30A2
ENSG00000158019	10.6622	14.4412	13.4549	11.6972	ENSG00000158019	BABAM2
ENSG00000158022	0.793469	0.354809	0.602648	1.1294	ENSG00000158022	TRIM63
ENSG00000158023	35.7688	48.3586	44.1718	53.3046	ENSG00000158023	WDR66
ENSG00000158042	21.8526	20.8446	16.1267	12.4117	ENSG00000158042	MRPL17
ENSG00000158050	0.882358	6.92191	1.79129	0.55624	ENSG00000158050	DUSP2
ENSG00000158055	46.9583	24.417	50.6965	13.042	ENSG00000158055	GRHL3
ENSG00000158062	7.45331	11.2949	8.00059	6.98192	ENSG00000158062	UBXN11
ENSG00000158077	0.104661	0.187471	0.169483	0.296188	ENSG00000158077	NLRP14
ENSG00000158079	4.88607	8.47647	6.73452	9.38645	ENSG00000158079	PTPDC1
ENSG00000158089	11.7847	31.7639	15.3513	11.3913	ENSG00000158089	GALNT14
ENSG00000158092	37.546	23.4003	49.9902	32.5561	ENSG00000158092	NCK1
ENSG00000158104	1.12686	1.36928	1.64995	1.25231	ENSG00000158104	HPD
ENSG00000158106	3.86975	5.81928	1.22455	0.845489	ENSG00000158106	RHPN1
ENSG00000158109	8.83593	6.0054	8.30367	8.08773	ENSG00000158109	TPRG1L
ENSG00000158113	1.94868	3.05709	3.42498	3.50381	ENSG00000158113	LRRC43
ENSG00000158122	7.44636	11.3158	8.50773	11.5727	ENSG00000158122	AAED1
ENSG00000158125	21.5663	51.8106	21.3396	40.2325	ENSG00000158125	XDH
ENSG00000158156	4.82416	4.7264	5.08486	7.59787	ENSG00000158156	XKR8
ENSG00000158158	7.91786	11.8533	7.92878	4.71659	ENSG00000158158	CNNM4
ENSG00000158161	10.027	10.6418	9.59132	11.0876	ENSG00000158161	EYA3
ENSG00000158163	2.90599	11.7262	7.49001	14.3454	ENSG00000158163	DZIP1L
ENSG00000158164	0	0	0	0.540433	ENSG00000158164	TMSB15A
ENSG00000158169	4.82619	13.4413	13.4338	12.585	ENSG00000158169	FANCC
ENSG00000158186	2.31981	1.37056	3.99593	4.00556	ENSG00000158186	MRAS
ENSG00000158195	20.0656	18.5787	16.7597	17.2146	ENSG00000158195	WASF2

ENSG00000158201	28.0463	29.3316	6.4453	14.1795	ENSG00000158201	ABHD3
ENSG00000158220	2.48554	3.44398	3.49597	3.21761	ENSG00000158220	ESYT3
ENSG00000158234	8.07046	5.6076	7.59754	5.53982	ENSG00000158234	FAIM
ENSG00000158246	24.3768	10.4591	18.7084	5.98471	ENSG00000158246	FAM46B
ENSG00000158258	0.822148	1.27614	0.758525	3.62489	ENSG00000158258	CLSTN2
ENSG00000158270	0.428473	0.831306	0.880302	5.34307	ENSG00000158270	COLEC12
ENSG00000158286	19.8908	19.3901	11.5974	15.5055	ENSG00000158286	RNF207
ENSG00000158290	14.0252	15.3246	12.2146	24.4247	ENSG00000158290	CUL4B
ENSG00000158292	9.89811	16.3146	12.2871	9.32768	ENSG00000158292	GPR153
ENSG00000158296	5.56982	8.43087	8.9591	7.33742	ENSG00000158296	SLC13A3
ENSG00000158301	3.87605	3.56176	5.09082	3.51151	ENSG00000158301	GPRASP2
ENSG00000158315	16.3066	14.9663	11.1346	8.02098	ENSG00000158315	RHBDL2
ENSG00000158321	9.58662	18.079	26.5119	24.9661	ENSG00000158321	AUTS2
ENSG00000158352	1.11058	2.8919	2.28357	3.31033	ENSG00000158352	SHROOM4
ENSG00000158373	79.0691	90.5071	37.2782	25.1981	ENSG00000158373	HIST1H2BD
ENSG00000158402	1.13849	7.82999	0.966784	2.55376	ENSG00000158402	CDC25C
ENSG00000158406	21.6422	50.9172	25.6695	19.2297	ENSG00000158406	HIST1H4H
ENSG00000158411	22.9274	32.3809	28.2732	30.6702	ENSG00000158411	MITD1
ENSG00000158417	20.0026	21.2265	23.5792	38.0656	ENSG00000158417	EIF5B
ENSG00000158423	0.532953	1.23863	1.01923	0.608493	ENSG00000158423	RIBC1
ENSG00000158427	7.09007	13.7959	12.5764	18.1831	ENSG00000158427	TMSB15B
ENSG00000158428	1.98292	3.16398	3.61089	5.74587	ENSG00000158428	CATIP
ENSG00000158435	31.5676	26.4735	21.1192	17.6105	ENSG00000158435	CNOT11
ENSG00000158445	0.168694	0.240997	0.305339	0.43852	ENSG00000158445	KCNB1
ENSG00000158457	2.4421	3.59249	0.52469	0.63454	ENSG00000158457	TSPAN33
ENSG00000158458	1.50881	2.75422	1.92116	3.16222	ENSG00000158458	NRG2
ENSG00000158467	6.24592	14.8873	14.3798	10.2941	ENSG00000158467	AHCYL2
ENSG00000158470	17.0271	16.438	10.2264	10.1188	ENSG00000158470	B4GALT5
ENSG00000158473	1.85812	7.39884	4.48572	2.3991	ENSG00000158473	CD1D
ENSG00000158477	0	0.0517396	0	0.0589305	ENSG00000158477	CD1A
ENSG00000158480	3.09613	2.61549	3.16171	2.32383	ENSG00000158480	SPATA2
ENSG00000158481	0	0.156695	0.106229	0.243008	ENSG00000158481	CD1C
ENSG00000158482	2.02674	5.13883	5.48445	8.54658	ENSG00000158482	SNX29P1
ENSG00000158483	4.01519	5.32799	8.3504	4.44566	ENSG00000158483	FAM86C1
ENSG00000158485	0	0.173357	0.0521969	0.130791	ENSG00000158485	CD1B
ENSG00000158486	0.978083	1.45636	1.68905	1.6126	ENSG00000158486	DNAH3
ENSG00000158488	0.0668316	0.897392	0.510642	1.17925	ENSG00000158488	CD1E
ENSG00000158497	0	0.218029	0	0.723166	ENSG00000158497	HMHB1
ENSG00000158516	0.127461	0.205132	0.220888	0.183915	ENSG00000158516	CPA2
ENSG00000158517	1.20785	2.76649	3.52611	4.94752	ENSG00000158517	NCF1
ENSG00000158525	0.12116	0.397261	0.100009	0.43001	ENSG00000158525	CPA5
ENSG00000158526	7.98516	7.33534	8.0366	6.36394	ENSG00000158526	TSR2
ENSG00000158528	0.09912	0.238381	0.254254	0.643948	ENSG00000158528	PPP1R9A
ENSG00000158545	14.9382	15.3431	18.7142	21.8315	ENSG00000158545	ZC3H18
ENSG00000158552	23.9198	18.6787	22.4976	18.5112	ENSG00000158552	ZFAND2B
ENSG00000158553	0.0188145	0.0544238	0.0820084	0.0206882	ENSG00000158553	POM121L2
ENSG00000158555	4.95828	7.7534	4.66345	7.43853	ENSG00000158555	GDPD5
ENSG00000158560	1.32449	2.26175	3.17923	2.87462	ENSG00000158560	DYNC1I1
ENSG00000158571	0.259639	0.509328	0.583061	0.203535	ENSG00000158571	PFKFB1
ENSG00000158578	0.254878	0.32122	0.278791	0.182873	ENSG00000158578	ALAS2
ENSG00000158604	55.8972	56.4368	39.0148	40.9791	ENSG00000158604	TMED4
ENSG00000158615	26.0954	22.4866	27.892	13.2707	ENSG00000158615	PPP1R15B
ENSG00000158623	0.701229	2.60138	6.31277	6.86361	ENSG00000158623	COPG2

ENSG00000158636	6.73467	15.6721	12.6552	18.3546	ENSG00000158636	EMSY
ENSG00000158639	0	0	0	0	ENSG00000158639	PAGE5
ENSG00000158669	84.7847	57.5948	56.9249	48.9197	ENSG00000158669	GPAT4
ENSG00000158683	0.287211	0.196033	0.275814	1.89013	ENSG00000158683	PKD1L1
ENSG00000158691	3.78159	4.36804	4.41906	4.92617	ENSG00000158691	ZSCAN12
ENSG00000158710	102.49	135.015	82.1338	87.4975	ENSG00000158710	TAGLN2
ENSG00000158711	8.17553	14.9424	15.4519	13.7825	ENSG00000158711	ELK4
ENSG00000158714	0.554393	0.358178	0.600747	0.84446	ENSG00000158714	SLAMF8
ENSG00000158715	2.361	3.90707	1.21092	1.56817	ENSG00000158715	SLC45A3
ENSG00000158716	11.6317	9.92091	9.24467	5.10128	ENSG00000158716	DUSP23
ENSG00000158717	6.17066	8.7141	8.53588	7.01791	ENSG00000158717	RNF166
ENSG00000158731	0	0	0	0	ENSG00000158731	OR10J6P
ENSG00000158747	71.1252	66.2922	28.8617	32.1882	ENSG00000158747	NBL1
ENSG00000158748	0	0.0547971	0.0495378	0.0311929	ENSG00000158748	HTR6
ENSG00000158764	0.418891	0.302236	0.286202	0.114223	ENSG00000158764	ITLN2
ENSG00000158769	186.833	140.724	90.0451	34.4213	ENSG00000158769	F11R
ENSG00000158773	29.097	20.0423	21.143	15.295	ENSG00000158773	USF1
ENSG00000158786	2.47452	0.423761	0.633148	1.13288	ENSG00000158786	PLA2G2F
ENSG00000158792	4.41331	4.02255	3.37969	2.45704	ENSG00000158792	SPATA2L
ENSG00000158793	35.5654	37.4146	33.8378	21.0656	ENSG00000158793	NIT1
ENSG00000158796	12.2759	12.6421	13.485	10.269	ENSG00000158796	DEDD
ENSG00000158805	12.7993	14.7686	26.1288	13.9821	ENSG00000158805	ZNF276
ENSG00000158806	1.32607	1.05311	0.840125	1.8159	ENSG00000158806	NPM2
ENSG00000158813	4.63597	6.26621	7.07931	13.2217	ENSG00000158813	EDA
ENSG00000158815	0.869081	0.822942	0.56476	1.08573	ENSG00000158815	FGF17
ENSG00000158816	0.837681	1.90606	1.92369	2.84595	ENSG00000158816	VWA5B1
ENSG00000158825	14.0836	4.7168	5.03228	10.3524	ENSG00000158825	CDA
ENSG00000158828	50.6895	20.7382	19.6592	22.2689	ENSG00000158828	PINK1
ENSG00000158850	24.6672	22.3576	19.1263	18.6386	ENSG00000158850	B4GALT3
ENSG00000158856	3.06685	2.29859	0.925398	1.26862	ENSG00000158856	DMTN
ENSG00000158859	1.08516	3.05754	2.4262	12.194	ENSG00000158859	ADAMTS4
ENSG00000158863	50.8938	64.4079	66.3213	72.8918	ENSG00000158863	FAM160B2
ENSG00000158864	39.5098	51.4419	43.5054	45.0282	ENSG00000158864	NDUFS2
ENSG00000158865	0.20552	1.09682	1.39045	1.7679	ENSG00000158865	SLC5A11
ENSG00000158869	2.34404	3.72585	4.03372	3.88829	ENSG00000158869	FCER1G
ENSG00000158874	0.238409	0.248294	1.40759	1.88668	ENSG00000158874	APOA2
ENSG00000158882	7.84298	4.89242	6.30858	3.93245	ENSG00000158882	TOMM40L
ENSG00000158887	0.872314	1.22991	1.97587	1.63085	ENSG00000158887	MPZ
ENSG00000158901	0.380038	1.88249	1.89953	2.07628	ENSG00000158901	WFDC8
ENSG00000158941	81.2639	77.9029	61.5248	68.7712	ENSG00000158941	CCAR2
ENSG00000158955	1.08652	1.89157	1.34117	3.48048	ENSG00000158955	WNT9B
ENSG00000158966	3.71668	4.29124	5.34344	3.4446	ENSG00000158966	CACHD1
ENSG00000158985	16.3168	24.8883	23.4511	22.4958	ENSG00000158985	CDC42SE2
ENSG00000158987	10.4959	15.2912	16.0005	15.8077	ENSG00000158987	RAPGEF6
ENSG00000159023	20.4872	22.1076	20.1505	13.6954	ENSG00000159023	EPB41
ENSG00000159055	3.62868	7.61859	4.67759	5.30379	ENSG00000159055	MIS18A
ENSG00000159063	47.0197	72.0913	47.1838	69.5382	ENSG00000159063	ALG8
ENSG00000159069	70.5296	57.0162	49.1573	31.3068	ENSG00000159069	FBXW5
ENSG00000159079	22.9731	20.4239	18.7043	12.0755	ENSG00000159079	C21orf59
ENSG00000159082	3.62333	6.06339	5.34782	9.2328	ENSG00000159082	SYNJ1
ENSG00000159086	10.7618	17.9052	16.894	16.479	ENSG00000159086	PAXBP1
ENSG00000159110	4.72525	8.87795	8.27889	11.7135	ENSG00000159110	IFNAR2
ENSG00000159111	17.9838	15.2472	14.0476	8.64234	ENSG00000159111	MRPL10
ENSG00000159123	0	0.118755	0	0	ENSG00000159123	DMRTC1

ENSG00000159128	29.1922	47.2584	17.5047	14.5657	ENSG00000159128	IFNGR2
ENSG00000159131	26.8673	45.0863	49.2038	39.4307	ENSG00000159131	GART
ENSG00000159140	109.846	137.575	133.656	143.764	ENSG00000159140	SON
ENSG00000159147	10.1987	14.7292	10.2611	15.6158	ENSG00000159147	DONSON
ENSG00000159164	0.476957	0	1.99066	3.34189	ENSG00000159164	SV2A
ENSG00000159166	206.489	104.811	124.172	66.0918	ENSG00000159166	LAD1
ENSG00000159167	0.244563	0.423537	0.892702	6.03172	ENSG00000159167	STC1
ENSG00000159173	2.17086	2.699	3.40209	4.63327	ENSG00000159173	TNNI1
ENSG00000159176	62.1209	57.2663	39.7213	32.9793	ENSG00000159176	CSRP1
ENSG00000159182	0	1.00888	1.70747	1.246	ENSG00000159182	PRAC1
ENSG00000159184	0.412256	0.640035	0.632411	1.4629	ENSG00000159184	HOXB13
ENSG00000159186	0	0.104472	0.188674	0.469142	ENSG00000159186	AC007383.6
ENSG00000159189	0.111646	0.350201	0.421122	0.509228	ENSG00000159189	C1QC
ENSG00000159197	0	0.224044	0.151861	0	ENSG00000159197	KCNE2
ENSG00000159199	35.8246	35.3012	28.6607	22.3995	ENSG00000159199	ATP5G1
ENSG00000159200	9.76337	10.9609	22.3308	20.4873	ENSG00000159200	RCAN1
ENSG00000159202	30.0996	31.8667	52.0819	35.9615	ENSG00000159202	UBE2Z
ENSG00000159208	7.51596	1.55641	1.67094	0.745629	ENSG00000159208	CIART
ENSG00000159210	29.354	30.3041	31.1375	37.7055	ENSG00000159210	SNF8
ENSG00000159212	0.230306	0.573792	0.460433	0.755723	ENSG00000159212	CLIC6
ENSG00000159214	7.4729	13.2282	14.9013	6.287	ENSG00000159214	CCDC24
ENSG00000159216	47.1241	58.2137	42.9415	83.0002	ENSG00000159216	RUNX1
ENSG00000159217	3.16425	4.63056	4.91013	7.25063	ENSG00000159217	IGF2BP1
ENSG00000159224	0	0	0	0.10355	ENSG00000159224	GIP
ENSG00000159228	31.1335	33.8765	26.038	18.0465	ENSG00000159228	CBR1
ENSG00000159231	1.07932	2.57276	0.946658	2.85145	ENSG00000159231	CBR3
ENSG00000159239	1.50468	3.04797	3.58068	1.82884	ENSG00000159239	C2ORF81
ENSG00000159247	1.54574	2.69189	0.720466	2.19288	ENSG00000159247	TUBBP5
ENSG00000159248	0.0978432	0.196143	0.102226	0.262947	ENSG00000159248	GJD2
ENSG00000159251	0.0131406	0.0254731	0.023333	0.234592	ENSG00000159251	ACTC1
ENSG00000159256	33.5874	39.9813	33.6337	37.836	ENSG00000159256	MORC3
ENSG00000159259	4.70595	10.516	8.26542	12.7107	ENSG00000159259	CHAF1B
ENSG00000159261	3.63923	4.74103	5.22462	6.27282	ENSG00000159261	CLDN14
ENSG00000159263	1.3188	2.65462	2.20349	3.70389	ENSG00000159263	SIM2
ENSG00000159267	9.92231	20.3114	15.5039	15.0478	ENSG00000159267	HLCS
ENSG00000159289	2.11638	2.75446	2.08433	1.74014	ENSG00000159289	GOLGA6A
ENSG00000159307	5.58307	10.6304	10.9933	16.7232	ENSG00000159307	SCUBE1
ENSG00000159314	50.7842	40.6131	43.8386	24.1727	ENSG00000159314	ARHGAP27
ENSG00000159322	30.6504	47.508	34.2286	28.2987	ENSG00000159322	ADPGK
ENSG00000159335	60.0554	53.4921	44.5212	114.237	ENSG00000159335	PTMS
ENSG00000159337	1.18979	1.809	1.23864	3.04358	ENSG00000159337	PLA2G4D
ENSG00000159339	1.20029	1.84909	0.652644	3.39599	ENSG00000159339	PADI4
ENSG00000159346	133.499	63.9505	39.9736	23.3992	ENSG00000159346	ADIPOR1
ENSG00000159348	217.575	122.031	119.534	34.176	ENSG00000159348	CYB5R1
ENSG00000159352	68.422	66.2016	64.8757	66.4786	ENSG00000159352	PSMD4
ENSG00000159363	109.582	51.4625	38.3043	35.0425	ENSG00000159363	ATP13A2
ENSG00000159374	1.88553	2.79548	1.71316	3.78948	ENSG00000159374	M1AP
ENSG00000159377	99.9347	82.739	60.2359	43.897	ENSG00000159377	PSMB4
ENSG00000159387	0.17139	0.525358	0.256104	0.416953	ENSG00000159387	IRX6
ENSG00000159388	20.2998	17.2718	31.2709	7.61467	ENSG00000159388	BTG2
ENSG00000159398	0.0819234	0.541567	0.231913	0.322142	ENSG00000159398	CES5A
ENSG00000159399	10.2947	13.1504	14.7958	13.9772	ENSG00000159399	HK2
ENSG00000159403	2.03771	7.75959	23.1813	92.9282	ENSG00000159403	C1R
ENSG00000159409	0.257238	0.51373	0.347815	0.438147	ENSG00000159409	CELF3

ENSG00000159423	9.00816	22.0488	13.9518	8.39766	ENSG00000159423	ALDH4A1
ENSG00000159433	2.42269	7.69816	7.43984	16.1555	ENSG00000159433	STARD9
ENSG00000159445	11.2117	11.1482	14.729	13.1925	ENSG00000159445	THEM4
ENSG00000159450	0.338828	0.0669924	0.269711	0.297797	ENSG00000159450	TCHH
ENSG00000159455	0	0	0	0.748081	ENSG00000159455	LCE2B
ENSG00000159459	30.8288	42.7039	29.536	45.0409	ENSG00000159459	UBR1
ENSG00000159461	84.4266	73.6535	52.7619	36.6848	ENSG00000159461	AMFR
ENSG00000159479	20.7197	20.7913	21.4847	14.167	ENSG00000159479	MED8
ENSG00000159495	0.0240844	0.0696494	0.139139	0.171685	ENSG00000159495	TGM7
ENSG00000159496	1.91447	3.83452	4.44904	7.21491	ENSG00000159496	RGL4
ENSG00000159516	0.507349	0.365148	0.220694	2.34706	ENSG00000159516	SPRR2G
ENSG00000159527	5.56377	1.40501	1.68497	1.22947	ENSG00000159527	PGLYRP3
ENSG00000159556	0.163791	3.06714	0.20999	0.132908	ENSG00000159556	ISL2
ENSG00000159579	32.9115	44.989	50.7511	65.0659	ENSG00000159579	RSPRY1
ENSG00000159588	0.885358	2.03058	2.4097	1.70713	ENSG00000159588	CCDC17
ENSG00000159592	69.6094	86.8021	87.0901	69.317	ENSG00000159592	GPBP1L1
ENSG00000159593	50.3171	57.323	48.5319	50.4913	ENSG00000159593	NAE1
ENSG00000159596	19.9175	16.3034	14.567	8.97763	ENSG00000159596	TMEM69
ENSG00000159618	2.72809	5.52191	3.10975	7.27254	ENSG00000159618	ADGRG5
ENSG00000159625	1.32096	1.88892	1.47892	1.92709	ENSG00000159625	DRC7
ENSG00000159640	0.788899	2.80787	2.90314	3.28812	ENSG00000159640	ACE
ENSG00000159648	1.12424	4.03044	2.37871	4.2712	ENSG00000159648	TEPP
ENSG00000159650	0.0374849	0.0501847	0.07876	0.0572452	ENSG00000159650	UROC1
ENSG00000159658	49.1015	34.5004	28.2297	25.4539	ENSG00000159658	EFCAB14
ENSG00000159674	3.26582	4.80381	7.74301	67.9641	ENSG00000159674	SPON2
ENSG00000159685	12.0333	13.1063	13.223	10.7476	ENSG00000159685	CHCHD6
ENSG00000159692	57.9868	69.279	76.8792	66.2563	ENSG00000159692	CTBP1
ENSG00000159708	1.61974	3.75588	3.93039	5.86804	ENSG00000159708	LRRC36
ENSG00000159712	0.606457	0.112017	0.137713	0.380653	ENSG00000159712	ANKRD18CP
ENSG00000159713	0.356441	0.171791	0.244874	0.314755	ENSG00000159713	TPPP3
ENSG00000159714	5.64086	8.71409	14.9795	6.27322	ENSG00000159714	ZDHHC1
ENSG00000159720	61.0226	25.9253	33.4316	27.5744	ENSG00000159720	ATP6V0D1
ENSG00000159723	0.51491	0.907259	0.745107	0.650736	ENSG00000159723	AGRP
ENSG00000159733	2.58479	4.65234	5.28882	10.4432	ENSG00000159733	ZFYVE28
ENSG00000159753	1.01718	1.17184	1.84916	1.01349	ENSG00000159753	CARMIL2
ENSG00000159761	0.237296	1.03046	1.3662	1.60501	ENSG00000159761	C16orf86
ENSG00000159763	0	0	0	0.130954	ENSG00000159763	PIP
ENSG00000159784	0.0766096	0.187354	0.353502	0.509506	ENSG00000159784	FAM131B
ENSG00000159788	34.712	47.769	52.4993	42.1465	ENSG00000159788	RGS12
ENSG00000159792	5.65	8.56531	7.97137	8.83467	ENSG00000159792	PSKH1
ENSG00000159840	60.2278	67.6595	68.094	82.3266	ENSG00000159840	ZYX
ENSG00000159842	20.9921	40.8375	32.6662	47.8347	ENSG00000159842	ABR
ENSG00000159860	0.257069	0.0236225	0.160341	0.206638	ENSG00000159860	FAM115D
ENSG00000159871	20.1662	14.5034	12.0939	28.9692	ENSG00000159871	LYPD5
ENSG00000159873	8.69535	5.03772	7.27462	6.6659	ENSG00000159873	CCDC117
ENSG00000159882	4.24603	4.95473	5.87284	6.0551	ENSG00000159882	ZNF230
ENSG00000159884	6.15112	3.91788	2.80217	1.55086	ENSG00000159884	CCDC107
ENSG00000159885	2.2192	3.95108	2.66303	2.34385	ENSG00000159885	ZNF222
ENSG00000159899	2.34546	7.38864	6.38686	9.8133	ENSG00000159899	NPR2
ENSG00000159904	0	0.0663692	0	0	ENSG00000159904	ZNF890P
ENSG00000159905	2.73892	5.15592	4.63372	5.81948	ENSG00000159905	ZNF221
ENSG00000159915	5.11491	10.3593	10.8544	21.9164	ENSG00000159915	ZNF233
ENSG00000159917	4.36866	7.57242	5.18719	10.3967	ENSG00000159917	ZNF235
ENSG00000159921	6.87161	7.11713	5.35764	12.4858	ENSG00000159921	GNE

ENSG00000159958	0.135409	0.781302	1.05896	0.809853	ENSG00000159958	TNFRSF13C
ENSG00000159961	0	0	0	0	ENSG00000159961	OR3A3
ENSG00000160007	13.2275	21.8338	29.4846	23.12	ENSG00000160007	ARHGAP35
ENSG00000160013	2.71915	5.10128	5.53838	15.393	ENSG00000160013	PTGIR
ENSG00000160014	70.8932	62.2334	38.6173	40.525	ENSG00000160014	CALM3
ENSG00000160049	19.8918	14.9409	29.837	18.5965	ENSG00000160049	DFFA
ENSG00000160050	5.28435	7.91571	9.05729	10.3695	ENSG00000160050	CCDC28B
ENSG00000160051	4.55557	5.18034	5.8173	4.85358	ENSG00000160051	IQCC
ENSG00000160055	15.661	17.2258	19.0755	12.0579	ENSG00000160055	TMEM234
ENSG00000160058	32.1332	24.9973	33.3137	24.697	ENSG00000160058	BSDC1
ENSG00000160062	3.08221	5.14587	5.95688	7.93064	ENSG00000160062	ZBTB8A
ENSG00000160072	36.3691	33.5618	41.5584	30.1371	ENSG00000160072	ATAD3B
ENSG00000160075	38.3085	26.3043	37.3123	24.8848	ENSG00000160075	SSU72
ENSG00000160087	30.7517	33.0118	38.3279	33.6066	ENSG00000160087	UBE2J2
ENSG00000160094	6.50504	13.5268	14.9223	23.3153	ENSG00000160094	ZNF362
ENSG00000160097	5.39338	3.04453	7.61857	4.40536	ENSG00000160097	FNDC5
ENSG00000160111	2.77206	5.40212	4.41053	7.34801	ENSG00000160111	CPAMD8
ENSG00000160113	29.7176	25.7339	24.8485	14.9379	ENSG00000160113	NR2F6
ENSG00000160117	4.17455	9.07518	8.42808	12.3766	ENSG00000160117	ANKLE1
ENSG00000160124	20.0392	22.035	28.9964	21.1744	ENSG00000160124	CCDC58
ENSG00000160131	16.7081	14.6149	16.6579	11.3556	ENSG00000160131	VMA21
ENSG00000160145	4.81287	6.50831	4.70026	10.947	ENSG00000160145	KALRN
ENSG00000160161	0.390053	0.260285	0.788342	0.627742	ENSG00000160161	CILP2
ENSG00000160172	1.69959	2.72901	4.89962	2.61082	ENSG00000160172	FAM86C2P
ENSG00000160179	13.4306	19.5712	20.6761	37.2501	ENSG00000160179	ABCG1
ENSG00000160180	0.0580087	0	0	0.0632291	ENSG00000160180	TFF3
ENSG00000160181	0.429572	1.4293	0.333554	1.01326	ENSG00000160181	TFF2
ENSG00000160182	0	0	0	0	ENSG00000160182	TFF1
ENSG00000160183	0.692273	1.46157	1.30021	3.5429	ENSG00000160183	TMPRSS3
ENSG00000160185	1.06991	1.55616	1.43353	1.93591	ENSG00000160185	UBASH3A
ENSG00000160188	1.06368	1.76642	1.31753	1.27369	ENSG00000160188	RSPH1
ENSG00000160190	10.4293	11.2483	6.3148	5.96874	ENSG00000160190	SLC37A1
ENSG00000160191	6.6433	12.2226	10.5052	17.3425	ENSG00000160191	PDE9A
ENSG00000160193	9.3752	9.39651	17.9033	10.2637	ENSG00000160193	WDR4
ENSG00000160194	23.7704	18.9285	24.4105	24.7379	ENSG00000160194	NDUFV3
ENSG00000160199	12.9028	28.6919	25.3529	38.6718	ENSG00000160199	PKNOX1
ENSG00000160200	10.6157	93.3802	137.554	34.1052	ENSG00000160200	CBS
ENSG00000160201	10.1846	20.2931	20.721	27.9657	ENSG00000160201	U2AF1
ENSG00000160202	0	0.0748312	0.102174	0	ENSG00000160202	CRYAA
ENSG00000160207	2.68651	2.42616	7.03009	3.55102	ENSG00000160207	HSF2BP
ENSG00000160208	12.5292	13.6417	18.9231	10.1927	ENSG00000160208	RRP1B
ENSG00000160209	108.68	106.409	89.8977	78.7091	ENSG00000160209	PDXK
ENSG00000160211	12.3708	6.24961	10.0608	24.1658	ENSG00000160211	G6PD
ENSG00000160213	56.2617	27.3846	35.8091	32.4092	ENSG00000160213	CSTB
ENSG00000160214	23.6127	22.2868	33.202	22.7087	ENSG00000160214	RRP1
ENSG00000160216	29.7885	35.0303	31.3297	28.1551	ENSG00000160216	AGPAT3
ENSG00000160218	23.7223	25.4821	25.2996	26.6425	ENSG00000160218	TRAPPC10
ENSG00000160219	0.789852	2.82036	2.87955	4.62674	ENSG00000160219	GAB3
ENSG00000160221	27.7868	25.0906	33.5281	24.6154	ENSG00000160221	C21orf33
ENSG00000160223	1.69257	4.32259	5.29759	2.81822	ENSG00000160223	ICOSLG
ENSG00000160224	0.787472	1.54293	1.22376	2.50463	ENSG00000160224	AIRE
ENSG00000160226	5.91988	9.52449	9.60864	6.60399	ENSG00000160226	C21orf2
ENSG00000160229	6.97514	16.3622	11.7287	20.7564	ENSG00000160229	ZNF66
ENSG00000160233	3.41029	3.33467	2.50049	3.27119	ENSG00000160233	LRRC3

ENSG00000160255	0.959914	3.39966	2.70377	5.44062	ENSG00000160255	ITGB2
ENSG00000160256	13.5512	14.6849	18.9535	12.904	ENSG00000160256	FAM207A
ENSG00000160271	26.725	24.0703	26.4302	19.6433	ENSG00000160271	RALGDS
ENSG00000160282	1.31135	1.51945	1.46099	3.10685	ENSG00000160282	FTCD
ENSG00000160284	3.63814	2.5704	3.28941	4.91562	ENSG00000160284	SPATC1L
ENSG00000160285	55.6702	74.0189	74.0493	95.8754	ENSG00000160285	LSS
ENSG00000160293	13.8355	22.2326	26.146	23.6968	ENSG00000160293	VAV2
ENSG00000160294	40.3902	52.0148	62.6668	60.6433	ENSG00000160294	MCM3AP
ENSG00000160298	2.02555	7.88943	3.39431	6.70478	ENSG00000160298	C21orf58
ENSG00000160299	7.56293	18.0233	19.7169	20.649	ENSG00000160299	PCNT
ENSG00000160305	27.1661	41.7393	43.8325	41.6538	ENSG00000160305	DIP2A
ENSG00000160307	2.40583	0.467949	0.798366	3.36365	ENSG00000160307	S100B
ENSG00000160310	73.7248	59.9318	54.8798	48.1586	ENSG00000160310	PRMT2
ENSG00000160318	0.800031	0.899982	0.21614	0.724538	ENSG00000160318	CLDND2
ENSG00000160321	11.185	14.5331	9.46689	21.8318	ENSG00000160321	ZNF208
ENSG00000160323	1.02752	3.60896	2.31423	1.51751	ENSG00000160323	ADAMTS13
ENSG00000160325	5.31173	4.17484	4.59177	3.12639	ENSG00000160325	CACFD1
ENSG00000160326	13.9034	13.9507	11.0847	10.3344	ENSG00000160326	SLC2A6
ENSG00000160339	0	0	0	0	ENSG00000160339	FCN2
ENSG00000160345	0.925065	2.06113	2.54844	1.25129	ENSG00000160345	C9orf116
ENSG00000160349	0	0	0	0	ENSG00000160349	LCN1
ENSG00000160352	14.6791	26.538	22.0028	29.6505	ENSG00000160352	ZNF714
ENSG00000160360	15.1887	8.36598	12.6704	14.2766	ENSG00000160360	GPSM1
ENSG00000160392	5.65742	4.75133	4.92489	6.06928	ENSG00000160392	C19orf47
ENSG00000160396	0.114326	0.19629	0.247826	0.409449	ENSG00000160396	HIPK4
ENSG00000160401	3.38831	3.06563	5.34188	3.09729	ENSG00000160401	CFAP157
ENSG00000160404	6.56278	6.01444	4.69652	3.24796	ENSG00000160404	TOR2A
ENSG00000160408	21.7229	18.1096	19.27	16.6597	ENSG00000160408	ST6GALNAC6
ENSG00000160410	36.203	32.9963	31.206	34.5901	ENSG00000160410	SHKBP1
ENSG00000160439	3.73612	2.69337	3.04044	3.60671	ENSG00000160439	RDH13
ENSG00000160445	12.7048	8.30377	10.9069	10.4582	ENSG00000160445	ZER1
ENSG00000160446	35.1356	32.1292	11.0131	7.86305	ENSG00000160446	ZDHHC12
ENSG00000160447	1.57604	3.99709	1.61966	2.29174	ENSG00000160447	PKN3
ENSG00000160460	1.31035	1.01526	1.41843	2.51037	ENSG00000160460	SPTBN4
ENSG00000160469	3.75001	3.52912	6.14658	8.60884	ENSG00000160469	BRSK1
ENSG00000160471	2.98706	9.27125	10.6149	11.0748	ENSG00000160471	COX6B2
ENSG00000160472	0.239124	0.803172	0.688269	0.843472	ENSG00000160472	TMEM190
ENSG00000160505	0.0170511	0.134482	0.167823	0.351782	ENSG00000160505	NLRP4
ENSG00000160539	0.13399	0.258288	0.280203	1.48138	ENSG00000160539	PLPP7
ENSG00000160551	40.7609	40.9594	44.9928	59.4604	ENSG00000160551	TAOK1
ENSG00000160563	10.3967	10.4464	10.8708	6.96756	ENSG00000160563	MED27
ENSG00000160570	16.8109	16.3956	12.6873	11.5834	ENSG00000160570	DEDD2
ENSG00000160584	16.7913	22.0584	21.3135	32.6766	ENSG00000160584	SIK3
ENSG00000160588	30.0029	8.82705	11.9813	6.15926	ENSG00000160588	MPZL3
ENSG00000160593	0.251821	0.492202	0.532444	0.79589	ENSG00000160593	JAML
ENSG00000160602	3.46908	6.40643	5.12237	6.38969	ENSG00000160602	NEK8
ENSG00000160606	11.9074	11.7089	10.8173	5.45148	ENSG00000160606	TLCD1
ENSG00000160613	40.4855	54.5283	69.1183	74.0116	ENSG00000160613	PCSK7
ENSG00000160633	15.3508	24.5526	39.0483	40.6627	ENSG00000160633	SAFB
ENSG00000160654	2.07241	4.77371	4.89606	9.32914	ENSG00000160654	CD3G
ENSG00000160678	6.70005	7.51598	7.32123	4.39935	ENSG00000160678	S100A1
ENSG00000160679	22.0847	29.7897	28.3126	25.5675	ENSG00000160679	CHTOP
ENSG00000160683	2.96171	3.10978	4.40169	1.37806	ENSG00000160683	CXCR5
ENSG00000160685	63.6701	51.1019	73.5563	20.4647	ENSG00000160685	ZBTB7B

ENSG00000160688	26.082	29.2059	46.67	29.9882	ENSG00000160688	FLAD1
ENSG00000160691	242.325	267.678	293.563	181.814	ENSG00000160691	SHC1
ENSG00000160695	19.4035	14.552	19.0099	17.8197	ENSG00000160695	VPS11
ENSG00000160703	16.6956	13.4321	11.8201	6.58107	ENSG00000160703	NLRX1
ENSG00000160710	53.8102	80.287	80.8913	81.8492	ENSG00000160710	ADAR
ENSG00000160712	19.6056	20.7241	16.8306	10.641	ENSG00000160712	IL6R
ENSG00000160714	34.965	32.0971	27.1768	14.6964	ENSG00000160714	UBE2Q1
ENSG00000160716	0.299822	1.4462	0.863892	0.72088	ENSG00000160716	CHRNB2
ENSG00000160741	16.2438	18.2862	19.2317	15.9244	ENSG00000160741	CRTC2
ENSG00000160746	31.6841	48.1106	18.9339	35.736	ENSG00000160746	ANO10
ENSG00000160752	337.101	203.463	65.2994	176.106	ENSG00000160752	FDPS
ENSG00000160753	16.1213	16.0564	15.1116	12.6759	ENSG00000160753	RUSC1
ENSG00000160766	3.84835	3.67684	2.40564	4.62478	ENSG00000160766	GBAP1
ENSG00000160767	4.93126	8.1277	6.27232	9.6089	ENSG00000160767	FAM189B
ENSG00000160781	4.31327	5.80134	11.3806	2.62321	ENSG00000160781	PAQR6
ENSG00000160783	19.2279	17.2095	14.7527	16.1876	ENSG00000160783	PMF1
ENSG00000160785	9.64123	5.81803	7.88518	6.31943	ENSG00000160785	SLC25A44
ENSG00000160789	489.042	573.172	263.896	337.343	ENSG00000160789	LMNA
ENSG00000160791	0	0.0303978	0	0	ENSG00000160791	CCR5
ENSG00000160796	190.106	104.323	71.6586	37.9928	ENSG00000160796	NBEAL2
ENSG00000160799	34.915	23.2393	22.0947	19.8389	ENSG00000160799	CCDC12
ENSG00000160801	0.485262	0.449409	0.91095	1.78853	ENSG00000160801	PTH1R
ENSG00000160803	13.6827	11.8126	15.8202	9.33118	ENSG00000160803	UBQLN4
ENSG00000160808	0.177216	0.169628	0.117968	0.221438	ENSG00000160808	MYL3
ENSG00000160813	20.5328	27.5109	18.2056	13.2107	ENSG00000160813	PPP1R35
ENSG00000160818	15.165	17.1137	21.7109	15.9464	ENSG00000160818	GPATCH4
ENSG00000160828	15.5552	18.494	19.887	19.7647	ENSG00000160828	STAG3L2
ENSG00000160838	0.336319	1.06614	1.07318	1.62838	ENSG00000160838	LRRC71
ENSG00000160844	0.445629	0.263499	0.183505	0	ENSG00000160844	GATS
ENSG00000160856	8.34326	22.1054	22.1474	33.8561	ENSG00000160856	FCRL3
ENSG00000160862	12.1325	1.27536	2.34369	5.67145	ENSG00000160862	AZGP1
ENSG00000160867	2.28383	7.07802	3.50562	4.73316	ENSG00000160867	FGFR4
ENSG00000160868	0.501872	0.776433	0.735371	1.1649	ENSG00000160868	CYP3A4
ENSG00000160870	1.63818	5.24663	3.34057	8.17297	ENSG00000160870	CYP3A7
ENSG00000160877	33.5805	28.2404	23.0026	18.9424	ENSG00000160877	NACC1
ENSG00000160882	0.188604	0.784081	0.652568	1.43763	ENSG00000160882	CYP11B1
ENSG00000160883	0	0.020772	0.0155559	0.987124	ENSG00000160883	HK3
ENSG00000160886	8.93193	24.0857	1.71051	3.48756	ENSG00000160886	LY6K
ENSG00000160888	33.5091	34.1118	29.4682	22.9112	ENSG00000160888	IER2
ENSG00000160908	9.8083	9.17751	10.3643	9.90443	ENSG00000160908	ZNF394
ENSG00000160917	22.3588	51.8489	62.8445	29.3735	ENSG00000160917	CPSF4
ENSG00000160932	110.585	240.86	80.881	86.7568	ENSG00000160932	LY6E
ENSG00000160948	45.2559	52.2716	40.1509	42.4863	ENSG00000160948	VPS28
ENSG00000160949	1.83816	4.00262	1.99422	3.47603	ENSG00000160949	TONSL
ENSG00000160951	0.164494	0.316927	0.250613	0.449935	ENSG00000160951	PTGER1
ENSG00000160953	19.0685	24.1696	23.8812	36.7273	ENSG00000160953	MUM1
ENSG00000160957	11.2605	18.4663	10.839	15.2594	ENSG00000160957	RECQL4
ENSG00000160959	17.5158	22.8155	24.8983	13.3339	ENSG00000160959	LRRC14
ENSG00000160961	18.0847	36.0023	37.5811	58.538	ENSG00000160961	ZNF333
ENSG00000160963	0.0184595	0.0533978	0.112648	0.123473	ENSG00000160963	COL26A1
ENSG00000160972	21.9806	27.6101	30.7604	20.3306	ENSG00000160972	PPP1R16A
ENSG00000160973	0.201789	0.205169	0.359859	0.194784	ENSG00000160973	FOXH1
ENSG00000160991	4.02724	4.83886	6.45175	10.1292	ENSG00000160991	ORAI2
ENSG00000160993	5.42197	6.16761	5.74411	6.51803	ENSG00000160993	ALKBH4

ENSG00000160994	0	0.0317839	0.0861963	0.0742576	ENSG00000160994	CCDC105
ENSG00000160999	0.739099	0.6939	0.971556	0.86393	ENSG00000160999	SH2B2
ENSG00000161010	25.2377	43.3072	41.2178	57.1479	ENSG00000161010	MRNIP
ENSG00000161011	167.114	101.323	116.046	73.6914	ENSG00000161011	SQSTM1
ENSG00000161013	107.392	98.0264	115.389	66.8295	ENSG00000161013	MGAT4B
ENSG00000161016	589.676	312.397	370.395	251.561	ENSG00000161016	RPL8
ENSG00000161021	5.7306	6.97192	10.1023	8.63279	ENSG00000161021	MAML1
ENSG00000161031	0.0250502	0	0.0436591	0	ENSG00000161031	PGLYRP2
ENSG00000161036	11.1887	12.5347	7.81459	9.0335	ENSG00000161036	LRWD1
ENSG00000161040	1.36074	2.93949	4.72843	3.78629	ENSG00000161040	FBXL13
ENSG00000161048	3.99563	6.05608	6.98718	7.17491	ENSG00000161048	NAPEPLD
ENSG00000161055	0	0	0	0	ENSG00000161055	SCGB3A1
ENSG00000161057	51.584	33.306	27.8922	26.8401	ENSG00000161057	PSMC2
ENSG00000161082	2.88949	3.48774	4.13331	7.66032	ENSG00000161082	CELF5
ENSG00000161091	48.1638	50.1982	52.5551	56.1686	ENSG00000161091	MFSD12
ENSG00000161103	0.403676	1.26021	0.848701	2.0473	ENSG00000161103	AC008132.1
ENSG00000161132	0.0507286	0.0489334	0.138315	0.16813	ENSG00000161132	Xxbac-B444P24.10
ENSG00000161133	0.241009	0.152477	1.39373	0.298604	ENSG00000161133	USP41
ENSG00000161149	2.10456	4.10141	4.23338	3.30158	ENSG00000161149	TUBA3FP
ENSG00000161179	14.8235	18.3613	20.3922	7.56917	ENSG00000161179	YDJC
ENSG00000161180	1.43969	0.0952069	0.0645543	0.687331	ENSG00000161180	CCDC116
ENSG00000161202	19.8534	21.9913	30.1829	27.7344	ENSG00000161202	DVL3
ENSG00000161203	102.318	96.5285	111.355	80.7002	ENSG00000161203	AP2M1
ENSG00000161204	23.2767	22.8496	35.2971	33.7189	ENSG00000161204	ABCF3
ENSG00000161217	82.0319	35.5856	53.0394	40.6381	ENSG00000161217	PCYT1A
ENSG00000161243	11.6412	26.6148	21.9927	27.1531	ENSG00000161243	FBXO27
ENSG00000161249	411.76	152.497	283.526	115.306	ENSG00000161249	DMKN
ENSG00000161265	4.79461	6.16078	10.0722	9.21467	ENSG00000161265	U2AF1L4
ENSG00000161267	13.2912	22.2539	17.5427	26.891	ENSG00000161267	BDH1
ENSG00000161270	0.542268	0.390863	0.398601	1.18515	ENSG00000161270	NPHS1
ENSG00000161277	0.778604	1.04573	0.722672	0.904831	ENSG00000161277	THAP8
ENSG00000161281	2.93561	4.25176	2.82523	7.48254	ENSG00000161281	COX7A1
ENSG00000161298	4.55719	5.09599	4.31182	4.79376	ENSG00000161298	ZNF382
ENSG00000161326	47.8755	18.1007	53.169	16.4439	ENSG00000161326	DUSP14
ENSG00000161328	0.582154	0.853399	2.06391	1.09657	ENSG00000161328	LRRC56
ENSG00000161381	2.22942	8.47659	5.90141	7.66087	ENSG00000161381	PLXDC1
ENSG00000161395	10.3373	11.4736	11.446	8.94978	ENSG00000161395	PGAP3
ENSG00000161405	0.341591	0.457183	0.337409	0.247962	ENSG00000161405	IKZF3
ENSG00000161509	0.43014	1.05541	0.803716	1.70689	ENSG00000161509	GRIN2C
ENSG00000161513	7.73874	11.9068	10.5857	8.61951	ENSG00000161513	FDXR
ENSG00000161526	61.079	43.9738	59.1876	43.842	ENSG00000161526	SAP30BP
ENSG00000161533	37.0793	20.0766	29.7749	20.6609	ENSG00000161533	ACOX1
ENSG00000161542	24.2382	21.9744	19.7403	23.3888	ENSG00000161542	PRPSAP1
ENSG00000161544	10.9723	7.12547	12.7176	8.23557	ENSG00000161544	CYGB
ENSG00000161547	86.9474	70.2743	67.9286	59.5882	ENSG00000161547	SRSF2
ENSG00000161551	9.03469	15.4823	17.4515	18.5021	ENSG00000161551	ZNF577
ENSG00000161558	2.05266	8.42162	6.41915	12.4806	ENSG00000161558	TMEM143
ENSG00000161570	2.44643	6.42515	6.40949	15.2325	ENSG00000161570	CCL5
ENSG00000161572	0.1754	0	0.203391	0.237301	ENSG00000161572	LYZL6
ENSG00000161573	2.12562	3.99522	3.63106	5.86544	ENSG00000161573	CCL16
ENSG00000161574	0	0	0	0	ENSG00000161574	CCL15-CCL14
ENSG00000161583	11.8487	18.1972	19.0607	16.1976	ENSG00000161583	TBC1D3G
ENSG00000161594	0.0637304	0.210827	0.0595555	0.104999	ENSG00000161594	KLHL10
ENSG00000161609	2.90048	1.82849	3.02955	5.90583	ENSG00000161609	CCDC155

ENSG00000161610	0	0.119384	0	0	ENSG00000161610	HCRT
ENSG00000161618	8.8681	14.4701	8.17773	8.0767	ENSG00000161618	ALDH16A1
ENSG00000161634	1.62596	2.99995	4.25519	6.51159	ENSG00000161634	DCD
ENSG00000161638	168.787	175.909	117.549	177.247	ENSG00000161638	ITGA5
ENSG00000161640	0.763581	1.29836	1.3908	2.58413	ENSG00000161640	SIGLEC11
ENSG00000161642	15.9801	20.3863	22.8617	18.6788	ENSG00000161642	ZNF385A
ENSG00000161643	1.90065	3.10187	2.97346	3.85201	ENSG00000161643	SIGLEC16
ENSG00000161647	15.0248	26.1096	21.0892	30.3928	ENSG00000161647	MPP3
ENSG00000161649	3.90111	7.21127	5.47582	15.7203	ENSG00000161649	CD300LG
ENSG00000161652	4.48728	10.7591	9.34338	17.5201	ENSG00000161652	IZUMO2
ENSG00000161653	2.28184	16.4064	4.07249	4.34359	ENSG00000161653	NAGS
ENSG00000161654	19.7559	22.2425	21.8314	18.2227	ENSG00000161654	LSM12
ENSG00000161664	1.74371	3.10442	3.55603	3.20036	ENSG00000161664	ASB16
ENSG00000161671	44.6799	45.5331	29.2266	25.652	ENSG00000161671	EMC10
ENSG00000161677	14.5627	17.3073	12.0819	13.2522	ENSG00000161677	JOSD2
ENSG00000161681	1.24964	1.0716	1.59365	6.25648	ENSG00000161681	SHANK1
ENSG00000161682	2.65528	2.50008	3.07915	4.3894	ENSG00000161682	FAM171A2
ENSG00000161692	4.08868	9.28578	4.34304	8.93235	ENSG00000161692	DBF4B
ENSG00000161714	22.991	42.3397	33.729	17.6433	ENSG00000161714	PLCD3
ENSG00000161791	5.66931	10.3733	9.71642	29.4567	ENSG00000161791	FMNL3
ENSG00000161798	0	0.302591	0	0.338339	ENSG00000161798	AQP5
ENSG00000161800	12.182	37.9365	8.80741	17.3991	ENSG00000161800	RACGAP1
ENSG00000161807	0.163285	0.1274	0.140148	0	ENSG00000161807	OR7G1
ENSG00000161813	21.7118	24.977	26.2424	27.0575	ENSG00000161813	LARP4
ENSG00000161835	0.971424	1.39575	1.83597	3.30926	ENSG00000161835	GRASP
ENSG00000161847	5.95966	7.90423	7.80761	10.4805	ENSG00000161847	RAVER1
ENSG00000161849	0.05368	0.0258696	0.233869	0.0883785	ENSG00000161849	KRT84
ENSG00000161850	0.0228875	0.121604	0.0916403	0.0462477	ENSG00000161850	KRT82
ENSG00000161860	3.16263	4.65951	4.01945	6.24005	ENSG00000161860	SYCE2
ENSG00000161888	5.19364	16.0676	5.17056	13.7317	ENSG00000161888	SPC24
ENSG00000161896	0.155832	0.204735	0.293506	0.328374	ENSG00000161896	IP6K3
ENSG00000161904	52.8258	68.6746	45.099	36.9746	ENSG00000161904	LEMD2
ENSG00000161905	1.78943	1.88292	3.99957	1.77183	ENSG00000161905	ALOX15
ENSG00000161911	0.118741	0.341865	0.364746	0.310242	ENSG00000161911	TREML1
ENSG00000161912	0.980845	3.43515	2.76634	3.71519	ENSG00000161912	ADCY10P1
ENSG00000161914	2.98351	5.42416	4.24236	5.51203	ENSG00000161914	ZNF653
ENSG00000161920	14.39	13.2728	11.5434	16.8556	ENSG00000161920	MED11
ENSG00000161921	21.3209	12.3604	11.9512	7.35954	ENSG00000161921	CXCL16
ENSG00000161929	4.12942	8.58554	7.61146	15.1564	ENSG00000161929	SCIMP
ENSG00000161939	1.38436	1.01458	1.68152	1.21095	ENSG00000161939	RNASEK-C17orf49
ENSG00000161940	0.755908	0.530991	2.65243	0.828654	ENSG00000161940	BCL6B
ENSG00000161944	0.882007	1.14531	0.787581	3.10451	ENSG00000161944	ASGR2
ENSG00000161955	2.95172	3.11653	3.74692	1.38696	ENSG00000161955	TNFSF13
ENSG00000161956	27.113	23.3564	31.8954	15.0614	ENSG00000161956	SENP3
ENSG00000161958	53.3316	25.5402	39.8524	18.9412	ENSG00000161958	FGF11
ENSG00000161960	590.418	659.961	647.808	306.325	ENSG00000161960	EIF4A1
ENSG00000161970	803.571	659.286	584.081	360.14	ENSG00000161970	RPL26
ENSG00000161973	0.13684	1.45035	1.54044	1.31999	ENSG00000161973	CCDC42
ENSG00000161980	4.24836	9.61988	9.03191	16.2435	ENSG00000161980	POLR3K
ENSG00000161981	8.185	8.46267	4.66233	4.39968	ENSG00000161981	SNRNP25
ENSG00000161992	0.252208	0.170173	0.131868	0.166156	ENSG00000161992	PRR35
ENSG00000161996	27.4862	45.1604	44.6363	50.5096	ENSG00000161996	WDR90
ENSG00000161999	27.1166	27.5636	24.8855	13.7229	ENSG00000161999	JMJD8
ENSG00000162004	3.18192	8.26778	9.04088	5.32288	ENSG00000162004	CCDC78

ENSG00000162006	0.235638	0.453052	1.19002	0.280135	ENSG00000162006	MSLNL
ENSG00000162009	0.0207662	0.0200211	0.0724038	0.0612669	ENSG00000162009	SSTR5
ENSG00000162032	20.9117	21.2373	13.2878	9.79469	ENSG00000162032	SPSB3
ENSG00000162039	0.433425	1.10966	1.08562	1.27494	ENSG00000162039	MEIOB
ENSG00000162040	5.16069	0.165806	0.399598	1.06432	ENSG00000162040	HS3ST6
ENSG00000162062	5.45942	7.23197	3.41885	4.23527	ENSG00000162062	C16orf59
ENSG00000162063	4.20878	16.441	3.53951	7.60856	ENSG00000162063	CCNF
ENSG00000162065	5.44623	6.34896	5.62092	6.92556	ENSG00000162065	TBC1D24
ENSG00000162066	18.6511	17.2915	18.9036	15.6659	ENSG00000162066	AMDHD2
ENSG00000162068	1.16444	0.93653	1.75804	4.82244	ENSG00000162068	NTN3
ENSG00000162069	22.3375	5.44763	9.50894	3.07415	ENSG00000162069	BICDL2
ENSG00000162073	14.261	24.8585	11.0104	6.3612	ENSG00000162073	PAQR4
ENSG00000162076	17.1855	16.1962	18.6921	11.3491	ENSG00000162076	FLYWCH2
ENSG00000162078	1.36545	0.117708	0.37299	0.201597	ENSG00000162078	ZG16B
ENSG00000162086	18.6841	23.2108	31.7515	24.5129	ENSG00000162086	ZNF75A
ENSG00000162104	16.5686	18.4613	18.5021	14.6741	ENSG00000162104	ADCY9
ENSG00000162105	9.68682	20.3722	14.7244	18.0091	ENSG00000162105	SHANK2
ENSG00000162129	10.7216	19.0097	9.66635	12.3701	ENSG00000162129	CLPB
ENSG00000162139	9.73912	20.9611	23.1277	24.0339	ENSG00000162139	NEU3
ENSG00000162144	26.7233	39.6264	55.9812	31.5153	ENSG00000162144	CYB561A3
ENSG00000162148	1.66511	1.8319	3.59447	3.71993	ENSG00000162148	PPP1R32
ENSG00000162174	5.69956	9.68154	11.6443	12.8288	ENSG00000162174	ASRGL1
ENSG00000162188	0.727098	1.58831	0.936006	1.38615	ENSG00000162188	GNG3
ENSG00000162191	30.1994	18.7902	27.6994	17.4907	ENSG00000162191	UBXN1
ENSG00000162194	27.5598	23.2049	22.6339	14.9358	ENSG00000162194	LBHD1
ENSG00000162222	19.0898	18.9189	23.9545	25.2078	ENSG00000162222	TTC9C
ENSG00000162227	12.0197	16.3032	14.7524	10.7391	ENSG00000162227	TAF6L
ENSG00000162231	25.5364	20.2262	31.4272	28.5301	ENSG00000162231	NXF1
ENSG00000162236	17.4449	15.054	17.6707	14.8713	ENSG00000162236	STX5
ENSG00000162241	4.91788	10.3831	9.64345	15.5727	ENSG00000162241	SLC25A45
ENSG00000162244	443.807	376.861	296.679	207.112	ENSG00000162244	RPL29
ENSG00000162267	0.135058	0.340122	0.216159	0.225524	ENSG00000162267	ITIH3
ENSG00000162290	5.63945	5.96243	4.32284	4.65273	ENSG00000162290	DCP1A
ENSG00000162298	34.744	32.4601	21.3319	19.3304	ENSG00000162298	SYVN1
ENSG00000162300	23.1059	17.769	21.8759	15.1712	ENSG00000162300	ZFPL1
ENSG00000162302	55.4558	54.4998	36.5643	32.3884	ENSG00000162302	RPS6KA4
ENSG00000162337	11.107	30.9978	19.1994	17.7698	ENSG00000162337	LRP5
ENSG00000162341	11.517	14.9321	15.8525	12.9503	ENSG00000162341	TPCN2
ENSG00000162344	0.0906926	0.0874304	0.138326	0.174367	ENSG00000162344	FGF19
ENSG00000162365	0.622803	2.28471	2.25062	3.00807	ENSG00000162365	CYP4A22
ENSG00000162366	2.80275	0.726653	5.12508	2.46143	ENSG00000162366	PDZK1IP1
ENSG00000162367	0.284745	1.43805	1.67567	2.91193	ENSG00000162367	TAL1
ENSG00000162368	52.153	25.3872	25.6147	30.5164	ENSG00000162368	CMPK1
ENSG00000162373	0.710232	0.422347	0.316438	0.646577	ENSG00000162373	BEND5
ENSG00000162374	0.977677	3.0912	2.29413	3.4192	ENSG00000162374	ELAVL4
ENSG00000162377	7.35273	6.59651	9.1561	4.637	ENSG00000162377	COA7
ENSG00000162378	11.4448	10.4237	8.69473	10.3163	ENSG00000162378	ZYG11B
ENSG00000162383	0.119558	0.278	0.769798	0.441136	ENSG00000162383	SLC1A7
ENSG00000162384	13.3935	16.7902	17.1708	16.3536	ENSG00000162384	C1orf123
ENSG00000162385	7.533	8.06742	10.1524	9.53382	ENSG00000162385	MAGOH
ENSG00000162390	8.52784	19.4003	13.49	18.1335	ENSG00000162390	ACOT11
ENSG00000162391	0.15847	0.91142	0.489707	0.573805	ENSG00000162391	FAM151A
ENSG00000162396	2.20503	1.99485	2.98965	1.1516	ENSG00000162396	PARS2
ENSG00000162398	0.0962063	0.216305	0.195538	0.0351578	ENSG00000162398	LEXM

ENSG00000162399	0.302802	0.63529	0.524322	1.03434	ENSG00000162399	BSND
ENSG00000162402	25.1164	44.0163	31.9218	34.2663	ENSG00000162402	USP24
ENSG00000162407	3.58967	4.66822	3.82779	12.2802	ENSG00000162407	PLPP3
ENSG00000162408	20.294	25.5916	25.7581	24.6559	ENSG00000162408	NOL9
ENSG00000162409	0.364271	0.884511	1.1761	0.967633	ENSG00000162409	PRKAA2
ENSG00000162413	77.7774	42.5148	26.2755	28.1286	ENSG00000162413	KLHL21
ENSG00000162415	1.48579	3.66046	4.87573	4.25873	ENSG00000162415	ZSWIM5
ENSG00000162419	4.84264	4.14723	4.35056	6.66999	ENSG00000162419	GMEB1
ENSG00000162426	0.0925544	0.559292	0.426916	0.838878	ENSG00000162426	SLC45A1
ENSG00000162430	27.4851	37.8879	17.3773	25.4248	ENSG00000162430	SELENON
ENSG00000162433	18.4833	12.2755	10.8031	12.3087	ENSG00000162433	AK4
ENSG00000162434	33.0659	41.1416	41.3819	35.0039	ENSG00000162434	JAK1
ENSG00000162437	3.70875	4.88329	3.7008	2.79942	ENSG00000162437	RAVER2
ENSG00000162438	1.60885	4.25795	3.86279	6.00389	ENSG00000162438	CTRC
ENSG00000162441	25.5094	18.3361	20.9086	17.1977	ENSG00000162441	LZIC
ENSG00000162444	4.29489	1.85329	0.783796	1.8136	ENSG00000162444	RBP7
ENSG00000162456	0.0732084	0.2426	0.251054	0.413635	ENSG00000162456	KNCN
ENSG00000162458	90.248	96.4502	127.353	84.2363	ENSG00000162458	FBLIM1
ENSG00000162460	0.114389	0.14802	0.0837414	0.333966	ENSG00000162460	TMEM82
ENSG00000162461	2.11193	3.50126	3.84597	4.22587	ENSG00000162461	SLC25A34
ENSG00000162482	0.484976	0.900841	0.962501	1.15489	ENSG00000162482	AKR7A3
ENSG00000162490	0.922306	2.15842	1.63389	3.47055	ENSG00000162490	DRAXIN
ENSG00000162493	29.0027	16.5185	21.2707	37.3838	ENSG00000162493	PDPN
ENSG00000162494	1.66982	3.65723	2.5	5.20094	ENSG00000162494	LRRC38
ENSG00000162496	39.5295	17.2832	6.93758	5.32069	ENSG00000162496	DHRS3
ENSG00000162510	1.48639	1.69783	2.55689	1.22206	ENSG00000162510	MATN1
ENSG00000162511	0.226377	0.169729	0.67788	0.788063	ENSG00000162511	LAPTM5
ENSG00000162512	13.2796	15.8423	12.6693	20.2944	ENSG00000162512	SDC3
ENSG00000162517	21.6229	23.1296	21.1553	14.9795	ENSG00000162517	PEF1
ENSG00000162520	5.28984	4.49256	9.46702	6.0923	ENSG00000162520	SYNC
ENSG00000162521	36.282	43.3256	44.6783	47.3362	ENSG00000162521	RBBP4
ENSG00000162522	33.893	28.3068	45.1808	14.9601	ENSG00000162522	KIAA1522
ENSG00000162526	1.54392	2.30263	4.84145	3.63288	ENSG00000162526	TSSK3
ENSG00000162542	9.32288	10.3007	7.59583	7.28091	ENSG00000162542	TMCO4
ENSG00000162543	0.0288274	0.0832564	0.176832	0.0951026	ENSG00000162543	UBXN10
ENSG00000162545	100.168	23.9678	6.0071	37.5094	ENSG00000162545	CAMK2N1
ENSG00000162551	0.377452	0.45247	0.359509	1.91403	ENSG00000162551	ALPL
ENSG00000162552	1.52566	2.5349	7.52278	3.34994	ENSG00000162552	WNT4
ENSG00000162571	2.35034	3.99037	3.37062	7.96352	ENSG00000162571	TTLL10
ENSG00000162572	0.883728	1.26933	2.13443	2.24302	ENSG00000162572	SCNN1D
ENSG00000162576	29.2481	18.5194	12.7814	89.0623	ENSG00000162576	MXRA8
ENSG00000162585	10.9543	13.0039	13.8414	16.815	ENSG00000162585	FAAP20
ENSG00000162591	2.3208	6.46524	4.82583	3.32513	ENSG00000162591	MEGF6
ENSG00000162592	0.0773499	0	0.0432467	0.0816561	ENSG00000162592	CCDC27
ENSG00000162594	1.35533	2.62393	2.29381	4.12719	ENSG00000162594	IL23R
ENSG00000162595	0.200211	0.471247	0.373784	0.37667	ENSG00000162595	DIRAS3
ENSG00000162598	0.429331	0.709876	0.743084	1.09679	ENSG00000162598	C1orf87
ENSG00000162599	15.8921	17.3401	23.2575	15.2512	ENSG00000162599	NFIA
ENSG00000162600	11.4839	19.0368	18.0471	12.1602	ENSG00000162600	OMA1
ENSG00000162601	12.7065	23.2776	20.8872	32.9226	ENSG00000162601	MYSM1
ENSG00000162604	54.361	58.3939	38.4889	44.5697	ENSG00000162604	TM2D1
ENSG00000162607	7.17939	14.2117	8.91609	8.67507	ENSG00000162607	USP1
ENSG00000162613	80.9718	107.21	98.4585	97.4711	ENSG00000162613	FUBP1
ENSG00000162614	3.60847	8.01292	7.80082	16.6529	ENSG00000162614	NEXN

ENSG00000162616	13.9974	11.1319	12.9501	53.406	ENSG00000162616	DNAJB4
ENSG00000162618	0.15152	0.119052	0.161135	2.59664	ENSG00000162618	ADGRL4
ENSG00000162620	0.886176	1.90911	0.919764	1.2265	ENSG00000162620	LRRIQ3
ENSG00000162621	0.0140178	0.0815325	0.0611183	0.0925828	ENSG00000162621	LRRC53
ENSG00000162623	16.7108	23.1527	24.4813	31.2867	ENSG00000162623	TYW3
ENSG00000162624	0.12441	0.43032	0.346929	0.636539	ENSG00000162624	LHX8
ENSG00000162627	6.65826	12.0526	6.81449	11.2629	ENSG00000162627	SNX7
ENSG00000162630	0.551506	1.34048	1.67162	3.74285	ENSG00000162630	B3GALT2
ENSG00000162631	3.47235	9.81459	1.54553	9.14233	ENSG00000162631	NTNG1
ENSG00000162636	2.58098	2.74706	1.61098	4.60989	ENSG00000162636	FAM102B
ENSG00000162639	1.30821	0.963077	1.35761	1.59582	ENSG00000162639	HENMT1
ENSG00000162641	1.97687	2.1187	1.33418	1.24011	ENSG00000162641	AKNAD1
ENSG00000162642	12.552	15.4936	18.3585	15.6238	ENSG00000162642	C1orf52
ENSG00000162643	1.37026	2.41502	2.47138	1.90091	ENSG00000162643	WDR63
ENSG00000162645	0.96441	0.856504	0.950219	2.01811	ENSG00000162645	GBP2
ENSG00000162650	3.79032	6.23659	5.86252	19.5358	ENSG00000162650	ATXN7L2
ENSG00000162654	4.16398	8.63949	8.29886	15.7037	ENSG00000162654	GBP4
ENSG00000162664	5.5538	10.6076	11.181	10.8617	ENSG00000162664	ZNF326
ENSG00000162669	0.322186	0.466826	0.806003	0.309521	ENSG00000162669	HFM1
ENSG00000162670	0.0190007	0	0	0.0214354	ENSG00000162670	BRINP3
ENSG00000162676	0.445537	0.0989468	0.214128	0.996721	ENSG00000162676	GFI1
ENSG00000162685	0.60686	0.760566	0.85377	0.812015	ENSG00000162685	LSP1P3
ENSG00000162687	0.116285	0.298163	1.3084	1.154	ENSG00000162687	KCNT2
ENSG00000162688	7.68639	8.61491	8.38981	8.45283	ENSG00000162688	AGL
ENSG00000162692	0.240325	0.265107	0.253342	2.79621	ENSG00000162692	VCAM1
ENSG00000162694	19.8452	37.0753	38.2304	57.5994	ENSG00000162694	EXTL2
ENSG00000162695	32.3833	34.5711	30.3388	23.5361	ENSG00000162695	SLC30A7
ENSG00000162699	0	0	0.0575587	0.216165	ENSG00000162699	DNAJA1P5
ENSG00000162702	12.6294	14.4445	12.3897	13.3635	ENSG00000162702	ZNF281
ENSG00000162704	66.2259	39.8089	34.0898	36.6677	ENSG00000162704	ARPC5
ENSG00000162706	0.231118	0.421308	0.639753	3.18915	ENSG00000162706	CADM3
ENSG00000162711	0.855206	0.673143	0.726316	0.931719	ENSG00000162711	NLRP3
ENSG00000162714	7.57555	18.4028	14.9479	12.8955	ENSG00000162714	ZNF496
ENSG00000162722	0.7843	2.1297	1.42975	2.58518	ENSG00000162722	TRIM58
ENSG00000162723	1.09341	0.400964	0.090599	0.208954	ENSG00000162723	SLAMF9
ENSG00000162727	0	0	0	0	ENSG00000162727	OR2M5
ENSG00000162728	0.350018	0.829822	0.735069	1.03892	ENSG00000162728	KCNJ9
ENSG00000162729	24.6001	42.3917	20.7774	20.5608	ENSG00000162729	IGSF8
ENSG00000162733	2.00805	1.06448	8.22865	57.2339	ENSG00000162733	DDR2
ENSG00000162734	65.8597	25.7891	30.8214	32.9577	ENSG00000162734	PEA15
ENSG00000162735	19.6107	18.9266	18.7386	11.3792	ENSG00000162735	PEX19
ENSG00000162736	50.8472	61.5359	55.6747	43.7792	ENSG00000162736	NCSTN
ENSG00000162738	6.65811	9.11035	8.78466	5.46611	ENSG00000162738	VANGL2
ENSG00000162739	0.845095	1.53669	1.93503	2.47596	ENSG00000162739	SLAMF6
ENSG00000162745	0.615006	2.21645	1.93881	8.30265	ENSG00000162745	OLFML2B
ENSG00000162746	0.793836	1.42303	0.518728	0.804133	ENSG00000162746	FCRLB
ENSG00000162747	0.0439841	0.127071	0.0765714	0.240463	ENSG00000162747	FCGR3B
ENSG00000162753	0.606475	0.543367	0.631942	0.822411	ENSG00000162753	SLC9C2
ENSG00000162755	1.10728	3.72311	2.48098	1.10157	ENSG00000162755	KLHDC9
ENSG00000162757	81.6082	17.9938	26.3527	22.6013	ENSG00000162757	C1orf74
ENSG00000162761	0.0767965	0.356725	0.248149	0.31354	ENSG00000162761	LMX1A
ENSG00000162763	0.180724	0.332265	0.485916	2.34721	ENSG00000162763	LRRC52
ENSG00000162769	12.3648	16.1494	12.0448	13.7043	ENSG00000162769	FLVCR1
ENSG00000162771	0.0240688	0.0460272	0.0416115	0	ENSG00000162771	FAM71A

ENSG00000162772	4.69948	4.23093	9.10866	3.68165	ENSG00000162772	ATF3
ENSG00000162775	10.3561	13.9439	13.8423	11.9675	ENSG00000162775	RBM15
ENSG00000162777	11.0501	9.98068	8.15902	3.0361	ENSG00000162777	DENND2D
ENSG00000162779	0.808852	1.95749	2.34178	2.50121	ENSG00000162779	AXDND1
ENSG00000162782	0.157636	0.122329	0.302928	0.207381	ENSG00000162782	TDRD5
ENSG00000162783	100.005	35.0075	42.0056	37.3309	ENSG00000162783	IER5
ENSG00000162804	1.02555	1.17143	1.29552	11.9443	ENSG00000162804	SNED1
ENSG00000162813	16.5116	11.7229	14.6521	11.8844	ENSG00000162813	BPNT1
ENSG00000162814	6.92905	16.6288	19.3609	26.6369	ENSG00000162814	SPATA17
ENSG00000162817	0.593439	0.818691	0.572067	3.3348	ENSG00000162817	C1orf115
ENSG00000162819	34.0919	23.6685	26.0789	18.624	ENSG00000162819	BROX
ENSG00000162825	212.455	226.258	256.464	510.182	ENSG00000162825	NBPF20
ENSG00000162836	2.8036	9.61053	8.47776	8.13948	ENSG00000162836	ACP6
ENSG00000162840	0	0	0	0	ENSG00000162840	MT2P1
ENSG00000162843	0.0345474	0.261969	0.532221	0.307697	ENSG00000162843	WDR64
ENSG00000162849	2.59787	5.65972	6.18083	7.58307	ENSG00000162849	KIF26B
ENSG00000162851	6.22302	5.03736	6.95554	5.23167	ENSG00000162851	TFB2M
ENSG00000162852	6.50818	7.6808	6.99881	8.1203	ENSG00000162852	CNST
ENSG00000162869	11.8099	16.1874	12.6316	19.8198	ENSG00000162869	PPP1R21
ENSG00000162873	0.265755	0.177442	0.255836	0.182906	ENSG00000162873	KLHDC8A
ENSG00000162877	0.106861	3.16457	2.37183	0.631503	ENSG00000162877	PM20D1
ENSG00000162878	0.764866	0.713371	0.259026	2.39649	ENSG00000162878	PKDCC
ENSG00000162881	0.0982124	0.124914	0.366993	0.675044	ENSG00000162881	OXER1
ENSG00000162882	1.32575	4.21454	4.22143	5.73301	ENSG00000162882	HAAO
ENSG00000162885	22.6272	33.3502	40.2788	32.5392	ENSG00000162885	B3GALNT2
ENSG00000162888	0.38548	0.535349	0.455218	0.830699	ENSG00000162888	C1orf147
ENSG00000162889	16.0838	22.2564	17.0109	26.4772	ENSG00000162889	MAPKAPK2
ENSG00000162891	0.111679	0.940933	1.29607	0.741854	ENSG00000162891	IL20
ENSG00000162892	0.335479	1.80331	2.51217	21.1127	ENSG00000162892	IL24
ENSG00000162894	0.846875	1.51649	1.10983	1.74931	ENSG00000162894	FCMR
ENSG00000162896	1.1554	0.880395	0.918879	1.36741	ENSG00000162896	PIGR
ENSG00000162897	1.16752	0.217995	0.39396	0.106125	ENSG00000162897	FCAMR
ENSG00000162909	246.918	276.011	130.093	169.109	ENSG00000162909	CAPN2
ENSG00000162910	26.3596	28.1745	25.9573	16.2434	ENSG00000162910	MRPL55
ENSG00000162913	2.08653	5.09948	4.57867	7.83939	ENSG00000162913	C1orf145
ENSG00000162923	39.8521	38.6593	42.1414	49.6901	ENSG00000162923	WDR26
ENSG00000162924	12.1263	11.5623	14.2576	17.0354	ENSG00000162924	REL
ENSG00000162927	4.02993	6.48458	6.91226	6.0077	ENSG00000162927	PUS10
ENSG00000162928	22.9215	17.3615	22.2336	12.9405	ENSG00000162928	PEX13
ENSG00000162929	17.2913	25.389	23.8707	37.0375	ENSG00000162929	KIAA1841
ENSG00000162931	3.71723	5.19993	6.30499	3.57656	ENSG00000162931	TRIM17
ENSG00000162944	0.712821	1.53557	1.72435	3.2942	ENSG00000162944	RFTN2
ENSG00000162946	1.72994	2.20015	1.75757	4.84726	ENSG00000162946	DISC1
ENSG00000162949	0.539648	0.8858	1.22062	1.6996	ENSG00000162949	CAPN13
ENSG00000162951	0.822034	1.07983	0.981968	0.621667	ENSG00000162951	LRRTM1
ENSG00000162959	37.3077	29.5365	26.3897	23.8606	ENSG00000162959	MEMO1
ENSG00000162961	41.51	28.0703	26.1279	28.9911	ENSG00000162961	DPY30
ENSG00000162971	6.88282	9.44487	10.7236	8.50937	ENSG00000162971	TYW5
ENSG00000162972	11.2185	12.7921	9.0788	7.89029	ENSG00000162972	MAIP1
ENSG00000162975	0.146218	0.164422	0.361001	0.328547	ENSG00000162975	KCNF1
ENSG00000162976	12.545	13.1835	6.46586	8.81151	ENSG00000162976	PQLC3
ENSG00000162980	34.1525	21.546	33.1312	24.6142	ENSG00000162980	ARL5A
ENSG00000162981	30.5179	9.93883	18.9924	9.57406	ENSG00000162981	FAM84A
ENSG00000162989	0.254349	0.722457	0.350163	1.19125	ENSG00000162989	KCNJ3

ENSG00000162992	0.083044	0.170916	0.104378	0.401388	ENSG00000162992	NEUROD1
ENSG00000162994	10.7373	19.5337	24.214	24.9492	ENSG00000162994	CLHC1
ENSG00000162997	0.982444	2.54366	2.20594	4.1137	ENSG00000162997	PRORSD1P
ENSG00000162998	0.26512	0.677285	0.887145	0.843185	ENSG00000162998	FRZB
ENSG00000162999	1.07166	2.46038	2.06053	3.49102	ENSG00000162999	DUSP19
ENSG00000163001	16.2216	31.7931	26.4983	28.8443	ENSG00000163001	CFAP36
ENSG00000163002	13.7822	20.6537	19.2212	27.3423	ENSG00000163002	NUP35
ENSG00000163006	4.73862	4.89417	3.90018	7.02147	ENSG00000163006	CCDC138
ENSG00000163009	1.19417	2.42257	2.78525	4.50985	ENSG00000163009	C2orf48
ENSG00000163012	0.0268536	0	0.32281	0.029548	ENSG00000163012	ZSWIM2
ENSG00000163013	3.91612	3.55312	5.14591	4.24519	ENSG00000163013	FBXO41
ENSG00000163016	0.323279	0.345088	0.939817	2.17901	ENSG00000163016	ALMS1P1
ENSG00000163017	1.83045	5.88007	5.73585	10.0424	ENSG00000163017	ACTG2
ENSG00000163026	3.23343	3.45853	3.01078	2.94673	ENSG00000163026	WDCP
ENSG00000163029	18.0564	38.8762	29.782	40.7627	ENSG00000163029	SMC6
ENSG00000163032	3.8608	14.362	15.1347	11.1064	ENSG00000163032	VSNL1
ENSG00000163040	6.06245	10.6944	7.02169	9.3728	ENSG00000163040	CCDC74A
ENSG00000163041	46.5142	34.915	28.3094	37.1355	ENSG00000163041	H3F3A
ENSG00000163046	1952.81	9843.36	3934.45	9586.2	ENSG00000163046	ANKRD30BL
ENSG00000163050	4.31952	4.04465	5.69647	5.29758	ENSG00000163050	COQ8A
ENSG00000163053	1.42323	3.50062	1.3548	1.21156	ENSG00000163053	SLC16A14
ENSG00000163060	0.204012	0.221556	0.103616	0.0718192	ENSG00000163060	TEKT4
ENSG00000163064	0.303359	0.191426	2.05688	6.87516	ENSG00000163064	EN1
ENSG00000163067	2.57293	1.93262	2.96426	2.69032	ENSG00000163067	ZNF2
ENSG00000163069	7.24066	12.4172	7.9671	13.575	ENSG00000163069	SGCB
ENSG00000163071	3.86105	10.2738	6.38086	5.53238	ENSG00000163071	SPATA18
ENSG00000163072	1.00536	2.70961	0.755354	0.608429	ENSG00000163072	NOSTRIN
ENSG00000163075	3.03405	5.68687	5.76245	8.77679	ENSG00000163075	CFAP221
ENSG00000163081	0.66555	0.831176	1.2202	1.69989	ENSG00000163081	CCDC140
ENSG00000163082	6.86603	5.32961	6.81134	6.76762	ENSG00000163082	SGPP2
ENSG00000163083	0.18741	0.329173	0.252838	0.375775	ENSG00000163083	INHBB
ENSG00000163092	0.0343767	0.129641	0.101221	0.147096	ENSG00000163092	XIRP2
ENSG00000163093	6.43561	9.36146	10.1768	15.1963	ENSG00000163093	BBS5
ENSG00000163098	0	0	0.0242903	0.0305928	ENSG00000163098	BIRC8
ENSG00000163104	20.1148	22.8735	19.1815	22.3609	ENSG00000163104	SMARCAD1
ENSG00000163106	0.387596	1.55761	0.441726	2.34786	ENSG00000163106	HPGDS
ENSG00000163110	90.6419	117.585	69.6518	71.7183	ENSG00000163110	PDLIM5
ENSG00000163113	5.90637	8.00924	9.43073	10.0166	ENSG00000163113	OTUD7B
ENSG00000163114	0.0422936	0.983099	0.0735831	0	ENSG00000163114	PDHA2
ENSG00000163116	0.769659	0.845009	0.874762	1.26533	ENSG00000163116	STPG2
ENSG00000163121	0.391201	0.186979	0.166813	0.305625	ENSG00000163121	NEURL3
ENSG00000163125	3.86489	4.4237	4.61723	3.80644	ENSG00000163125	RPRD2
ENSG00000163126	1.97948	2.55055	4.31342	2.8191	ENSG00000163126	ANKRD23
ENSG00000163131	6.08731	7.89899	4.5197	8.67159	ENSG00000163131	CTSS
ENSG00000163132	0.4379	1.74626	2.21357	4.15025	ENSG00000163132	MSX1
ENSG00000163138	22.4529	34.0253	36.3292	43.8638	ENSG00000163138	PACRGL
ENSG00000163141	19.4761	7.37637	13.6841	6.13442	ENSG00000163141	BNIPL
ENSG00000163145	0.618166	0.828305	1.88134	1.42276	ENSG00000163145	C1QTNF7
ENSG00000163154	0.203766	0.606082	0.879855	0.84974	ENSG00000163154	TNFAIP8L2
ENSG00000163155	4.72492	4.55929	4.62746	3.30539	ENSG00000163155	LYSMD1
ENSG00000163156	26.4213	22.0997	24.3412	21.9253	ENSG00000163156	SCNM1
ENSG00000163157	0.922069	0.64285	0.330901	0.272626	ENSG00000163157	TMOD4
ENSG00000163159	23.594	13.6208	14.7996	9.76786	ENSG00000163159	VPS72
ENSG00000163161	19.5324	26.3947	30.3389	23.7886	ENSG00000163161	ERCC3

ENSG00000163162	93.6357	103.389	81.6913	78.2336	ENSG00000163162	RNF149
ENSG00000163166	27.6808	27.1987	30.2103	31.3988	ENSG00000163166	IWS1
ENSG00000163170	14.9226	18.7085	12.6267	7.86764	ENSG00000163170	BOLA3
ENSG00000163171	12.3501	23.9078	28.4694	28.4821	ENSG00000163171	CDC42EP3
ENSG00000163191	1391.88	608.999	443.52	325.495	ENSG00000163191	S100A11
ENSG00000163202	30.0349	5.56366	4.29016	49.1976	ENSG00000163202	LCE3D
ENSG00000163206	0	0	0	0	ENSG00000163206	SMCP
ENSG00000163207	172.952	5.90767	16.3684	28.5475	ENSG00000163207	IVL
ENSG00000163209	206.478	2.61069	4.9677	31.0743	ENSG00000163209	SPRR3
ENSG00000163214	12.0825	19.6321	22.6237	27.3258	ENSG00000163214	DHX57
ENSG00000163216	20.5139	12.1731	19.8158	9.27605	ENSG00000163216	SPRR2D
ENSG00000163217	0.0364157	0.356852	0.03365	0	ENSG00000163217	BMP10
ENSG00000163218	5.89262	1.3036	6.60806	1.70382	ENSG00000163218	PGLYRP4
ENSG00000163219	6.57954	18.0766	7.6535	10.8134	ENSG00000163219	ARHGAP25
ENSG00000163220	1185.08	162.357	644.511	254.105	ENSG00000163220	S100A9
ENSG00000163221	2.90429	2.08858	1.8859	2.48653	ENSG00000163221	S100A12
ENSG00000163235	81.5611	49.4237	18.4597	27.8866	ENSG00000163235	TGFA
ENSG00000163239	0.169695	0	0.0773568	0.0614129	ENSG00000163239	TDRD10
ENSG00000163249	10.8251	14.9361	8.68188	11.4099	ENSG00000163249	CCNYL1
ENSG00000163251	3.82825	6.60969	4.83979	3.53666	ENSG00000163251	FZD5
ENSG00000163254	0	0	0	0	ENSG00000163254	CRYGC
ENSG00000163257	10.235	15.1912	17.9002	16.7601	ENSG00000163257	DCAF16
ENSG00000163263	0	0.430647	0.388992	0.238144	ENSG00000163263	C1orf189
ENSG00000163273	0.197973	0.423913	0.276508	0.749295	ENSG00000163273	NPPC
ENSG00000163281	12.0817	12.071	11.7635	10.0532	ENSG00000163281	GNPDA2
ENSG00000163283	0.665343	0.64331	0.675721	1.46986	ENSG00000163283	ALPP
ENSG00000163285	0.0704558	0.271924	0.18441	0.337589	ENSG00000163285	GABRG1
ENSG00000163286	0.107446	0.0428541	0.0387435	0.0488416	ENSG00000163286	ALPPL2
ENSG00000163288	0.232539	0.127512	0.216513	0.234282	ENSG00000163288	GABRB1
ENSG00000163291	15.3675	20.3047	16.0791	15.9538	ENSG00000163291	PAQR3
ENSG00000163293	33.0751	16.3421	12.6039	7.63478	ENSG00000163293	NIPAL1
ENSG00000163295	0.021696	0	0	0.0238412	ENSG00000163295	ALPI
ENSG00000163297	114.606	445.258	65.1803	249.656	ENSG00000163297	ANTXR2
ENSG00000163312	5.7223	5.33857	5.25407	3.96	ENSG00000163312	HELQ
ENSG00000163319	29.1645	26.7897	32.1604	23.6359	ENSG00000163319	MRPS18C
ENSG00000163320	25.4026	29.3571	22.4412	19.1774	ENSG00000163320	CGGBP1
ENSG00000163322	7.28015	11.7887	12.4002	20.6176	ENSG00000163322	ABRAXAS1
ENSG00000163328	8.68259	8.85611	8.23794	12.5884	ENSG00000163328	GPR155
ENSG00000163331	0.13199	2.77795	5.26309	0.570253	ENSG00000163331	DAPL1
ENSG00000163344	3.37641	3.03167	5.64162	1.66981	ENSG00000163344	PMVK
ENSG00000163346	31.0574	26.0018	27.8764	21.418	ENSG00000163346	PBXIP1
ENSG00000163347	81.8942	14.7855	128.163	14.175	ENSG00000163347	CLDN1
ENSG00000163348	13.6349	15.4347	15.9615	9.45588	ENSG00000163348	PYGO2
ENSG00000163349	10.4658	12.8298	14.0388	11.1574	ENSG00000163349	HIPK1
ENSG00000163352	0.957959	0.377033	1.63561	0.605566	ENSG00000163352	LENEP
ENSG00000163354	0.487901	2.15091	0.862203	1.21671	ENSG00000163354	DCST2
ENSG00000163357	2.0174	3.16452	2.13287	4.58907	ENSG00000163357	DCST1
ENSG00000163359	1.56139	1.92186	20.2746	1209.81	ENSG00000163359	COL6A3
ENSG00000163362	23.4478	25.4058	40.4832	23.5331	ENSG00000163362	INAVA
ENSG00000163374	22.6228	26.6108	28.4663	21.9036	ENSG00000163374	YY1AP1
ENSG00000163376	1.52268	0.91833	2.25031	1.06278	ENSG00000163376	KBTBD8
ENSG00000163377	0.195911	0.282977	0.404953	0.56334	ENSG00000163377	FAM19A4
ENSG00000163378	38.3316	70.5384	37.0813	37.2473	ENSG00000163378	EOGT
ENSG00000163380	0.573113	1.23718	0.789875	1.53477	ENSG00000163380	LMOD3

ENSG00000163382	42.5627	31.8192	30.5998	16.6651	ENSG00000163382	NAXE
ENSG00000163386	44.3949	48.6541	59.9184	74.1186	ENSG00000163386	NBPF10
ENSG00000163389	11.5006	16.1668	19.1106	12.7395	ENSG00000163389	POGLUT1
ENSG00000163393	16.6851	48.5481	41.3144	19.747	ENSG00000163393	SLC22A15
ENSG00000163394	0.0332406	0.128112	0	0.327897	ENSG00000163394	CCKAR
ENSG00000163395	1.33259	1.51272	0.229286	1.17355	ENSG00000163395	IGFN1
ENSG00000163399	116.904	144.087	149.412	120.978	ENSG00000163399	ATP1A1
ENSG00000163406	2.81041	2.78886	3.08195	2.49864	ENSG00000163406	SLC15A2
ENSG00000163412	0.986257	1.39537	1.05052	1.37113	ENSG00000163412	EIF4E3
ENSG00000163421	0.31475	0.250048	0.16396	0.267652	ENSG00000163421	PROK2
ENSG00000163424	0.17059	0.0302105	0.219029	0.222002	ENSG00000163424	C3orf30
ENSG00000163428	8.45292	9.1117	11.2037	10.4343	ENSG00000163428	LRRC58
ENSG00000163430	81.8446	115.711	104.96	222.159	ENSG00000163430	FSTL1
ENSG00000163431	0.124316	0.170655	0.154281	0.464451	ENSG00000163431	LMOD1
ENSG00000163435	98.2487	5.17286	5.85846	8.91805	ENSG00000163435	ELF3
ENSG00000163440	0	0	0	0.160642	ENSG00000163440	PDCL2
ENSG00000163444	30.558	24.9337	23.8427	20.2759	ENSG00000163444	TMEM183A
ENSG00000163449	0.994664	1.86118	1.43224	2.45252	ENSG00000163449	TMEM169
ENSG00000163453	117.971	253.261	136.854	162.037	ENSG00000163453	IGFBP7
ENSG00000163462	3.10402	4.85901	5.44968	6.56495	ENSG00000163462	TRIM46
ENSG00000163463	82.5706	51.8578	53.1607	31.2281	ENSG00000163463	KRTCAP2
ENSG00000163464	1.73223	0.197417	0.079046	0.492935	ENSG00000163464	CXCR1
ENSG00000163466	330.541	284.209	223.828	206.156	ENSG00000163466	ARPC2
ENSG00000163467	1.63055	2.92399	3.00256	3.05075	ENSG00000163467	TSACC
ENSG00000163468	148.636	117.807	111.158	95.8836	ENSG00000163468	CCT3
ENSG00000163472	35.5081	12.8988	21.4827	5.11773	ENSG00000163472	TMEM79
ENSG00000163479	88.7682	94.8312	50.0412	46.8869	ENSG00000163479	SSR2
ENSG00000163481	19.2796	13.1839	25.1517	9.31335	ENSG00000163481	RNF25
ENSG00000163482	19.1459	19.3675	28.1345	26.3368	ENSG00000163482	STK36
ENSG00000163485	0.166905	0.251107	0.224636	0.376955	ENSG00000163485	ADORA1
ENSG00000163486	16.1169	22.8498	16.9337	16.9439	ENSG00000163486	SRGAP2
ENSG00000163491	2.3822	4.16272	3.81653	13.2387	ENSG00000163491	NEK10
ENSG00000163492	0.385146	1.00245	0.798807	1.31509	ENSG00000163492	CCDC141
ENSG00000163497	1.77226	0.901162	0.72823	1.29033	ENSG00000163497	FEV
ENSG00000163499	0.646845	0.297333	0.429149	0.165722	ENSG00000163499	CRYBA2
ENSG00000163501	0.0835015	0	0.0970049	0.0610878	ENSG00000163501	IHH
ENSG00000163507	5.35801	15.3718	2.88525	8.81624	ENSG00000163507	KIAA1524
ENSG00000163508	0.128429	0.6603	0.389127	0.468798	ENSG00000163508	EOMES
ENSG00000163510	5.55025	6.45602	7.71279	7.4075	ENSG00000163510	CWC22
ENSG00000163512	24.7226	47.6645	68.5444	29.918	ENSG00000163512	AZI2
ENSG00000163513	126.738	63.721	34.5188	45.9745	ENSG00000163513	TGFBR2
ENSG00000163515	0	0.192859	0.174202	0.108434	ENSG00000163515	RETNLB
ENSG00000163516	30.1854	41.5761	47.8603	29.052	ENSG00000163516	ANKZF1
ENSG00000163517	12.4556	13.949	15.162	10.9142	ENSG00000163517	HDAC11
ENSG00000163518	0.407134	1.00886	0.527458	1.16386	ENSG00000163518	FCRL4
ENSG00000163519	0.118755	0.115281	0.159352	0.32813	ENSG00000163519	TRAT1
ENSG00000163520	0.76289	2.21045	4.62973	24.006	ENSG00000163520	FBLN2
ENSG00000163521	8.4462	16.354	12.2142	23.1591	ENSG00000163521	GLB1L
ENSG00000163527	117.997	196.878	97.6022	80.7733	ENSG00000163527	STT3B
ENSG00000163528	4.74134	6.6214	6.21443	4.07664	ENSG00000163528	CHCHD4
ENSG00000163530	0.159739	0.472013	0.189151	0.444291	ENSG00000163530	DPPA2
ENSG00000163531	2.56577	5.76472	4.07194	3.39775	ENSG00000163531	NFASC
ENSG00000163534	1.5267	2.77419	2.41517	4.32151	ENSG00000163534	FCRL1
ENSG00000163535	6.86199	21.7676	11.4462	25.9604	ENSG00000163535	SGO2

ENSG00000163536	1.71792	5.71095	2.24547	1.30975	ENSG00000163536	SERPINI1
ENSG00000163539	39.1095	62.5686	54.4762	67.6173	ENSG00000163539	CLASP2
ENSG00000163541	27.0671	30.6233	25.6392	26.3346	ENSG00000163541	SUCLG1
ENSG00000163545	10.546	8.99704	6.82903	10.4008	ENSG00000163545	NUAK2
ENSG00000163554	1.228	1.36189	2.80616	3.92117	ENSG00000163554	SPTA1
ENSG00000163558	45.5443	37.0955	42.0231	31.6648	ENSG00000163558	PRKCI
ENSG00000163563	0.122649	0.196885	0.531464	0.395576	ENSG00000163563	MNDA
ENSG00000163564	1.35515	2.59051	2.60193	4.11854	ENSG00000163564	PYHIN1
ENSG00000163565	32.3699	80.6778	64.7436	56.4653	ENSG00000163565	IFI16
ENSG00000163568	0.560413	1.16026	1.10888	1.58585	ENSG00000163568	AIM2
ENSG00000163576	3.3609	2.88314	2.55523	4.46091	ENSG00000163576	EFHB
ENSG00000163577	5.5495	3.22579	6.01639	3.40096	ENSG00000163577	EIF5A2
ENSG00000163581	0.075537	0.10316	0.736075	0.11759	ENSG00000163581	SLC2A2
ENSG00000163584	58.105	73.0923	93.4553	38.8288	ENSG00000163584	RPL22L1
ENSG00000163586	0.0617689	0.0595226	0.134521	0.237078	ENSG00000163586	FABP1
ENSG00000163590	3.7246	1.82641	1.87536	1.76708	ENSG00000163590	PPM1L
ENSG00000163596	5.51875	10.2868	10.7022	14.1774	ENSG00000163596	ICA1L
ENSG00000163599	0.114496	0.0856328	0.193941	0.389499	ENSG00000163599	CTLA4
ENSG00000163600	0.087718	0.140372	0.0490112	0.229308	ENSG00000163600	ICOS
ENSG00000163602	2.36529	3.16852	3.99527	3.62847	ENSG00000163602	RYBP
ENSG00000163605	41.8604	44.6519	47.3842	46.3577	ENSG00000163605	PPP4R2
ENSG00000163606	0.612543	0.750794	0.29524	0.541954	ENSG00000163606	CD200R1
ENSG00000163607	11.0116	8.97365	9.52651	8.4465	ENSG00000163607	GTPBP8
ENSG00000163608	24.7653	37.3823	39.6711	33.2126	ENSG00000163608	NEPRO
ENSG00000163611	7.32429	14.6436	9.56964	9.62792	ENSG00000163611	SPICE1
ENSG00000163612	0	0	0.251435	0.0819544	ENSG00000163612	FAM86KP
ENSG00000163617	5.6697	8.40304	9.88501	12.494	ENSG00000163617	CCDC191
ENSG00000163618	1.98966	6.22725	3.46767	8.26537	ENSG00000163618	CADPS
ENSG00000163623	0.0218202	0.147439	0.0667086	0.280749	ENSG00000163623	NKX6-1
ENSG00000163624	19.8192	20.8902	14.9983	4.3654	ENSG00000163624	CDS1
ENSG00000163625	41.0336	61.335	58.8699	66.7175	ENSG00000163625	WDFY3
ENSG00000163626	8.87386	9.56999	8.9482	10.9602	ENSG00000163626	COX18
ENSG00000163629	45.1298	68.586	46.6793	35.5893	ENSG00000163629	PTPN13
ENSG00000163630	1.92926	6.319	4.27636	6.52297	ENSG00000163630	SYNPR
ENSG00000163631	0.590765	0.653904	0.397051	0.674821	ENSG00000163631	ALB
ENSG00000163632	1.55529	3.3719	4.30155	5.12865	ENSG00000163632	C3orf49
ENSG00000163633	17.6692	28.1737	26.9938	40.3986	ENSG00000163633	C4orf36
ENSG00000163634	24.82	20.1928	18.9858	17.0154	ENSG00000163634	THOC7
ENSG00000163635	18.4562	28.4123	23.1209	30.5398	ENSG00000163635	ATXN7
ENSG00000163636	53.2906	41.7565	35.1747	35.6489	ENSG00000163636	PSMD6
ENSG00000163637	8.492	8.16538	13.4996	21.754	ENSG00000163637	PRICKLE2
ENSG00000163638	11.8436	14.1758	13.8753	25.3898	ENSG00000163638	ADAMTS9
ENSG00000163644	6.91177	9.16204	7.82308	15.8548	ENSG00000163644	PPM1K
ENSG00000163645	0.16183	0.601322	0.28	0.845617	ENSG00000163645	ERICH6
ENSG00000163646	0.756445	1.98733	1.73257	2.5787	ENSG00000163646	CLRN1
ENSG00000163655	18.7715	32.5634	20.5474	29.4447	ENSG00000163655	GMPS
ENSG00000163659	78.5718	78.9512	55.5645	52.5458	ENSG00000163659	TIPARP
ENSG00000163660	71.959	116.822	106.678	77.954	ENSG00000163660	CCNL1
ENSG00000163661	0.203923	0.336899	7.68987	16.8711	ENSG00000163661	PTX3
ENSG00000163666	0.500517	0.633021	0.711641	0.768657	ENSG00000163666	HESX1
ENSG00000163673	0.533068	1.06211	0.812035	1.94598	ENSG00000163673	DCLK3
ENSG00000163681	96.7138	87.5825	73.5384	77.9403	ENSG00000163681	SLMAP
ENSG00000163682	407.897	359.443	342.809	279.035	ENSG00000163682	RPL9
ENSG00000163683	5.81465	8.18974	9.18829	12.8901	ENSG00000163683	SMIM14

ENSG00000163684	15.0304	20.4246	26.6158	25.8113	ENSG00000163684	RPP14
ENSG00000163686	8.49579	14.6342	22.2514	17.6779	ENSG00000163686	ABHD6
ENSG00000163687	1.01267	2.21376	1.70915	2.83874	ENSG00000163687	DNASE1L3
ENSG00000163689	18.3786	37.0859	6.10358	17.7913	ENSG00000163689	C3orf67
ENSG00000163694	23.4924	19.4696	10.6334	13.6635	ENSG00000163694	RBM47
ENSG00000163697	25.9527	47.6813	60.5345	98.7312	ENSG00000163697	APBB2
ENSG00000163701	24.5731	35.2815	24.723	24.0186	ENSG00000163701	IL17RE
ENSG00000163702	28.775	24.2546	17.3731	20.1118	ENSG00000163702	IL17RC
ENSG00000163703	16.0624	24.6446	12.9336	15.4538	ENSG00000163703	CRELD1
ENSG00000163704	1.92417	2.58666	4.23209	2.9146	ENSG00000163704	PRRT3
ENSG00000163705	3.73771	1.83524	2.85213	15.2267	ENSG00000163705	FANCD2OS
ENSG00000163710	5.18037	5.66944	3.74829	7.3495	ENSG00000163710	PCOLCE2
ENSG00000163714	62.4333	89.0292	81.1876	72.6504	ENSG00000163714	U2SURP
ENSG00000163719	13.6232	21.3956	19.8944	19.1074	ENSG00000163719	MTMR14
ENSG00000163728	19.6739	23.7208	22.1378	22.8459	ENSG00000163728	TTC14
ENSG00000163734	9.37227	3.71709	2.33368	15.0464	ENSG00000163734	CXCL3
ENSG00000163735	3.29656	1.08927	1.70987	51.3853	ENSG00000163735	CXCL5
ENSG00000163736	29.5963	0.17943	0	0.302928	ENSG00000163736	PPBP
ENSG00000163737	0	0	0	0	ENSG00000163737	PF4
ENSG00000163738	11.7439	30.8694	19.3572	23.0448	ENSG00000163738	MTHFD2L
ENSG00000163739	17.473	5.57136	4.26564	96.2232	ENSG00000163739	CXCL1
ENSG00000163743	6.29945	9.7042	8.94255	9.27756	ENSG00000163743	RCHY1
ENSG00000163746	0.925082	2.74908	0.634614	1.31462	ENSG00000163746	PLSCR2
ENSG00000163749	0.765205	1.05803	1.32942	2.17766	ENSG00000163749	CCDC158
ENSG00000163751	0	0	0.027627	0.0347734	ENSG00000163751	CPA3
ENSG00000163754	7.98547	11.6811	14.142	12.0743	ENSG00000163754	GYG1
ENSG00000163755	8.52093	9.50805	6.41542	9.00459	ENSG00000163755	HPS3
ENSG00000163762	0.759671	1.31216	0.464755	2.10922	ENSG00000163762	TM4SF18
ENSG00000163781	21.0666	38.9878	25.0251	37.8941	ENSG00000163781	TOPBP1
ENSG00000163785	55.6912	58.9107	56.907	53.8819	ENSG00000163785	RYK
ENSG00000163788	40.0315	31.8457	21.5128	33.355	ENSG00000163788	SNRK
ENSG00000163792	0.0412216	0.120543	0	0.134967	ENSG00000163792	TCF23
ENSG00000163793	0.947765	2.29661	2.27954	3.34651	ENSG00000163793	DNAJC5G
ENSG00000163794	0.571465	0.62775	1.68856	0.973581	ENSG00000163794	UCN
ENSG00000163795	8.55823	7.57368	10.3769	6.20425	ENSG00000163795	ZNF513
ENSG00000163798	20.1792	26.1902	25.502	42.8823	ENSG00000163798	SLC4A1AP
ENSG00000163803	2.66047	5.32752	4.66321	2.95832	ENSG00000163803	PLB1
ENSG00000163806	5.66949	6.45475	10.5932	13.4	ENSG00000163806	SPDYA
ENSG00000163807	13.0019	11.0041	10.9548	12.0709	ENSG00000163807	KIAA1143
ENSG00000163808	1.24869	6.0164	1.12535	4.38612	ENSG00000163808	KIF15
ENSG00000163810	1.17579	1.11106	0.847882	1.13855	ENSG00000163810	TGM4
ENSG00000163811	47.6394	63.6411	66.1707	53.1698	ENSG00000163811	WDR43
ENSG00000163812	63.8291	45.8885	43.5866	28.6886	ENSG00000163812	ZDHHC3
ENSG00000163814	149.932	153.308	97.6343	83.6367	ENSG00000163814	CDCP1
ENSG00000163815	0.380099	0.272565	0.228038	0.467008	ENSG00000163815	CLEC3B
ENSG00000163817	7.87022	12.5352	10.0247	23.9763	ENSG00000163817	SLC6A20
ENSG00000163818	7.10252	7.34171	8.72335	7.712	ENSG00000163818	LZTFL1
ENSG00000163820	10.0307	11.1975	11.6619	9.78126	ENSG00000163820	FYCO1
ENSG00000163823	0.104156	0.0617318	0.112771	0.164335	ENSG00000163823	CCR1
ENSG00000163825	0.0446661	0	0	0.0976617	ENSG00000163825	RTP3
ENSG00000163827	1.03293	1.54976	1.26763	3.32458	ENSG00000163827	LRRC2
ENSG00000163832	21.4079	29.1144	30.35	26.6629	ENSG00000163832	ELP6
ENSG00000163833	0.149718	0.296631	0.303285	0.50559	ENSG00000163833	FBXO40
ENSG00000163840	11.2506	18.4089	16.1631	16.7524	ENSG00000163840	DTX3L

ENSG00000163848	18.7823	21.2952	24.9715	19.991	ENSG00000163848	ZNF148
ENSG00000163864	0.966516	2.61553	2.79855	1.32153	ENSG00000163864	NMNAT3
ENSG00000163866	24.1424	15.8665	18.1987	16.4461	ENSG00000163866	SMIM12
ENSG00000163867	19.1915	24.0772	23.2633	30.5586	ENSG00000163867	ZMYM6
ENSG00000163870	39.2107	39.7008	31.0907	23.9202	ENSG00000163870	TPRA1
ENSG00000163872	20.3585	25.5412	25.9828	27.6251	ENSG00000163872	YEATS2
ENSG00000163873	0.213796	0.182561	0.259704	0.465304	ENSG00000163873	GRIK3
ENSG00000163874	32.6191	61.212	63.163	25.9197	ENSG00000163874	ZC3H12A
ENSG00000163875	34.6102	19.2132	16.0327	16.877	ENSG00000163875	MEAF6
ENSG00000163877	15.4138	17.8752	15.4964	23.6881	ENSG00000163877	SNIP1
ENSG00000163879	0.526101	1.11945	1.26782	1.8344	ENSG00000163879	DNALI1
ENSG00000163882	63.7066	70.413	56.666	66.2869	ENSG00000163882	POLR2H
ENSG00000163884	19.1247	26.8238	49.5827	39.4303	ENSG00000163884	KLF15
ENSG00000163885	4.83584	4.1302	6.08234	8.95387	ENSG00000163885	CFAP100
ENSG00000163888	0.0876088	0.440223	0.240896	0.611814	ENSG00000163888	CAMK2N2
ENSG00000163898	9.20837	1.04302	1.97388	2.69686	ENSG00000163898	LIPH
ENSG00000163900	22.5668	22.4272	23.0534	18.2747	ENSG00000163900	TMEM41A
ENSG00000163902	230.085	269.612	138.555	122.849	ENSG00000163902	RPN1
ENSG00000163904	21.3896	18.2558	22.8045	58.1057	ENSG00000163904	SENP2
ENSG00000163909	0.0150216	0.115914	0.118988	0.984308	ENSG00000163909	HEYL
ENSG00000163913	12.3542	27.5157	29.2455	41.3492	ENSG00000163913	IFT122
ENSG00000163914	0.177445	0.503841	0.420536	0.721547	ENSG00000163914	RHO
ENSG00000163915	22.5357	56.561	23.482	61.3386	ENSG00000163915	IGF2BP2-AS1
ENSG00000163918	11.9954	24.9579	10.3614	16.1106	ENSG00000163918	RFC4
ENSG00000163923	13.957	27.6328	19.7402	24.2092	ENSG00000163923	RPL39L
ENSG00000163930	37.9276	57.3421	52.4675	31.5566	ENSG00000163930	BAP1
ENSG00000163931	77.6426	109.172	57.4746	54.6368	ENSG00000163931	TKT
ENSG00000163932	2.60026	2.37243	3.38802	3.58456	ENSG00000163932	PRKCD
ENSG00000163933	17.2509	29.965	21.6669	13.3375	ENSG00000163933	RFT1
ENSG00000163935	4.81085	6.6907	4.77609	8.74248	ENSG00000163935	SFMBT1
ENSG00000163938	78.1391	90.815	106.229	69.6188	ENSG00000163938	GNL3
ENSG00000163939	34.2547	40.6389	44.4343	45.4877	ENSG00000163939	PBRM1
ENSG00000163945	8.91508	18.5195	20.9227	20.6088	ENSG00000163945	UVSSA
ENSG00000163946	28.7024	52.23	46.7147	50.5151	ENSG00000163946	FAM208A
ENSG00000163947	10.7123	10.9101	8.3025	8.06557	ENSG00000163947	ARHGEF3
ENSG00000163950	19.8128	18.1729	18.6363	16.018	ENSG00000163950	SLBP
ENSG00000163956	85.4844	91.8523	57.8347	34.709	ENSG00000163956	LRPAP1
ENSG00000163958	0.385801	1.048	0.612722	0.977136	ENSG00000163958	ZDHHC19
ENSG00000163959	18.9255	13.0823	16.831	19.6577	ENSG00000163959	SLC51A
ENSG00000163960	11.1571	14.6527	14.62	19.8182	ENSG00000163960	UBXN7
ENSG00000163961	7.12993	12.0343	6.82528	9.34738	ENSG00000163961	RNF168
ENSG00000163964	8.67013	11.6449	9.81195	11.9111	ENSG00000163964	PIGX
ENSG00000163975	60.2931	33.2419	10.7203	30.4726	ENSG00000163975	MELTF
ENSG00000163982	0	0.0321958	0.133607	0.376813	ENSG00000163982	OTOP1
ENSG00000163993	137.39	5.23665	18.0897	16.5846	ENSG00000163993	S100P
ENSG00000163995	10.2273	0.468518	0.515857	2.1065	ENSG00000163995	ABLIM2
ENSG00000164002	2.75359	3.38344	2.825	2.66256	ENSG00000164002	EXO5
ENSG00000164007	0.308795	0.869268	0.703111	1.09971	ENSG00000164007	CLDN19
ENSG00000164008	8.98873	8.38544	11.7311	12.6475	ENSG00000164008	C1orf50
ENSG00000164010	4.48748	10.3456	8.65912	5.835	ENSG00000164010	ERMAP
ENSG00000164011	1.839	2.9927	3.13328	4.03422	ENSG00000164011	ZNF691
ENSG00000164022	28.6463	23.7386	23.5673	15.2707	ENSG00000164022	AIMP1
ENSG00000164023	53.9393	48.2139	30.0182	25.3472	ENSG00000164023	SGMS2
ENSG00000164024	40.3014	55.0546	38.1046	38.2943	ENSG00000164024	METAP1

ENSG00000164031	26.2472	34.7036	31.7906	30.7468	ENSG00000164031	DNAJB14
ENSG00000164032	76.1887	125.731	35.0552	45.5342	ENSG00000164032	H2AFZ
ENSG00000164035	10.8154	12.9271	10.8798	17.7661	ENSG00000164035	EMCN
ENSG00000164037	2.12376	3.81177	2.18531	4.86558	ENSG00000164037	SLC9B1
ENSG00000164038	8.36367	10.9158	11.2629	10.2647	ENSG00000164038	SLC9B2
ENSG00000164039	14.1805	14.6787	20.2202	14.1878	ENSG00000164039	BDH2
ENSG00000164040	17.6844	17.6635	15.2064	21.353	ENSG00000164040	PGRMC2
ENSG00000164045	4.29401	6.28327	2.48149	5.4404	ENSG00000164045	CDC25A
ENSG00000164047	0.748258	1.25826	0.730685	0.101155	ENSG00000164047	CAMP
ENSG00000164048	11.5637	12.4408	14.3937	13.8627	ENSG00000164048	ZNF589
ENSG00000164049	1.48315	3.09614	3.72596	3.15166	ENSG00000164049	FBXW12
ENSG00000164050	128.23	172.259	215.949	90.4144	ENSG00000164050	PLXNB1
ENSG00000164051	10.5693	7.11914	10.3814	4.53416	ENSG00000164051	CCDC51
ENSG00000164053	4.1591	8.24297	6.01627	5.27141	ENSG00000164053	ATRIP
ENSG00000164054	55.4626	95.3859	53.3391	55.3566	ENSG00000164054	SHISA5
ENSG00000164056	1.27125	1.67185	3.06103	10.3185	ENSG00000164056	SPRY1
ENSG00000164061	0.292316	0.323445	0.373442	0.396677	ENSG00000164061	BSN
ENSG00000164062	58.394	79.3552	68.1415	45.7024	ENSG00000164062	APEH
ENSG00000164066	10.612	20.54	20.7064	36.8029	ENSG00000164066	INTU
ENSG00000164068	18.0886	22.2917	22.8943	22.6153	ENSG00000164068	RNF123
ENSG00000164070	13.962	14.413	13.1494	7.63168	ENSG00000164070	HSPA4L
ENSG00000164073	22.0935	30.0525	24.1022	29.3484	ENSG00000164073	MFSD8
ENSG00000164074	5.35943	8.31487	7.04178	8.97467	ENSG00000164074	ABHD18
ENSG00000164076	1.16209	0.327559	0.0815893	0.38714	ENSG00000164076	CAMKV
ENSG00000164077	7.61595	5.8748	8.34642	5.8824	ENSG00000164077	MON1A
ENSG00000164078	33.9293	96.2878	21.4542	39.3856	ENSG00000164078	MST1R
ENSG00000164080	9.65698	9.78345	12.1399	13.1512	ENSG00000164080	RAD54L2
ENSG00000164081	26.6494	36.7495	17.8041	14.994	ENSG00000164081	TEX264
ENSG00000164082	0.397737	0.516249	0.657729	0.794405	ENSG00000164082	GRM2
ENSG00000164086	59.2222	57.8087	54.1792	31.5341	ENSG00000164086	DUSP7
ENSG00000164087	1.97109	7.28523	3.12876	2.89128	ENSG00000164087	POC1A
ENSG00000164088	2.14778	4.91405	3.94821	4.11765	ENSG00000164088	PPM1M
ENSG00000164089	1.64805	2.41736	2.05335	4.16248	ENSG00000164089	ETNPPL
ENSG00000164091	19.973	23.723	27.2676	19.6847	ENSG00000164091	WDR82
ENSG00000164093	7.93533	8.59372	0.512724	1.38878	ENSG00000164093	PITX2
ENSG00000164096	58.7714	14.377	14.7098	20.234	ENSG00000164096	C4orf3
ENSG00000164099	16.958	25.4037	24.7243	13.2897	ENSG00000164099	PRSS12
ENSG00000164100	0.491681	0.636127	0.92627	0.582617	ENSG00000164100	NDST3
ENSG00000164104	14.097	57.9341	16.8337	23.7516	ENSG00000164104	HMGB2
ENSG00000164105	2.58183	7.29182	3.28692	5.68042	ENSG00000164105	SAP30
ENSG00000164106	1.53913	3.66242	4.04409	6.9331	ENSG00000164106	SCRG1
ENSG00000164107	0.101958	0.159751	0.411848	2.27825	ENSG00000164107	HAND2
ENSG00000164109	5.86965	20.8015	3.63258	5.58943	ENSG00000164109	MAD2L1
ENSG00000164111	96.506	137.225	66.6312	138.995	ENSG00000164111	ANXA5
ENSG00000164112	0.596892	1.40692	1.37034	1.406	ENSG00000164112	TMEM155
ENSG00000164113	0.0846968	0.0855687	0.0257851	0.0649327	ENSG00000164113	ADAD1
ENSG00000164114	7.58597	7.54674	10.1666	11.8939	ENSG00000164114	MAP9
ENSG00000164116	2.15229	0.37399	0.706518	1.9545	ENSG00000164116	GUCY1A3
ENSG00000164117	10.3312	7.54354	6.64823	6.76266	ENSG00000164117	FBXO8
ENSG00000164118	6.71172	16.8546	11.0765	9.63738	ENSG00000164118	CEP44
ENSG00000164120	21.2917	3.67096	0.744717	2.53977	ENSG00000164120	HPGD
ENSG00000164122	0.132229	0.0872274	0.157526	0.0994887	ENSG00000164122	ASB5
ENSG00000164123	0.357311	0.283943	0.214166	0.741156	ENSG00000164123	C4orf45
ENSG00000164124	7.4993	8.55355	6.76786	5.08367	ENSG00000164124	TMEM144

ENSG00000164125	1.66084	2.80772	3.11428	20.2383	ENSG00000164125	FAM198B
ENSG00000164128	0.342987	0.455644	0.376665	1.03184	ENSG00000164128	NPY1R
ENSG00000164129	0.123341	0.178144	0.134527	0.236519	ENSG00000164129	NPY5R
ENSG00000164134	34.2867	38.6642	43.8034	39.3031	ENSG00000164134	NAA15
ENSG00000164136	4.09459	6.00975	3.48671	6.8329	ENSG00000164136	IL15
ENSG00000164142	19.0302	22.6385	22.2421	11.3621	ENSG00000164142	FAM160A1
ENSG00000164144	22.4214	23.2787	19.3124	23.6173	ENSG00000164144	ARFIP1
ENSG00000164151	11.419	17.2146	18.5146	20.6789	ENSG00000164151	ICE1
ENSG00000164161	0.217205	1.39544	1.45166	1.41565	ENSG00000164161	HHIP
ENSG00000164162	20.4676	34.2597	33.7607	31.5713	ENSG00000164162	ANAPC10
ENSG00000164163	60.0565	58.4393	47.9394	38.6623	ENSG00000164163	ABCE1
ENSG00000164164	23.0445	35.8704	41.4062	47.2236	ENSG00000164164	OTUD4
ENSG00000164167	11.5078	18.9932	14.55	12.2252	ENSG00000164167	LSM6
ENSG00000164168	26.4829	24.26	22.017	17.7367	ENSG00000164168	TMEM184C
ENSG00000164169	6.49125	6.63053	6.46811	5.70463	ENSG00000164169	PRMT9
ENSG00000164171	164.713	245.281	37.2818	115.721	ENSG00000164171	ITGA2
ENSG00000164172	16.759	15.5678	11.3878	11.5271	ENSG00000164172	MOCS2
ENSG00000164175	0.481816	0.156289	0.0712509	0	ENSG00000164175	SLC45A2
ENSG00000164176	0.0569659	0.286742	0.401389	3.29375	ENSG00000164176	EDIL3
ENSG00000164180	18.4589	31.248	22.9958	18.2764	ENSG00000164180	TMEM161B
ENSG00000164181	13.9182	14.27	12.0857	3.85681	ENSG00000164181	ELOVL7
ENSG00000164182	13.5597	17.4254	17.7831	14.0291	ENSG00000164182	NDUFAF2
ENSG00000164185	0.20121	0.878133	1.31148	1.06984	ENSG00000164185	ZNF474
ENSG00000164187	10.2016	11.0065	10.6325	7.93203	ENSG00000164187	LMBRD2
ENSG00000164188	0.140904	0.396311	0.153713	0.661849	ENSG00000164188	RANBP3L
ENSG00000164190	10.633	21.2825	21.5739	24.2503	ENSG00000164190	NIPBL
ENSG00000164197	7.14276	11.4952	9.86231	15.0809	ENSG00000164197	RNF180
ENSG00000164199	3.46324	12.0059	10.0542	19.2346	ENSG00000164199	ADGRV1
ENSG00000164209	19.4328	15.2835	22.1322	13.4092	ENSG00000164209	SLC25A46
ENSG00000164211	59.6945	60.5452	30.1494	49.4166	ENSG00000164211	STARD4
ENSG00000164219	9.00935	18.5203	12.5858	11.5178	ENSG00000164219	PGGT1B
ENSG00000164220	0.763737	1.9183	1.10562	4.99011	ENSG00000164220	F2RL2
ENSG00000164221	5.55941	3.53674	5.09147	5.32022	ENSG00000164221	CCDC112
ENSG00000164236	0.378443	1.32516	1.29465	2.2854	ENSG00000164236	ANKRD33B
ENSG00000164237	2.00315	6.59057	3.90871	8.58558	ENSG00000164237	CMBL
ENSG00000164241	4.31434	7.61797	9.11446	7.18993	ENSG00000164241	C5orf63
ENSG00000164244	25.2027	22.1471	19.398	32.577	ENSG00000164244	PRRC1
ENSG00000164251	48.6714	45.4391	38.8948	17.1374	ENSG00000164251	F2RL1
ENSG00000164252	8.3122	11.6316	13.0543	10.8117	ENSG00000164252	AGGF1
ENSG00000164253	25.9347	58.4325	67.505	53.3291	ENSG00000164253	WDR41
ENSG00000164256	1.2426	3.8271	2.85698	5.70763	ENSG00000164256	PRDM9
ENSG00000164258	52.1587	49.4521	41.8877	32.2328	ENSG00000164258	NDUFS4
ENSG00000164265	9.57193	9.23899	10.9483	32.1627	ENSG00000164265	SCGB3A2
ENSG00000164266	8.87386	0.629684	0.72589	2.40369	ENSG00000164266	SPINK1
ENSG00000164270	0.31895	0.780483	0.591434	1.01582	ENSG00000164270	HTR4
ENSG00000164283	1.1147	7.5574	0.123559	4.17888	ENSG00000164283	ESM1
ENSG00000164284	10.5693	22.1636	18.3588	9.88984	ENSG00000164284	GRPEL2
ENSG00000164287	1.56264	3.56529	4.49915	6.33525	ENSG00000164287	CDC20B
ENSG00000164291	12.0123	11.1943	8.66495	12.727	ENSG00000164291	ARSK
ENSG00000164292	5.18476	7.44299	4.59554	20.4564	ENSG00000164292	RHOBTB3
ENSG00000164294	14.4841	40.5151	19.8597	25.3075	ENSG00000164294	GPX8
ENSG00000164296	3.11916	5.3819	6.38298	5.91989	ENSG00000164296	TIGD6
ENSG00000164299	0	0	0.0644444	0.0332199	ENSG00000164299	SPZ1
ENSG00000164300	35.3249	41.7106	31.0892	21.1631	ENSG00000164300	SERINC5

ENSG00000164303	0.848766	2.2215	1.65387	2.22528	ENSG00000164303	ENPP6
ENSG00000164304	0.39387	0.94616	1.36757	0.582433	ENSG00000164304	CAGE1
ENSG00000164305	20.5325	14.7655	8.26474	12.1534	ENSG00000164305	CASP3
ENSG00000164306	7.40689	17.3245	9.15696	12.929	ENSG00000164306	PRIMPOL
ENSG00000164307	18.5739	54.5832	30.6365	33.8457	ENSG00000164307	ERAP1
ENSG00000164308	5.77272	45.0207	18.8759	30.2144	ENSG00000164308	ERAP2
ENSG00000164309	0.776077	0.436172	0.789908	0.541554	ENSG00000164309	CMYA5
ENSG00000164318	1.29761	1.91744	3.94148	2.95159	ENSG00000164318	EGFLAM
ENSG00000164323	14.0096	15.9487	19.1185	16.5396	ENSG00000164323	CFAP97
ENSG00000164325	0.162149	0.219205	0.25611	0.0725508	ENSG00000164325	TMEM174
ENSG00000164326	0	0	0	0	ENSG00000164326	CARTPT
ENSG00000164327	26.0442	36.0007	29.4068	43.2393	ENSG00000164327	RICTOR
ENSG00000164329	32.4504	57.3916	57.5381	58.3483	ENSG00000164329	PAPD4
ENSG00000164330	1.77708	3.2656	2.85731	12.3831	ENSG00000164330	EBF1
ENSG00000164331	9.39355	19.1755	18.8096	13.1852	ENSG00000164331	ANKRA2
ENSG00000164332	17.4943	18.8759	24.0583	20.886	ENSG00000164332	UBLCP1
ENSG00000164334	0	0	0.0428542	0.10757	ENSG00000164334	FAM170A
ENSG00000164338	15.7363	16.9034	21.1947	11.2063	ENSG00000164338	UTP15
ENSG00000164342	2.71268	3.94995	4.92851	2.18626	ENSG00000164342	TLR3
ENSG00000164344	0.09254	0.638834	0.18445	0.89498	ENSG00000164344	KLKB1
ENSG00000164346	38.7832	26.0293	23.3505	19.9856	ENSG00000164346	NSA2
ENSG00000164347	26.2602	31.7537	24.0676	27.6949	ENSG00000164347	GFM2
ENSG00000164362	0.340794	0.0221762	0.117905	0.286185	ENSG00000164362	TERT
ENSG00000164363	0	0	0.0390119	0.048998	ENSG00000164363	SLC6A18
ENSG00000164366	9.17411	14.3385	13.6588	20.5967	ENSG00000164366	CCDC127
ENSG00000164379	24.1792	7.29607	2.66752	4.5392	ENSG00000164379	FOXQ1
ENSG00000164385	0.562868	0.689101	0.993213	1.64121	ENSG00000164385	LINC01600
ENSG00000164393	1.18664	0.402647	0.269516	0.629422	ENSG00000164393	ADGRF2
ENSG00000164398	1.97053	1.52205	2.11862	3.41619	ENSG00000164398	ACSL6
ENSG00000164399	0.308213	0.476977	0.53095	0.584262	ENSG00000164399	IL3
ENSG00000164400	5.47352	4.00969	2.38403	11.2287	ENSG00000164400	CSF2
ENSG00000164402	28.226	27.0086	19.4073	22.886	ENSG00000164402	SEPT8
ENSG00000164403	2.37725	2.95726	3.70327	6.30153	ENSG00000164403	SHROOM1
ENSG00000164404	0.338251	0.322427	0.218699	0.06894	ENSG00000164404	GDF9
ENSG00000164405	128.418	83.8662	56.0421	50.0031	ENSG00000164405	UQCRQ
ENSG00000164406	1.69094	4.27426	3.17352	3.72643	ENSG00000164406	LEAP2
ENSG00000164411	0.756479	1.167	1.43664	2.42606	ENSG00000164411	GJB7
ENSG00000164414	14.9675	14.1339	13.9269	10.0398	ENSG00000164414	SLC35A1
ENSG00000164418	1.16008	2.23337	2.45625	4.39904	ENSG00000164418	GRIK2
ENSG00000164430	4.25633	9.17234	6.53832	8.27677	ENSG00000164430	MB21D1
ENSG00000164434	1.35538	2.28898	2.12477	3.85999	ENSG00000164434	FABP7
ENSG00000164438	0.156353	0.0374723	0.0680377	0.214924	ENSG00000164438	TLX3
ENSG00000164440	0.243201	0.416982	0.801374	0.93454	ENSG00000164440	TXLNB
ENSG00000164442	18.3032	4.04514	6.68648	21.3078	ENSG00000164442	CITED2
ENSG00000164451	0.207273	0.186942	0.313718	0.794503	ENSG00000164451	FAM26D
ENSG00000164458	0	0.0373604	0	0	ENSG00000164458	T
ENSG00000164463	6.62708	8.0941	8.42362	9.00111	ENSG00000164463	CREBRF
ENSG00000164465	27.0114	26.9357	26.7802	33.8653	ENSG00000164465	DCBLD1
ENSG00000164466	28.5951	37.1536	29.1157	45.0947	ENSG00000164466	SFXN1
ENSG00000164483	11.2575	28.6892	25.1977	53.5032	ENSG00000164483	SAMD3
ENSG00000164484	9.46693	21.4328	14.0149	19.1547	ENSG00000164484	TMEM200A
ENSG00000164485	0.190876	0.328059	0.298357	0.743727	ENSG00000164485	IL22RA2
ENSG00000164488	0.621401	0.527222	0.547232	1.26558	ENSG00000164488	DACT2
ENSG00000164494	2.94032	3.56079	2.30386	2.41259	ENSG00000164494	PDSS2

ENSG00000164500	0	0.107155	0.0483728	0.0609253	ENSG00000164500	C7orf72
ENSG00000164506	22.3791	25.5568	21.675	25.9809	ENSG00000164506	STXBP5
ENSG00000164508	0.303929	0.291333	0.263044	0.162447	ENSG00000164508	HIST1H2AA
ENSG00000164509	0.914335	6.20942	5.64734	6.33552	ENSG00000164509	IL31RA
ENSG00000164512	1.06136	1.57662	1.46709	2.29998	ENSG00000164512	ANKRD55
ENSG00000164520	23.6881	10.4319	10.0949	4.2308	ENSG00000164520	RAET1E
ENSG00000164530	0.674424	0.161515	0.291584	0.0563345	ENSG00000164530	PI16
ENSG00000164532	0	0	0	0.0756663	ENSG00000164532	TBX20
ENSG00000164535	23.8543	27.3945	29.2752	30.0107	ENSG00000164535	DAGLB
ENSG00000164542	8.26804	7.53186	5.27138	5.62676	ENSG00000164542	KIAA0895
ENSG00000164543	58.6511	47.8244	34.4673	34.6093	ENSG00000164543	STK17A
ENSG00000164548	28.0895	46.3527	48.1945	48.1743	ENSG00000164548	TRA2A
ENSG00000164556	0.289092	0.208879	0.377635	0.59372	ENSG00000164556	FAM183BP
ENSG00000164574	11.5272	17.8146	16.3749	19.0336	ENSG00000164574	GALNT10
ENSG00000164576	16.1474	18.1112	18.0426	14.3449	ENSG00000164576	SAP30L
ENSG00000164587	459.217	370.693	255.588	190.771	ENSG00000164587	RPS14
ENSG00000164588	0.0497008	0.191522	0.15626	0.729477	ENSG00000164588	HCN1
ENSG00000164591	1.37905	2.22921	1.64156	2.37861	ENSG00000164591	MYOZ3
ENSG00000164597	40.3514	60.2442	51.3522	50.3037	ENSG00000164597	COG5
ENSG00000164600	0.105499	0.126961	0.0917737	0.25992	ENSG00000164600	NEUROD6
ENSG00000164603	6.34238	4.99964	5.38161	7.9799	ENSG00000164603	BMT2
ENSG00000164604	2.64161	3.18151	2.51472	3.93036	ENSG00000164604	GPR85
ENSG00000164609	28.0916	16.3227	13.7564	13.8416	ENSG00000164609	SLU7
ENSG00000164610	8.77772	10.7215	11.7115	12.1078	ENSG00000164610	RP9
ENSG00000164611	13.9468	60.5073	11.5434	16.7987	ENSG00000164611	PTTG1
ENSG00000164615	13.6726	13.6603	12.3982	7.33441	ENSG00000164615	CAMLG
ENSG00000164616	0.0452904	0.163876	0.395111	0.247207	ENSG00000164616	FBXL21
ENSG00000164619	1.06446	2.34208	1.81387	21.4816	ENSG00000164619	BMPER
ENSG00000164620	7.31891	6.93801	8.1833	4.57391	ENSG00000164620	RELL2
ENSG00000164626	0.0722321	0.0557029	0.117465	0.0833611	ENSG00000164626	KCNK5
ENSG00000164627	2.0176	5.00901	4.10848	6.86862	ENSG00000164627	KIF6
ENSG00000164631	14.6654	10.5517	18.8119	15.2565	ENSG00000164631	ZNF12
ENSG00000164638	2.27043	3.6542	6.29553	4.42838	ENSG00000164638	SLC29A4
ENSG00000164645	0	0.0578231	0.104856	0.392823	ENSG00000164645	TEX47
ENSG00000164647	10.7712	30.4182	5.60071	21.3758	ENSG00000164647	STEAP1
ENSG00000164649	5.66014	15.7059	9.57736	20.1504	ENSG00000164649	CDCA7L
ENSG00000164651	0.107521	0.037438	0.152302	4.15627	ENSG00000164651	SP8
ENSG00000164654	16.887	22.2475	20.6713	12.3158	ENSG00000164654	MIOS
ENSG00000164659	3.53144	9.605	5.21086	10.9212	ENSG00000164659	KIAA1324L
ENSG00000164663	2.91184	4.80337	5.53526	6.64661	ENSG00000164663	USP49
ENSG00000164669	0.753202	2.52351	2.07757	2.52062	ENSG00000164669	INTS4P1
ENSG00000164674	1.53349	3.16301	1.96021	2.10779	ENSG00000164674	SYTL3
ENSG00000164675	0.345644	0.369179	0.712562	0.715619	ENSG00000164675	IQUB
ENSG00000164683	0.380511	1.81328	1.46436	3.66437	ENSG00000164683	HEY1
ENSG00000164684	3.05762	3.17958	3.15452	2.51834	ENSG00000164684	ZNF704
ENSG00000164687	25.584	27.5225	91.2526	18.9284	ENSG00000164687	FABP5
ENSG00000164690	0.0733749	0.288318	0.132768	0.466719	ENSG00000164690	SHH
ENSG00000164691	0.579461	0.55879	0.511623	0.335415	ENSG00000164691	TAGAP
ENSG00000164692	1.43588	2.63783	25	2234.67	ENSG00000164692	COL1A2
ENSG00000164694	0.0353089	0.158428	0.0559308	0.474241	ENSG00000164694	FNDC1
ENSG00000164695	7.09635	5.23285	6.43231	3.2678	ENSG00000164695	CHMP4C
ENSG00000164707	1.77967	7.17118	5.06459	7.93636	ENSG00000164707	SLC13A4
ENSG00000164708	0	0	0	0	ENSG00000164708	PGAM2
ENSG00000164713	36.8038	32.8189	39.7973	38.4202	ENSG00000164713	BRI3

ENSG00000164715	14.88	11.9994	10.6053	9.20061	ENSG00000164715	LMTK2
ENSG00000164729	0.346855	0.309347	0.181133	0.175858	ENSG00000164729	SLC35G3
ENSG00000164733	492.5	471.897	273.406	387.476	ENSG00000164733	CTSB
ENSG00000164736	0.340963	0.763689	0.684228	1.31001	ENSG00000164736	SOX17
ENSG00000164740	0.17592	0	0.303907	0.508965	ENSG00000164740	SEPT7P5
ENSG00000164741	3.72431	18.9512	5.11257	43.8635	ENSG00000164741	DLC1
ENSG00000164742	0.557989	0.549996	0.683216	1.20019	ENSG00000164742	ADCY1
ENSG00000164743	1.12995	0.466433	0.632425	0.529928	ENSG00000164743	C8orf48
ENSG00000164744	1.03845	1.34591	1.63383	1.38568	ENSG00000164744	SUN3
ENSG00000164746	0.921518	3.2683	1.11374	1.17943	ENSG00000164746	C7orf57
ENSG00000164749	2.2653	3.48606	1.74271	7.06183	ENSG00000164749	HNF4G
ENSG00000164751	15.835	12.2614	10.2978	9.56308	ENSG00000164751	PEX2
ENSG00000164754	51.413	74.0727	40.0215	37.95	ENSG00000164754	RAD21
ENSG00000164756	1.43128	3.61523	3.69455	5.03541	ENSG00000164756	SLC30A8
ENSG00000164758	7.38086	14.1954	7.05626	6.9779	ENSG00000164758	MED30
ENSG00000164761	0.575713	1.08559	0.455405	29.9329	ENSG00000164761	TNFRSF11B
ENSG00000164764	2.36484	4.97539	5.45363	7.53401	ENSG00000164764	SBSPON
ENSG00000164776	5.5085	7.92612	9.30542	12.0753	ENSG00000164776	PHKG1
ENSG00000164778	0.4109	0.910595	0.602873	1.18305	ENSG00000164778	EN2
ENSG00000164794	1.52377	3.73049	3.01131	6.50714	ENSG00000164794	KCNV1
ENSG00000164796	4.16609	7.86983	6.32468	9.3948	ENSG00000164796	CSMD3
ENSG00000164808	14.9916	33.2176	25.3162	40.9457	ENSG00000164808	SPIDR
ENSG00000164815	14.795	23.6376	20.5643	14.5183	ENSG00000164815	ORC5
ENSG00000164816	0	0	0	0	ENSG00000164816	DEFA5
ENSG00000164818	13.0008	20.2326	16.2197	14.5073	ENSG00000164818	DNAAF5
ENSG00000164821	0	0	0	0	ENSG00000164821	DEFA4
ENSG00000164822	0.166994	0.319963	0.722128	0	ENSG00000164822	DEFA6
ENSG00000164823	5.71613	9.70543	6.43576	4.25294	ENSG00000164823	OSGIN2
ENSG00000164825	9.90256	3.26661	4.91471	3.98381	ENSG00000164825	DEFB1
ENSG00000164828	94.7783	131.788	97.9126	87.8272	ENSG00000164828	SUN1
ENSG00000164830	20.1946	25.8632	20.6328	21.2811	ENSG00000164830	OXR1
ENSG00000164841	0.178924	0.483904	0.2807	0.32019	ENSG00000164841	TMEM74
ENSG00000164845	1.87715	1.698	1.7632	1.08366	ENSG00000164845	FAM86FP
ENSG00000164849	1.19689	3.16789	4.88588	6.05553	ENSG00000164849	GPR146
ENSG00000164850	1.05202	1.3799	3.16145	3.43055	ENSG00000164850	GPER1
ENSG00000164853	0.510022	0.504703	0.644243	0.614085	ENSG00000164853	UNCX
ENSG00000164855	36.3678	14.643	24.6834	12.9909	ENSG00000164855	TMEM184A
ENSG00000164867	3.41443	3.9086	5.41442	10.1	ENSG00000164867	NOS3
ENSG00000164871	1.41164	5.58671	3.18059	5.69838	ENSG00000164871	SPAG11B
ENSG00000164877	25.1942	57.0231	38.7692	38.7783	ENSG00000164877	MICALL2
ENSG00000164879	0.85485	1.38554	2.05776	0.755191	ENSG00000164879	CA3
ENSG00000164880	40.0848	52.7289	55.5395	55.5173	ENSG00000164880	INTS1
ENSG00000164885	6.87995	5.0325	5.14193	4.74448	ENSG00000164885	CDK5
ENSG00000164889	46.3959	56.2354	65.2808	47.4154	ENSG00000164889	SLC4A2
ENSG00000164893	0.571311	1.82342	0.666995	0.880649	ENSG00000164893	SLC7A13
ENSG00000164896	29.4075	25.2263	29.1092	22.4482	ENSG00000164896	FASTK
ENSG00000164897	18.088	20.9655	12.8256	8.05483	ENSG00000164897	TMUB1
ENSG00000164898	4.3157	10.0994	7.93671	10.6594	ENSG00000164898	FMC1
ENSG00000164900	0.198633	0.553125	0.239345	1.57309	ENSG00000164900	GBX1
ENSG00000164902	16.8913	9.62984	15.999	14.1185	ENSG00000164902	PHAX
ENSG00000164904	23.6619	54.2969	28.3786	43.2625	ENSG00000164904	ALDH7A1
ENSG00000164916	21.2229	24.0331	26.2719	29.1797	ENSG00000164916	FOXK1
ENSG00000164919	156.331	138.667	81.7478	86.0029	ENSG00000164919	COX6C
ENSG00000164920	2.68177	4.23055	2.35651	2.28811	ENSG00000164920	OSR2

ENSG00000164924	498.539	299.503	273.022	244.722	ENSG00000164924	YWHAZ
ENSG00000164929	1.32032	3.43212	4.43959	10.7917	ENSG00000164929	BAALC
ENSG00000164930	49.1857	68.3929	79.8575	21.4005	ENSG00000164930	FZD6
ENSG00000164932	1.89746	3.54208	3.84777	42.0619	ENSG00000164932	CTHRC1
ENSG00000164933	12.8727	15.6788	16.3057	15.751	ENSG00000164933	SLC25A32
ENSG00000164934	25.5339	18.906	22.0042	17.5941	ENSG00000164934	DCAF13
ENSG00000164935	0	0.18965	0.218752	0.48396	ENSG00000164935	DCSTAMP
ENSG00000164938	8.5609	6.87402	12.0216	9.09413	ENSG00000164938	TP53INP1
ENSG00000164941	44.1367	65.4601	55.0859	62.9967	ENSG00000164941	INTS8
ENSG00000164944	17.1701	21.9237	16.4835	25.9534	ENSG00000164944	VIRMA
ENSG00000164946	0.219139	0.368438	0.998433	0.706711	ENSG00000164946	FREM1
ENSG00000164949	2.2634	1.53158	0.216104	6.42403	ENSG00000164949	GEM
ENSG00000164951	36.9519	55.0474	28.1205	31.7817	ENSG00000164951	PDP1
ENSG00000164953	11.5717	19.5201	19.4575	21.2399	ENSG00000164953	TMEM67
ENSG00000164961	19.2207	17.7349	17.3444	18.1191	ENSG00000164961	WASHC5
ENSG00000164967	9.37108	7.94162	8.14111	3.92779	ENSG00000164967	RPP25L
ENSG00000164970	7.43551	6.55082	9.89869	9.29875	ENSG00000164970	FAM219A
ENSG00000164972	0.624848	2.60731	1.30188	0.878222	ENSG00000164972	C9orf24
ENSG00000164975	14.6294	12.9804	13.9839	18.3989	ENSG00000164975	SNAPC3
ENSG00000164976	15.2175	25.685	25.7841	32.969	ENSG00000164976	KIAA1161
ENSG00000164978	12.2346	8.5478	8.99621	7.11635	ENSG00000164978	NUDT2
ENSG00000164983	4.26059	5.68247	3.83531	5.06541	ENSG00000164983	TMEM65
ENSG00000164985	16.076	49.1583	39.4577	61.6921	ENSG00000164985	PSIP1
ENSG00000164989	5.67412	11.5516	12.8145	20.3141	ENSG00000164989	CCDC171
ENSG00000165006	22.1655	12.6334	19.4473	12.3225	ENSG00000165006	UBAP1
ENSG00000165023	0.0613629	0.118387	0.128435	0.14868	ENSG00000165023	DIRAS2
ENSG00000165025	2.76565	8.75945	3.37928	1.76785	ENSG00000165025	SYK
ENSG00000165028	1.48235	1.737	1.98126	3.14705	ENSG00000165028	NIPSNAP3B
ENSG00000165029	52.8252	52.4218	35.5636	70.3653	ENSG00000165029	ABCA1
ENSG00000165030	7.08493	5.29641	16.3528	4.90795	ENSG00000165030	NFIL3
ENSG00000165046	3.28778	10.4433	6.95021	10.6802	ENSG00000165046	LETM2
ENSG00000165055	28.6334	37.177	37.0181	46.969	ENSG00000165055	METTL2B
ENSG00000165059	0	0.0722753	0	0.0402491	ENSG00000165059	PRKACG
ENSG00000165060	1.4678	3.36462	5.3343	4.91147	ENSG00000165060	FXN
ENSG00000165061	4.13507	4.77042	3.94499	7.32302	ENSG00000165061	ZMAT4
ENSG00000165066	3.42563	1.02427	1.17673	6.44178	ENSG00000165066	NKX6-3
ENSG00000165071	0.500862	1.12844	0.346881	1.52698	ENSG00000165071	TMEM71
ENSG00000165072	2.2316	13.7366	1.69456	6.26793	ENSG00000165072	MAMDC2
ENSG00000165076	0.487175	0.812002	1.09644	0.828517	ENSG00000165076	PRSS37
ENSG00000165078	5.87286	9.34584	2.39838	3.84836	ENSG00000165078	CPA6
ENSG00000165084	2.72554	5.85413	5.98067	9.88581	ENSG00000165084	C8orf34
ENSG00000165091	2.22879	3.28099	3.80187	5.36701	ENSG00000165091	TMC1
ENSG00000165092	0.233209	0.376407	0.645104	0.391084	ENSG00000165092	ALDH1A1
ENSG00000165097	9.60074	6.85133	5.82506	8.05766	ENSG00000165097	KDM1B
ENSG00000165102	40.5379	53.3328	38.642	44.8439	ENSG00000165102	HGSNAT
ENSG00000165105	39.4806	79.4706	73.8808	138.682	ENSG00000165105	RASEF
ENSG00000165113	1.19504	0.854913	1.37266	2.50486	ENSG00000165113	GKAP1
ENSG00000165115	5.5941	10.829	9.31027	8.95153	ENSG00000165115	KIF27
ENSG00000165118	7.5558	10.2198	9.13906	10.4341	ENSG00000165118	C9orf64
ENSG00000165119	210.549	191.594	187.477	179.502	ENSG00000165119	HNRNPK
ENSG00000165120	0.103821	0.252743	0.180655	0.341713	ENSG00000165120	SSMEM1
ENSG00000165121	0.374398	0.57493	0.63462	0.461874	ENSG00000165121	RP11-213G2.3
ENSG00000165124	0.131326	0.444898	1.64967	2.00859	ENSG00000165124	SVEP1
ENSG00000165125	0.450271	0.224212	0.152829	0.347659	ENSG00000165125	TRPV6

ENSG00000165131	0.0465144	0	0.121129	0.0503106	ENSG00000165131	C7orf34
ENSG00000165138	7.42092	11.9754	11.0872	12.0845	ENSG00000165138	ANKS6
ENSG00000165140	0.199142	0.106	0.0957338	0.130767	ENSG00000165140	FBP1
ENSG00000165152	8.40921	10.4663	7.67601	4.28172	ENSG00000165152	TMEM246
ENSG00000165156	19.5931	20.4899	25.0379	25.5867	ENSG00000165156	ZHX1
ENSG00000165164	0	0.0755813	0.0546688	0.017248	ENSG00000165164	CFAP47
ENSG00000165168	0.0974455	0.213717	0.166217	0.162543	ENSG00000165168	CYBB
ENSG00000165169	23.7485	13.6371	11.4254	13.5992	ENSG00000165169	DYNLT3
ENSG00000165171	3.42521	2.46109	1.20825	0.890006	ENSG00000165171	METTL27
ENSG00000165175	24.4298	35.3201	23.5019	15.2048	ENSG00000165175	MID1IP1
ENSG00000165178	0	0.0857609	0.132615	0	ENSG00000165178	NCF1C
ENSG00000165181	0.768553	3.01363	1.80588	3.89475	ENSG00000165181	C9orf84
ENSG00000165182	0.100069	0.556954	0.17498	0.0714118	ENSG00000165182	CXorf58
ENSG00000165185	0.960233	1.45559	1.24725	1.99772	ENSG00000165185	KIAA1958
ENSG00000165186	0.390565	0.773964	0.695061	1.21946	ENSG00000165186	PTCHD1
ENSG00000165188	0.6654	0.664552	0.408834	0.484874	ENSG00000165188	RNF183
ENSG00000165192	2.58633	5.81344	4.79558	8.85971	ENSG00000165192	ASB11
ENSG00000165194	0.0333574	2.2642	0.316396	1.74541	ENSG00000165194	PCDH19
ENSG00000165195	6.31962	7.44142	8.61214	6.73288	ENSG00000165195	PIGA
ENSG00000165197	0.140384	0.300291	0.44112	0.253221	ENSG00000165197	VEGFD
ENSG00000165202	0.112861	0	0.196332	0.0615303	ENSG00000165202	OR1Q1
ENSG00000165204	0	0	0.104153	0.39148	ENSG00000165204	OR1K1
ENSG00000165209	13.3763	10.5785	11.6343	10.7464	ENSG00000165209	STRBP
ENSG00000165215	1.43451	4.02834	4.37184	6.14772	ENSG00000165215	CLDN3
ENSG00000165219	37.9656	43.8994	43.9338	37.7169	ENSG00000165219	GAPVD1
ENSG00000165233	20.7927	25.4389	12.3025	11.2013	ENSG00000165233	CARD19
ENSG00000165238	1.46362	2.3356	3.0741	5.96005	ENSG00000165238	WNK2
ENSG00000165240	0	3.37E-08	9.02E-08	0	ENSG00000165240	ATP7A
ENSG00000165244	0.881286	2.39742	0.337744	2.11175	ENSG00000165244	ZNF367
ENSG00000165246	12.9168	16.8258	22.7136	1.10165	ENSG00000165246	NLGN4Y
ENSG00000165259	1.88544	2.84476	3.42051	3.47931	ENSG00000165259	HDX
ENSG00000165264	18.2717	17.378	7.28719	11.019	ENSG00000165264	NDUFB6
ENSG00000165269	0.068774	0.266149	1.04311	0.388111	ENSG00000165269	AQP7
ENSG00000165271	31.5116	31.1855	33.8551	30.6963	ENSG00000165271	NOL6
ENSG00000165272	50.7612	249.999	40.8565	29.6254	ENSG00000165272	AQP3
ENSG00000165275	9.71833	17.2616	22.0601	28.0754	ENSG00000165275	TRMT10B
ENSG00000165280	269.066	201.838	130.597	168.397	ENSG00000165280	VCP
ENSG00000165282	16.9196	24.7775	18.2107	11.0516	ENSG00000165282	PIGO
ENSG00000165283	33.8461	32.304	39.8122	21.5301	ENSG00000165283	STOML2
ENSG00000165288	8.14663	11.7295	12.7877	13.8018	ENSG00000165288	BRWD3
ENSG00000165300	0.176645	0.279419	0.328849	1.89453	ENSG00000165300	SLITRK5
ENSG00000165304	12.0849	32.2444	11.8925	22.8165	ENSG00000165304	MELK
ENSG00000165309	5.21853	9.85764	7.34702	14.8535	ENSG00000165309	ARMC3
ENSG00000165312	3.16207	3.38902	4.93662	3.00107	ENSG00000165312	OTUD1
ENSG00000165322	17.7187	23.0309	12.6317	21.0756	ENSG00000165322	ARHGAP12
ENSG00000165323	0.316939	0.463005	0.622821	0.971969	ENSG00000165323	FAT3
ENSG00000165325	0.119675	0.512746	0.66215	1.80012	ENSG00000165325	DEUP1
ENSG00000165338	3.62934	6.46568	6.46437	10.8995	ENSG00000165338	HECTD2
ENSG00000165349	0	0.168598	0.0435494	0.137189	ENSG00000165349	SLC7A3
ENSG00000165355	5.08788	4.78432	4.1598	4.85285	ENSG00000165355	FBXO33
ENSG00000165359	1.33849	4.36982	3.42431	2.80391	ENSG00000165359	INTS6L
ENSG00000165370	0	0	0.0330317	0	ENSG00000165370	GPR101
ENSG00000165376	0.0563993	0.413313	0.319779	0.521832	ENSG00000165376	CLDN2
ENSG00000165379	0.572512	0.566109	1.03681	6.45928	ENSG00000165379	LRFN5

ENSG00000165383	0.798906	1.33788	1.86124	3.26491	ENSG00000165383	LRRC18
ENSG00000165388	0.201048	0.729094	0.244868	0.393184	ENSG00000165388	ZNF488
ENSG00000165389	8.08949	6.31596	5.55308	7.49216	ENSG00000165389	SPTSSA
ENSG00000165390	154.903	107.459	112.874	67.3244	ENSG00000165390	ANXA8
ENSG00000165392	6.6784	12.7657	14.5751	10.7152	ENSG00000165392	WRN
ENSG00000165406	7.71773	7.0478	9.03402	9.50831	ENSG00000165406	MARCH8
ENSG00000165409	0.229095	1.04081	0.704095	1.48849	ENSG00000165409	TSHR
ENSG00000165410	7.47425	4.7969	4.98388	11.7315	ENSG00000165410	CFL2
ENSG00000165416	19.8075	18.4747	18.1909	23.5504	ENSG00000165416	SUGT1
ENSG00000165417	5.83508	7.77209	9.82502	8.87253	ENSG00000165417	GTF2A1
ENSG00000165424	1.10664	0.991373	1.38855	7.75714	ENSG00000165424	ZCCHC24
ENSG00000165434	2.64747	2.58393	1.94265	4.23969	ENSG00000165434	PGM2L1
ENSG00000165443	0.326535	0.309755	0.119453	0.68074	ENSG00000165443	PHYHIPL
ENSG00000165449	2.34239	12.5883	2.3385	3.33367	ENSG00000165449	SLC16A9
ENSG00000165457	0	0	0.114617	0	ENSG00000165457	FOLR2
ENSG00000165458	95.0304	62.5452	105.024	88.4965	ENSG00000165458	INPPL1
ENSG00000165462	0.614084	0.471176	0.482981	0.464407	ENSG00000165462	PHOX2A
ENSG00000165471	0.305444	0.823445	0.797925	0.586156	ENSG00000165471	MBL2
ENSG00000165474	157.639	693.399	501.105	200.531	ENSG00000165474	GJB2
ENSG00000165475	5.05739	6.03018	2.84705	3.51871	ENSG00000165475	CRYL1
ENSG00000165476	70.1614	38.2227	18.6243	25.5854	ENSG00000165476	REEP3
ENSG00000165478	0.121703	0.133401	0.317719	0.329118	ENSG00000165478	HEPACAM
ENSG00000165480	1.39589	5.45616	1.18805	3.20428	ENSG00000165480	SKA3
ENSG00000165487	20.6353	22.2754	21.6583	29.1442	ENSG00000165487	MICU2
ENSG00000165490	3.75607	11.6673	3.56862	8.0265	ENSG00000165490	DDIAS
ENSG00000165494	22.2076	37.1384	37.936	19.1408	ENSG00000165494	PCF11
ENSG00000165495	6.25686	23.1057	13.9734	41.2211	ENSG00000165495	PKNOX2
ENSG00000165496	0	0.0770195	0.139199	0.173791	ENSG00000165496	RPL10L
ENSG00000165501	5.83313	5.94945	5.30783	3.58633	ENSG00000165501	LRR1
ENSG00000165502	115.886	71.4221	47.77	47.388	ENSG00000165502	RPL36AL
ENSG00000165506	3.90998	4.52156	5.12705	2.57237	ENSG00000165506	DNAAF2
ENSG00000165507	5.71924	5.74506	5.01868	10.5327	ENSG00000165507	C10orf10
ENSG00000165509	0.0292634	0	0.0575312	0.242186	ENSG00000165509	MAGEC3
ENSG00000165511	0.557696	1.20151	1.48033	1.871	ENSG00000165511	C10orf25
ENSG00000165512	2.68969	5.19711	5.12623	3.30726	ENSG00000165512	ZNF22
ENSG00000165516	25.0873	29.8976	27.7755	22.9571	ENSG00000165516	KLHDC2
ENSG00000165521	1.93016	2.91718	3.14052	6.95014	ENSG00000165521	EML5
ENSG00000165525	28.7275	37.7415	36.9823	48.8996	ENSG00000165525	NEMF
ENSG00000165526	14.6144	22.7815	25.3716	25.123	ENSG00000165526	RPUSD4
ENSG00000165527	58.3012	56.1779	54.6528	31.0194	ENSG00000165527	ARF6
ENSG00000165533	13.0726	17.0258	21.0271	18.1077	ENSG00000165533	TTC8
ENSG00000165548	3.84674	1.90613	3.20752	1.92463	ENSG00000165548	TMEM63C
ENSG00000165553	0.0300782	0.0869582	0.104813	0.0329902	ENSG00000165553	NGB
ENSG00000165555	0.978776	1.11744	1.4467	0.737147	ENSG00000165555	NOXRED1
ENSG00000165556	0.0138278	0.227089	0.192043	0.209427	ENSG00000165556	CDX2
ENSG00000165566	3.00557	2.07403	1.86704	3.19523	ENSG00000165566	AMER2
ENSG00000165568	1.46766	5.9605	3.03859	4.4676	ENSG00000165568	AKR1E2
ENSG00000165572	3.30488	4.96738	4.40843	5.12304	ENSG00000165572	KBTBD6
ENSG00000165583	0.13298	0.707185	0.510932	0.881636	ENSG00000165583	SSX5
ENSG00000165584	1.63324	3.11634	2.38126	3.92602	ENSG00000165584	SSX3
ENSG00000165588	0.0508622	0.255729	0.230312	0.710747	ENSG00000165588	OTX2
ENSG00000165591	3.37064	3.11211	1.54256	0.624875	ENSG00000165591	FAAH2
ENSG00000165606	0.240372	0.154039	0.0695839	0.0868955	ENSG00000165606	DRGX
ENSG00000165609	36.8666	40.2246	35.1159	23.726	ENSG00000165609	NUDT5

ENSG00000165617	0.304061	0.540452	0.805994	2.88213	ENSG00000165617	DACT1
ENSG00000165621	0.376957	0.726512	1.16849	0.81656	ENSG00000165621	OXGR1
ENSG00000165623	0	0	0	0.0931134	ENSG00000165623	UCMA
ENSG00000165626	4.08963	3.29154	2.80596	5.37345	ENSG00000165626	BEND7
ENSG00000165629	106.295	114.047	77.2078	106.151	ENSG00000165629	ATP5C1
ENSG00000165630	13.9088	12.1081	13.7179	10.6082	ENSG00000165630	PRPF18
ENSG00000165632	1.36637	1.63341	2.29627	3.09743	ENSG00000165632	TAF3
ENSG00000165633	1.41287	2.40081	2.1877	7.41118	ENSG00000165633	VSTM4
ENSG00000165637	151.96	88.992	82.6854	65.4526	ENSG00000165637	VDAC2
ENSG00000165643	0.0858524	0.0820608	0.0752008	0	ENSG00000165643	SOHLH1
ENSG00000165644	19.2456	17.0662	16.5895	9.60095	ENSG00000165644	COMTD1
ENSG00000165646	4.96825	4.59178	3.78432	3.86586	ENSG00000165646	SLC18A2
ENSG00000165650	30.4487	33.4278	23.2143	22.031	ENSG00000165650	PDZD8
ENSG00000165655	6.28918	4.65297	13.8816	7.03606	ENSG00000165655	ZNF503
ENSG00000165659	0.167254	0.454573	0.40975	0.434279	ENSG00000165659	DACH1
ENSG00000165660	9.33789	7.08099	7.42583	5.42812	ENSG00000165660	ABRAXAS2
ENSG00000165661	4.97649	8.38853	7.53761	5.25442	ENSG00000165661	QSOX2
ENSG00000165669	32.2792	35.1424	35.8866	21.1424	ENSG00000165669	FAM204A
ENSG00000165671	26.9017	37.3764	40.8071	37.6379	ENSG00000165671	NSD1
ENSG00000165672	44.8056	51.116	27.5932	28.8809	ENSG00000165672	PRDX3
ENSG00000165675	5.35718	5.45677	6.18327	4.24666	ENSG00000165675	ENOX2
ENSG00000165678	48.6744	41.3948	40.8363	23.9163	ENSG00000165678	GHITM
ENSG00000165682	0.463936	0.93043	0.962434	1.91981	ENSG00000165682	CLEC1B
ENSG00000165684	6.56042	6.50477	9.04748	8.09984	ENSG00000165684	SNAPC4
ENSG00000165685	3.34803	11.5941	10.8326	27.3239	ENSG00000165685	TMEM52B
ENSG00000165688	30.4044	28.9992	28.0673	25.8613	ENSG00000165688	PMPCA
ENSG00000165689	32.3401	37.8994	42.2887	35.9442	ENSG00000165689	SDCCAG3
ENSG00000165694	0.026729	0.184898	0.117017	0.146694	ENSG00000165694	FRMD7
ENSG00000165695	0.732789	0.647638	0.878754	0.336311	ENSG00000165695	AK8
ENSG00000165698	2.67105	4.14968	4.43991	4.79411	ENSG00000165698	SPACA9
ENSG00000165699	17.7	22.0711	21.9324	19.9379	ENSG00000165699	TSC1
ENSG00000165702	0.808045	1.03857	0.821984	1.31862	ENSG00000165702	GFI1B
ENSG00000165704	4.15701	7.85264	4.84005	10.1671	ENSG00000165704	HPRT1
ENSG00000165714	3.12509	4.24006	4.75216	5.38792	ENSG00000165714	BORCS5
ENSG00000165716	2.29624	1.44925	4.1052	0.972921	ENSG00000165716	FAM69B
ENSG00000165724	20.5397	22.5125	24.0416	11.7318	ENSG00000165724	ZMYND19
ENSG00000165730	0.0371584	0.0677739	0.0724443	0.038653	ENSG00000165730	STOX1
ENSG00000165731	0.251842	1.06718	0.869397	0.598236	ENSG00000165731	RET
ENSG00000165732	54.9446	38.353	72.8509	40.6318	ENSG00000165732	DDX21
ENSG00000165733	10.042	12.4108	13.2334	13.1649	ENSG00000165733	BMS1
ENSG00000165752	4.3991	5.18752	4.84459	5.23871	ENSG00000165752	STK32C
ENSG00000165757	2.00011	0.863336	2.28905	15.219	ENSG00000165757	JCAD
ENSG00000165762	0	0.0543679	0	0.123193	ENSG00000165762	OR4K2
ENSG00000165775	7.9392	8.26102	7.12869	9.54089	ENSG00000165775	FUNDC2
ENSG00000165782	9.99425	8.92379	8.1925	8.37908	ENSG00000165782	TMEM55B
ENSG00000165792	26.3518	36.1406	29.9179	21.5598	ENSG00000165792	METTL17
ENSG00000165794	6.12453	0.499659	0.582793	0.930585	ENSG00000165794	SLC39A2
ENSG00000165795	45.4	15.9479	12.6262	23.2921	ENSG00000165795	NDRG2
ENSG00000165799	32.9538	11.1881	6.67674	11.023	ENSG00000165799	RNASE7
ENSG00000165801	8.52681	16.7231	11.1587	26.9274	ENSG00000165801	ARHGEF40
ENSG00000165802	24.7926	23.4964	29.0275	22.3104	ENSG00000165802	NSMF
ENSG00000165804	21.2177	25.5565	24.2496	17.4588	ENSG00000165804	ZNF219
ENSG00000165805	6.31507	17.1633	14.6872	30.6767	ENSG00000165805	C12orf50
ENSG00000165806	6.9446	7.35428	6.73819	6.39161	ENSG00000165806	CASP7

ENSG00000165807	1.7553	1.03855	0.88575	1.0876	ENSG00000165807	PPP1R36
ENSG00000165810	4.09311	6.42167	7.55529	9.95679	ENSG00000165810	BTNL9
ENSG00000165813	23.988	20.5547	19.4182	24.8898	ENSG00000165813	CCDC186
ENSG00000165816	0.765742	1.86422	1.20215	1.01291	ENSG00000165816	VWA2
ENSG00000165819	34.8619	43.2135	36.0516	35.6271	ENSG00000165819	METTL3
ENSG00000165821	0.413741	1.19884	1.32556	2.10525	ENSG00000165821	SALL2
ENSG00000165828	1.35162	3.2442	3.517	4.3327	ENSG00000165828	PRAP1
ENSG00000165832	13.7914	15.6805	15.6739	8.36047	ENSG00000165832	TRUB1
ENSG00000165837	3.74943	5.44672	4.10905	5.67376	ENSG00000165837	ERICH6B
ENSG00000165841	0.0595689	0.241836	0.253465	0.154589	ENSG00000165841	CYP2C19
ENSG00000165861	8.31795	7.99111	13.3827	9.59981	ENSG00000165861	ZFYVE1
ENSG00000165862	0.0369516	0.133016	0.0536505	0.0409064	ENSG00000165862	PNLIPRP2
ENSG00000165863	0.751243	1.03305	0.415189	1.61818	ENSG00000165863	C10orf82
ENSG00000165868	0.48017	3.40798	6.76019	2.41905	ENSG00000165868	HSPA12A
ENSG00000165874	0.148183	0.275315	0.165642	0.169526	ENSG00000165874	FAM35BP
ENSG00000165879	0.983863	0.486151	0.636135	0.878188	ENSG00000165879	FRAT1
ENSG00000165886	8.89064	8.38799	4.95696	5.77139	ENSG00000165886	UBTD1
ENSG00000165887	1.72494	0.452718	0.419662	0.428711	ENSG00000165887	ANKRD2
ENSG00000165891	4.92699	18.171	7.32321	12.2282	ENSG00000165891	E2F7
ENSG00000165895	3.81231	2.89234	3.8119	8.09016	ENSG00000165895	ARHGAP42
ENSG00000165898	10.0523	9.82003	5.99653	5.1191	ENSG00000165898	ISCA2
ENSG00000165899	0	0.277849	0.120481	0.460735	ENSG00000165899	OTOGL
ENSG00000165905	1.7467	21.8285	15.8794	12.142	ENSG00000165905	LARGE2
ENSG00000165912	41.3549	50.8889	37.8494	22.7614	ENSG00000165912	PACSIN3
ENSG00000165914	21.1469	39.3969	37.8919	59.6104	ENSG00000165914	TTC7B
ENSG00000165915	49.4534	48.4599	35.3815	40.5848	ENSG00000165915	SLC39A13
ENSG00000165916	63.4159	47.4341	34.5973	39.4399	ENSG00000165916	PSMC3
ENSG00000165917	1.03696	1.6696	1.90548	1.59024	ENSG00000165917	RAPSN
ENSG00000165923	2.59494	7.12101	6.01638	8.15092	ENSG00000165923	AGBL2
ENSG00000165929	11.2062	13.7106	17.0929	10.404	ENSG00000165929	TC2N
ENSG00000165934	29.2367	32.1544	29.8067	35.9408	ENSG00000165934	CPSF2
ENSG00000165935	3.25336	2.16274	2.98495	2.14138	ENSG00000165935	SMCO2
ENSG00000165943	11.5724	9.39643	8.46861	5.24223	ENSG00000165943	MOAP1
ENSG00000165948	15.4369	26.3537	18.5789	23.4049	ENSG00000165948	IFI27L1
ENSG00000165949	154.742	103.298	39.8541	75.1401	ENSG00000165949	IFI27
ENSG00000165953	0	0	0.0337712	0	ENSG00000165953	SERPINA12
ENSG00000165959	11.322	23.7044	7.24072	9.00023	ENSG00000165959	CLMN
ENSG00000165966	0.0901628	0.312418	0.147347	0.30568	ENSG00000165966	PDZRN4
ENSG00000165970	0.0678788	0.0796352	0.108709	0.174647	ENSG00000165970	SLC6A5
ENSG00000165972	8.01121	12.5375	12.7019	17.9105	ENSG00000165972	CCDC38
ENSG00000165973	0.563227	2.35869	2.49427	2.85933	ENSG00000165973	NELL1
ENSG00000165983	4.81542	7.02589	7.6402	3.00761	ENSG00000165983	PTER
ENSG00000165985	0.466748	1.00515	1.54822	1.12443	ENSG00000165985	C1QL3
ENSG00000165995	2.36025	4.59673	3.82088	4.86353	ENSG00000165995	CACNB2
ENSG00000165996	7.95785	15.2405	8.0792	6.90456	ENSG00000165996	HACD1
ENSG00000165997	6.23484	7.50985	8.20711	6.63754	ENSG00000165997	ARL5B
ENSG00000166002	0.554118	0.939668	1.08931	3.04449	ENSG00000166002	SMCO4
ENSG00000166004	7.87538	17.6371	13.318	14.2396	ENSG00000166004	CEP295
ENSG00000166006	0.680717	3.03761	2.70695	3.48819	ENSG00000166006	KCNC2
ENSG00000166007	0	0	0	0.0747637	ENSG00000166007	TRIM51HP
ENSG00000166008	0.0264856	0	0.0460838	0.0643849	ENSG00000166008	MAGEA9
ENSG00000166012	113.91	179.965	167.186	134.996	ENSG00000166012	TAF1D
ENSG00000166013	0	0.0443284	0	0	ENSG00000166013	TRIM53BP
ENSG00000166016	3.09641	1.46609	3.49044	1.82099	ENSG00000166016	ABTB2

ENSG00000166024	7.9883	8.88216	7.55504	6.59304	ENSG00000166024	R3HCC1L
ENSG00000166025	95.8766	82.0603	73.4664	74.5339	ENSG00000166025	AMOTL1
ENSG00000166033	142.707	280.409	110.876	197.121	ENSG00000166033	HTRA1
ENSG00000166035	0.751811	1.37758	1.62255	3.61212	ENSG00000166035	LIPC
ENSG00000166037	16.2876	31.3074	26.0451	22.9428	ENSG00000166037	CEP57
ENSG00000166046	21.5185	10.1642	15.2986	12.8089	ENSG00000166046	TCP11L2
ENSG00000166049	0.0186257	0.0666013	0.0451624	0.110125	ENSG00000166049	PASD1
ENSG00000166068	12.1252	21.7226	20.1161	25.4786	ENSG00000166068	SPRED1
ENSG00000166069	0.303554	1.31178	0.994174	1.95918	ENSG00000166069	TMCO5A
ENSG00000166073	8.53216	16.7664	6.43455	17.8017	ENSG00000166073	GPR176
ENSG00000166086	2.58419	3.8605	7.64523	12.7595	ENSG00000166086	JAM3
ENSG00000166090	0	0.0432352	0.0390793	0.147246	ENSG00000166090	IL25
ENSG00000166091	0.193972	0.381375	0.351488	0.676679	ENSG00000166091	CMTM5
ENSG00000166104	0.0902622	0.105645	0.197414	0.498957	ENSG00000166104	hsa-mir-7162
ENSG00000166105	4.40801	10.496	10.9521	13.5435	ENSG00000166105	GLB1L3
ENSG00000166106	3.22311	0.499843	0.476235	1.51881	ENSG00000166106	ADAMTS15
ENSG00000166111	1.07366	1.56567	0.414308	0.896711	ENSG00000166111	SVOP
ENSG00000166118	1.25303	1.15115	0.337612	1.18079	ENSG00000166118	SPATA19
ENSG00000166123	10.081	25.5041	34.8424	16.9093	ENSG00000166123	GPT2
ENSG00000166126	2.0908	1.78887	1.83276	0.498161	ENSG00000166126	AMN
ENSG00000166128	18.1157	6.11365	9.53813	13.8344	ENSG00000166128	RAB8B
ENSG00000166130	19.7058	29.242	14.867	25.8399	ENSG00000166130	IKBIP
ENSG00000166133	6.01501	5.0421	6.03148	3.87997	ENSG00000166133	RPUSD2
ENSG00000166135	5.87424	7.9306	7.47712	8.91741	ENSG00000166135	HIF1AN
ENSG00000166136	94.6816	73.1742	62.242	45.0953	ENSG00000166136	NDUFB8
ENSG00000166140	18.0459	18.3826	12.5036	12.1693	ENSG00000166140	ZFYVE19
ENSG00000166143	0.272157	0.2833	0.65146	0.403792	ENSG00000166143	PPP1R14D
ENSG00000166145	217.044	159.931	116.386	48.1258	ENSG00000166145	SPINT1
ENSG00000166147	3.11175	4.31441	3.97313	122.226	ENSG00000166147	FBN1
ENSG00000166148	0	0	0	0.0415941	ENSG00000166148	AVPR1A
ENSG00000166152	0.114228	0.110004	0	0.249066	ENSG00000166152	C16orf78
ENSG00000166153	1.20097	3.39422	2.62319	3.04268	ENSG00000166153	DEPDC4
ENSG00000166157	0.947526	0.529979	0.101674	0.420987	ENSG00000166157	TPTE
ENSG00000166159	0.691282	1.38971	2.14086	0.835316	ENSG00000166159	LRTM2
ENSG00000166160	0	0	0	0	ENSG00000166160	OPN1MW2
ENSG00000166164	36.1481	39.5848	37.3299	42.6076	ENSG00000166164	BRD7
ENSG00000166165	13.4457	7.55535	29.5254	15.2119	ENSG00000166165	CKB
ENSG00000166166	5.54326	5.46069	6.61943	2.77353	ENSG00000166166	TRMT61A
ENSG00000166167	11.8754	11.3865	10.5791	9.41954	ENSG00000166167	BTRC
ENSG00000166169	12.6264	17.8948	21.3443	12.9151	ENSG00000166169	POLL
ENSG00000166170	16.9549	11.4378	16.1458	9.88255	ENSG00000166170	BAG5
ENSG00000166171	14.8202	12.3015	13.35	13.2062	ENSG00000166171	DPCD
ENSG00000166173	17.7908	25.0936	28.5498	11.5361	ENSG00000166173	LARP6
ENSG00000166181	38.7275	35.8441	39.1982	33.2852	ENSG00000166181	API5
ENSG00000166183	7.00368	2.73118	3.00138	2.13433	ENSG00000166183	ASPG
ENSG00000166188	3.16059	4.22894	7.54611	3.89312	ENSG00000166188	ZNF319
ENSG00000166189	17.6567	12.3208	12.6349	9.62841	ENSG00000166189	HPS6
ENSG00000166192	2.64626	7.69957	7.55922	8.50301	ENSG00000166192	SENP8
ENSG00000166197	24.236	25.2804	36.0566	27.7392	ENSG00000166197	NOLC1
ENSG00000166199	27.7439	23.9446	26.3613	17.5215	ENSG00000166199	ALKBH3
ENSG00000166200	37.2984	44.6298	40.3789	48.6223	ENSG00000166200	COPS2
ENSG00000166206	0.432236	2.54084	1.52457	1.63505	ENSG00000166206	GABRB3
ENSG00000166211	0.124515	0.179699	0.274571	0.447645	ENSG00000166211	SPIC
ENSG00000166220	0.388719	0.16248	0.28389	1.05032	ENSG00000166220	TBATA

ENSG00000166224	39.5279	38.1079	45.313	21.841	ENSG00000166224	SGPL1
ENSG00000166225	19.2829	15.737	18.1831	17.5271	ENSG00000166225	FRS2
ENSG00000166226	115.51	100.133	90.2892	86.6146	ENSG00000166226	CCT2
ENSG00000166228	25.6827	39.3181	26.6123	37.583	ENSG00000166228	PCBD1
ENSG00000166233	37.9574	44.6761	48.9799	59.8889	ENSG00000166233	ARIH1
ENSG00000166246	0.290432	0.162053	0.445485	0.713301	ENSG00000166246	C16orf71
ENSG00000166250	7.75613	12.4354	21.4613	30.1585	ENSG00000166250	CLMP
ENSG00000166257	0.774408	1.2628	1.95062	2.59694	ENSG00000166257	SCN3B
ENSG00000166260	18.6199	28.6361	30.3311	25.1526	ENSG00000166260	COX11
ENSG00000166261	8.0747	15.6411	13.8505	6.80107	ENSG00000166261	ZNF202
ENSG00000166262	8.98555	19.2277	14.9371	26.9658	ENSG00000166262	FAM227B
ENSG00000166263	5.00446	8.86956	7.28699	9.82696	ENSG00000166263	STXBP4
ENSG00000166265	0.43459	1.70546	5.32083	3.1075	ENSG00000166265	CYYR1
ENSG00000166266	14.8623	18.712	16.5769	19.3648	ENSG00000166266	CUL5
ENSG00000166268	0.722257	0.172345	0.37642	0.285981	ENSG00000166268	MYRFL
ENSG00000166272	14.4328	7.6949	13.8358	8.71563	ENSG00000166272	WBP1L
ENSG00000166275	9.28136	4.58377	6.00559	5.59974	ENSG00000166275	BORCS7
ENSG00000166278	0.483689	0.353366	0.534279	0.467155	ENSG00000166278	C2
ENSG00000166289	5.22867	6.53696	8.04878	3.36199	ENSG00000166289	PLEKHF1
ENSG00000166292	0.0980251	0.125936	0.619342	0.596137	ENSG00000166292	TMEM100
ENSG00000166295	28.598	27.027	29.3614	15.2669	ENSG00000166295	ANAPC16
ENSG00000166311	10.6109	12.8397	6.86938	11.2272	ENSG00000166311	SMPD1
ENSG00000166313	3.80287	3.31022	3.1102	7.12603	ENSG00000166313	APBB1
ENSG00000166317	0.18819	0.561848	0.396877	1.0332	ENSG00000166317	SYNPO2L
ENSG00000166321	8.82194	26.6741	23.5066	28.9278	ENSG00000166321	NUDT13
ENSG00000166323	1.75542	4.07858	3.26316	8.7949	ENSG00000166323	C11orf65
ENSG00000166326	9.82108	14.5133	18.4741	13.5262	ENSG00000166326	TRIM44
ENSG00000166329	0	0	0	0	ENSG00000166329	CCDC182
ENSG00000166333	29.3681	32.3955	19.511	34.5615	ENSG00000166333	ILK
ENSG00000166337	47.0276	36.7136	28.6044	24.0886	ENSG00000166337	TAF10
ENSG00000166340	27.4399	38.389	31.8202	44.8848	ENSG00000166340	TPP1
ENSG00000166341	0.376691	0.335112	0.581571	7.23727	ENSG00000166341	DCHS1
ENSG00000166342	4.78591	4.41452	6.15036	41.5348	ENSG00000166342	NETO1
ENSG00000166343	1.17759	4.22717	3.36982	5.64823	ENSG00000166343	MSS51
ENSG00000166347	10.3438	7.37947	5.52636	6.38	ENSG00000166347	CYB5A
ENSG00000166348	14.7212	19.144	19.6293	24.1271	ENSG00000166348	USP54
ENSG00000166349	1.77931	2.31356	1.52879	1.05409	ENSG00000166349	RAG1
ENSG00000166351	0	0	0	0	ENSG00000166351	POTED
ENSG00000166352	10.6942	13.5115	12.2451	11.8014	ENSG00000166352	C11orf74
ENSG00000166359	0.29955	0.67345	0.943894	0.512846	ENSG00000166359	WDR88
ENSG00000166363	0.117197	0.070606	0.0573892	0.981985	ENSG00000166363	OR10A5
ENSG00000166368	0.163766	0.315247	0.237431	0.595465	ENSG00000166368	OR2D2
ENSG00000166377	44.6025	92.9741	99.939	196.501	ENSG00000166377	ATP9B
ENSG00000166387	10.6433	16.4844	21.6282	11.169	ENSG00000166387	PPFIBP2
ENSG00000166391	0.0416856	0.0821312	0.10396	0.074953	ENSG00000166391	MOGAT2
ENSG00000166394	86.8109	25.684	17.6983	15.8524	ENSG00000166394	CYB5R2
ENSG00000166396	521.643	75.2639	78.0551	75.43	ENSG00000166396	SERPINB7
ENSG00000166398	5.34796	8.35321	7.52766	12.8133	ENSG00000166398	KIAA0355
ENSG00000166401	19.336	17.3042	22.1242	15.7691	ENSG00000166401	SERPINB8
ENSG00000166402	1.51862	0.700322	0.904892	2.78145	ENSG00000166402	TUB
ENSG00000166405	3.13929	3.15236	5.36691	6.88679	ENSG00000166405	RIC3
ENSG00000166407	0.156172	0.342355	0.485108	0.520988	ENSG00000166407	LMO1
ENSG00000166408	0.580859	0.912706	0.706889	0.368589	ENSG00000166408	OR5P1P
ENSG00000166411	33.2807	37.4353	39.4409	42.0959	ENSG00000166411	IDH3A

ENSG00000166415	4.00741	18.0923	14.6394	23.5697	ENSG00000166415	WDR72
ENSG00000166426	0	0	0	0	ENSG00000166426	CRABP1
ENSG00000166428	0.63347	2.45418	2.07843	2.97471	ENSG00000166428	PLD4
ENSG00000166432	0.347379	0.791202	0.829255	1.47418	ENSG00000166432	ZMAT1
ENSG00000166435	18.7407	20.9967	20.5562	23.2913	ENSG00000166435	XRRA1
ENSG00000166436	1.27843	6.63861	10.9306	2.69349	ENSG00000166436	TRIM66
ENSG00000166439	11.7449	11.2696	8.11339	7.71625	ENSG00000166439	RNF169
ENSG00000166441	582.599	448.063	415.076	276.144	ENSG00000166441	RPL27A
ENSG00000166444	20.6637	59.9814	45.9402	76.2518	ENSG00000166444	ST5
ENSG00000166446	5.38855	7.1669	7.187	12.2762	ENSG00000166446	CDYL2
ENSG00000166448	1.24748	2.23903	1.77415	2.82193	ENSG00000166448	TMEM130
ENSG00000166450	0.433293	0.981963	0.959516	1.69259	ENSG00000166450	PRTG
ENSG00000166451	4.70587	11.4695	7.86578	11.695	ENSG00000166451	CENPN
ENSG00000166452	12.9435	19.0464	14.9278	17.671	ENSG00000166452	AKIP1
ENSG00000166454	32.149	13.8772	19.7662	10.3477	ENSG00000166454	ATMIN
ENSG00000166455	0.98723	1.0333	1.45321	1.59985	ENSG00000166455	C16orf46
ENSG00000166471	72.6147	70.8264	31.04	37.2737	ENSG00000166471	TMEM41B
ENSG00000166473	3.4856	5.48411	5.57926	10.0806	ENSG00000166473	PKD1L2
ENSG00000166477	15.0911	14.5675	15.9305	20.5202	ENSG00000166477	LEO1
ENSG00000166478	20.8343	14.4556	12.5827	16.405	ENSG00000166478	ZNF143
ENSG00000166479	42.9761	71.5597	67.5581	64.0137	ENSG00000166479	TMX3
ENSG00000166482	0.562876	1.21486	1.36537	3.342	ENSG00000166482	MFAP4
ENSG00000166483	24.0966	41.4126	18.3397	25.2348	ENSG00000166483	WEE1
ENSG00000166484	7.64774	4.83525	7.13307	6.42776	ENSG00000166484	MAPK7
ENSG00000166492	0	0	0	0.256094	ENSG00000166492	FAM86GP
ENSG00000166501	0.845391	1.65019	0.99459	1.59977	ENSG00000166501	PRKCB
ENSG00000166503	25.2299	25.0356	21.2722	22.4823	ENSG00000166503	HDGFL3
ENSG00000166507	13.2916	14.1817	13.739	10.2213	ENSG00000166507	NDST2
ENSG00000166508	20.2495	45.2986	14.3667	29.4072	ENSG00000166508	MCM7
ENSG00000166509	2.78194	6.513	6.27368	10.0937	ENSG00000166509	CLEC3A
ENSG00000166510	8.43317	6.96038	4.01959	3.95528	ENSG00000166510	CCDC68
ENSG00000166523	2.2333	5.42673	4.61357	7.98923	ENSG00000166523	CLEC4E
ENSG00000166526	17.8634	20.0022	27.9639	26.408	ENSG00000166526	ZNF3
ENSG00000166527	0.235036	0.142079	0.193776	0.571982	ENSG00000166527	CLEC4D
ENSG00000166529	7.4357	7.19752	10.6261	7.87874	ENSG00000166529	ZSCAN21
ENSG00000166530	0	0	0	0	ENSG00000166530	HSBP1P2
ENSG00000166532	36.474	41.0362	46.7019	35.5535	ENSG00000166532	RIMKLB
ENSG00000166535	799.673	90.6027	136.876	153.985	ENSG00000166535	A2ML1
ENSG00000166546	2.18121	2.95853	3.62715	6.00843	ENSG00000166546	BEAN1
ENSG00000166548	8.73508	16.5107	16.3534	15.8274	ENSG00000166548	TK2
ENSG00000166557	73.5783	59.6219	39.8605	31.5025	ENSG00000166557	TMED3
ENSG00000166558	0	0.0434982	0.107301	0.619048	ENSG00000166558	SLC38A8
ENSG00000166562	36.4043	31.8892	17.3308	14.124	ENSG00000166562	SEC11C
ENSG00000166569	1.23783	2.04115	1.41187	2.56531	ENSG00000166569	CPLX4
ENSG00000166573	0.0582694	0.0560737	0	0.190529	ENSG00000166573	GALR1
ENSG00000166575	17.0368	29.1967	17.2943	31.4663	ENSG00000166575	TMEM135
ENSG00000166578	1.27668	1.62252	1.62231	4.43347	ENSG00000166578	IQCD
ENSG00000166579	57.3349	48.1699	57.2356	58.4999	ENSG00000166579	NDEL1
ENSG00000166582	4.49647	3.90544	8.22925	4.34926	ENSG00000166582	CENPV
ENSG00000166589	3.33875	0.353124	0.290548	0.971024	ENSG00000166589	CDH16
ENSG00000166592	25.5344	3.44742	4.48546	6.30542	ENSG00000166592	RRAD
ENSG00000166595	39.5467	25.6607	19.9099	14.8161	ENSG00000166595	FAM96B
ENSG00000166596	1.28503	1.72488	1.91945	2.41839	ENSG00000166596	CFAP52
ENSG00000166598	530.995	958.086	348.746	554.041	ENSG00000166598	HSP90B1

ENSG00000166603	0.121729	0.0781638	0.141307	0.136686	ENSG00000166603	MC4R
ENSG00000166619	80.5454	100.129	104.857	62.2188	ENSG00000166619	BLCAP
ENSG00000166634	1.76261	0.714773	0.38387	0.0535335	ENSG00000166634	SERPINB12
ENSG00000166664	0.792671	3.47553	0.920231	1.79301	ENSG00000166664	CHRFAM7A
ENSG00000166667	1.4527	3.27063	3.01274	6.62472	ENSG00000166667	SPDYE6
ENSG00000166669	8.50545	16.8246	19.2175	23.4703	ENSG00000166669	ATF7IP2
ENSG00000166670	84.458	35.6355	7.88398	34.7201	ENSG00000166670	MMP10
ENSG00000166676	2.79143	5.4744	5.06759	10.3798	ENSG00000166676	TVP23A
ENSG00000166681	55.1133	47.4962	35.9171	44.8797	ENSG00000166681	BEX3
ENSG00000166682	1.9667	3.72028	3.60336	3.29043	ENSG00000166682	TMPRSS5
ENSG00000166685	20.2079	29.3274	26.7252	40.1506	ENSG00000166685	COG1
ENSG00000166689	14.834	2.03013	2.58823	3.90423	ENSG00000166689	PLEKHA7
ENSG00000166693	0	0.256759	0.116003	0	ENSG00000166693	OR5M13P
ENSG00000166704	15.0015	18.7047	18.9602	30.9791	ENSG00000166704	ZNF606
ENSG00000166707	2.06697	1.99963	2.11543	3.00496	ENSG00000166707	ZCCHC18
ENSG00000166710	665.943	1349.24	525.618	605.989	ENSG00000166710	B2M
ENSG00000166716	6.16647	7.10756	8.13929	6.93344	ENSG00000166716	ZNF592
ENSG00000166734	36.1837	47.8045	34.8191	61.5913	ENSG00000166734	CASC4
ENSG00000166736	0	0.024435	0	0	ENSG00000166736	HTR3A
ENSG00000166741	0.483249	0.912162	10.949	67.509	ENSG00000166741	NNMT
ENSG00000166743	0.217533	0.297613	0.409427	0.270947	ENSG00000166743	ACSM1
ENSG00000166747	51.8328	46.8918	48.2281	59.7481	ENSG00000166747	AP1G1
ENSG00000166748	0.156115	0.337938	0.243688	0.173561	ENSG00000166748	AGBL1
ENSG00000166750	57.6631	57.8513	74.2136	47.3672	ENSG00000166750	SLFN5
ENSG00000166762	10.3537	20.7516	24.9836	21.1589	ENSG00000166762	CATSPER2
ENSG00000166763	0.108865	0.114222	0.458239	0.0408599	ENSG00000166763	STRCP1
ENSG00000166780	4.61474	11.9898	6.12195	17.6517	ENSG00000166780	C16orf45
ENSG00000166783	11.8044	20.9893	17.2359	24.2181	ENSG00000166783	MARF1
ENSG00000166787	0.21487	0.309539	0	0.261497	ENSG00000166787	SAA3P
ENSG00000166788	8.091	15.138	12.7523	12.0881	ENSG00000166788	SAAL1
ENSG00000166793	4.27454	3.87376	2.93677	4.20297	ENSG00000166793	YPEL4
ENSG00000166794	349.238	330.003	168.877	161.297	ENSG00000166794	PPIB
ENSG00000166796	0.214179	1.12287	0.498057	1.06065	ENSG00000166796	LDHC
ENSG00000166797	22.5327	28.7003	20.0685	23.483	ENSG00000166797	FAM96A
ENSG00000166800	0.65117	1.32996	1.35916	2.76952	ENSG00000166800	LDHAL6A
ENSG00000166801	12.323	26.5542	23.0044	20.4635	ENSG00000166801	FAM111A
ENSG00000166803	8.36213	13.3367	8.9711	16.8526	ENSG00000166803	PCLAF
ENSG00000166813	1.82036	4.9007	5.54823	6.66999	ENSG00000166813	KIF7
ENSG00000166816	1.85831	1.72617	1.02591	1.96727	ENSG00000166816	LDHD
ENSG00000166819	0.406904	1.21603	0.751282	1.27363	ENSG00000166819	PLIN1
ENSG00000166821	7.84304	7.87151	6.64759	5.82401	ENSG00000166821	PEX11A
ENSG00000166822	18.773	16.5334	12.2547	12.4853	ENSG00000166822	TMEM170A
ENSG00000166823	0.307895	0.366051	0.38917	0.578571	ENSG00000166823	MESP1
ENSG00000166825	6.54403	60.4789	22.3431	299.153	ENSG00000166825	ANPEP
ENSG00000166828	2.71592	1.32986	1.21859	1.78791	ENSG00000166828	SCNN1G
ENSG00000166831	0.0327171	0.357025	0.228206	0.5376	ENSG00000166831	RBPMS2
ENSG00000166833	9.2578	13.9701	28.3383	17.4044	ENSG00000166833	NAV2
ENSG00000166839	4.8349	12.8474	9.50849	14.0175	ENSG00000166839	ANKDD1A
ENSG00000166840	3.23432	6.05794	6.10438	9.5875	ENSG00000166840	GLYATL1
ENSG00000166845	6.67848	13.4282	10.3398	14.6861	ENSG00000166845	C18orf54
ENSG00000166847	31.48	29.6803	37.7921	31.3228	ENSG00000166847	DCTN5
ENSG00000166848	20.5915	15.8196	17.6202	16.6283	ENSG00000166848	TERF2IP
ENSG00000166851	6.9997	24.1281	4.15542	8.723	ENSG00000166851	PLK1
ENSG00000166855	19.5579	25.718	27.4155	26.1022	ENSG00000166855	CLPX

ENSG00000166856	0.236629	0.35827	0.47108	0.259321	ENSG00000166856	GPR182
ENSG00000166860	2.72057	3.30843	3.51416	2.38265	ENSG00000166860	ZBTB39
ENSG00000166862	0.568803	1.64786	1.68075	3.24396	ENSG00000166862	CACNG2
ENSG00000166863	0.214579	0.0684014	0.0995699	0.124804	ENSG00000166863	TAC3
ENSG00000166866	0.0449455	1.10288	0.852227	0.791634	ENSG00000166866	MYO1A
ENSG00000166869	4.86735	11.5144	10.3457	14.4341	ENSG00000166869	CHP2
ENSG00000166881	8.09923	18.7067	9.54634	8.47593	ENSG00000166881	NEMP1
ENSG00000166884	0	0	0.050451	0.0632291	ENSG00000166884	OR4D6
ENSG00000166886	18.7682	22.9639	25.3788	12.9109	ENSG00000166886	NAB2
ENSG00000166887	23.2328	35.8435	40.4847	40.1896	ENSG00000166887	VPS39
ENSG00000166888	63.4689	95.8317	86.1784	73.5995	ENSG00000166888	STAT6
ENSG00000166889	7.97129	10.1931	13.6589	9.14509	ENSG00000166889	PATL1
ENSG00000166896	1.22707	3.09275	1.09202	2.38732	ENSG00000166896	ATP23
ENSG00000166897	3.1197	4.03852	5.4569	3.09105	ENSG00000166897	ELFN2
ENSG00000166900	34.1202	13.9148	13.4658	19.7975	ENSG00000166900	STX3
ENSG00000166902	18.0934	19.42	14.4991	13.6847	ENSG00000166902	MRPL16
ENSG00000166908	40.9425	23.4677	23.3937	13.5524	ENSG00000166908	PIP4K2C
ENSG00000166912	10.1021	14.9335	10.6418	15.877	ENSG00000166912	MTMR10
ENSG00000166913	52.5342	60.3698	61.9644	57.584	ENSG00000166913	YWHAB
ENSG00000166920	22.973	1.32809	0.828345	2.2817	ENSG00000166920	C15orf48
ENSG00000166922	11.635	5.64207	11.864	42.2368	ENSG00000166922	SCG5
ENSG00000166923	0.111826	0.122119	1.52997	137.061	ENSG00000166923	GREM1
ENSG00000166924	0.526622	1.9452	2.34077	1.76742	ENSG00000166924	NYAP1
ENSG00000166925	25.2021	23.192	19.5762	16.7386	ENSG00000166925	TSC22D4
ENSG00000166926	0	0	0	0.136889	ENSG00000166926	MS4A6E
ENSG00000166927	2.29698	4.86029	4.40601	10.3672	ENSG00000166927	MS4A7
ENSG00000166928	0.0436292	0.157596	0.0190136	0.430425	ENSG00000166928	MS4A14
ENSG00000166930	0.215507	1.57429	0.453091	1.12501	ENSG00000166930	MS4A5
ENSG00000166938	6.86788	14.9838	10.8262	16.1016	ENSG00000166938	DIS3L
ENSG00000166946	30.9198	19.2386	15.3882	14.981	ENSG00000166946	CCNDBP1
ENSG00000166947	4.80371	11.1804	9.24961	17.3071	ENSG00000166947	EPB42
ENSG00000166948	0.025953	0.175107	0.384455	0.227935	ENSG00000166948	TGM6
ENSG00000166949	28.3759	57.848	25.8234	49.572	ENSG00000166949	SMAD3
ENSG00000166959	0.562375	0.586498	0.719461	0.671692	ENSG00000166959	MS4A8
ENSG00000166960	0.948711	0.903057	0.300704	0.502842	ENSG00000166960	CCDC178
ENSG00000166961	0.0531838	0.447411	0.782278	1.01595	ENSG00000166961	MS4A15
ENSG00000166963	0.508341	1.00541	1.61814	5.93574	ENSG00000166963	MAP1A
ENSG00000166965	6.34431	19.2127	12.2522	10.6546	ENSG00000166965	RCCD1
ENSG00000166971	20.7742	19.087	20.7034	10.58	ENSG00000166971	AKTIP
ENSG00000166974	8.35083	3.77656	2.76311	7.78725	ENSG00000166974	MAPRE2
ENSG00000166979	4.13832	11.5867	9.94309	9.51415	ENSG00000166979	EVA1C
ENSG00000166984	0	0	0.157584	1.37155	ENSG00000166984	TCP10L2
ENSG00000166986	66.6642	174.047	195.021	77.1164	ENSG00000166986	MARS
ENSG00000166987	7.00975	13.1819	16.1892	17.9013	ENSG00000166987	MBD6
ENSG00000166997	9.27202	13.2228	10.595	19.0632	ENSG00000166997	CNPY4
ENSG00000167004	416.18	633.547	321.371	385.393	ENSG00000167004	PDIA3
ENSG00000167005	39.9853	48.051	37.812	44.19	ENSG00000167005	NUDT21
ENSG00000167011	1.02374	1.46833	1.60752	2.63259	ENSG00000167011	NAT16
ENSG00000167014	0.233254	1.41737	1.16977	6.03163	ENSG00000167014	TERB2
ENSG00000167034	0.187403	0.990416	0.927805	0.540425	ENSG00000167034	NKX3-1
ENSG00000167037	0.532587	1.05811	0.922191	1.36337	ENSG00000167037	SGSM1
ENSG00000167046	0.38397	0.171502	0.101921	0.22459	ENSG00000167046	RP11-93B14.6
ENSG00000167065	9.29765	15.7968	14.1158	21.6133	ENSG00000167065	DUSP18
ENSG00000167074	3.17585	7.1336	5.32651	2.12951	ENSG00000167074	TEF

ENSG00000167077	3.48829	7.7531	5.29828	10.1107	ENSG00000167077	MEI1
ENSG00000167080	0.372574	1.34225	8.6921	0.482533	ENSG00000167080	B4GALNT2
ENSG00000167081	16.9952	27.404	13.6322	31.1264	ENSG00000167081	PBX3
ENSG00000167083	0	0.273796	0.248157	0.31072	ENSG00000167083	GNGT2
ENSG00000167085	84.8971	51.2131	41.2127	30.7843	ENSG00000167085	PHB
ENSG00000167088	27.6575	23.7116	21.1128	15.4926	ENSG00000167088	SNRPD1
ENSG00000167094	0.801431	1.55306	1.32135	1.89107	ENSG00000167094	TTC16
ENSG00000167098	0.146415	0	0.126783	0	ENSG00000167098	SUN5
ENSG00000167100	0.795258	1.83686	1.52997	5.01778	ENSG00000167100	SAMD14
ENSG00000167103	10.9873	21.9235	19.6428	17.4554	ENSG00000167103	PIP5KL1
ENSG00000167104	0.129427	0.132347	0	0.237944	ENSG00000167104	BPIFB6
ENSG00000167105	3.0583	5.61342	3.21154	3.29754	ENSG00000167105	TMEM92
ENSG00000167106	11.3469	13.3673	16.0058	11.8256	ENSG00000167106	FAM102A
ENSG00000167107	44.1142	64.4655	65.855	43.4719	ENSG00000167107	ACSF2
ENSG00000167110	17015.8	11868.5	10186.7	5372.34	ENSG00000167110	GOLGA2
ENSG00000167112	184.897	137.61	111.028	63.8365	ENSG00000167112	TRUB2
ENSG00000167113	27.1925	31.3034	34.0079	29.3413	ENSG00000167113	COQ4
ENSG00000167114	45.0489	24.2956	20.6341	13.8069	ENSG00000167114	SLC27A4
ENSG00000167118	13.9557	10.723	12.9514	8.88526	ENSG00000167118	URM1
ENSG00000167123	86.2094	94.04	85.2049	160.545	ENSG00000167123	CERCAM
ENSG00000167130	17.0913	16.3767	9.20964	4.93854	ENSG00000167130	DOLPP1
ENSG00000167131	0.961279	0.851644	0.561269	0.518862	ENSG00000167131	CCDC103
ENSG00000167136	5.40518	2.88609	3.78533	3.27593	ENSG00000167136	ENDOG
ENSG00000167139	0.19327	0.185911	0.112006	0.140228	ENSG00000167139	TBC1D21
ENSG00000167157	0.773802	0.325726	0.37897	1.58649	ENSG00000167157	PRRX2
ENSG00000167165	3.77697	5.64311	13.0936	2.25322	ENSG00000167165	UGT1A6
ENSG00000167173	12.395	14.5064	7.01517	14.0935	ENSG00000167173	C15orf39
ENSG00000167178	2.85528	5.4893	4.12924	6.14398	ENSG00000167178	ISLR2
ENSG00000167182	1.51899	1.54133	1.47408	1.97064	ENSG00000167182	SP2
ENSG00000167183	7.24646	0.44108	1.09923	0.626643	ENSG00000167183	PRR15L
ENSG00000167186	6.77226	9.59523	8.54717	8.81524	ENSG00000167186	COQ7
ENSG00000167191	0.443635	0.629313	0.536696	1.03067	ENSG00000167191	GPRC5B
ENSG00000167193	37.8813	28.5423	32.3551	29.9088	ENSG00000167193	CRK
ENSG00000167194	0.21166	0.194232	0	0.215252	ENSG00000167194	C16orf92
ENSG00000167195	0.503287	0	0	0.0998795	ENSG00000167195	GOLGA6C
ENSG00000167196	27.6646	39.928	39.46	27.8542	ENSG00000167196	FBXO22
ENSG00000167202	16.6015	23.1803	30.7761	43.9998	ENSG00000167202	TBC1D2B
ENSG00000167207	2.95266	3.86785	12.5243	2.32852	ENSG00000167207	NOD2
ENSG00000167208	0.743959	1.67465	1.39206	1.87206	ENSG00000167208	SNX20
ENSG00000167210	0.10621	0.109833	0.204394	0.456829	ENSG00000167210	LOXHD1
ENSG00000167216	4.82934	8.97892	10.649	15.4015	ENSG00000167216	KATNAL2
ENSG00000167220	10.9026	16.7642	16.6103	16.5099	ENSG00000167220	HDHD2
ENSG00000167230	0.102684	0.188248	0.839435	0.798703	ENSG00000167230	C17orf78
ENSG00000167232	25.521	26.0048	28.3029	34.6366	ENSG00000167232	ZNF91
ENSG00000167236	0	0.607746	0.365896	1.12189	ENSG00000167236	CCL23
ENSG00000167244	0.371428	0.882057	0.865265	1.79102	ENSG00000167244	IGF2
ENSG00000167257	5.08404	6.19153	8.89448	6.87961	ENSG00000167257	RNF214
ENSG00000167258	26.553	32.696	42.3292	33.0846	ENSG00000167258	CDK12
ENSG00000167261	0.869437	1.16831	0.510086	0.993288	ENSG00000167261	DPEP2
ENSG00000167264	19.9604	17.7492	18.2533	16.8333	ENSG00000167264	DUS2
ENSG00000167272	31.8403	35.1339	28.0398	30.6913	ENSG00000167272	POP5
ENSG00000167280	11.2297	19.4772	20.7667	14.7393	ENSG00000167280	ENGASE
ENSG00000167281	1.07038	2.06476	2.5052	3.40534	ENSG00000167281	RBFOX3
ENSG00000167283	47.2707	34.3399	25.8631	20.6222	ENSG00000167283	ATP5L

ENSG00000167286	0.0739528	0	0	0	ENSG00000167286	CD3D
ENSG00000167291	10.3429	14.6331	24.884	15.5173	ENSG00000167291	TBC1D16
ENSG00000167302	20.6642	17.6572	27.1085	16.0269	ENSG00000167302	TEPSIN
ENSG00000167306	51.8354	9.07423	4.77767	6.26036	ENSG00000167306	MYO5B
ENSG00000167311	0.154334	0.184753	0.892893	0.479427	ENSG00000167311	ART5
ENSG00000167315	2.35685	4.24186	9.18629	6.53651	ENSG00000167315	ACAA2
ENSG00000167323	38.5707	53.3682	54.0309	44.2992	ENSG00000167323	STIM1
ENSG00000167325	30.8908	57.5936	22.8376	34.2114	ENSG00000167325	RRM1
ENSG00000167332	0.446066	1.52433	1.1716	1.97378	ENSG00000167332	OR51E2
ENSG00000167333	6.47308	7.59342	7.35343	4.88418	ENSG00000167333	TRIM68
ENSG00000167346	0	0.225756	0.174084	0.213646	ENSG00000167346	MMP26
ENSG00000167359	0.0660652	0.762453	0.229651	0.503119	ENSG00000167359	OR51I1
ENSG00000167360	0	0	0	0	ENSG00000167360	OR51Q1
ENSG00000167363	5.05677	8.67856	10.2384	14.9384	ENSG00000167363	FN3K
ENSG00000167371	0.753834	1.02381	1.19724	3.73665	ENSG00000167371	PRRT2
ENSG00000167377	4.84804	4.25213	9.30478	7.59789	ENSG00000167377	ZNF23
ENSG00000167378	17.5267	12.1523	16.7615	16.7892	ENSG00000167378	IRGQ
ENSG00000167380	8.72787	9.15613	11.7206	11.9316	ENSG00000167380	ZNF226
ENSG00000167383	7.65801	5.69089	10.3618	5.35744	ENSG00000167383	ZNF229
ENSG00000167384	5.58016	7.20227	7.86575	10.5726	ENSG00000167384	ZNF180
ENSG00000167390	0	0	0	0	ENSG00000167390	POM121L3P
ENSG00000167393	12.0116	19.1167	12.176	12.4176	ENSG00000167393	PPP2R3B
ENSG00000167394	8.78028	5.6138	6.84305	5.45103	ENSG00000167394	ZNF668
ENSG00000167395	9.15809	7.67773	8.88584	6.45811	ENSG00000167395	ZNF646
ENSG00000167397	21.7691	29.5595	17.1412	25.7691	ENSG00000167397	VKORC1
ENSG00000167414	0	0.621358	0.553552	0	ENSG00000167414	GNG8
ENSG00000167419	3.98369	10.8961	9.30946	20.2481	ENSG00000167419	LPO
ENSG00000167434	1.16159	3.3954	1.30717	2.28897	ENSG00000167434	CA4
ENSG00000167447	11.0658	9.32381	7.66486	6.20158	ENSG00000167447	SMG8
ENSG00000167460	381	361.631	161.478	394.768	ENSG00000167460	TPM4
ENSG00000167461	20.1634	26.8662	21.2705	16.2139	ENSG00000167461	RAB8A
ENSG00000167468	56.035	49.1321	52.8151	36.3289	ENSG00000167468	GPX4
ENSG00000167470	24.1544	40.538	42.4468	24.9035	ENSG00000167470	MIDN
ENSG00000167476	1.15009	0.910038	1.32766	1.23135	ENSG00000167476	JSRP1
ENSG00000167483	4.32475	7.58643	7.06438	11.1432	ENSG00000167483	FAM129C
ENSG00000167487	2.27316	3.45931	3.18758	3.54801	ENSG00000167487	KLHL26
ENSG00000167491	43.1586	44.5591	58.4098	63.1036	ENSG00000167491	GATAD2A
ENSG00000167494	0	0	0	0	ENSG00000167494	NOS2P2
ENSG00000167508	140.626	108.559	27.5109	104.32	ENSG00000167508	MVD
ENSG00000167513	2.92485	7.32028	3.0975	5.23888	ENSG00000167513	CDT1
ENSG00000167515	21.8258	16.1381	12.3924	8.65739	ENSG00000167515	TRAPPC2L
ENSG00000167522	34.951	87.624	100.306	106.718	ENSG00000167522	ANKRD11
ENSG00000167523	4.52312	9.17746	12.0937	9.51129	ENSG00000167523	SPATA33
ENSG00000167524	11.9883	19.8826	24.4623	21.6202	ENSG00000167524	SGK494
ENSG00000167525	2.03612	4.63612	4.17888	4.84196	ENSG00000167525	PROCA1
ENSG00000167526	855.549	631.665	597.737	367.815	ENSG00000167526	RPL13
ENSG00000167528	4.66099	8.15542	7.74791	3.94429	ENSG00000167528	ZNF641
ENSG00000167531	0.0478836	0.0922062	0.0416703	0.104622	ENSG00000167531	LALBA
ENSG00000167535	18.7797	18.4321	22.9327	17.6046	ENSG00000167535	CACNB3
ENSG00000167536	2.50454	6.44711	2.5812	3.29856	ENSG00000167536	DHRS13
ENSG00000167543	44.0713	48.1347	33.9578	31.1357	ENSG00000167543	TP53I13
ENSG00000167548	28.1075	39.7409	52.5178	62.51	ENSG00000167548	KMT2D
ENSG00000167549	41.1818	33.433	19.316	23.2919	ENSG00000167549	CORO6
ENSG00000167550	1.39342	1.90182	1.12671	1.16193	ENSG00000167550	RHEBL1

ENSG00000167552	134.337	36.1343	32.6783	83.233	ENSG00000167552	TUBA1A
ENSG00000167553	237.37	224.347	108.766	90.6031	ENSG00000167553	TUBA1C
ENSG00000167554	7.62751	11.1004	12.1074	17.9265	ENSG00000167554	ZNF610
ENSG00000167555	30.2715	24.7346	48.3703	33.0838	ENSG00000167555	ZNF528
ENSG00000167562	10.688	12.9684	11.6847	8.86379	ENSG00000167562	ZNF701
ENSG00000167565	13.5711	18.3857	14.6897	8.07433	ENSG00000167565	SERTAD3
ENSG00000167566	8.21632	14.8155	15.2697	15.2774	ENSG00000167566	NCKAP5L
ENSG00000167578	11.3723	15.819	12.7965	17.4811	ENSG00000167578	RAB4B
ENSG00000167580	0.194214	0.311896	0.346853	0.709692	ENSG00000167580	AQP2
ENSG00000167588	1.06077	1.67931	1.09367	0.888028	ENSG00000167588	GPD1
ENSG00000167595	12.9519	21.6168	24.5474	25.6604	ENSG00000167595	PROSER3
ENSG00000167600	5.3956	23.2214	6.03377	3.76795	ENSG00000167600	CYP2S1
ENSG00000167601	16.6141	80.0785	32.368	44.0568	ENSG00000167601	AXL
ENSG00000167604	10.7856	13.8373	11.4615	13.0515	ENSG00000167604	NFKBID
ENSG00000167608	3.42339	4.64329	1.72368	1.68632	ENSG00000167608	TMC4
ENSG00000167612	0.0687535	0.0892412	0.136178	0.138313	ENSG00000167612	ANKRD33
ENSG00000167613	0.233848	0.244949	0.286938	0.32704	ENSG00000167613	LAIR1
ENSG00000167614	1.09565	1.1237	1.29485	0.752864	ENSG00000167614	TTYH1
ENSG00000167615	11.7622	24.2333	22.5489	29.8783	ENSG00000167615	LENG8
ENSG00000167617	6.90641	6.48352	5.20337	7.25698	ENSG00000167617	CDC42EP5
ENSG00000167618	0	0	0	0.0366664	ENSG00000167618	LAIR2
ENSG00000167619	8.64632	15.6982	11.5962	19.8701	ENSG00000167619	TMEM145
ENSG00000167625	6.80344	7.08434	6.37746	9.5965	ENSG00000167625	ZNF526
ENSG00000167632	7.42339	11.3297	8.22316	13.9465	ENSG00000167632	TRAPPC9
ENSG00000167633	0	0	0	0	ENSG00000167633	KIR3DL1
ENSG00000167634	0.00591224	0.0414758	0	0	ENSG00000167634	NLRP7
ENSG00000167635	30.2657	34.0195	53.8302	32.3656	ENSG00000167635	ZNF146
ENSG00000167637	19.7484	29.1135	29.7003	39.8123	ENSG00000167637	ZNF283
ENSG00000167641	1.02965	2.04679	2.81584	2.13665	ENSG00000167641	PPP1R14A
ENSG00000167642	443.459	503.98	263.089	132.698	ENSG00000167642	SPINT2
ENSG00000167644	273.554	175.852	84.8476	53.4889	ENSG00000167644	C19orf33
ENSG00000167645	39.1688	56.2047	32.1782	34.3379	ENSG00000167645	YIF1B
ENSG00000167646	2.1984	3.64766	4.10023	1.33554	ENSG00000167646	DNAAF3
ENSG00000167653	12.0845	0.397334	0.329241	0.71898	ENSG00000167653	PSCA
ENSG00000167654	1.44048	2.86193	2.6949	4.26052	ENSG00000167654	ATCAY
ENSG00000167656	57.7003	20.9695	2.04635	4.41967	ENSG00000167656	LY6D
ENSG00000167657	48.0395	27.9396	36.1684	28.8471	ENSG00000167657	DAPK3
ENSG00000167658	605.609	495.89	603.854	434.912	ENSG00000167658	EEF2
ENSG00000167664	0.656244	1.32057	1.83569	2.04243	ENSG00000167664	TMIGD2
ENSG00000167670	4.67147	10.4172	5.79607	10.8147	ENSG00000167670	CHAF1A
ENSG00000167671	40.6122	33.1013	34.3681	26.3446	ENSG00000167671	UBXN6
ENSG00000167674	29.7559	28.6114	27.8245	30.2685	ENSG00000167674	HDGFL2
ENSG00000167676	1.19203	2.59289	3.11266	0.95285	ENSG00000167676	PLIN4
ENSG00000167680	3.48189	21.1573	24.2905	62.3717	ENSG00000167680	SEMA6B
ENSG00000167685	6.87516	9.47301	12.2794	14.3901	ENSG00000167685	ZNF444
ENSG00000167693	56.3802	55.8384	58.5404	71.5312	ENSG00000167693	NXN
ENSG00000167695	13.5446	22.2435	17.1074	8.03364	ENSG00000167695	FAM57A
ENSG00000167699	40.081	37.8103	32.7745	30.1761	ENSG00000167699	GLOD4
ENSG00000167700	22.2204	23.9503	18.4668	11.3512	ENSG00000167700	MFSD3
ENSG00000167701	2.17168	1.35235	2.81846	1.77412	ENSG00000167701	GPT
ENSG00000167702	44.1582	39.1633	51.3365	18.3025	ENSG00000167702	KIFC2
ENSG00000167703	11.6371	18.9942	33.1136	17.4745	ENSG00000167703	SLC43A2
ENSG00000167705	3.74433	3.54913	2.94282	2.20458	ENSG00000167705	RILP
ENSG00000167711	0.380063	0.741217	0.267846	0.561701	ENSG00000167711	SERPINF2

ENSG00000167716	15.1226	10.5442	12.11	14.1002	ENSG00000167716	WDR81
ENSG00000167720	5.96384	7.04373	5.88985	6.74068	ENSG00000167720	SRR
ENSG00000167721	19.8476	19.3131	21.6156	15.8191	ENSG00000167721	TSR1
ENSG00000167723	12.1554	13.3356	12.8239	25.5744	ENSG00000167723	TRPV3
ENSG00000167733	8.49387	15.1064	12.3566	15.9313	ENSG00000167733	HSD11B1L
ENSG00000167740	6.75541	8.51663	8.21261	6.5318	ENSG00000167740	CYB5D2
ENSG00000167741	12.9877	3.76508	5.60583	4.83354	ENSG00000167741	GGT6
ENSG00000167747	44.0142	67.346	72.3103	45.5891	ENSG00000167747	C19orf48
ENSG00000167748	0.146858	0.994159	0.250122	0.572325	ENSG00000167748	KLK1
ENSG00000167749	1.97529	2.13129	12.3171	3.79553	ENSG00000167749	KLK4
ENSG00000167751	4.27398	5.50655	6.1921	10.3797	ENSG00000167751	KLK2
ENSG00000167754	1334.14	261.544	94.8909	124.437	ENSG00000167754	KLK5
ENSG00000167755	88.8527	5.42375	4.34876	19.9613	ENSG00000167755	KLK6
ENSG00000167757	248.314	40.7697	23.6025	34.4442	ENSG00000167757	KLK11
ENSG00000167759	23.7615	2.10515	2.63189	3.99001	ENSG00000167759	KLK13
ENSG00000167765	0.756261	2.21555	2.38487	2.97853	ENSG00000167765	AC018755.1
ENSG00000167766	84.0472	72.5775	49.6305	76.459	ENSG00000167766	ZNF83
ENSG00000167767	24.4464	3.54741	4.83421	7.14677	ENSG00000167767	KRT80
ENSG00000167768	0.0452673	0.174558	1.73975	0.274293	ENSG00000167768	KRT1
ENSG00000167769	0.868034	1.36998	1.1533	1.52078	ENSG00000167769	ACER1
ENSG00000167770	32.0501	41.5779	34.0498	37.9339	ENSG00000167770	OTUB1
ENSG00000167771	1.13196	4.28507	3.03477	3.86454	ENSG00000167771	RCOR2
ENSG00000167772	111.718	29.1481	11.4627	44.7235	ENSG00000167772	ANGPTL4
ENSG00000167774	0.951576	0.634949	0	0	ENSG00000167774	NDUFA7
ENSG00000167775	10.734	22.1227	11.9173	14.0169	ENSG00000167775	CD320
ENSG00000167778	14.7655	14.8658	14.5144	15.6555	ENSG00000167778	SPRYD3
ENSG00000167779	18.0572	151.918	13.9572	13.8751	ENSG00000167779	IGFBP6
ENSG00000167780	0.0316769	0.424433	0.110373	0.173662	ENSG00000167780	SOAT2
ENSG00000167785	4.54199	8.96003	9.94673	5.2134	ENSG00000167785	ZNF558
ENSG00000167791	0	0	0.0598927	0	ENSG00000167791	CABP2
ENSG00000167792	88.6533	103.653	106.506	62.7614	ENSG00000167792	NDUFV1
ENSG00000167797	10.3934	15.4288	9.08406	6.41435	ENSG00000167797	CDK2AP2
ENSG00000167798	0.26188	0.198351	0.41054	0.644169	ENSG00000167798	C3P1
ENSG00000167799	3.71376	2.79231	2.1466	1.73083	ENSG00000167799	NUDT8
ENSG00000167800	0.112081	0.21594	0.195198	0.163655	ENSG00000167800	TBX10
ENSG00000167807	0.477853	1.07014	1.39754	1.64468	ENSG00000167807	CTD-2369P2.10
ENSG00000167815	70.0016	54.2747	33.8854	35.1552	ENSG00000167815	PRDX2
ENSG00000167822	0	0	0	0	ENSG00000167822	OR8J3
ENSG00000167825	0.198196	0.444764	0.574127	0.574993	ENSG00000167825	OR5I1
ENSG00000167840	4.57864	2.80809	4.22173	3.17004	ENSG00000167840	ZNF232
ENSG00000167842	15.46	20.0831	16.7519	16.1548	ENSG00000167842	MIS12
ENSG00000167850	0.0764278	0	0	0.0418373	ENSG00000167850	CD300C
ENSG00000167851	0.480604	0.379175	0.269906	0.528444	ENSG00000167851	CD300A
ENSG00000167858	0.0787847	0.367138	0.421562	1.13043	ENSG00000167858	TEKT1
ENSG00000167861	2.56056	2.55384	1.80966	2.31099	ENSG00000167861	HID1
ENSG00000167862	16.5835	11.2939	10.1625	7.93659	ENSG00000167862	MRPL58
ENSG00000167863	9896.07	6919.24	5661.89	3208.7	ENSG00000167863	ATP5H
ENSG00000167874	1.23515	1.67737	4.10999	2.93454	ENSG00000167874	TMEM88
ENSG00000167880	55.8632	31.5165	35.3488	20.641	ENSG00000167880	EVPL
ENSG00000167881	23.2654	28.1189	31.6358	34.8614	ENSG00000167881	SRP68
ENSG00000167889	0.29428	1.60298	0.931502	2.71192	ENSG00000167889	MGAT5B
ENSG00000167895	3.23464	6.7742	5.22953	15.6184	ENSG00000167895	TMC8
ENSG00000167900	5.16665	13.0025	2.84062	5.73883	ENSG00000167900	TK1
ENSG00000167904	25.8278	43.2002	35.6852	40.3124	ENSG00000167904	TMEM68

ENSG00000167910	0.0566634	0.183643	0.0990878	0.209321	ENSG00000167910	CYP7A1
ENSG00000167914	17.4678	5.00547	4.49994	10.1352	ENSG00000167914	GSDMA
ENSG00000167916	6.33364	0.261342	0.0262488	0.793262	ENSG00000167916	KRT24
ENSG00000167920	5.6024	8.9806	8.80389	5.22907	ENSG00000167920	TMEM99
ENSG00000167925	8.54863	9.42536	8.35803	7.554	ENSG00000167925	GHDC
ENSG00000167930	30.0051	39.5652	35.5289	30.3231	ENSG00000167930	FAM234A
ENSG00000167941	0.223298	0.56018	0.753516	0.8785	ENSG00000167941	SOST
ENSG00000167945	0.444923	0.339903	0.568545	0.377915	ENSG00000167945	PRR25
ENSG00000167962	23.5806	45.0459	54.2375	21.3519	ENSG00000167962	ZNF598
ENSG00000167964	4.76085	9.56994	16.4516	6.30765	ENSG00000167964	RAB26
ENSG00000167965	12.8766	10.2718	15.7	14.0052	ENSG00000167965	MLST8
ENSG00000167967	19.0684	18.9634	20.2809	12.4565	ENSG00000167967	E4F1
ENSG00000167968	2.87912	1.1283	1.90035	0.806816	ENSG00000167968	DNASE1L2
ENSG00000167969	11.061	22.0287	20.691	9.0711	ENSG00000167969	ECI1
ENSG00000167970	2.88847	0.631349	1.15543	0	ENSG00000167970	AC009065.1
ENSG00000167971	1.80933	0.189157	0.694622	0.840538	ENSG00000167971	CASKIN1
ENSG00000167972	0.335114	0.303849	0.409801	0.551955	ENSG00000167972	ABCA3
ENSG00000167977	24.8747	14.4999	20.9135	13.641	ENSG00000167977	KCTD5
ENSG00000167978	73.5974	99.8376	138.029	205.909	ENSG00000167978	SRRM2
ENSG00000167981	2.05474	1.91383	3.55305	1.56554	ENSG00000167981	ZNF597
ENSG00000167984	0.486302	0.81477	0.895758	1.26404	ENSG00000167984	NLRC3
ENSG00000167985	14.1201	11.2515	12.8162	11.9582	ENSG00000167985	SDHAF2
ENSG00000167986	77.4591	96.7178	85.7748	96.9809	ENSG00000167986	DDB1
ENSG00000167987	12.2142	9.60802	12.305	10.842	ENSG00000167987	VPS37C
ENSG00000167992	2.95491	7.43497	5.75627	15.2062	ENSG00000167992	VWCE
ENSG00000167994	2.13451	0.379232	0.8905	0.806508	ENSG00000167994	RAB3IL1
ENSG00000167995	2.20309	3.43896	8.06624	6.94152	ENSG00000167995	BEST1
ENSG00000167996	260.027	120.13	282.044	358.116	ENSG00000167996	FTH1
ENSG00000168000	19.621	18.7878	14.009	10.164	ENSG00000168000	BSCL2
ENSG00000168002	29.5112	23.1194	21.7116	15.525	ENSG00000168002	POLR2G
ENSG00000168003	221.472	745.427	756.934	145.959	ENSG00000168003	SLC3A2
ENSG00000168004	0.2126	0.249623	0.240901	0.393549	ENSG00000168004	HRASLS5
ENSG00000168005	8.82015	10.8272	7.91342	13.0495	ENSG00000168005	C11orf84
ENSG00000168010	20.2436	55.6101	37.3138	52.08	ENSG00000168010	ATG16L2
ENSG00000168014	23.3479	44.3379	44.0279	59.9987	ENSG00000168014	C2CD3
ENSG00000168016	4.26727	9.56669	19.8091	12.759	ENSG00000168016	TRANK1
ENSG00000168026	3.0758	10.2283	6.32256	9.84164	ENSG00000168026	TTC21A
ENSG00000168028	491.587	511.147	356.131	222.341	ENSG00000168028	RPSA
ENSG00000168032	12.4163	6.55043	7.25658	6.50722	ENSG00000168032	ENTPD3
ENSG00000168036	285.01	229.552	160.076	165.854	ENSG00000168036	CTNNB1
ENSG00000168038	6.50829	12.5722	13.4162	18.4654	ENSG00000168038	ULK4
ENSG00000168040	11.8049	12.6907	8.58474	8.19766	ENSG00000168040	FADD
ENSG00000168056	12.1962	16.9003	12.6146	23.484	ENSG00000168056	LTBP3
ENSG00000168060	1.30254	4.47904	3.57361	1.88272	ENSG00000168060	NAALADL1
ENSG00000168061	3.75089	5.73755	4.43206	3.06611	ENSG00000168061	SAC3D1
ENSG00000168062	0.257837	0.694479	0.426611	0.899972	ENSG00000168062	BATF2
ENSG00000168065	1.14457	1.82684	1.6034	1.68	ENSG00000168065	SLC22A11
ENSG00000168066	65.4849	97.5547	123.287	100.18	ENSG00000168066	SF1
ENSG00000168067	8.6645	10.7033	8.81902	7.52957	ENSG00000168067	MAP4K2
ENSG00000168070	0.402007	0.423604	1.02231	0.166723	ENSG00000168070	MAJIN
ENSG00000168071	6.46824	15.1457	9.62783	17.1462	ENSG00000168071	CCDC88B
ENSG00000168077	8.84358	26.2185	5.42856	7.42707	ENSG00000168077	SCARA3
ENSG00000168078	3.3127	12.271	1.76257	5.66407	ENSG00000168078	PBK
ENSG00000168079	0.47091	1.08797	0.957087	1.60941	ENSG00000168079	SCARA5

ENSG00000168081	0.243022	0.288029	0.533509	0.240375	ENSG00000168081	PNOC
ENSG00000168090	23.5492	27.8882	22.325	29.7068	ENSG00000168090	COPS6
ENSG00000168092	49.4298	53.4325	52.1269	53.1354	ENSG00000168092	PAFAH1B2
ENSG00000168096	17.299	29.967	30.8948	28.6655	ENSG00000168096	ANKS3
ENSG00000168101	9.46115	6.99033	5.46586	5.7965	ENSG00000168101	NUDT16L1
ENSG00000168116	4.8155	7.60042	6.3312	9.56334	ENSG00000168116	KIAA1586
ENSG00000168118	18.0873	14.1638	13.8418	11.8744	ENSG00000168118	RAB4A
ENSG00000168122	0	0.0747072	0	0	ENSG00000168122	ZNF355P
ENSG00000168124	0	0.382684	0.345792	0.288583	ENSG00000168124	OR1F1
ENSG00000168126	0.266297	0.0640255	0.115706	0.0724196	ENSG00000168126	OR2W6P
ENSG00000168129	0.259385	0.124856	0.337022	0.139219	ENSG00000168129	AC098817.5
ENSG00000168131	0.19718	0.237293	0.0428948	0.324946	ENSG00000168131	OR2B2
ENSG00000168135	0.190541	0.053449	0.166022	0.149373	ENSG00000168135	KCNJ4
ENSG00000168137	59.4618	125.715	138.103	143.72	ENSG00000168137	SETD5
ENSG00000168140	6.8948	7.7198	8.78899	15.7025	ENSG00000168140	VASN
ENSG00000168143	45.0036	46.8964	50.074	22.2727	ENSG00000168143	FAM83B
ENSG00000168148	0.321653	0	0.139139	0.171685	ENSG00000168148	HIST3H3
ENSG00000168152	3.7179	8.91374	6.94084	5.2438	ENSG00000168152	THAP9
ENSG00000168158	0	0.284837	0.102968	0.0645115	ENSG00000168158	OR2C1
ENSG00000168159	64.4155	52.4018	69.1138	48.1091	ENSG00000168159	RNF187
ENSG00000168172	16.8348	17.6091	16.5514	33.8586	ENSG00000168172	HOOK3
ENSG00000168175	50.7622	39.6424	46.251	44.7744	ENSG00000168175	MAPK1IP1L
ENSG00000168209	221.288	390.41	478.126	94.7872	ENSG00000168209	DDIT4
ENSG00000168214	19.7461	27.8765	13.9407	32.431	ENSG00000168214	RBPJ
ENSG00000168216	24.8752	20.4026	13.3132	10.771	ENSG00000168216	LMBRD1
ENSG00000168228	6.73657	10.2483	8.83613	10.3992	ENSG00000168228	ZCCHC4
ENSG00000168229	0.0186387	0.166446	0.108661	0.305824	ENSG00000168229	PTGDR
ENSG00000168234	10.37	15.937	15.9251	17.6035	ENSG00000168234	TTC39C
ENSG00000168237	4.37044	9.25196	8.99905	6.94097	ENSG00000168237	GLYCTK
ENSG00000168242	12.5199	37.2575	8.70588	10.7087	ENSG00000168242	HIST1H2BI
ENSG00000168243	0.743224	1.72255	1.30782	2.65182	ENSG00000168243	GNG4
ENSG00000168246	6.75906	5.29756	8.19562	6.68301	ENSG00000168246	UBTD2
ENSG00000168255	38.945	92.9223	84.2682	105.871	ENSG00000168255	POLR2J3
ENSG00000168256	9.14455	7.04017	10.7854	9.32226	ENSG00000168256	NKIRAS2
ENSG00000168259	37.3902	49.2066	54.5324	75.0755	ENSG00000168259	DNAJC7
ENSG00000168260	0.529017	0.561255	0.71921	0.633084	ENSG00000168260	C14orf183
ENSG00000168263	0.102377	0.641421	0.735997	1.46122	ENSG00000168263	KCNV2
ENSG00000168264	145.497	82.5554	111.27	54.9826	ENSG00000168264	IRF2BP2
ENSG00000168267	0.1533	0.109475	0.10012	0.247408	ENSG00000168267	PTF1A
ENSG00000168268	21.9149	28.9059	29.5565	33.7738	ENSG00000168268	NT5DC2
ENSG00000168269	0.0565842	0.136195	0.122426	0.430832	ENSG00000168269	FOXI1
ENSG00000168273	5.80985	6.83004	8.83758	3.41968	ENSG00000168273	SMIM4
ENSG00000168274	39.3637	78.934	39.2932	27.0362	ENSG00000168274	HIST1H2AE
ENSG00000168275	16.3704	11.9163	9.58768	6.7536	ENSG00000168275	COA6
ENSG00000168280	0.0279804	0.0980381	0.0830385	0.184153	ENSG00000168280	KIF5C
ENSG00000168282	30.4772	29.2914	24.1319	13.2101	ENSG00000168282	MGAT2
ENSG00000168283	22.129	14.709	16.5404	10.4536	ENSG00000168283	BMI1
ENSG00000168286	7.31356	6.49956	7.74894	5.58936	ENSG00000168286	THAP11
ENSG00000168288	58.9231	43.7555	43.3558	23.0946	ENSG00000168288	MMADHC
ENSG00000168291	24.4482	25.1971	21.0977	26.3739	ENSG00000168291	PDHB
ENSG00000168297	6.2623	19.2751	21.4458	16.9457	ENSG00000168297	PXK
ENSG00000168298	99.7414	225.364	98.0362	85.535	ENSG00000168298	HIST1H1E
ENSG00000168300	31.7475	33.6521	35.0929	39.5596	ENSG00000168300	PCMTD1
ENSG00000168301	4.66009	8.72843	7.24779	9.09037	ENSG00000168301	KCTD6

ENSG00000168303	3.00549	5.10584	5.15421	7.56318	ENSG00000168303	MPLKIP
ENSG00000168306	0.516676	2.05821	1.26538	2.91549	ENSG00000168306	ACOX2
ENSG00000168309	0.575007	0.944018	0.904794	1.29159	ENSG00000168309	FAM107A
ENSG00000168310	10.8295	17.1152	10.9113	17.8093	ENSG00000168310	IRF2
ENSG00000168314	3.59898	2.17382	3.90895	2.94134	ENSG00000168314	MOBP
ENSG00000168329	0.514214	0.580653	0.233035	0.819968	ENSG00000168329	CX3CR1
ENSG00000168333	0.0932693	0.394761	0.227158	0.192897	ENSG00000168333	C8orf22
ENSG00000168334	0.0705457	0.0680552	0.107687	0.0291546	ENSG00000168334	XIRP1
ENSG00000168348	0.090874	0.310404	0.158698	0.540036	ENSG00000168348	INSM2
ENSG00000168350	3.15244	1.27634	0.615062	1.88144	ENSG00000168350	DEGS2
ENSG00000168356	0.220383	0.482492	0.332622	0.664764	ENSG00000168356	SCN11A
ENSG00000168374	83.885	64.6485	52.7944	75.4162	ENSG00000168374	ARF4
ENSG00000168379	0	1.3374	0.0273378	0.10145	ENSG00000168379	HLA-DPB2
ENSG00000168384	0.015404	0.0454515	0.0767526	0.116139	ENSG00000168384	HLA-DPA1
ENSG00000168385	124.027	163.115	171.173	195.638	ENSG00000168385	SEPT2
ENSG00000168386	14.5406	10.5129	29.0346	21.3126	ENSG00000168386	FILIP1L
ENSG00000168389	74.0931	82.2816	62.7024	35.7277	ENSG00000168389	MFSD2A
ENSG00000168393	17.6748	37.895	16.1826	26.9239	ENSG00000168393	DTYMK
ENSG00000168394	8.41631	11.0199	9.61481	3.74213	ENSG00000168394	TAP1
ENSG00000168395	8.42928	15.9524	17.1591	19.0613	ENSG00000168395	ING5
ENSG00000168397	36.6102	49.1281	54.2916	49.8303	ENSG00000168397	ATG4B
ENSG00000168398	2.54746	13.201	7.1202	4.99804	ENSG00000168398	BDKRB2
ENSG00000168404	7.12077	12.5219	5.15828	12.4157	ENSG00000168404	MLKL
ENSG00000168405	0.301954	1.17597	0.344811	2.77822	ENSG00000168405	CMAHP
ENSG00000168411	16.7649	26.3749	21.1265	33.5739	ENSG00000168411	RFWD3
ENSG00000168412	0.0459323	0.0442287	0.159908	0.0502009	ENSG00000168412	MTNR1A
ENSG00000168418	0.233396	0.643223	0.417336	0.586479	ENSG00000168418	KCNG4
ENSG00000168421	4.60472	8.64564	8.97942	14.3234	ENSG00000168421	RHOH
ENSG00000168427	0.291489	0.448769	0.527014	0.741424	ENSG00000168427	KLHL30
ENSG00000168434	14.3145	22.0667	22.3224	31.3778	ENSG00000168434	COG7
ENSG00000168438	11.8764	18.5161	19.0611	19.0359	ENSG00000168438	CDC40
ENSG00000168439	88.8972	68.6572	58.9388	60.1462	ENSG00000168439	STIP1
ENSG00000168447	10.6875	4.58772	5.23264	5.59455	ENSG00000168447	SCNN1B
ENSG00000168452	1.73819	2.04805	0.757621	0.267292	ENSG00000168452	PPT2
ENSG00000168453	97.6205	64.6156	105.728	50.3519	ENSG00000168453	HR
ENSG00000168454	0.30836	0.972751	0.397653	1.39251	ENSG00000168454	TXNDC2
ENSG00000168461	33.3299	31.9901	28.5786	55.3556	ENSG00000168461	RAB31
ENSG00000168468	2.91793	7.62575	6.64023	18.8413	ENSG00000168468	ATF6B
ENSG00000168476	34.2354	57.1336	36.6437	18.4199	ENSG00000168476	REEP4
ENSG00000168477	0.421548	0.529132	1.07915	0.527541	ENSG00000168477	TNXB
ENSG00000168481	1.38771	0.296693	0.553964	0.947218	ENSG00000168481	LGI3
ENSG00000168484	0.847026	2.89378	1.6033	3.02449	ENSG00000168484	SFTPC
ENSG00000168487	39.3541	54.2676	54.4347	57.4302	ENSG00000168487	BMP1
ENSG00000168488	39.3887	60.3605	79.3187	72.5059	ENSG00000168488	ATXN2L
ENSG00000168490	3.22584	1.06905	0.725035	0.885331	ENSG00000168490	PHYHIP
ENSG00000168491	0.516845	1.11019	0.752355	1.10126	ENSG00000168491	CCDC110
ENSG00000168495	14.0379	11.1664	13.3859	13.8983	ENSG00000168495	POLR3D
ENSG00000168496	7.04175	8.13669	3.16894	10.43	ENSG00000168496	FEN1
ENSG00000168497	1.62197	2.02768	0.457827	0.691429	ENSG00000168497	CAVIN2
ENSG00000168502	11.5174	41.8772	40.957	37.6913	ENSG00000168502	MTCL1
ENSG00000168505	0.132159	0.128893	0.161151	0.522043	ENSG00000168505	GBX2
ENSG00000168509	0.0687763	0.0764003	0.0690527	0.148367	ENSG00000168509	HFE2
ENSG00000168515	0	0	0.15215	0	ENSG00000168515	SCGB1D1
ENSG00000168517	7.53751	8.62327	7.83835	5.07137	ENSG00000168517	HEXIM2

ENSG00000168522	52.515	66.7718	68.1694	62.6327	ENSG00000168522	FNTA
ENSG00000168528	56.9967	73.2959	53.1144	30.793	ENSG00000168528	SERINC2
ENSG00000168530	0.196562	0.204731	0.305775	1.81563	ENSG00000168530	MYL1
ENSG00000168538	21.9324	26.4219	28.0394	23.9335	ENSG00000168538	TRAPPC11
ENSG00000168539	0.376234	0.356452	0.506543	0.550954	ENSG00000168539	CHRM1
ENSG00000168542	0.283388	0.192929	12.5671	813.437	ENSG00000168542	COL3A1
ENSG00000168546	0.957557	1.04948	1.15291	3.76906	ENSG00000168546	GFRA2
ENSG00000168556	8.99375	6.59646	3.8305	3.96184	ENSG00000168556	ING2
ENSG00000168564	13.2904	6.21321	7.91148	3.97741	ENSG00000168564	CDKN2AIP
ENSG00000168566	5.09872	6.53316	5.75754	6.72454	ENSG00000168566	SNRNP48
ENSG00000168569	10.4885	13.5324	12.293	8.28392	ENSG00000168569	TMEM223
ENSG00000168575	270.261	140.286	96.8284	62.8441	ENSG00000168575	SLC20A2
ENSG00000168582	0	0	0	0	ENSG00000168582	CRYGA
ENSG00000168589	0.472109	1.08587	0.65773	2.68176	ENSG00000168589	DYNLRB2
ENSG00000168591	27.7479	26.604	25.7208	26.1931	ENSG00000168591	TMUB2
ENSG00000168594	1.08564	1.50241	1.1385	4.09129	ENSG00000168594	ADAM29
ENSG00000168610	37.7384	52.1672	51.3384	42.7021	ENSG00000168610	STAT3
ENSG00000168612	5.6992	6.75489	6.59454	7.36576	ENSG00000168612	ZSWIM1
ENSG00000168614	66.6942	122.444	117.125	177.621	ENSG00000168614	NBPF9
ENSG00000168615	200.937	177.97	101.004	123.781	ENSG00000168615	ADAM9
ENSG00000168619	2.25926	4.4213	4.59799	8.67064	ENSG00000168619	ADAM18
ENSG00000168621	3.56423	1.22075	1.53411	14.4322	ENSG00000168621	GDNF
ENSG00000168630	1.39721	1.29985	0	0	ENSG00000168630	SPINT5P
ENSG00000168631	0.109392	0.11982	0.103573	0.0760426	ENSG00000168631	DPCR1
ENSG00000168634	0.171145	0.123618	0.111737	0.233977	ENSG00000168634	WFDC13
ENSG00000168646	0.121177	0.174436	0.661482	4.05657	ENSG00000168646	AXIN2
ENSG00000168653	123.838	84.3781	55.4133	64.7497	ENSG00000168653	NDUFS5
ENSG00000168658	2.41828	6.15366	6.38214	8.9877	ENSG00000168658	VWA3B
ENSG00000168661	3.14402	2.05043	2.36244	3.46508	ENSG00000168661	ZNF30
ENSG00000168671	0.135058	0.723259	0.350927	2.0245	ENSG00000168671	UGT3A2
ENSG00000168672	52.7743	34.7331	18.6672	11.006	ENSG00000168672	FAM84B
ENSG00000168675	1.07569	8.50539	1.92727	11.7733	ENSG00000168675	LDLRAD4
ENSG00000168676	11.0232	15.7416	17.0242	21.1958	ENSG00000168676	KCTD19
ENSG00000168679	3.38192	5.5248	6.53267	8.07776	ENSG00000168679	SLC16A4
ENSG00000168685	5.86487	15.606	11.7159	27.769	ENSG00000168685	IL7R
ENSG00000168701	29.6457	21.5653	17.1579	12.9817	ENSG00000168701	TMEM208
ENSG00000168702	0.0869745	0.24212	0.248054	0.234605	ENSG00000168702	LRP1B
ENSG00000168703	75.4865	9.09881	7.14375	20.8255	ENSG00000168703	WFDC12
ENSG00000168710	16.9603	17.7788	18.4782	19.5168	ENSG00000168710	AHCYL1
ENSG00000168724	17.7347	24.1182	19.0294	22.8502	ENSG00000168724	DNAJC21
ENSG00000168734	10.897	13.1359	14.5633	22.3017	ENSG00000168734	PKIG
ENSG00000168743	2.3639	5.46594	2.01891	1.72796	ENSG00000168743	NPNT
ENSG00000168746	1.6858	3.96315	3.35414	3.76347	ENSG00000168746	LINC01620
ENSG00000168748	0	0.0412359	0.0901478	0.155846	ENSG00000168748	CA7
ENSG00000168754	1.45959	5.00991	4.51373	7.69968	ENSG00000168754	FAM178B
ENSG00000168757	0	0	0.0341145	0	ENSG00000168757	TSPY2
ENSG00000168758	13.3078	23.705	22.9048	21.3337	ENSG00000168758	SEMA4C
ENSG00000168763	4.57977	5.33522	9.10714	4.42709	ENSG00000168763	CNNM3
ENSG00000168765	0.970717	6.43183	3.84408	3.19748	ENSG00000168765	GSTM4
ENSG00000168769	16.3522	18.168	20.416	20.2562	ENSG00000168769	TET2
ENSG00000168772	0.533662	0.508413	0.560022	1.4	ENSG00000168772	CXXC4
ENSG00000168778	8.42273	10.9645	6.8355	9.84888	ENSG00000168778	TCTN2
ENSG00000168779	0.386952	0.670352	0.72127	4.55349	ENSG00000168779	SHOX2
ENSG00000168781	30.7411	76.0229	72.5226	65.7104	ENSG00000168781	PPIP5K1

ENSG00000168785	12.2154	31.1142	16.4759	43.244	ENSG00000168785	TSPAN5
ENSG00000168787	0	0.0114325	0.0103321	0.0258921	ENSG00000168787	OR12D2
ENSG00000168792	6.92511	6.43703	6.62142	4.96871	ENSG00000168792	ABHD15
ENSG00000168795	6.04761	6.25436	6.68328	4.44398	ENSG00000168795	ZBTB5
ENSG00000168802	22.4719	22.0803	21.3804	14.7198	ENSG00000168802	CHTF8
ENSG00000168803	5.38276	9.69052	8.34692	8.67918	ENSG00000168803	ADAL
ENSG00000168806	4.42789	3.11756	3.08024	1.96436	ENSG00000168806	LCMT2
ENSG00000168807	4.60895	6.26692	3.10004	5.22268	ENSG00000168807	SNTB2
ENSG00000168811	0.620179	0.89167	0.655429	1.03889	ENSG00000168811	IL12A
ENSG00000168813	3.15001	6.61983	5.97934	8.72008	ENSG00000168813	ZNF507
ENSG00000168818	17.861	17.9496	18.5169	21.0402	ENSG00000168818	STX18
ENSG00000168824	45.5824	42.4903	51.2024	55.436	ENSG00000168824	HGNC:18790
ENSG00000168826	2.54497	2.76767	3.71615	3.06908	ENSG00000168826	ZBTB49
ENSG00000168827	34.1119	38.7532	40.4496	47.8371	ENSG00000168827	GFM1
ENSG00000168828	0	0	0	0	ENSG00000168828	OR13J1
ENSG00000168830	0.288776	0.471205	0.225898	0.533396	ENSG00000168830	HTR1E
ENSG00000168843	0.157816	0.490076	0.346101	0.40781	ENSG00000168843	FSTL5
ENSG00000168852	5.22375	2.58524	1.4634	3.5518	ENSG00000168852	TPTE2P5
ENSG00000168872	29.4228	32.8376	39.2315	37.5283	ENSG00000168872	DDX19A
ENSG00000168874	0.924579	0.475734	0.686733	1.52911	ENSG00000168874	ATOH8
ENSG00000168875	0	0	0	0	ENSG00000168875	SOX14
ENSG00000168876	8.93548	8.08667	9.25167	6.0655	ENSG00000168876	ANKRD49
ENSG00000168878	1.01927	2.5774	1.45802	2.73672	ENSG00000168878	SFTPB
ENSG00000168883	21.0854	33.1139	31.1672	30.7542	ENSG00000168883	USP39
ENSG00000168884	15.6075	17.3937	15.6771	13.4055	ENSG00000168884	TNIP2
ENSG00000168887	12.2865	19.6899	17.4088	18.5179	ENSG00000168887	C2orf68
ENSG00000168890	8.95989	9.09391	11.155	6.73588	ENSG00000168890	TMEM150A
ENSG00000168894	83.1599	57.6839	46.7893	35.0839	ENSG00000168894	RNF181
ENSG00000168899	1.96976	1.82121	2.65027	3.00984	ENSG00000168899	VAMP5
ENSG00000168903	0.1138	0.329835	0.29822	0.628457	ENSG00000168903	BTNL3
ENSG00000168904	5.82494	10.0107	11.6161	12.0487	ENSG00000168904	LRRC28
ENSG00000168906	60.2755	111.527	119.248	93.0233	ENSG00000168906	MAT2A
ENSG00000168907	13.3096	17.3356	9.91073	2.94059	ENSG00000168907	PLA2G4F
ENSG00000168913	0.112493	0.541326	0.342466	0.367996	ENSG00000168913	ENHO
ENSG00000168916	1.61655	5.52515	8.85342	10.347	ENSG00000168916	ZNF608
ENSG00000168917	3.42367	3.67904	3.82494	4.70036	ENSG00000168917	SLC35G2
ENSG00000168918	15.9863	17.377	27.6345	9.71	ENSG00000168918	INPP5D
ENSG00000168924	53.4754	39.5795	51.3792	42.3591	ENSG00000168924	LETM1
ENSG00000168925	0.860579	0.806775	0.319629	1.64703	ENSG00000168925	CTRB1
ENSG00000168928	0.222215	0.62023	0.385381	0.471585	ENSG00000168928	CTRB2
ENSG00000168930	0.0652559	0.166708	0.0902346	0.0863386	ENSG00000168930	TRIM49
ENSG00000168936	27.1372	34.2654	40.4969	17.1498	ENSG00000168936	TMEM129
ENSG00000168938	22.8278	18.4269	16.3618	10.664	ENSG00000168938	PPIC
ENSG00000168939	0.435092	0.886519	1.41625	1.44732	ENSG00000168939	SPRY3
ENSG00000168944	6.43252	19.4641	11.5055	8.31707	ENSG00000168944	CEP120
ENSG00000168952	0.813155	1.47833	1.09346	4.36728	ENSG00000168952	STXBP6
ENSG00000168955	2.01049	3.628	2.29686	4.73389	ENSG00000168955	TM4SF20
ENSG00000168958	40.7175	40.1817	32.2939	39.9954	ENSG00000168958	MFF
ENSG00000168959	0.0963861	0.339138	0.534545	1.11621	ENSG00000168959	GRM5
ENSG00000168961	3.60576	3.04873	1.33113	4.17743	ENSG00000168961	LGALS9
ENSG00000168967	0.303751	0.919758	0.634095	1.33671	ENSG00000168967	PMCHL1
ENSG00000168970	10.9339	17.0784	14.0759	6.94095	ENSG00000168970	JMJD7-PLA2G4B
ENSG00000168992	0	0.0726974	0.178174	0	ENSG00000168992	OR7E102P
ENSG00000168993	0.0560286	0.0741945	0.179042	0.220164	ENSG00000168993	CPLX1

ENSG00000168994	26.4513	17.2039	24.4992	15.8436	ENSG00000168994	PXDC1
ENSG00000168995	0.0792619	0.499604	0.379412	0.894592	ENSG00000168995	SIGLEC7
ENSG00000169006	0.368034	0.638182	0.70508	0.967338	ENSG00000169006	NTSR2
ENSG00000169016	7.86189	8.43044	10.404	9.04768	ENSG00000169016	E2F6
ENSG00000169018	79.2888	51.7527	67.7916	28.9406	ENSG00000169018	FEM1B
ENSG00000169019	11.9741	9.58831	9.21911	6.26631	ENSG00000169019	COMMD8
ENSG00000169020	130.66	108.252	60.4885	74.3975	ENSG00000169020	ATP5I
ENSG00000169021	30.6201	23.4806	17.9482	12.7724	ENSG00000169021	UQCRFS1
ENSG00000169026	0.834909	0.975406	0.895566	3.36075	ENSG00000169026	MFSD7
ENSG00000169031	1.46756	3.82423	4.19148	4.45618	ENSG00000169031	COL4A3
ENSG00000169032	50.0591	32.146	20.7863	36.8178	ENSG00000169032	MAP2K1
ENSG00000169035	1455.19	32.3877	34.4149	51.2758	ENSG00000169035	KLK7
ENSG00000169040	0.448843	0.626258	0.09992	0.0832404	ENSG00000169040	PMCHL2
ENSG00000169045	309.891	411.099	433.574	397.198	ENSG00000169045	HNRNPH1
ENSG00000169047	6.79726	16.0177	15.923	15.7885	ENSG00000169047	IRS1
ENSG00000169057	5.34683	5.94737	6.83639	8.21241	ENSG00000169057	MECP2
ENSG00000169059	0	0.10264	0	0	ENSG00000169059	VCX3A
ENSG00000169062	15.826	17.2144	23.2453	16.7889	ENSG00000169062	UPF3A
ENSG00000169064	0.234824	1.25119	1.2551	1.35668	ENSG00000169064	ZBBX
ENSG00000169067	0.295627	0.0950118	0.154621	0.0867587	ENSG00000169067	ACTBL2
ENSG00000169071	0.280986	0.161171	1.26338	3.08887	ENSG00000169071	ROR2
ENSG00000169075	0.629995	0.955413	0.976734	1.91032	ENSG00000169075	BRD7P3
ENSG00000169083	0.687044	1.22295	1.37526	4.82784	ENSG00000169083	AR
ENSG00000169084	20.2605	25.6831	19.0197	29.1149	ENSG00000169084	DHRSX
ENSG00000169085	1.35045	2.85571	5.84183	7.90324	ENSG00000169085	C8orf46
ENSG00000169087	11.1534	25.9547	26.6184	38.7749	ENSG00000169087	HSPBAP1
ENSG00000169093	7.78362	11.4842	9.2745	11.6448	ENSG00000169093	ASMTL
ENSG00000169100	54.9018	57.4371	58.0837	40.9799	ENSG00000169100	SLC25A6
ENSG00000169105	2.70232	6.09485	3.24187	5.34705	ENSG00000169105	CHST14
ENSG00000169116	0.882832	0.347493	0.250309	0.506857	ENSG00000169116	PARM1
ENSG00000169118	13.6248	14.4222	19.1507	11.2358	ENSG00000169118	CSNK1G1
ENSG00000169122	0.825665	1.6473	3.54563	8.02976	ENSG00000169122	FAM110B
ENSG00000169126	2.73318	9.49011	5.8355	9.80182	ENSG00000169126	ARMC4
ENSG00000169129	27.2811	26.8238	17.6956	22.0547	ENSG00000169129	AFAP1L2
ENSG00000169131	8.56939	14.1606	12.3578	8.77948	ENSG00000169131	ZNF354A
ENSG00000169136	10.4969	10.374	16.5536	15.0507	ENSG00000169136	ATF5
ENSG00000169139	24.1171	17.9216	21.1215	20.7802	ENSG00000169139	UBE2V2
ENSG00000169154	0.0425756	0	0	0	ENSG00000169154	GOT1L1
ENSG00000169155	10.4796	10.2691	12.8534	8.74958	ENSG00000169155	ZBTB43
ENSG00000169164	0	2.58523	1.73105	0.384047	ENSG00000169164	RP11-167P23.2
ENSG00000169169	3.81086	6.58267	5.4317	16.4205	ENSG00000169169	CPT1C
ENSG00000169174	38.7977	145.042	32.9317	59.9972	ENSG00000169174	PCSK9
ENSG00000169180	69.384	105.958	110.585	94.8191	ENSG00000169180	XPO6
ENSG00000169181	0.510946	1.13326	0.907036	1.98972	ENSG00000169181	GSG1L
ENSG00000169184	9.63283	10.7387	7.77515	13.5655	ENSG00000169184	MN1
ENSG00000169188	7.42346	6.89225	7.75019	4.60512	ENSG00000169188	APEX2
ENSG00000169189	26.1499	36.6934	37.4019	34.4557	ENSG00000169189	NSMCE1
ENSG00000169193	8.2321	6.62316	7.40032	6.97362	ENSG00000169193	CCDC126
ENSG00000169194	0	0.088929	0.075397	0.0504664	ENSG00000169194	IL13
ENSG00000169202	0	0	0	0.0734341	ENSG00000169202	OR10G1P
ENSG00000169203	9.32436	14.0204	17.1084	28.9929	ENSG00000169203	RP11-231C14.4
ENSG00000169208	0	0	0	0	ENSG00000169208	OR10G3
ENSG00000169213	1.53272	5.97882	3.31151	14.5741	ENSG00000169213	RAB3B
ENSG00000169214	0	0.276955	0	0.125488	ENSG00000169214	OR6F1

ENSG00000169217	36.0825	25.7287	26.0649	18.4558	ENSG00000169217	CD2BP2
ENSG00000169218	0.210172	0.316595	0.262355	0.772693	ENSG00000169218	RSPO1
ENSG00000169220	7.70845	23.5101	12.1934	7.09622	ENSG00000169220	RGS14
ENSG00000169221	16.4217	16.4516	16.9704	16.9573	ENSG00000169221	TBC1D10B
ENSG00000169223	91.5747	129.101	69.939	51.784	ENSG00000169223	LMAN2
ENSG00000169224	2.0535	3.61279	2.56198	6.0022	ENSG00000169224	GCSAML
ENSG00000169228	6.68258	8.15085	13.513	9.21608	ENSG00000169228	RAB24
ENSG00000169230	65.0965	52.5238	37.5755	23.5681	ENSG00000169230	PRELID1
ENSG00000169231	21.3721	35.535	40.5005	26.4866	ENSG00000169231	THBS3
ENSG00000169239	8.17734	17.2989	18.68	27.0632	ENSG00000169239	CA5B
ENSG00000169241	53.0124	60.2953	40.3085	30.335	ENSG00000169241	SLC50A1
ENSG00000169242	38.4266	22.8493	31.5489	7.22691	ENSG00000169242	EFNA1
ENSG00000169245	0.204772	0.492813	8.21775	0.760348	ENSG00000169245	CXCL10
ENSG00000169246	50.5302	111.576	116.876	127.325	ENSG00000169246	NPIPB3
ENSG00000169247	45.1938	23.4049	8.20362	15.5282	ENSG00000169247	SH3TC2
ENSG00000169248	0.426971	1.10556	3.02938	0.542214	ENSG00000169248	CXCL11
ENSG00000169249	5.3537	5.92953	9.10045	12.7959	ENSG00000169249	ZRSR2
ENSG00000169251	27.6521	17.9413	26.4219	21.431	ENSG00000169251	NMD3
ENSG00000169252	36.5573	16.0441	13.6328	13.9629	ENSG00000169252	ADRB2
ENSG00000169253	0	0	0.271055	0	ENSG00000169253	RP11-220D10.1
ENSG00000169255	3.05917	6.4662	4.03315	7.6113	ENSG00000169255	B3GALNT1
ENSG00000169258	6.14498	5.61395	4.01484	5.08837	ENSG00000169258	GPRIN1
ENSG00000169260	0	0	0	1.82E-08	ENSG00000169260	ZNF311
ENSG00000169271	0	0	0.447802	0	ENSG00000169271	HSPB3
ENSG00000169282	2.31736	4.6554	3.43948	6.07126	ENSG00000169282	KCNAB1
ENSG00000169288	15.5633	15.1555	12.5876	12.3025	ENSG00000169288	MRPL1
ENSG00000169291	2.13241	0.982165	1.31868	1.8097	ENSG00000169291	SHE
ENSG00000169297	0.0838133	0.162972	0.097109	0.596005	ENSG00000169297	NR0B1
ENSG00000169299	18.7014	15.1634	16.9443	9.37782	ENSG00000169299	PGM2
ENSG00000169302	0.636114	1.3919	0.835157	2.08192	ENSG00000169302	STK32A
ENSG00000169306	1.13784	1.87534	1.45463	1.59	ENSG00000169306	IL1RAPL1
ENSG00000169313	0.0322884	0.311751	0.225384	0.282183	ENSG00000169313	P2RY12
ENSG00000169314	0.241914	0.518682	0.644378	1.20676	ENSG00000169314	C22orf15
ENSG00000169325	0	0	0	0	ENSG00000169325	GUSBP12
ENSG00000169327	0	0	0.0435135	0.109211	ENSG00000169327	OR5AU1
ENSG00000169330	0.601283	0.597988	0.745628	1.29205	ENSG00000169330	KIAA1024
ENSG00000169340	0.421349	0.846542	0.45772	1.97297	ENSG00000169340	PDILT
ENSG00000169344	0.36212	0.682514	0.288424	1.44148	ENSG00000169344	UMOD
ENSG00000169347	0.561556	0.967709	0.976052	1.93694	ENSG00000169347	GP2
ENSG00000169359	32.84	47.9819	32.5727	22.2251	ENSG00000169359	SLC33A1
ENSG00000169371	15.1207	32.1574	32.1398	42.6732	ENSG00000169371	SNUPN
ENSG00000169372	4.52262	7.27336	6.57439	11.1955	ENSG00000169372	CRADD
ENSG00000169375	13.426	28.3168	26.5094	30.5111	ENSG00000169375	SIN3A
ENSG00000169379	6.14826	7.48046	9.62982	11.0031	ENSG00000169379	ARL13B
ENSG00000169385	0	0	0	0.282994	ENSG00000169385	RNASE2
ENSG00000169393	0	0.333668	0	0.185463	ENSG00000169393	ELSPBP1
ENSG00000169397	0	0	0	0	ENSG00000169397	RNASE3
ENSG00000169398	78.1048	111.014	88.9163	170.826	ENSG00000169398	PTK2
ENSG00000169402	2.24971	3.80742	3.9188	6.12537	ENSG00000169402	RSPH10B2
ENSG00000169403	11.0224	16.1107	6.0722	4.93229	ENSG00000169403	PTAFR
ENSG00000169410	10.6507	15.8463	16.6921	12.5065	ENSG00000169410	PTPN9
ENSG00000169413	0	0	0	0	ENSG00000169413	RNASE6
ENSG00000169418	0.421096	0.438756	0.274754	1.88039	ENSG00000169418	NPR1
ENSG00000169427	0.0607286	0.0976506	0.106122	0.317005	ENSG00000169427	KCNK9

ENSG00000169429	7.56461	2.74207	2.96975	70.3097	ENSG00000169429	CXCL8
ENSG00000169432	1.25398	4.85282	4.19597	2.07145	ENSG00000169432	SCN9A
ENSG00000169435	6.73183	10.8436	13.0046	9.91159	ENSG00000169435	RASSF6
ENSG00000169436	28.0365	93.8297	13.2476	36.4997	ENSG00000169436	COL22A1
ENSG00000169439	3.54306	1.40423	6.17268	27.1414	ENSG00000169439	SDC2
ENSG00000169442	2.16599	1.30725	1.61524	0.178576	ENSG00000169442	CD52
ENSG00000169446	7.19034	6.51391	4.83398	4.4656	ENSG00000169446	MMGT1
ENSG00000169469	580.983	122.957	129.856	160.344	ENSG00000169469	SPRR1B
ENSG00000169474	194.389	39.6537	34.3761	76.3118	ENSG00000169474	SPRR1A
ENSG00000169484	0	0.0644378	0	0	ENSG00000169484	OR4K14
ENSG00000169488	0	0	0	0.107268	ENSG00000169488	OR4K15
ENSG00000169490	33.0907	24.8281	13.9178	10.8597	ENSG00000169490	TM2D2
ENSG00000169495	2.85932	5.61579	5.79294	9.47099	ENSG00000169495	HTRA4
ENSG00000169499	17.1203	25.0625	18.8548	33.8669	ENSG00000169499	PLEKHA2
ENSG00000169504	74.9792	57.2329	75.9774	70.4163	ENSG00000169504	CLIC4
ENSG00000169507	2.3268	5.29527	5.33975	5.04076	ENSG00000169507	SLC38A11
ENSG00000169508	0.774465	1.98819	1.57139	2.91531	ENSG00000169508	GPR183
ENSG00000169509	154.895	11.8527	5.92996	34.5201	ENSG00000169509	CRCT1
ENSG00000169515	3.16456	10.6983	22.2375	14.5804	ENSG00000169515	CCDC8
ENSG00000169519	15.1807	21.2825	12.593	16.494	ENSG00000169519	METTL15
ENSG00000169548	0.0260836	0	0.0227286	0.0572689	ENSG00000169548	ZNF280A
ENSG00000169550	8.94338	2.07862	4.81431	1.59465	ENSG00000169550	MUC15
ENSG00000169551	0.233588	0.123547	0.220798	0.259566	ENSG00000169551	CT55
ENSG00000169554	2.04663	2.60931	2.53897	42.0504	ENSG00000169554	ZEB2
ENSG00000169562	0.391365	0.340478	0.752832	1.10054	ENSG00000169562	GJB1
ENSG00000169564	21.7266	18.2727	15.9104	25.9869	ENSG00000169564	PCBP1
ENSG00000169567	140.29	127.964	102.348	63.6644	ENSG00000169567	HINT1
ENSG00000169570	2.72973	2.77748	4.10888	3.96092	ENSG00000169570	DTWD2
ENSG00000169575	0.087116	0.08372	0.0836786	0.205242	ENSG00000169575	VPREB1
ENSG00000169583	24.6343	5.06164	4.76595	7.07711	ENSG00000169583	CLIC3
ENSG00000169592	24.4007	29.5468	19.6173	17.5899	ENSG00000169592	INO80E
ENSG00000169594	53.8016	63.7761	63.4334	43.802	ENSG00000169594	BNC1
ENSG00000169598	4.90406	6.75245	6.25367	11.2586	ENSG00000169598	DFFB
ENSG00000169599	17.9027	18.7393	11.9013	15.0329	ENSG00000169599	NFU1
ENSG00000169604	7.60978	15.0054	18.179	45.5532	ENSG00000169604	ANTXR1
ENSG00000169605	0.0792665	0.685161	0.795725	1.17671	ENSG00000169605	GKN1
ENSG00000169607	3.28802	13.4128	4.11115	9.13055	ENSG00000169607	CKAP2L
ENSG00000169609	24.3623	41.3684	37.9253	53.016	ENSG00000169609	C15orf40
ENSG00000169612	13.5396	8.79769	12.2634	6.35466	ENSG00000169612	FAM103A1
ENSG00000169618	0	0.147109	0.0939514	0.039789	ENSG00000169618	PROKR1
ENSG00000169621	2.56698	6.90135	7.32262	9.00515	ENSG00000169621	APLF
ENSG00000169627	94.2043	38.5949	37.4437	24.3857	ENSG00000169627	BOLA2B
ENSG00000169629	9.42629	9.95157	12.9397	11.792	ENSG00000169629	RGPD8
ENSG00000169635	1.68967	2.75438	2.71079	2.14501	ENSG00000169635	HIC2
ENSG00000169641	32.102	32.2075	41.325	41.6507	ENSG00000169641	LUZP1
ENSG00000169660	8.28751	22.2458	17.1295	19.7576	ENSG00000169660	HEXDC
ENSG00000169662	0	0	0	0	ENSG00000169662	BCRP6
ENSG00000169668	0.996424	1.09517	0.600632	0.760296	ENSG00000169668	BCRP2
ENSG00000169676	0.0936409	0.512763	0.51006	0.308581	ENSG00000169676	DRD5
ENSG00000169679	8.84024	43.2161	6.97698	18.771	ENSG00000169679	BUB1
ENSG00000169682	32.907	29.8231	24.2583	28.1665	ENSG00000169682	SPNS1
ENSG00000169683	10.0259	12.4866	3.46907	6.38361	ENSG00000169683	LRRC45
ENSG00000169684	2.09167	6.0595	2.31044	2.91167	ENSG00000169684	CHRNA5
ENSG00000169688	0	1.01442	0.914505	1.67199	ENSG00000169688	MT1B

ENSG00000169689	19.8633	18.3916	8.75127	9.50302	ENSG00000169689	CENPX
ENSG00000169692	25.2221	33.6954	23.7006	12.4726	ENSG00000169692	AGPAT2
ENSG00000169696	10.8116	14.88	18.0005	14.7393	ENSG00000169696	ASPSCR1
ENSG00000169704	0.071134	0.205204	0.123608	0.154586	ENSG00000169704	GP9
ENSG00000169710	184.956	222.365	54.3307	243.004	ENSG00000169710	FASN
ENSG00000169714	88.1475	69.1814	68.5034	51.9797	ENSG00000169714	CNBP
ENSG00000169715	23.0895	188.162	25.0721	71.3217	ENSG00000169715	MT1E
ENSG00000169717	0	0	0	0	ENSG00000169717	ACTRT2
ENSG00000169718	67.6587	50.526	72.975	38.1346	ENSG00000169718	DUS1L
ENSG00000169727	52.3353	40.0066	34.2422	57.2827	ENSG00000169727	GPS1
ENSG00000169733	21.8333	24.544	24.9595	15.5113	ENSG00000169733	RFNG
ENSG00000169738	22.3209	17.5026	13.181	9.29936	ENSG00000169738	DCXR
ENSG00000169740	6.10571	8.82688	7.74507	7.90546	ENSG00000169740	ZNF32
ENSG00000169744	1.32464	2.9572	1.67354	6.33094	ENSG00000169744	LDB2
ENSG00000169750	6.22208	12.3263	8.41194	7.68	ENSG00000169750	RAC3
ENSG00000169752	30.0424	44.2777	44.235	69.0925	ENSG00000169752	NRG4
ENSG00000169756	40.1501	34.1337	40.4792	76.8822	ENSG00000169756	LIMS1
ENSG00000169758	2.91896	5.30676	4.83756	9.21427	ENSG00000169758	TMEM266
ENSG00000169760	0.274126	0.240898	0.103049	1.0419	ENSG00000169760	NLGN1
ENSG00000169762	16.145	41.0163	23.4285	42.3834	ENSG00000169762	TAPT1
ENSG00000169763	0.24387	0.23405	0	0	ENSG00000169763	PRYP3
ENSG00000169764	95.621	61.3454	51.3909	65.0941	ENSG00000169764	UGP2
ENSG00000169777	0.0872626	0	0	0.094487	ENSG00000169777	TAS2R1
ENSG00000169783	0.622429	0.858619	0.810701	1.45272	ENSG00000169783	LINGO1
ENSG00000169789	0.0217339	0.0871339	0.0786819	0	ENSG00000169789	PRY
ENSG00000169800	0	0	0	0.00530398	ENSG00000169800	RBMY1F
ENSG00000169807	0.0217339	0.0871339	0.0786819	0	ENSG00000169807	PRY2
ENSG00000169811	0	0	0	0	ENSG00000169811	RBMY1HP
ENSG00000169813	66.6644	70.9584	63.9322	53.7901	ENSG00000169813	HNRNPF
ENSG00000169814	7.14113	7.64719	4.03426	4.2271	ENSG00000169814	BTD
ENSG00000169826	3.2163	5.78628	7.77801	10.6847	ENSG00000169826	CSGALNACT2
ENSG00000169836	0.0111445	0.130661	0.134691	0.25831	ENSG00000169836	TACR3
ENSG00000169840	0.0345191	0.0664814	0.0300486	0.0756083	ENSG00000169840	GSX1
ENSG00000169849	0	0	0	0	ENSG00000169849	TSPY14P
ENSG00000169851	15.557	36.8453	11.6127	31.108	ENSG00000169851	PCDH7
ENSG00000169855	17.4403	36.3407	48.3961	40.3405	ENSG00000169855	ROBO1
ENSG00000169856	0.1812	0.348492	0.366743	0.936457	ENSG00000169856	ONECUT1
ENSG00000169857	8.05957	6.48957	6.18855	6.01666	ENSG00000169857	AVEN
ENSG00000169860	5.10595	4.58253	6.15028	1.18091	ENSG00000169860	P2RY1
ENSG00000169861	0	0	0	0	ENSG00000169861	IGHV1OR21-1
ENSG00000169862	0.102564	0.341909	0.25736	0.797775	ENSG00000169862	CTNND2
ENSG00000169871	17.5872	22.2914	22.572	34.8881	ENSG00000169871	TRIM56
ENSG00000169876	0.626599	3.878	4.93079	5.42626	ENSG00000169876	MUC17
ENSG00000169877	0	0	0	0	ENSG00000169877	AHSP
ENSG00000169884	0.469313	0.509996	0.636875	0.452822	ENSG00000169884	WNT10B
ENSG00000169885	0.255342	0.345987	1.47515	0.184428	ENSG00000169885	CALML6
ENSG00000169891	4.01521	8.93631	7.95766	13.2793	ENSG00000169891	REPS2
ENSG00000169894	0.436419	0.711846	0.276869	0.931109	ENSG00000169894	MUC3A
ENSG00000169895	13.3709	11.8372	12.7677	20.4944	ENSG00000169895	SYAP1
ENSG00000169896	0.419015	0.528059	0.65307	1.58465	ENSG00000169896	ITGAM
ENSG00000169900	0.158776	0	0.137896	0	ENSG00000169900	PYDC1
ENSG00000169902	40.8326	38.1341	29.5759	45.1874	ENSG00000169902	TPST1
ENSG00000169903	0.0813056	0.154494	0.232781	0.150768	ENSG00000169903	TM4SF4
ENSG00000169905	75.6598	60.7444	66.56	53.8485	ENSG00000169905	TOR1AIP2

ENSG00000169906	0.177158	0.862751	0.755746	1.48853	ENSG00000169906	S100G
ENSG00000169908	271.625	96.1002	36.6805	44.4473	ENSG00000169908	TM4SF1
ENSG00000169914	4.69332	8.90006	7.92381	12.9225	ENSG00000169914	OTUD3
ENSG00000169918	1.43727	5.99588	2.62551	7.50335	ENSG00000169918	OTUD7A
ENSG00000169919	12.6596	24.7856	16.4555	18.5484	ENSG00000169919	GUSB
ENSG00000169925	3.33933	8.69945	9.4092	9.62434	ENSG00000169925	BRD3
ENSG00000169926	29.1682	32.455	38.2367	18.7524	ENSG00000169926	KLF13
ENSG00000169933	0.192658	0.309723	0.272206	0.439085	ENSG00000169933	FRMPD4
ENSG00000169946	2.94943	6.63217	6.68836	11.3524	ENSG00000169946	ZFPM2
ENSG00000169951	2.86267	4.28387	3.38129	3.16176	ENSG00000169951	ZNF764
ENSG00000169953	0.307964	0.671012	1.00751	1.04441	ENSG00000169953	HSFY2
ENSG00000169955	3.16386	3.88636	4.17972	3.93678	ENSG00000169955	ZNF747
ENSG00000169957	13.1757	16.1963	24.0222	9.77707	ENSG00000169957	ZNF768
ENSG00000169962	3.25309	4.75211	2.20254	2.68918	ENSG00000169962	TAS1R3
ENSG00000169964	5.76492	9.97245	8.47171	5.31173	ENSG00000169964	TMEM42
ENSG00000169967	20.2824	18.7164	24.9828	19.068	ENSG00000169967	MAP3K2
ENSG00000169972	19.0798	12.1345	13.5221	6.77433	ENSG00000169972	PUSL1
ENSG00000169976	43.5646	28.7987	21.6777	18.5293	ENSG00000169976	SF3B5
ENSG00000169981	8.32733	7.6171	7.52749	5.59656	ENSG00000169981	ZNF35
ENSG00000169989	0.246708	0.237836	0.273665	0.0739246	ENSG00000169989	TIGD4
ENSG00000169991	33.0804	28.8061	49.34	20.3275	ENSG00000169991	IFFO2
ENSG00000169992	4.46481	8.32361	12.4196	18.7653	ENSG00000169992	NLGN2
ENSG00000169994	0.0839387	0.0525456	0.0569802	0.526678	ENSG00000169994	MYO7B
ENSG00000170004	42.576	51.3575	66.8761	67.7445	ENSG00000170004	CHD3
ENSG00000170006	67.0543	55.2611	31.5472	25.6476	ENSG00000170006	TMEM154
ENSG00000170011	0.200548	0.552052	0.268118	0.765019	ENSG00000170011	MYRIP
ENSG00000170017	68.0275	106.963	40.4369	37.3526	ENSG00000170017	ALCAM
ENSG00000170027	68.0505	38.2391	74.6606	54.6774	ENSG00000170027	YWHAG
ENSG00000170035	27.5746	25.4685	22.5916	28.7812	ENSG00000170035	UBE2E3
ENSG00000170037	19.2752	26.2799	25.0087	30.2244	ENSG00000170037	CNTROB
ENSG00000170043	18.7741	11.2487	16.4911	20.1507	ENSG00000170043	TRAPPC1
ENSG00000170044	2.77756	3.71786	2.29133	3.0256	ENSG00000170044	ZPLD1
ENSG00000170049	2.32926	3.21971	5.92498	5.94186	ENSG00000170049	KCNAB3
ENSG00000170054	0.228792	0.0501204	0.0452995	0.333948	ENSG00000170054	SERPINA9
ENSG00000170074	4.72377	5.1378	4.34963	2.13908	ENSG00000170074	FAM153A
ENSG00000170075	0.585213	0.947661	0.962836	1.28274	ENSG00000170075	GPR37L1
ENSG00000170085	11.3955	19.0404	17.2764	29.0483	ENSG00000170085	SIMC1
ENSG00000170088	14.1972	13.1924	14.0922	10.5273	ENSG00000170088	TMEM192
ENSG00000170089	16.4328	31.846	20.8735	21.2014	ENSG00000170089	RP11-423H2.1
ENSG00000170091	0.228582	0.298029	0.455021	0.477975	ENSG00000170091	HGNC:24955
ENSG00000170092	1.27938	2.10749	2.08736	6.25868	ENSG00000170092	SPDYE5
ENSG00000170099	0.0927054	0.623533	0.600344	0.676592	ENSG00000170099	SERPINA6
ENSG00000170100	7.49252	6.25576	8.99312	6.73581	ENSG00000170100	ZNF778
ENSG00000170113	15.0886	7.38155	6.90902	7.91784	ENSG00000170113	NIPA1
ENSG00000170122	0.21868	0.0823723	0.230347	0.119426	ENSG00000170122	FOXD4
ENSG00000170128	0	0	0.0848248	0	ENSG00000170128	GPR25
ENSG00000170142	47.4434	45.332	44.1184	40.2101	ENSG00000170142	UBE2E1
ENSG00000170144	15.2905	26.3025	23.6552	34.8165	ENSG00000170144	HNRNPA3
ENSG00000170145	6.60065	7.23086	5.37041	9.65799	ENSG00000170145	SIK2
ENSG00000170152	0	0	0	0	ENSG00000170152	RP11-374M1.7
ENSG00000170153	0.337919	1.13189	0.437597	3.41037	ENSG00000170153	RNF150
ENSG00000170160	4.67566	17.0381	13.7663	25.7128	ENSG00000170160	CCDC144A
ENSG00000170162	0.10043	0.0655519	0.0583159	0.440574	ENSG00000170162	VGLL2
ENSG00000170165	0.261075	0.533212	0.491436	0.371464	ENSG00000170165	CR848007.1

ENSG00000170166	0.594656	0	0.040742	0.88476	ENSG00000170166	HOXD4
ENSG00000170175	22.2887	27.892	13.1533	12.5504	ENSG00000170175	CHRNB1
ENSG00000170178	0	0.0731968	0.132267	2.31457	ENSG00000170178	HOXD12
ENSG00000170180	0.489965	1.49971	2.01101	3.79417	ENSG00000170180	GYPA
ENSG00000170185	11.9282	7.68304	9.23018	6.90401	ENSG00000170185	USP38
ENSG00000170190	3.18496	16.7153	7.798	6.00818	ENSG00000170190	SLC16A5
ENSG00000170191	2.30784	2.83812	2.4863	3.02324	ENSG00000170191	NANP
ENSG00000170209	1.63032	1.82613	3.62905	1.57399	ENSG00000170209	ANKK1
ENSG00000170214	0.23003	0.348461	0.181788	1.09492	ENSG00000170214	ADRA1B
ENSG00000170215	0.820841	0	0	0	ENSG00000170215	FAM27B
ENSG00000170217	0.937918	1.32422	1.11012	1.34051	ENSG00000170217	RP11-12A20.2
ENSG00000170222	3.93012	6.41556	6.77806	3.6875	ENSG00000170222	ADPRM
ENSG00000170231	0.251579	0.545738	0.703089	0.700488	ENSG00000170231	FABP6
ENSG00000170234	9.57246	18.4048	10.9888	26.7632	ENSG00000170234	PWWP2A
ENSG00000170236	2.47075	4.19005	4.75116	5.59883	ENSG00000170236	USP50
ENSG00000170242	29.7174	28.6836	31.8134	32.4084	ENSG00000170242	USP47
ENSG00000170248	237.504	175.91	147.286	146.285	ENSG00000170248	PDCD6IP
ENSG00000170255	0	0	0	0	ENSG00000170255	MRGPRX1
ENSG00000170260	4.97302	8.86559	6.70412	6.93232	ENSG00000170260	ZNF212
ENSG00000170262	1.2417	3.3738	2.52585	4.83676	ENSG00000170262	MRAP
ENSG00000170264	2.22767	4.35394	4.21072	7.1046	ENSG00000170264	FAM161A
ENSG00000170265	15.8897	28.1862	25.5905	15.1355	ENSG00000170265	ZNF282
ENSG00000170266	46.336	65.0274	50.4403	35.9407	ENSG00000170266	GLB1
ENSG00000170270	2.45207	2.58758	2.04305	1.87905	ENSG00000170270	GON7
ENSG00000170271	12.8078	18.372	19.9308	26.9597	ENSG00000170271	FAXDC2
ENSG00000170275	50.493	69.5719	33.6075	37.5062	ENSG00000170275	CRTAP
ENSG00000170276	0.0621472	0	0.111457	0.0899456	ENSG00000170276	HSPB2
ENSG00000170279	0	0.125477	0	0	ENSG00000170279	C7orf33
ENSG00000170289	2.5974	7.39982	5.82577	9.93146	ENSG00000170289	CNGB3
ENSG00000170290	0.186658	0.35837	0.240115	0.0997448	ENSG00000170290	SLN
ENSG00000170291	13.6804	9.28539	12.536	7.57082	ENSG00000170291	ELP5
ENSG00000170293	1.96542	0.935424	1.03743	0.669965	ENSG00000170293	CMTM8
ENSG00000170296	90.098	36.1824	42.6817	39.4401	ENSG00000170296	GABARAP
ENSG00000170298	2.64004	25.9072	11.788	37.7521	ENSG00000170298	LGALS9B
ENSG00000170310	35.938	36.7616	26.646	34.2042	ENSG00000170310	STX8
ENSG00000170312	11.2809	52.9854	4.78045	19.126	ENSG00000170312	CDK1
ENSG00000170315	212.799	176.838	150.708	130.368	ENSG00000170315	UBB
ENSG00000170322	19.6257	26.5544	24.7045	17.3835	ENSG00000170322	NFRKB
ENSG00000170323	0.372448	1.00743	1.06275	1.32594	ENSG00000170323	FABP4
ENSG00000170324	0.929486	2.05466	2.19029	2.89055	ENSG00000170324	FRMPD2
ENSG00000170325	4.65922	5.20816	2.18001	4.70156	ENSG00000170325	PRDM10
ENSG00000170340	43.2881	27.4282	17.7053	16.1692	ENSG00000170340	B3GNT2
ENSG00000170345	50.6665	192.161	22.1352	28.0389	ENSG00000170345	FOS
ENSG00000170348	255.084	280.58	121.441	68.7353	ENSG00000170348	TMED10
ENSG00000170356	2.12405	0	0	0	ENSG00000170356	OR2A20P
ENSG00000170364	20.2068	28.5381	26.097	30.6533	ENSG00000170364	SETMAR
ENSG00000170365	10.564	24.6427	31.2354	22.23	ENSG00000170365	SMAD1
ENSG00000170367	0	0	0.0755054	0	ENSG00000170367	CST5
ENSG00000170369	0.176306	0	0	0	ENSG00000170369	CST2
ENSG00000170370	1.06298	1.35061	1.34685	3.94794	ENSG00000170370	EMX2
ENSG00000170373	0.313882	0.200973	0.272281	0.112903	ENSG00000170373	CST1
ENSG00000170374	0.129803	0.399004	0.464371	0.304276	ENSG00000170374	SP7
ENSG00000170379	2.67932	4.35981	4.52897	8.38158	ENSG00000170379	TCAF2
ENSG00000170381	0.139743	0.294468	0.963305	0.511509	ENSG00000170381	SEMA3E

ENSG00000170382	0.291986	0.87242	0.598633	2.08096	ENSG00000170382	LRRN2
ENSG00000170385	21.0086	25.0632	39.1694	12.0487	ENSG00000170385	SLC30A1
ENSG00000170390	0.0310091	0.123073	0.178171	1.47378	ENSG00000170390	DCLK2
ENSG00000170396	0.0343634	0.154726	0.181663	0.705994	ENSG00000170396	ZNF804A
ENSG00000170409	0	0	0	0	ENSG00000170409	CTA-313A17.2
ENSG00000170412	12.0665	14.704	10.0936	6.45053	ENSG00000170412	GPRC5C
ENSG00000170417	91.6728	192.711	194.845	385.458	ENSG00000170417	TMEM182
ENSG00000170419	0.332277	0.566756	0.521216	1.08815	ENSG00000170419	VSTM2A
ENSG00000170421	59.2807	158.582	75.9432	43.8401	ENSG00000170421	KRT8
ENSG00000170423	10.8628	0.467345	0.748247	1.19007	ENSG00000170423	KRT78
ENSG00000170425	9.03205	36.4927	13.2399	13.2342	ENSG00000170425	ADORA2B
ENSG00000170426	3.20939	1.53995	1.27182	1.91581	ENSG00000170426	SDR9C7
ENSG00000170430	8.32237	12.1136	9.22252	9.5328	ENSG00000170430	MGMT
ENSG00000170439	0.0481686	0	0	0.0843526	ENSG00000170439	METTL7B
ENSG00000170442	1.07049	1.15124	1.85744	0.532288	ENSG00000170442	KRT86
ENSG00000170445	43.2019	32.9562	41.3121	35.6098	ENSG00000170445	HARS
ENSG00000170448	6.85643	10.3349	13.7989	14.3465	ENSG00000170448	NFXL1
ENSG00000170454	3.35085	1.48545	3.40579	1.71112	ENSG00000170454	KRT75
ENSG00000170456	3.69395	6.19636	5.66355	11.6574	ENSG00000170456	DENND5B
ENSG00000170458	1.42882	1.07606	1.09993	0.280485	ENSG00000170458	CD14
ENSG00000170464	2.35251	6.03973	4.58208	8.78979	ENSG00000170464	DNAJC18
ENSG00000170465	90.6548	3.97996	18.481	19.0691	ENSG00000170465	KRT6C
ENSG00000170468	5.86465	5.53407	6.81797	4.87541	ENSG00000170468	RIOX1
ENSG00000170469	2.3702	5.35571	4.37823	2.90935	ENSG00000170469	SPATA24
ENSG00000170471	31.707	31.6341	34.1227	32.986	ENSG00000170471	RALGAPB
ENSG00000170473	21.8215	22.058	18.038	11.4952	ENSG00000170473	PYM1
ENSG00000170476	1.21552	2.14273	2.29971	3.99264	ENSG00000170476	MZB1
ENSG00000170477	9.88521	0.321291	0.0561276	1.34625	ENSG00000170477	KRT4
ENSG00000170482	2.67269	2.32987	2.26021	2.88896	ENSG00000170482	SLC23A1
ENSG00000170484	0.401203	0.257989	0.232018	0.717195	ENSG00000170484	KRT74
ENSG00000170485	49.676	23.3585	36.3292	38.485	ENSG00000170485	NPAS2
ENSG00000170486	1.00054	1.08025	1.0839	0.940704	ENSG00000170486	KRT72
ENSG00000170498	2.10934	1.36679	1.81289	13.9834	ENSG00000170498	KISS1
ENSG00000170500	2.96748	3.33763	6.7048	68.816	ENSG00000170500	LONRF2
ENSG00000170502	13.6997	22.9246	19.202	30.0935	ENSG00000170502	NUDT9
ENSG00000170509	0.397111	0.933055	0.844617	1.07435	ENSG00000170509	HSD17B13
ENSG00000170515	88.842	82.2087	80.2477	48.0492	ENSG00000170515	PA2G4
ENSG00000170516	1.30607	2.52926	3.41388	4.1246	ENSG00000170516	COX7B2
ENSG00000170522	27.3697	42.0498	11.3381	19.7868	ENSG00000170522	ELOVL6
ENSG00000170523	0	0	0.0309825	0	ENSG00000170523	KRT83
ENSG00000170525	11.7871	10.4737	15.5551	26.4196	ENSG00000170525	PFKFB3
ENSG00000170537	7.13942	14.3271	6.63463	11.6761	ENSG00000170537	TMC7
ENSG00000170540	78.7015	136.62	38.2115	41.2055	ENSG00000170540	ARL6IP1
ENSG00000170542	7.66793	7.19998	6.01476	11.7068	ENSG00000170542	SERPINB9
ENSG00000170545	31.1119	19.9268	20.089	20.5591	ENSG00000170545	SMAGP
ENSG00000170549	2.35649	1.29926	10.3285	3.35631	ENSG00000170549	IRX1
ENSG00000170558	0.413624	0.537703	0.862366	9.91639	ENSG00000170558	CDH2
ENSG00000170561	16.3713	14.3087	28.3294	11.0906	ENSG00000170561	IRX2
ENSG00000170571	29.6284	51.2908	24.3835	13.2634	ENSG00000170571	EMB
ENSG00000170577	0.0511169	0.190294	0.0888407	0.257523	ENSG00000170577	SIX2
ENSG00000170579	4.71105	7.31181	7.75845	17.764	ENSG00000170579	DLGAP1
ENSG00000170581	76.2222	102.79	105.081	137.51	ENSG00000170581	STAT2
ENSG00000170584	9.36239	15.64	14.4507	9.04057	ENSG00000170584	NUDCD2
ENSG00000170604	6.68849	6.01745	8.22772	4.89542	ENSG00000170604	IRF2BP1

ENSG00000170605	0.21563	0.623785	0.439354	0.882188	ENSG00000170605	OR9K2
ENSG00000170606	82.3444	65.5378	72.2529	52.4268	ENSG00000170606	HSPA4
ENSG00000170608	0.139776	0.109295	0.172909	0	ENSG00000170608	FOXA3
ENSG00000170613	0.0670517	0.064796	0.0799546	0.125941	ENSG00000170613	FAM71B
ENSG00000170615	0.795367	0.942101	1.00821	0.615745	ENSG00000170615	SLC26A5
ENSG00000170616	0.258928	0.343924	0.427076	0.569371	ENSG00000170616	SCRT1
ENSG00000170619	14.5552	12.2064	13.3445	7.96366	ENSG00000170619	COMMD5
ENSG00000170624	0.38683	0.152535	0.515265	9.36643	ENSG00000170624	SGCD
ENSG00000170627	0.696283	2.084	2.1622	2.24416	ENSG00000170627	GTSF1
ENSG00000170629	5.88301	13.6344	12.4532	19.8904	ENSG00000170629	DPY19L2P2
ENSG00000170631	3.65126	7.79223	7.06112	9.528	ENSG00000170631	ZNF16
ENSG00000170632	21.137	24.7306	22.8724	23.099	ENSG00000170632	ARMC10
ENSG00000170633	12.4768	13.008	14.3746	12.4229	ENSG00000170633	RNF34
ENSG00000170634	10.6218	14.9803	14.2173	16.7768	ENSG00000170634	ACYP2
ENSG00000170638	19.6023	28.5367	24.6101	16.9337	ENSG00000170638	TRABD
ENSG00000170647	1.07202	0.826435	1.2831	1.98182	ENSG00000170647	TMEM133
ENSG00000170653	4.25698	9.98421	10.8959	13.5184	ENSG00000170653	ATF7
ENSG00000170667	2.04495	1.23284	2.31491	2.30365	ENSG00000170667	RASA4B
ENSG00000170677	35.5962	16.0735	16.043	11.8325	ENSG00000170677	SOCS6
ENSG00000170681	0.593237	0.555384	0.519693	1.99064	ENSG00000170681	CAVIN4
ENSG00000170683	0.575579	0.332346	0.100121	0.125488	ENSG00000170683	OR10A3
ENSG00000170684	0.625353	1.56721	1.81969	1.25597	ENSG00000170684	ZNF296
ENSG00000170688	1.62278	1.31316	1.723	1.16109	ENSG00000170688	OR5E1P
ENSG00000170689	0.0530797	0.102185	0.230889	0.173866	ENSG00000170689	HOXB9
ENSG00000170703	0.500306	1.07622	2.02773	2.26078	ENSG00000170703	TTLL6
ENSG00000170727	29.1031	28.2616	33.7888	23.9522	ENSG00000170727	BOP1
ENSG00000170734	10.8395	14.835	17.6231	11.3538	ENSG00000170734	POLH
ENSG00000170743	0.0343054	0.176904	0.253263	0.180422	ENSG00000170743	SYT9
ENSG00000170745	2.63023	3.70988	3.32456	4.49778	ENSG00000170745	KCNS3
ENSG00000170748	1.13898	0.623424	1.43799	8.87613	ENSG00000170748	RBMXL2
ENSG00000170759	88.2442	63.1488	61.7639	55.1563	ENSG00000170759	KIF5B
ENSG00000170775	0.49686	1.01625	2.5579	0.682005	ENSG00000170775	GPR37
ENSG00000170776	69.119	83.111	60.6399	114.256	ENSG00000170776	AKAP13
ENSG00000170777	0.0669504	0.277636	0.193671	0.337098	ENSG00000170777	TPD52L3
ENSG00000170779	18.2154	25.352	12.2728	14.9868	ENSG00000170779	CDCA4
ENSG00000170782	0.248433	0.179269	0.270017	0.946904	ENSG00000170782	OR10A4
ENSG00000170786	9.84747	16.1909	6.325	5.25033	ENSG00000170786	SDR16C5
ENSG00000170788	2.76489	4.15333	3.11588	8.51936	ENSG00000170788	DYDC1
ENSG00000170790	0.174221	0.209454	0.397689	1.05399	ENSG00000170790	OR10A2
ENSG00000170791	19.1195	20.8888	19.8636	18.5129	ENSG00000170791	CHCHD7
ENSG00000170801	0.0278338	0.0629866	0.0903335	1.58528	ENSG00000170801	HTRA3
ENSG00000170802	21.0846	21.0877	14.2356	12.292	ENSG00000170802	FOXN2
ENSG00000170803	0.061886	0.119086	0.161432	0.741369	ENSG00000170803	OR2AG1
ENSG00000170807	0.285023	0.36345	0.311795	0.764389	ENSG00000170807	LMOD2
ENSG00000170819	0.170828	0.327255	0	0.54346	ENSG00000170819	BFSP2
ENSG00000170820	0.275848	1.04044	1.00455	1.39807	ENSG00000170820	FSHR
ENSG00000170827	0.131018	0.153627	0.421822	0.132658	ENSG00000170827	CELP
ENSG00000170832	22.0543	29.4924	30.4983	38.8015	ENSG00000170832	USP32
ENSG00000170835	1.08964	0.756305	0.890444	0.349854	ENSG00000170835	CEL
ENSG00000170836	4.92751	4.25093	4.59643	4.3027	ENSG00000170836	PPM1D
ENSG00000170837	0.419303	0.503881	0.335935	0.747875	ENSG00000170837	GPR27
ENSG00000170848	1.73506	1.44626	1.68643	4.04055	ENSG00000170848	PSG6
ENSG00000170852	17.7875	30.9191	20.405	24.4592	ENSG00000170852	KBTBD2
ENSG00000170854	22.0801	26.0548	32.7804	16.7956	ENSG00000170854	RIOX2

ENSG00000170855	10.6435	7.58714	11.6828	4.43186	ENSG00000170855	TRIAP1
ENSG00000170858	0.00527241	0.0101636	0.00924141	0.017363	ENSG00000170858	LILRP2
ENSG00000170860	4.06838	4.79968	2.39091	3.52188	ENSG00000170860	LSM3
ENSG00000170866	0.0111762	0.0215246	0	0	ENSG00000170866	LILRA3
ENSG00000170871	15.2351	13.128	13.0582	13.6816	ENSG00000170871	KIAA0232
ENSG00000170873	49.5309	74.9643	63.8836	80.0631	ENSG00000170873	MTSS1
ENSG00000170876	80.673	123.773	85.7901	44.5506	ENSG00000170876	TMEM43
ENSG00000170881	21.044	21.9053	18.7239	6.5802	ENSG00000170881	RNF139
ENSG00000170889	9.24947	14.556	15.5378	8.66882	ENSG00000170889	RPS9
ENSG00000170890	0.772359	1.48222	0.22302	1.52032	ENSG00000170890	PLA2G1B
ENSG00000170891	0	0.364892	0.114039	0.706403	ENSG00000170891	CYTL1
ENSG00000170892	1.51921	0.0206544	0.0163054	0	ENSG00000170892	TSEN34
ENSG00000170893	0.109555	0.0783507	0.159079	0.175344	ENSG00000170893	TRH
ENSG00000170899	7.58652	15.4984	15.7823	14.0891	ENSG00000170899	GSTA4
ENSG00000170903	6.64731	7.24431	13.5335	8.40352	ENSG00000170903	MSANTD4
ENSG00000170906	6.25364	4.86093	4.30662	4.47814	ENSG00000170906	NDUFA3
ENSG00000170909	0.0673209	0.124011	0.116879	0.167476	ENSG00000170909	OSCAR
ENSG00000170915	0.659784	3.68564	1.05868	2.22464	ENSG00000170915	PAQR8
ENSG00000170917	6.16924	13.7236	12.2769	29.7962	ENSG00000170917	NUDT6
ENSG00000170920	0.0665741	0	0	0	ENSG00000170920	OR7G3
ENSG00000170921	73.2946	108.315	170.856	111.732	ENSG00000170921	TANC2
ENSG00000170923	0	0.056838	0	0	ENSG00000170923	OR7G2
ENSG00000170925	0.285981	0.688376	0.580711	1.74377	ENSG00000170925	TEX13B
ENSG00000170927	0.114427	0.306197	0.309053	0.466056	ENSG00000170927	PKHD1
ENSG00000170929	0	0	0	0	ENSG00000170929	OR1M1
ENSG00000170935	0.24725	0	0.213159	0	ENSG00000170935	NCBP2L
ENSG00000170946	15.7127	23.5431	24.3692	24.0288	ENSG00000170946	DNAJC24
ENSG00000170948	0	0	0.0632729	0.0954319	ENSG00000170948	MBD3L1
ENSG00000170949	21.6058	27.0501	27.2773	27.2045	ENSG00000170949	ZNF160
ENSG00000170950	0	0.130808	0.0295579	0.0743805	ENSG00000170950	PGK2
ENSG00000170953	0	0	0	0	ENSG00000170953	OR8B12
ENSG00000170954	10.2422	11.5172	9.27227	11.2159	ENSG00000170954	ZNF415
ENSG00000170955	46.8291	40.3965	11.2241	23.3293	ENSG00000170955	CAVIN3
ENSG00000170956	0.236641	0.0815275	0.307697	0.706281	ENSG00000170956	CEACAM3
ENSG00000170959	1.10469	2.82491	2.99425	4.11733	ENSG00000170959	DCDC1
ENSG00000170961	10.8956	14.6944	0.853038	39.5123	ENSG00000170961	HAS2
ENSG00000170962	0.13374	0.041204	0.0745093	0.12126	ENSG00000170962	PDGFD
ENSG00000170965	6.95259	3.10865	1.25448	0.677428	ENSG00000170965	PLAC1
ENSG00000170967	0.126898	0.163185	0.20258	0.394619	ENSG00000170967	DDI1
ENSG00000170989	15.4561	4.59283	1.10171	2.95505	ENSG00000170989	S1PR1
ENSG00000171004	1.36501	2.29253	0.923342	0.253428	ENSG00000171004	HS6ST2
ENSG00000171014	0	0	0	0.0604902	ENSG00000171014	OR4D5
ENSG00000171016	2.35332	1.79457	1.97817	4.40924	ENSG00000171016	PYGO1
ENSG00000171017	20.834	14.181	13.3631	10.6691	ENSG00000171017	LRRC8E
ENSG00000171033	1.57244	3.13388	0.943341	2.23063	ENSG00000171033	PKIA
ENSG00000171044	7.11413	8.92049	7.74957	9.6802	ENSG00000171044	XKR6
ENSG00000171045	7.95742	12.7546	13.7524	11.4101	ENSG00000171045	TSNARE1
ENSG00000171049	1.14102	2.49938	2.63442	2.88879	ENSG00000171049	FPR2
ENSG00000171051	2.69743	2.99893	3.19208	4.90702	ENSG00000171051	FPR1
ENSG00000171053	1.21808	3.51042	2.61678	5.26825	ENSG00000171053	PATE1
ENSG00000171054	0	0	0	0	ENSG00000171054	OR13H1
ENSG00000171055	28.0981	27.316	21.7249	33.6379	ENSG00000171055	FEZ2
ENSG00000171056	2.98974	7.06309	6.80136	3.90101	ENSG00000171056	SOX7
ENSG00000171060	0.473619	1.40244	1.20939	1.5191	ENSG00000171060	C8orf74

ENSG00000171067	27.6409	27.1913	22.8405	28.8282	ENSG00000171067	C11orf24
ENSG00000171084	0.468121	1.17061	2.13676	0.786671	ENSG00000171084	FAM86JP
ENSG00000171094	0.626551	0.795355	1.16411	1.03282	ENSG00000171094	ALK
ENSG00000171097	11.1988	19.6914	8.65219	19.7651	ENSG00000171097	KYAT1
ENSG00000171100	4.17428	6.82476	5.47344	4.12138	ENSG00000171100	MTM1
ENSG00000171101	0	0.458205	0.0424592	0.098111	ENSG00000171101	SIGLEC17P
ENSG00000171102	0	0	0	0	ENSG00000171102	OBP2B
ENSG00000171103	6.09865	6.57027	9.89948	5.79771	ENSG00000171103	TRMT61B
ENSG00000171105	9.33591	6.43532	5.32385	9.77619	ENSG00000171105	INSR
ENSG00000171109	33.6379	35.3329	46.4811	31.3058	ENSG00000171109	MFN1
ENSG00000171115	0.235077	0.555457	0.393519	1.04531	ENSG00000171115	GIMAP8
ENSG00000171116	0.255542	0	0	0	ENSG00000171116	HSFX1
ENSG00000171119	0.547117	0.157789	0.285217	0.41726	ENSG00000171119	NRTN
ENSG00000171121	0.207664	1.17026	0.535962	1.38149	ENSG00000171121	KCNMB3
ENSG00000171124	34.886	26.1687	17.6016	21.1623	ENSG00000171124	FUT3
ENSG00000171126	0.146209	0.171647	0.18119	0.130954	ENSG00000171126	KCNG3
ENSG00000171129	0.558345	2.28722	1.04612	0.50374	ENSG00000171129	HSFX2
ENSG00000171130	4.22198	1.86237	0.864423	1.11061	ENSG00000171130	ATP6V0E2
ENSG00000171132	5.05337	11.9291	15.8972	20.6973	ENSG00000171132	PRKCE
ENSG00000171133	0	0	0.0513673	0	ENSG00000171133	OR2K2
ENSG00000171135	13.9754	12.2919	13.4435	4.06829	ENSG00000171135	JAGN1
ENSG00000171136	0	0.130257	0.117572	0	ENSG00000171136	RLN3
ENSG00000171148	16.0248	22.2504	21.6326	17.6501	ENSG00000171148	TADA3
ENSG00000171150	4.05146	4.32063	4.81129	14.1888	ENSG00000171150	SOCS5
ENSG00000171155	14.8399	12.0589	5.59097	6.80521	ENSG00000171155	C1GALT1C1
ENSG00000171159	48.8668	24.0222	23.3178	13.7202	ENSG00000171159	C9orf16
ENSG00000171160	5.05853	7.18633	7.82534	4.73906	ENSG00000171160	MORN4
ENSG00000171161	10.8658	12.1529	14.8529	8.76223	ENSG00000171161	ZNF672
ENSG00000171163	34.32	35.784	39.9514	24.4588	ENSG00000171163	ZNF692
ENSG00000171169	4.71917	3.12292	4.79315	4.04569	ENSG00000171169	NAIF1
ENSG00000171174	3.1586	4.5775	4.55062	5.85482	ENSG00000171174	RBKS
ENSG00000171180	0	0	0	0	ENSG00000171180	OR2M4
ENSG00000171189	0.78429	0.957865	1.78801	2.65453	ENSG00000171189	GRIK1
ENSG00000171195	0.124714	0.154133	0.434409	0.406802	ENSG00000171195	MUC7
ENSG00000171199	0	0.113418	0.100855	0	ENSG00000171199	OPRPN
ENSG00000171201	0.100374	0	0.135838	0.335326	ENSG00000171201	SMR3B
ENSG00000171202	22.8914	17.7785	13.4508	11.8481	ENSG00000171202	TMEM126A
ENSG00000171204	19.3184	16.8795	16.1876	12.5779	ENSG00000171204	TMEM126B
ENSG00000171206	18.9591	38.5411	28.2379	25.4132	ENSG00000171206	TRIM8
ENSG00000171208	21.061	24.5632	14.0458	9.59356	ENSG00000171208	NETO2
ENSG00000171209	0	0	0	0	ENSG00000171209	CSN3
ENSG00000171217	1.13703	4.40439	2.32293	2.43807	ENSG00000171217	CLDN20
ENSG00000171219	27.378	19.2938	11.0239	9.9263	ENSG00000171219	CDC42BPG
ENSG00000171222	24.982	13.7343	13.1963	11.4827	ENSG00000171222	SCAND1
ENSG00000171223	133.782	142.343	116.661	52.6679	ENSG00000171223	JUNB
ENSG00000171224	1.50195	2.08625	1.63738	1.19607	ENSG00000171224	C10orf35
ENSG00000171227	1.38793	2.78024	1.717	3.7432	ENSG00000171227	TMEM37
ENSG00000171234	0.830299	1.1059	1.14675	1.25929	ENSG00000171234	UGT2B7
ENSG00000171236	3.1569	5.33676	2.12105	3.27436	ENSG00000171236	LRG1
ENSG00000171241	2.87138	12.7391	2.82009	9.32491	ENSG00000171241	SHCBP1
ENSG00000171243	0.253394	0.382211	0.512341	0.631005	ENSG00000171243	SOSTDC1
ENSG00000171246	0.563545	0.418917	0.211672	0.631894	ENSG00000171246	NPTX1
ENSG00000171262	3.8484	5.44486	6.22866	8.49186	ENSG00000171262	FAM98B
ENSG00000171282	0.562555	2.64052	2.58756	4.87474	ENSG00000171282	RP11-1055B8.7

ENSG00000171291	6.94086	11.4332	9.68092	15.4899	ENSG00000171291	ZNF439
ENSG00000171295	14.5085	22.0897	16.2689	23.9332	ENSG00000171295	ZNF440
ENSG00000171298	24.3354	41.8527	60.6262	13.6201	ENSG00000171298	GAA
ENSG00000171302	47.8586	57.2751	27.9244	30.1325	ENSG00000171302	CANT1
ENSG00000171303	0.611382	1.09773	0.980552	2.09405	ENSG00000171303	KCNK3
ENSG00000171307	33.2055	35.3392	24.4932	24.7317	ENSG00000171307	ZDHHC16
ENSG00000171310	16.4357	24.6975	20.0717	19.9775	ENSG00000171310	CHST11
ENSG00000171311	16.3959	20.5283	19.7084	15.2332	ENSG00000171311	EXOSC1
ENSG00000171314	191.526	140.983	89.8577	82.2012	ENSG00000171314	PGAM1
ENSG00000171316	14.5316	18.3216	22.8703	21.5712	ENSG00000171316	CHD7
ENSG00000171320	3.76661	9.43429	3.87995	8.77771	ENSG00000171320	ESCO2
ENSG00000171345	964.348	407.098	13.8409	74.5109	ENSG00000171345	KRT19
ENSG00000171346	737.9	477.178	58.9179	166.825	ENSG00000171346	KRT15
ENSG00000171357	2.12181	6.2858	5.08264	6.45702	ENSG00000171357	LURAP1
ENSG00000171360	0.150221	0.0459216	0.020758	0.165907	ENSG00000171360	KRT38
ENSG00000171365	12.7679	6.73644	4.86943	5.52341	ENSG00000171365	CLCN5
ENSG00000171368	4.17876	1.45209	1.66692	2.43323	ENSG00000171368	TPPP
ENSG00000171385	1.33055	0.448683	0.77819	1.08734	ENSG00000171385	KCND3
ENSG00000171388	0.290961	3.04801	0.0905786	1.05075	ENSG00000171388	APLN
ENSG00000171396	0	0	0.148052	0	ENSG00000171396	KRTAP4-4
ENSG00000171401	113.402	2.79792	0.54011	1.72861	ENSG00000171401	KRT13
ENSG00000171402	0	0.303617	0	0.338298	ENSG00000171402	XAGE3
ENSG00000171403	0.739873	0.285524	0.254944	0.425846	ENSG00000171403	KRT9
ENSG00000171405	0.882007	1.12612	2.00614	1.81681	ENSG00000171405	XAGE5
ENSG00000171408	0.317315	0.680346	0.619439	4.36994	ENSG00000171408	PDE7B
ENSG00000171421	24.537	15.6347	19.0144	9.21149	ENSG00000171421	MRPL36
ENSG00000171425	6.9697	6.70166	6.68823	4.81379	ENSG00000171425	ZNF581
ENSG00000171428	2.55396	1.89355	1.92072	1.52322	ENSG00000171428	NAT1
ENSG00000171431	0.0822056	0	0.0143206	0.0181861	ENSG00000171431	KRT20
ENSG00000171433	0	0	0	0	ENSG00000171433	GLOD5
ENSG00000171435	0.328508	0.936092	0.65996	0.984678	ENSG00000171435	KSR2
ENSG00000171443	10.5347	4.99316	6.12531	4.36497	ENSG00000171443	ZNF524
ENSG00000171444	28.5514	29.139	42.218	30.4115	ENSG00000171444	MCC
ENSG00000171446	0	0	0.093307	0.0391215	ENSG00000171446	KRT27
ENSG00000171448	1.57217	1.60008	2.07162	2.14996	ENSG00000171448	ZBTB26
ENSG00000171450	0.0223392	0.347209	0.137134	0.252067	ENSG00000171450	CDK5R2
ENSG00000171451	1.56681	1.46335	1.53373	4.4437	ENSG00000171451	DSEL
ENSG00000171453	17.7081	19.3075	22.2171	17.4297	ENSG00000171453	POLR1C
ENSG00000171456	18.8869	33.2271	34.772	45.3023	ENSG00000171456	ASXL1
ENSG00000171459	0	0.0321361	0.0580758	0	ENSG00000171459	OR1L6
ENSG00000171462	8.37332	25.3903	17.867	8.22197	ENSG00000171462	DLK2
ENSG00000171466	28.8261	34.5063	36.0969	33.7744	ENSG00000171466	ZNF562
ENSG00000171467	8.07446	10.4994	7.32945	15.7875	ENSG00000171467	ZNF318
ENSG00000171469	38.0702	43.8455	55.7225	33.0903	ENSG00000171469	ZNF561
ENSG00000171471	0.974483	1.7579	1.79204	2.378	ENSG00000171471	MAP1LC3B2
ENSG00000171475	10.494	10.3649	10.3231	15.6724	ENSG00000171475	WIPF2
ENSG00000171476	211.924	28.8228	17.2917	41.4153	ENSG00000171476	HOPX
ENSG00000171478	0	0	0	0	ENSG00000171478	SPACA5B
ENSG00000171481	0	0.0537111	0.118518	0	ENSG00000171481	OR1L3
ENSG00000171483	0	0.0772503	0.017522	0.0228706	ENSG00000171483	SSX6
ENSG00000171484	0	0	0.0540033	0	ENSG00000171484	OR1B1
ENSG00000171487	0.133889	0.341464	0.845709	0.722368	ENSG00000171487	NLRP5
ENSG00000171488	12.6307	27.7549	7.92227	17.248	ENSG00000171488	LRRC8C
ENSG00000171489	10.1445	26.0479	21.435	6.52098	ENSG00000171489	SPACA5

ENSG00000171490	65.2991	52.0555	69.0484	38.4418	ENSG00000171490	RSL1D1
ENSG00000171492	23.7256	29.7141	26.8113	10.193	ENSG00000171492	LRRC8D
ENSG00000171495	0.056961	0.564632	0.203962	0.12661	ENSG00000171495	MROH2B
ENSG00000171496	0	0.0553909	0	0.188232	ENSG00000171496	OR1L8
ENSG00000171497	14.0723	13.6596	14.9383	14.0116	ENSG00000171497	PPID
ENSG00000171501	0	0	0	0	ENSG00000171501	OR1N2
ENSG00000171502	0.252907	0.64776	0.331165	2.52667	ENSG00000171502	COL24A1
ENSG00000171503	10.0985	16.0598	13.5885	13.9158	ENSG00000171503	ETFDH
ENSG00000171505	0.668316	0.642722	0.116152	0.0765044	ENSG00000171505	OR1N1
ENSG00000171509	0.741281	0.983368	1.98776	1.34952	ENSG00000171509	RXFP1
ENSG00000171517	14.2239	38.73	19.4578	8.61666	ENSG00000171517	LPAR3
ENSG00000171522	5.27002	5.47882	2.52449	4.04709	ENSG00000171522	PTGER4
ENSG00000171530	76.8946	50.7213	57.1262	55.6869	ENSG00000171530	TBCA
ENSG00000171532	0.567704	0.836588	0.921792	0.833759	ENSG00000171532	NEUROD2
ENSG00000171533	1.25225	0.75441	0.96901	1.70092	ENSG00000171533	MAP6
ENSG00000171540	0.0295622	0.0712975	0.225308	0.0813393	ENSG00000171540	OTP
ENSG00000171551	0	0.0534739	0.0355218	0.0217817	ENSG00000171551	ECEL1
ENSG00000171552	88.4993	54.4817	34.6059	33.8149	ENSG00000171552	BCL2L1
ENSG00000171557	0.261684	0.991113	0.983331	0.34232	ENSG00000171557	FGG
ENSG00000171560	0.0690515	0.0710728	0.0473457	0.130477	ENSG00000171560	FGA
ENSG00000171561	0.117596	0.169743	0.10227	0.320391	ENSG00000171561	OR2AT4
ENSG00000171564	0.896114	1.10564	1.16375	2.02328	ENSG00000171564	FGB
ENSG00000171566	48.5253	50.0366	53.4103	27.7199	ENSG00000171566	PLRG1
ENSG00000171570	0.542837	0.202499	0	0.304266	ENSG00000171570	RAB4B-EGLN2
ENSG00000171574	6.22595	7.42909	10.9272	6.33107	ENSG00000171574	ZNF584
ENSG00000171587	5.17375	11.9492	8.61954	6.74933	ENSG00000171587	DSCAM
ENSG00000171595	0.0283019	0.0432053	0.0782215	0.0492784	ENSG00000171595	DNAI2
ENSG00000171596	0.791748	2.01931	1.85223	3.38088	ENSG00000171596	NMUR1
ENSG00000171603	130.201	240.085	157.81	141.108	ENSG00000171603	CLSTN1
ENSG00000171604	13.0496	19.1516	13.7748	38.7725	ENSG00000171604	CXXC5
ENSG00000171606	23.1524	32.2242	35.8812	24.4402	ENSG00000171606	ZNF274
ENSG00000171608	10.9598	18.0302	16.6681	36.8949	ENSG00000171608	PIK3CD
ENSG00000171611	0	0.0831634	0	0.374855	ENSG00000171611	PTCRA
ENSG00000171612	3.57609	4.61552	4.09103	4.90767	ENSG00000171612	SLC25A33
ENSG00000171617	31.7024	17.6657	14.7108	41.4764	ENSG00000171617	ENC1
ENSG00000171621	8.42129	5.01664	11.3462	6.98678	ENSG00000171621	SPSB1
ENSG00000171631	1.13691	1.10789	1.08	1.42781	ENSG00000171631	P2RY6
ENSG00000171634	40.5915	31.3422	32.0285	89.4463	ENSG00000171634	BPTF
ENSG00000171643	0.158583	0.211907	0.261233	0.260345	ENSG00000171643	S100Z
ENSG00000171649	6.15759	5.80539	6.43191	4.63503	ENSG00000171649	ZIK1
ENSG00000171657	1.46272	3.90341	3.21497	6.13312	ENSG00000171657	GPR82
ENSG00000171658	4.16632	19.0334	6.39491	10.2767	ENSG00000171658	NMRAL2P
ENSG00000171659	0.295195	0.708229	1.05001	0.778886	ENSG00000171659	GPR34
ENSG00000171680	108.857	186.574	97.4928	64.0281	ENSG00000171680	PLEKHG5
ENSG00000171681	30.1891	49.0295	36.9768	48.3493	ENSG00000171681	ATF7IP
ENSG00000171695	0.0862465	0.0704158	0.127258	0.0795399	ENSG00000171695	LKAAEAR1
ENSG00000171700	11.0822	8.86811	5.87575	7.242	ENSG00000171700	RGS19
ENSG00000171703	12.4535	17.7595	22.6639	13.1624	ENSG00000171703	TCEA2
ENSG00000171711	0	0	0	0	ENSG00000171711	DEFB4A
ENSG00000171714	0.17155	0.164019	0.147492	0.372595	ENSG00000171714	ANO5
ENSG00000171720	33.685	28.2327	28.6012	26.2955	ENSG00000171720	HDAC3
ENSG00000171722	0.297968	0.374443	0.553176	0.841563	ENSG00000171722	SPATA46
ENSG00000171723	11.5749	18.569	19.8918	25.9453	ENSG00000171723	GPHN
ENSG00000171724	0.0707394	0.45074	0.345356	1.76038	ENSG00000171724	VAT1L

ENSG00000171729	19.8344	17.7612	10.7706	9.02396	ENSG00000171729	TMEM51
ENSG00000171735	16.0522	22.7446	17.2578	21.6529	ENSG00000171735	CAMTA1
ENSG00000171747	1.37664	1.84921	2.39674	1.44209	ENSG00000171747	LGALS4
ENSG00000171757	1.63638	3.09337	2.04261	4.34614	ENSG00000171757	LRRC34
ENSG00000171759	3.73953	7.79177	8.17466	11.2363	ENSG00000171759	PAH
ENSG00000171763	7.33836	9.0094	11.4906	6.73439	ENSG00000171763	SPATA5L1
ENSG00000171766	2.57723	4.89902	4.31751	6.91645	ENSG00000171766	GATM
ENSG00000171772	0	0.0411033	0.154197	0.233401	ENSG00000171772	SYCE1
ENSG00000171773	0.661708	0.41149	0.679701	1.23054	ENSG00000171773	NXNL1
ENSG00000171777	0.788387	1.30233	1.21759	1.52114	ENSG00000171777	RASGRP4
ENSG00000171786	0.569017	0.518755	0.55978	0.956163	ENSG00000171786	NHLH1
ENSG00000171790	1.36101	3.07871	4.17529	3.20682	ENSG00000171790	SLFNL1
ENSG00000171791	1.00839	1.32755	1.42086	1.20827	ENSG00000171791	BCL2
ENSG00000171792	8.55242	18.2496	15.0202	13.3135	ENSG00000171792	RHNO1
ENSG00000171793	38.3812	45.913	50.4006	53.2423	ENSG00000171793	CTPS1
ENSG00000171794	0	0.150211	0.181017	0.0567715	ENSG00000171794	UTF1
ENSG00000171798	0.185342	0.80244	0.37736	1.67852	ENSG00000171798	KNDC1
ENSG00000171804	0.0543118	0.129919	0.234535	0.145178	ENSG00000171804	WDR87
ENSG00000171806	3.31117	2.93054	3.82054	1.86966	ENSG00000171806	METTL18
ENSG00000171811	1.17162	0.554021	1.09354	2.04771	ENSG00000171811	CFAP46
ENSG00000171812	0.459889	1.64301	1.18128	0.954452	ENSG00000171812	COL8A2
ENSG00000171813	13.6637	8.47914	11.048	5.17208	ENSG00000171813	PWWP2B
ENSG00000171815	0.0109211	0.0105287	0.00951881	0.0120005	ENSG00000171815	PCDHB1
ENSG00000171817	1.17614	1.2878	2.19691	3.81898	ENSG00000171817	ZNF540
ENSG00000171819	0.573936	1.44521	2.00814	1.74553	ENSG00000171819	ANGPTL7
ENSG00000171823	3.98044	5.57279	3.82054	16.3039	ENSG00000171823	FBXL14
ENSG00000171824	46.8076	67.098	54.6657	71.4089	ENSG00000171824	EXOSC10
ENSG00000171827	3.31716	4.51546	3.1859	1.75753	ENSG00000171827	ZNF570
ENSG00000171840	6.46519	1.70447	2.61992	2.94047	ENSG00000171840	NINJ2
ENSG00000171843	7.93392	14.1911	14.0036	18.8209	ENSG00000171843	MLLT3
ENSG00000171847	0.368479	0.74142	0.497485	0.459374	ENSG00000171847	FAM90A1
ENSG00000171848	4.95695	15.3755	2.78161	18.5142	ENSG00000171848	RRM2
ENSG00000171853	42.3469	70.78	81.3226	74.8818	ENSG00000171853	TRAPPC12
ENSG00000171855	0	0.373485	0.403778	0.665417	ENSG00000171855	IFNB1
ENSG00000171858	302.43	309.694	317.88	180.184	ENSG00000171858	RPS21
ENSG00000171860	0.196411	0.512773	1.07805	0.613439	ENSG00000171860	C3AR1
ENSG00000171861	10.6109	11.8253	14.4395	12.5326	ENSG00000171861	MRM3
ENSG00000171862	40.4935	51.7176	51.9386	44.3624	ENSG00000171862	PTEN
ENSG00000171863	489.315	366.77	295.059	191.098	ENSG00000171863	RPS7
ENSG00000171864	0.685865	1.67729	1.04365	1.8263	ENSG00000171864	PRND
ENSG00000171865	14.6584	16.905	17.2967	14.0778	ENSG00000171865	RNASEH1
ENSG00000171867	379.822	467.103	320.76	181.529	ENSG00000171867	PRNP
ENSG00000171872	0.17155	0.735216	0.878618	1.14975	ENSG00000171872	KLF17
ENSG00000171873	0.288842	0.139164	0.0359146	0.203801	ENSG00000171873	ADRA1D
ENSG00000171877	6.24849	6.70373	1.76299	5.37987	ENSG00000171877	FRMD5
ENSG00000171885	0.102091	0.850996	0.035575	0.693557	ENSG00000171885	AQP4
ENSG00000171903	11.0827	15.1481	2.05718	6.49393	ENSG00000171903	CYP4F11
ENSG00000171914	5.80665	7.45647	6.97491	22.3379	ENSG00000171914	TLN2
ENSG00000171916	6.25525	41.981	17.7461	36.6572	ENSG00000171916	LGALS9C
ENSG00000171928	53.3017	44.647	39.526	31.1664	ENSG00000171928	TVP23B
ENSG00000171931	2.20924	3.9378	4.02114	5.66713	ENSG00000171931	FBXW10
ENSG00000171936	0.0655639	0	0	0.0926074	ENSG00000171936	OR10H3
ENSG00000171940	25.1695	23.7021	23.9204	21.6209	ENSG00000171940	ZNF217
ENSG00000171942	0	0.0898861	0.159784	0.0833746	ENSG00000171942	OR10H2

ENSG00000171943	3.48712	4.27964	3.41445	4.17598	ENSG00000171943	SRGAP2C
ENSG00000171944	0.196692	0.445104	0.569846	0.214011	ENSG00000171944	OR52A5
ENSG00000171951	0.269415	0.0413834	0.486384	0.577782	ENSG00000171951	SCG2
ENSG00000171953	13.4717	19.9402	14.3631	16.4718	ENSG00000171953	ATPAF2
ENSG00000171954	1.79741	0.525362	0.842563	0.8574	ENSG00000171954	CYP4F22
ENSG00000171956	0.395289	1.50067	1.86399	3.38146	ENSG00000171956	FOXB1
ENSG00000171960	14.3538	22.4708	14.4505	15.0906	ENSG00000171960	PPIH
ENSG00000171962	11.6296	28.2003	24.5642	44.2099	ENSG00000171962	DRC3
ENSG00000171970	5.46168	5.80209	5.89277	4.67831	ENSG00000171970	ZNF57
ENSG00000171984	3.67842	4.79124	4.01905	6.6099	ENSG00000171984	C20orf196
ENSG00000171987	0	0.100689	0.181886	0.228274	ENSG00000171987	C11orf40
ENSG00000171988	36.6652	51.3189	32.7068	43.9399	ENSG00000171988	JMJD1C
ENSG00000171989	2.69687	2.30178	2.0149	2.84373	ENSG00000171989	LDHAL6B
ENSG00000171992	3.17092	8.36882	13.1155	8.62555	ENSG00000171992	SYNPO
ENSG00000171999	0.0700764	0	0.121778	0.152339	ENSG00000171999	OR52P2P
ENSG00000172000	0.130431	0	0.187689	0.208325	ENSG00000172000	ZNF556
ENSG00000172005	22.8743	0.917075	0.166059	3.82408	ENSG00000172005	MAL
ENSG00000172006	5.78923	9.5241	9.82143	15.2505	ENSG00000172006	ZNF554
ENSG00000172007	3.52509	8.2213	7.43259	7.04607	ENSG00000172007	RAB33B
ENSG00000172009	24.8507	28.2783	25.6872	23.3152	ENSG00000172009	THOP1
ENSG00000172014	0.480324	1.17681	0.306868	0.234693	ENSG00000172014	ANKRD20A4
ENSG00000172016	0.121785	0.245467	0.221636	0	ENSG00000172016	REG3A
ENSG00000172020	0.313488	1.18142	0.7014	1.52096	ENSG00000172020	GAP43
ENSG00000172023	0.247051	0.349102	0.107047	0.37425	ENSG00000172023	REG1B
ENSG00000172031	3.0011	2.42003	2.24357	2.99783	ENSG00000172031	EPHX4
ENSG00000172037	43.8233	121.283	154.536	191.294	ENSG00000172037	LAMB2
ENSG00000172046	16.0193	22.4297	27.6295	17.6115	ENSG00000172046	USP19
ENSG00000172053	74.3755	79.7083	66.5152	70.3078	ENSG00000172053	QARS
ENSG00000172057	29.9037	26.2731	22.7675	15.5109	ENSG00000172057	ORMDL3
ENSG00000172058	3.90243	7.55916	5.65863	8.88912	ENSG00000172058	SERF1A
ENSG00000172059	3.73591	3.45882	9.08072	3.17949	ENSG00000172059	KLF11
ENSG00000172061	0.0673199	0.113347	0.11712	5.65484	ENSG00000172061	LRRC15
ENSG00000172062	4.16941	4.61996	11.4263	6.427	ENSG00000172062	SMN1
ENSG00000172071	14.6048	22.9335	14.4044	15.842	ENSG00000172071	EIF2AK3
ENSG00000172073	0.0816378	0.392344	0.212676	0.177015	ENSG00000172073	TEX37
ENSG00000172081	13.9909	20.7615	17.8961	21.8399	ENSG00000172081	MOB3A
ENSG00000172086	13.2255	11.8144	15.0876	7.2579	ENSG00000172086	KRCC1
ENSG00000172113	14.3045	23.8776	20.0211	21.1353	ENSG00000172113	NME6
ENSG00000172115	57.05	36.8247	44.9282	27.2812	ENSG00000172115	CYCS
ENSG00000172116	0	0	0	0.0816963	ENSG00000172116	CD8B
ENSG00000172123	7.32584	8.97124	9.66297	11.623	ENSG00000172123	SLFN12
ENSG00000172137	2.46896	0.655766	0.286169	1.02974	ENSG00000172137	CALB2
ENSG00000172139	0.788853	1.00745	0.924051	1.15241	ENSG00000172139	SLC9C1
ENSG00000172146	0	0	0	0	ENSG00000172146	OR1A1
ENSG00000172148	0	0	0	0	ENSG00000172148	ABCG4C005255.6
ENSG00000172150	0	0	0	0	ENSG00000172150	OR1A2
ENSG00000172154	0	0	0.159161	0	ENSG00000172154	OR8I2
ENSG00000172155	0	0	0	0.529736	ENSG00000172155	LCE1D
ENSG00000172156	0.175992	0.182865	0.416151	0.499561	ENSG00000172156	CCL11
ENSG00000172159	0.705285	0.914345	1.26648	1.25452	ENSG00000172159	FRMD3
ENSG00000172164	6.86925	7.97262	17.5227	106.021	ENSG00000172164	SNTB1
ENSG00000172167	4.7651	12.2059	8.20167	12.9748	ENSG00000172167	MTBP
ENSG00000172171	15.4473	14.769	16.2923	17.4308	ENSG00000172171	TEFM
ENSG00000172172	20.2576	22.8192	17.2079	12.8392	ENSG00000172172	MRPL13

ENSG00000172175	28.4618	31.6164	26.5409	20.373	ENSG00000172175	MALT1
ENSG00000172179	0.0434315	0.209129	0.0378059	0.142482	ENSG00000172179	PRL
ENSG00000172183	19.028	13.6273	12.329	18.371	ENSG00000172183	ISG20
ENSG00000172186	0	0	0.317266	0.268684	ENSG00000172186	HMGN1P35
ENSG00000172188	0	0	0	0	ENSG00000172188	OR4C11
ENSG00000172197	7.61705	26.0767	5.35157	5.54237	ENSG00000172197	MBOAT1
ENSG00000172199	0.0673525	0.0323857	0	0.0366268	ENSG00000172199	OR8U1
ENSG00000172201	1.1252	0.140091	0.785734	1.14867	ENSG00000172201	ID4
ENSG00000172208	0	0.175088	0.105489	0.0660749	ENSG00000172208	OR4X2
ENSG00000172209	1.84741	5.75858	3.64836	5.45638	ENSG00000172209	GPR22
ENSG00000172215	0.917652	1.7289	1.96067	1.28411	ENSG00000172215	CXCR6
ENSG00000172216	40.1679	39.4928	56.5107	32.3898	ENSG00000172216	CEBPB
ENSG00000172232	0.366853	0.832876	0.536884	1.75632	ENSG00000172232	AZU1
ENSG00000172236	0	0	0	0	ENSG00000172236	TPSAB1
ENSG00000172238	0.0508416	0	0	0.0144594	ENSG00000172238	ATOH1
ENSG00000172239	42.2101	35.2674	35.8522	22.9717	ENSG00000172239	PAIP1
ENSG00000172243	2.55248	5.29207	4.97259	8.23153	ENSG00000172243	CLEC7A
ENSG00000172244	1.41844	6.09724	3.36302	3.16489	ENSG00000172244	C5orf34
ENSG00000172247	0.241349	0.167582	0.270258	0.528911	ENSG00000172247	C1QTNF4
ENSG00000172260	3.18424	8.64499	6.61318	15.0974	ENSG00000172260	NEGR1
ENSG00000172262	22.9175	32.4939	37.1806	38.6427	ENSG00000172262	ZNF131
ENSG00000172264	5.69433	9.34708	10.0069	12.1846	ENSG00000172264	MACROD2
ENSG00000172269	21.9879	32.0836	20.2262	18.0425	ENSG00000172269	DPAGT1
ENSG00000172270	370.755	491.297	251.157	152.528	ENSG00000172270	BSG
ENSG00000172273	20.5917	30.7656	36.1178	51.5424	ENSG00000172273	HINFP
ENSG00000172283	0.24387	0.23405	0	0	ENSG00000172283	PRYP4
ENSG00000172288	0	0	0	0	ENSG00000172288	CDY1
ENSG00000172289	0	0	0.0511351	0.0640783	ENSG00000172289	OR10V1
ENSG00000172292	26.7741	31.7483	28.3035	10.89	ENSG00000172292	CERS6
ENSG00000172294	0	0.0213295	0	0.00818209	ENSG00000172294	CSPG4P4Y
ENSG00000172296	20.4414	29.5589	37.2551	52.1509	ENSG00000172296	SPTLC3
ENSG00000172297	0	0.118845	0.21926	0.332232	ENSG00000172297	GOLGA2P3Y
ENSG00000172301	17.2468	12.513	10.1021	10.4215	ENSG00000172301	COPRS
ENSG00000172315	5.96996	8.0325	10.0006	9.05334	ENSG00000172315	TP53RK
ENSG00000172318	0.465386	0.688421	0.680191	1.54673	ENSG00000172318	B3GALT1
ENSG00000172320	0	0.224044	0	0	ENSG00000172320	OR5A1
ENSG00000172322	0.759746	1.67355	1.49477	2.25654	ENSG00000172322	CLEC12A
ENSG00000172324	0	0.228389	0.103203	0.4526	ENSG00000172324	OR5A2
ENSG00000172331	7.66371	4.84847	2.39427	8.42961	ENSG00000172331	BPGM
ENSG00000172332	0	0	0.0659958	0.104546	ENSG00000172332	AC012005.2
ENSG00000172336	17.2559	15.4757	10.4203	8.86674	ENSG00000172336	POP7
ENSG00000172339	5.98018	9.75667	9.68193	14.6261	ENSG00000172339	ALG14
ENSG00000172340	14.2468	20.2942	13.7643	16.2254	ENSG00000172340	SUCLG2
ENSG00000172342	0	0.0213295	0	0.00818209	ENSG00000172342	CSPG4P3Y
ENSG00000172345	11.6373	13.6356	16.9149	7.05799	ENSG00000172345	STARD5
ENSG00000172346	0.849682	2.32705	1.55471	2.92952	ENSG00000172346	CSDC2
ENSG00000172348	0.0685427	0.132191	0.104577	0.264357	ENSG00000172348	RCAN2
ENSG00000172349	1.09293	2.83333	3.93152	3.64806	ENSG00000172349	IL16
ENSG00000172350	1.44878	2.0551	1.40186	3.43928	ENSG00000172350	ABCG4
ENSG00000172352	0	0	0	0	ENSG00000172352	CDY1B
ENSG00000172354	60.3732	51.847	43.5043	43.3614	ENSG00000172354	GNB2
ENSG00000172361	0.830561	0.858294	0.920215	0.437185	ENSG00000172361	CFAP53
ENSG00000172362	0.116017	0.0558235	0.151893	0.126458	ENSG00000172362	OR5B12
ENSG00000172365	0	0	0	0.0635802	ENSG00000172365	OR5B2

ENSG00000172366	7.15293	9.26711	9.16517	5.21476	ENSG00000172366	MCRIP2
ENSG00000172367	0.0838895	0.435154	0.209241	0.269194	ENSG00000172367	PDZD3
ENSG00000172375	5.06085	6.15891	6.0596	7.81476	ENSG00000172375	C2CD2L
ENSG00000172377	0.13213	0.0635378	0.0574127	0.215623	ENSG00000172377	OR9I1
ENSG00000172379	1.86983	3.06921	2.68722	7.23607	ENSG00000172379	ARNT2
ENSG00000172380	55.8412	46.8478	37.3712	34.1324	ENSG00000172380	GNG12
ENSG00000172381	0	0	0	0	ENSG00000172381	OR6Q1
ENSG00000172382	35.5286	7.54715	8.66284	9.44779	ENSG00000172382	PRSS27
ENSG00000172399	0.0638325	0.0410271	0.185461	0.518152	ENSG00000172399	MYOZ2
ENSG00000172403	0.459705	1.21334	2.56835	1.54698	ENSG00000172403	SYNPO2
ENSG00000172404	0.738347	2.42508	2.24717	2.53517	ENSG00000172404	DNAJB7
ENSG00000172409	9.58226	5.81638	7.05529	3.47788	ENSG00000172409	CLP1
ENSG00000172410	0	0	0.0810419	0	ENSG00000172410	INSL5
ENSG00000172421	0	0.072292	0.294886	0.0410867	ENSG00000172421	EFCAB3
ENSG00000172425	0.32439	0.530343	0.757616	0.5456	ENSG00000172425	TTC36
ENSG00000172426	1.16499	1.43297	1.25752	1.16535	ENSG00000172426	RSPH9
ENSG00000172428	34.3572	24.1823	26.6734	19.3335	ENSG00000172428	COPS9
ENSG00000172432	73.1061	102.36	120.8	74.7862	ENSG00000172432	GTPBP2
ENSG00000172456	8.31316	13.6609	13.8706	12.4327	ENSG00000172456	FGGY
ENSG00000172457	0	0	0	0	ENSG00000172457	OR9G4
ENSG00000172458	0.651417	0.663056	1.29566	0.472565	ENSG00000172458	IL17D
ENSG00000172459	0.0598846	0.115247	0.0520767	0	ENSG00000172459	OR5AR1
ENSG00000172460	0.145417	0.139862	0.301203	0.275554	ENSG00000172460	PRSS30P
ENSG00000172461	0.13635	0.206582	0.420827	0.537633	ENSG00000172461	FUT9
ENSG00000172464	0.0655639	0.0707909	0.0589332	0.214011	ENSG00000172464	OR5AP2
ENSG00000172465	6.49881	4.46681	3.20692	4.98426	ENSG00000172465	TCEAL1
ENSG00000172466	21.1775	22.9989	21.7834	20.7328	ENSG00000172466	ZNF24
ENSG00000172468	0.190018	0.0886427	0.440814	0.55547	ENSG00000172468	HSFY1
ENSG00000172469	9.44436	18.2589	10.8927	11.0953	ENSG00000172469	MANEA
ENSG00000172476	0.712386	1.88859	1.70703	1.91394	ENSG00000172476	RAB40A
ENSG00000172478	26.553	3.45045	4.68379	9.61545	ENSG00000172478	C2orf54
ENSG00000172482	0.893642	1.93763	1.74538	3.01	ENSG00000172482	AGXT
ENSG00000172487	0.0283695	0.0546426	0.0249353	0	ENSG00000172487	OR8J1
ENSG00000172489	0	0.0867347	0.0522571	0.0982057	ENSG00000172489	OR5T3
ENSG00000172493	31.4352	23.4306	25.1169	34.6584	ENSG00000172493	AFF1
ENSG00000172497	0.10079	0.0957017	0.0864439	0	ENSG00000172497	ACOT12
ENSG00000172500	32.7606	34.0007	34.6693	23.8743	ENSG00000172500	FIBP
ENSG00000172508	1.71039	2.5304	2.43344	4.35777	ENSG00000172508	CARNS1
ENSG00000172519	0.0533528	0.212343	0.0675991	0.507503	ENSG00000172519	OR10H5
ENSG00000172524	0.00462984	0.00875722	0.0165025	0	ENSG00000172524	TRIM40
ENSG00000172530	12.3333	15.811	19.805	22.0423	ENSG00000172530	BANP
ENSG00000172531	67.1444	49.3213	29.7867	21.7799	ENSG00000172531	PPP1CA
ENSG00000172534	7.87845	7.86789	6.28205	8.57649	ENSG00000172534	HCFC1
ENSG00000172538	0	0	0	0	ENSG00000172538	FAM170B
ENSG00000172543	1.14062	5.68257	5.13625	9.65185	ENSG00000172543	CTSW
ENSG00000172548	14.9941	13.1119	23.6849	7.88385	ENSG00000172548	NIPAL4
ENSG00000172551	2.26687	0	1.72777	2.3071	ENSG00000172551	MUCL1
ENSG00000172554	1.67588	6.6888	4.56953	6.11565	ENSG00000172554	SNTG2
ENSG00000172568	0.0263889	0	0.0459885	0.0869029	ENSG00000172568	FNDC9
ENSG00000172572	0.135562	0.203889	0.469291	0.931428	ENSG00000172572	PDE3A
ENSG00000172575	1.16663	3.09515	2.70967	5.26484	ENSG00000172575	RASGRP1
ENSG00000172578	2.01015	3.47541	3.84557	6.94002	ENSG00000172578	KLHL6
ENSG00000172586	18.5009	12.4811	10.7848	8.26084	ENSG00000172586	CHCHD1
ENSG00000172590	49.937	62.7776	42.027	40.556	ENSG00000172590	MRPL52

ENSG00000172594	7.33785	5.85212	7.80926	4.40042	ENSG00000172594	SMPDL3A
ENSG00000172602	2.06981	3.97335	3.46421	5.81525	ENSG00000172602	RND1
ENSG00000172613	11.7636	16.67	14.1442	15.0564	ENSG00000172613	RAD9A
ENSG00000172638	17.8705	29.7609	16.982	45.9144	ENSG00000172638	EFEMP2
ENSG00000172640	0.167288	0.429345	0.679059	0.243246	ENSG00000172640	OR10AD1
ENSG00000172650	4.82173	9.78978	11.7976	13.6608	ENSG00000172650	AGAP5
ENSG00000172653	0.0219817	0.117319	0.150472	0.202654	ENSG00000172653	C17orf66
ENSG00000172660	12.5504	24.5826	29.0635	22.5314	ENSG00000172660	TAF15
ENSG00000172661	6.64161	6.40745	9.30862	8.36609	ENSG00000172661	WASHC2C
ENSG00000172663	16.9617	21.898	24.2416	14.4369	ENSG00000172663	TMEM134
ENSG00000172667	7.13955	4.90436	6.75741	11.3778	ENSG00000172667	ZMAT3
ENSG00000172671	3.2352	6.31611	5.5717	6.26532	ENSG00000172671	ZFAND4
ENSG00000172673	0.0437501	0.0555756	0.0489487	0.0330727	ENSG00000172673	THEMIS
ENSG00000172680	0	0.0566449	0.051193	0	ENSG00000172680	MOS
ENSG00000172687	10.5853	18.842	18.3004	18.9258	ENSG00000172687	ZNF738
ENSG00000172689	0.938348	2.40877	1.97473	4.73906	ENSG00000172689	MS4A10
ENSG00000172716	1.33473	7.3957	1.42285	14.3704	ENSG00000172716	SLFN11
ENSG00000172717	0.866702	2.87521	2.19743	2.34277	ENSG00000172717	FAM71D
ENSG00000172724	0.488129	0.7555	1.03288	0.686741	ENSG00000172724	CCL19
ENSG00000172725	59.7252	57.0983	35.9569	31.5663	ENSG00000172725	CORO1B
ENSG00000172728	10.5662	21.388	13.2908	17.2978	ENSG00000172728	FUT10
ENSG00000172731	4.79761	3.06686	1.04867	2.42992	ENSG00000172731	LRRC20
ENSG00000172732	34.1706	45.4637	43.2091	24.084	ENSG00000172732	MUS81
ENSG00000172733	0.133691	0.258995	0.116544	1.14921	ENSG00000172733	PURG
ENSG00000172738	2.95589	2.61531	3.83816	2.39781	ENSG00000172738	TMEM217
ENSG00000172742	8.97E-06	0.317689	1.39E-05	1.21E-05	ENSG00000172742	OR4D9
ENSG00000172746	0.232616	0.486317	0	0	ENSG00000172746	RPL12P13
ENSG00000172748	8.06208	8.63837	14.3455	10.4348	ENSG00000172748	ZNF596
ENSG00000172752	0.0970347	0.163908	0.169772	0.33549	ENSG00000172752	COL6A5
ENSG00000172757	423.93	292	179.791	223.07	ENSG00000172757	CFL1
ENSG00000172765	37.2298	29.5331	30.4863	37.3503	ENSG00000172765	TMCC1
ENSG00000172766	8.55304	12.4372	9.55411	11.9891	ENSG00000172766	NAA16
ENSG00000172769	0	0	0	0	ENSG00000172769	OR5B3
ENSG00000172771	1.52761	1.9488	1.89937	2.93985	ENSG00000172771	EFCAB12
ENSG00000172772	0.0396154	0.0763161	0.034492	0.0867161	ENSG00000172772	OR10W1
ENSG00000172774	0.189966	0.121829	0	0.137864	ENSG00000172774	OR1S1
ENSG00000172775	42.2912	54.615	54.7889	51.5063	ENSG00000172775	FAM192A
ENSG00000172780	14.8846	15.6555	14.3758	10.3972	ENSG00000172780	RAB43
ENSG00000172782	1.45238	3.70707	4.80003	5.95884	ENSG00000172782	FADS6
ENSG00000172785	33.3938	31.843	46.6785	25.5451	ENSG00000172785	CBWD1
ENSG00000172789	0.472843	1.41165	1.02261	3.39094	ENSG00000172789	HOXC5
ENSG00000172794	0.605597	0.721036	0.775273	1.44013	ENSG00000172794	RAB37
ENSG00000172795	16.0606	21.9856	16.734	19.5101	ENSG00000172795	DCP2
ENSG00000172799	0	0	0.131265	0	ENSG00000172799	ZBTB8OSP2
ENSG00000172803	3.88453	5.95819	5.67629	3.03892	ENSG00000172803	SNX32
ENSG00000172809	486.299	352.134	269.679	211.203	ENSG00000172809	RPL38
ENSG00000172817	0.606138	0.443461	2.58761	23.2355	ENSG00000172817	CYP7B1
ENSG00000172818	23.9755	5.97363	12.6208	2.49157	ENSG00000172818	OVOL1
ENSG00000172819	55.9884	33.1535	65.1428	20.2752	ENSG00000172819	RARG
ENSG00000172824	4.28688	1.77387	4.14486	2.67763	ENSG00000172824	CES4A
ENSG00000172828	4.80019	9.39457	8.9001	9.57139	ENSG00000172828	CES3
ENSG00000172830	41.1387	51.6484	39.4452	18.3024	ENSG00000172830	SSH3
ENSG00000172831	124.358	45.3683	55.4347	27.1159	ENSG00000172831	CES2
ENSG00000172840	9.88036	11.6271	8.14432	14.3497	ENSG00000172840	PDP2

ENSG00000172845	30.3175	32.4702	28.6076	95.6768	ENSG00000172845	SP3
ENSG00000172850	2.05115	3.2431	2.47841	1.71742	ENSG00000172850	LSM2
ENSG00000172867	0.0462364	0.0891794	0.121174	0.304748	ENSG00000172867	KRT2
ENSG00000172869	17.6344	27.4461	27.0142	23.1586	ENSG00000172869	DMXL1
ENSG00000172878	3.08009	8.93626	8.01786	6.99996	ENSG00000172878	METAP1D
ENSG00000172888	5.12026	9.29448	15.3021	12.1011	ENSG00000172888	ZNF621
ENSG00000172889	11.4732	17.1095	6.00537	4.51725	ENSG00000172889	EGFL7
ENSG00000172890	58.9637	66.7973	73.8936	56.7457	ENSG00000172890	NADSYN1
ENSG00000172893	107.19	105.976	27.259	44.5445	ENSG00000172893	DHCR7
ENSG00000172900	1.32918	2.01876	2.04831	4.44438	ENSG00000172900	FLJ42102
ENSG00000172901	0.204046	0.703055	0.975951	0.798538	ENSG00000172901	LVRN
ENSG00000172912	2.29809	0.885059	1.55035	2.81436	ENSG00000172912	COX6B1P3
ENSG00000172915	0.226883	0.7114	1.10127	2.07146	ENSG00000172915	NBEA
ENSG00000172922	9.49735	9.97129	9.68194	9.5114	ENSG00000172922	RNASEH2C
ENSG00000172927	6.24572	1.72386	3.88741	9.59191	ENSG00000172927	MYEOV
ENSG00000172932	41.834	49.2479	40.683	36.8362	ENSG00000172932	ANKRD13D
ENSG00000172935	0.217258	0.0942209	0.295473	1.92888	ENSG00000172935	MRGPRF
ENSG00000172936	8.99217	6.80101	8.31187	9.41052	ENSG00000172936	MYD88
ENSG00000172938	0	0	0	0	ENSG00000172938	MRGPRD
ENSG00000172939	45.3065	31.7326	38.7795	35.9798	ENSG00000172939	OXSR1
ENSG00000172940	0.489924	1.13994	1.03214	1.41117	ENSG00000172940	SLC22A13
ENSG00000172943	5.67178	6.76896	6.7779	6.87685	ENSG00000172943	PHF8
ENSG00000172954	30.1624	51.4247	42.8189	69.9718	ENSG00000172954	LCLAT1
ENSG00000172955	3.00842	6.2679	4.7885	5.06073	ENSG00000172955	ADH6
ENSG00000172967	0.0338925	0.0653101	0.0299605	0.226994	ENSG00000172967	XKR3
ENSG00000172969	0.424724	3.16E-08	1.08121	1.0758	ENSG00000172969	FRG2C
ENSG00000172971	0	0	0	0	ENSG00000172971	UNC93B3
ENSG00000172974	1.18672	0.644444	0.845051	0.354306	ENSG00000172974	AC007318.5
ENSG00000172977	23.2029	31.0383	27.3407	22.0368	ENSG00000172977	KAT5
ENSG00000172985	0.276996	0.237216	3.14461	14.6592	ENSG00000172985	SH3RF3
ENSG00000172986	1.34022	1.58891	2.20527	4.00748	ENSG00000172986	GXYLT2
ENSG00000172987	0	0.0389299	0	0.058822	ENSG00000172987	HPSE2
ENSG00000172992	23.5929	28.3469	23.3934	19.3237	ENSG00000172992	DCAKD
ENSG00000172995	0.73506	2.21179	1.45636	3.27565	ENSG00000172995	ARPP21
ENSG00000173011	7.19205	5.52272	7.73297	3.73998	ENSG00000173011	TADA2B
ENSG00000173013	0.495089	0.276276	0.522234	0.457693	ENSG00000173013	CCDC96
ENSG00000173020	38.2739	30.9503	36.1468	18.9858	ENSG00000173020	GRK2
ENSG00000173039	38.6982	30.2685	38.6521	23.9434	ENSG00000173039	RELA
ENSG00000173040	5.55539	11.0803	10.0523	10.5691	ENSG00000173040	EVC2
ENSG00000173041	12.8355	28.4444	16.9314	25.0523	ENSG00000173041	ZNF680
ENSG00000173064	20.0532	25.917	27.2529	42.7467	ENSG00000173064	HECTD4
ENSG00000173065	12.4604	10.6485	8.12056	13.6111	ENSG00000173065	FAM222B
ENSG00000173068	2.15205	3.24216	3.15173	9.38015	ENSG00000173068	BNC2
ENSG00000173077	8.63285	21.3047	20.6857	32.7237	ENSG00000173077	DEC1
ENSG00000173080	0.368166	2.68326	0.915151	1.66453	ENSG00000173080	RXFP4
ENSG00000173083	5.51326	12.4496	5.63751	7.14661	ENSG00000173083	HPSE
ENSG00000173085	9.30336	12.947	6.18008	5.15725	ENSG00000173085	COQ2
ENSG00000173088	5.26959	12.1134	10.9436	13.4122	ENSG00000173088	C10orf131
ENSG00000173093	0.198794	0.112997	0.0260726	0.34864	ENSG00000173093	CCDC63
ENSG00000173110	12.7032	0.140767	0.247774	2.91576	ENSG00000173110	HSPA6
ENSG00000173113	102.115	85.1918	48.0554	41.117	ENSG00000173113	TRMT112
ENSG00000173114	0.675761	1.97177	2.31476	3.63426	ENSG00000173114	LRRN3
ENSG00000173120	40.8201	48.6377	62.1954	67.0213	ENSG00000173120	KDM2A
ENSG00000173124	1.07657	1.60534	1.8879	2.74908	ENSG00000173124	ACSM6

ENSG00000173137	10.5863	17.2288	10.6753	17.9766	ENSG00000173137	ADCK5
ENSG00000173141	10.7864	12.0534	11.8926	10.9598	ENSG00000173141	MRPL57
ENSG00000173145	17.7765	22.731	19.8712	15.713	ENSG00000173145	NOC3L
ENSG00000173153	35.24	34.8734	39.989	21.2221	ENSG00000173153	ESRRA
ENSG00000173156	79.5991	29.011	57.7105	18.0208	ENSG00000173156	RHOD
ENSG00000173157	0.128801	0.482148	0.310927	0.887662	ENSG00000173157	ADAMTS20
ENSG00000173163	22.0073	20.4142	16.5611	18.332	ENSG00000173163	COMMD1
ENSG00000173166	6.50691	14.2852	7.13509	25.5154	ENSG00000173166	RAPH1
ENSG00000173171	30.9265	21.6881	18.9549	11.7396	ENSG00000173171	MTX1
ENSG00000173175	0.40687	0.630197	1.19554	1.22154	ENSG00000173175	ADCY5
ENSG00000173193	11.9993	31.7333	26.3975	39.6545	ENSG00000173193	PARP14
ENSG00000173198	15.1908	32.7326	32.3132	68.5516	ENSG00000173198	CYSLTR1
ENSG00000173200	4.1573	10.9617	10.1371	19.9465	ENSG00000173200	PARP15
ENSG00000173207	16.174	52.4577	19.7916	18.1965	ENSG00000173207	CKS1B
ENSG00000173208	0.0597165	0.0987587	0.141776	0.159965	ENSG00000173208	ABCD2
ENSG00000173209	29.3616	48.3994	33.5169	37.8428	ENSG00000173209	AHSA2
ENSG00000173210	28.6196	7.65678	5.75203	24.8139	ENSG00000173210	ABLIM3
ENSG00000173212	5.46172	13.873	16.5395	44.4345	ENSG00000173212	MAB21L3
ENSG00000173213	0.279222	1.15219	0.0528753	0.353434	ENSG00000173213	TUBB8P12
ENSG00000173214	5.84376	7.67349	8.65116	7.7934	ENSG00000173214	MFSD4B
ENSG00000173218	22.5935	30.1248	14.8465	9.69764	ENSG00000173218	VANGL1
ENSG00000173221	15.1714	8.75251	8.90181	17.7858	ENSG00000173221	GLRX
ENSG00000173226	8.86561	14.1411	11.0013	9.50818	ENSG00000173226	IQCB1
ENSG00000173227	0.922699	2.81525	3.11955	3.1387	ENSG00000173227	SYT12
ENSG00000173230	43.1854	54.9141	55.9324	56.8694	ENSG00000173230	GOLGB1
ENSG00000173231	0	0	0	0	ENSG00000173231	TERF1P1
ENSG00000173237	0.269358	0.254181	0.499938	0.638326	ENSG00000173237	C11orf86
ENSG00000173239	1.02362	0.387921	0.841905	0.175694	ENSG00000173239	LIPM
ENSG00000173250	0.159383	0.375682	0.4946	0.273233	ENSG00000173250	GPR151
ENSG00000173253	0.0451096	0.108718	0.0786316	0.189952	ENSG00000173253	DMRT2
ENSG00000173258	5.50221	13.7997	11.6987	21.9038	ENSG00000173258	ZNF483
ENSG00000173261	0.786175	0.746225	2.93769	1.51849	ENSG00000173261	PLAC8L1
ENSG00000173262	2689.52	1849.59	1673.16	988.987	ENSG00000173262	SLC2A14
ENSG00000173264	20.6424	21.0228	18.019	15.5056	ENSG00000173264	GPR137
ENSG00000173267	56.3721	9.20559	5.13787	5.98148	ENSG00000173267	SNCG
ENSG00000173269	13.7836	40.2342	14.0032	11.2573	ENSG00000173269	MMRN2
ENSG00000173272	88.6728	99.0281	63.5614	56.1371	ENSG00000173272	MZT2A
ENSG00000173273	18.1319	34.6102	34.7551	42.1224	ENSG00000173273	TNKS
ENSG00000173275	2.56375	4.45487	4.70101	2.94232	ENSG00000173275	ZNF449
ENSG00000173276	10.4038	11.6971	14.2803	15.051	ENSG00000173276	ZBTB21
ENSG00000173281	9.83718	3.20694	6.16707	5.79734	ENSG00000173281	PPP1R3B
ENSG00000173285	0	0	0	0.0619297	ENSG00000173285	OR10K1
ENSG00000173295	4.75347	10.7912	19.8929	10.9832	ENSG00000173295	FAM86B3P
ENSG00000173302	0.140536	0.045339	0.0407693	0.256411	ENSG00000173302	GPR148
ENSG00000173320	2.88155	2.79573	2.40488	0.989475	ENSG00000173320	STOX2
ENSG00000173327	19.8244	21.2318	24.8167	24.2683	ENSG00000173327	MAP3K11
ENSG00000173334	35.29	30.7088	20.221	14.0303	ENSG00000173334	TRIB1
ENSG00000173335	0	0.0349097	0	0.0396636	ENSG00000173335	CST9
ENSG00000173338	0.646489	1.72871	0.446655	0.404767	ENSG00000173338	KCNK7
ENSG00000173349	0.0711699	0.0390735	0	0.0694172	ENSG00000173349	SFT2D3
ENSG00000173357	0	0	0.0451639	0.113318	ENSG00000173357	AC007967.3
ENSG00000173366	0.198082	0.175076	0	0.0209447	ENSG00000173366	TLR9
ENSG00000173369	0.312573	0.300705	0.441511	0.552788	ENSG00000173369	C1QB
ENSG00000173372	0	0	0	0	ENSG00000173372	C1QA

ENSG00000173376	0.830152	1.60881	1.36029	6.17016	ENSG00000173376	NDNF
ENSG00000173389	0.367283	1.83049	1.64215	1.71075	ENSG00000173389	IQCF1
ENSG00000173391	2.81504	5.17567	4.34754	6.55581	ENSG00000173391	OLR1
ENSG00000173401	3.45855	5.83171	3.7343	3.24278	ENSG00000173401	GLIPR1L1
ENSG00000173402	36.4739	45.4997	33.7771	30.4091	ENSG00000173402	DAG1
ENSG00000173404	26.4263	11.319	8.21972	17.1391	ENSG00000173404	INSM1
ENSG00000173406	0.561274	1.47816	0.856896	1.27761	ENSG00000173406	DAB1
ENSG00000173409	13.3683	14.3779	10.1055	8.76812	ENSG00000173409	ARV1
ENSG00000173418	36.3661	32.1366	23.8925	21.8732	ENSG00000173418	NAA20
ENSG00000173421	2.35325	1.85269	2.83816	9.15015	ENSG00000173421	CCDC36
ENSG00000173431	0.109961	0.425592	0.189464	1.17768	ENSG00000173431	RNASE8
ENSG00000173432	5.03534	3.45048	33.9234	4.73569	ENSG00000173432	SAA1
ENSG00000173436	18.8326	31.5317	25.3084	40.6192	ENSG00000173436	MINOS1
ENSG00000173442	22.3488	42.3113	22.0254	24.6111	ENSG00000173442	EHBP1L1
ENSG00000173451	4.90056	8.27937	5.64715	4.13563	ENSG00000173451	THAP2
ENSG00000173452	0.42627	0.430077	0.440457	0.498043	ENSG00000173452	TMEM196
ENSG00000173456	6.70228	11.0225	6.68242	6.40972	ENSG00000173456	RNF26
ENSG00000173457	123.67	142.935	97.0704	59.7039	ENSG00000173457	PPP1R14B
ENSG00000173464	0.0552017	0.318996	0.047939	0.361202	ENSG00000173464	RNASE11
ENSG00000173465	24.5584	18.7985	17.3425	8.63536	ENSG00000173465	SSSCA1
ENSG00000173467	1.56586	2.21947	3.23861	4.11231	ENSG00000173467	AGR3
ENSG00000173473	27.2812	34.0708	45.6795	43.0669	ENSG00000173473	SMARCC1
ENSG00000173480	12.2506	16.6609	21.9061	21.2044	ENSG00000173480	ZNF417
ENSG00000173482	34.7589	51.1972	59.686	82.0959	ENSG00000173482	PTPRM
ENSG00000173486	54.5358	53.2345	30.8829	33.5255	ENSG00000173486	FKBP2
ENSG00000173503	0.0274983	0.0159269	0.0264951	0.0206416	ENSG00000173503	LTA
ENSG00000173511	14.2293	15.529	8.00603	12.546	ENSG00000173511	VEGFB
ENSG00000173517	11.8714	27.9189	28.4158	63.8894	ENSG00000173517	PEAK1
ENSG00000173530	19.2772	6.77962	5.62081	9.93143	ENSG00000173530	TNFRSF10D
ENSG00000173531	9.67614	16.0007	27.5422	10.6306	ENSG00000173531	MST1
ENSG00000173535	3.82119	4.31198	2.83836	4.32368	ENSG00000173535	TNFRSF10C
ENSG00000173540	16.9817	19.9913	14.9927	12.2174	ENSG00000173540	GMPPB
ENSG00000173542	7.09738	9.75509	8.6286	14.3985	ENSG00000173542	MOB1B
ENSG00000173545	19.1583	12.5597	13.7281	11.041	ENSG00000173545	ZNF622
ENSG00000173546	1.92007	27.8453	96.5725	39.2248	ENSG00000173546	CSPG4
ENSG00000173548	28.7301	23.2753	34.7463	14.4726	ENSG00000173548	SNX33
ENSG00000173557	0	0.068153	0	0.0775632	ENSG00000173557	C2orf70
ENSG00000173559	36.7797	57.1812	85.2603	64.4659	ENSG00000173559	NABP1
ENSG00000173566	4.47499	3.97861	6.10333	2.12672	ENSG00000173566	NUDT18
ENSG00000173567	2.69836	2.17324	2.06539	1.66015	ENSG00000173567	ADGRF3
ENSG00000173572	0.017447	0	0.0608432	0.0767618	ENSG00000173572	NLRP13
ENSG00000173575	107.38	158.474	131.152	141.482	ENSG00000173575	CHD2
ENSG00000173578	1.25039	2.87319	3.25691	3.91037	ENSG00000173578	XCR1
ENSG00000173581	2.57294	2.43951	3.72262	3.27239	ENSG00000173581	CCDC106
ENSG00000173585	0.0220465	0.298073	0.0384309	0.218021	ENSG00000173585	CCR9
ENSG00000173588	12.0892	29.544	26.1748	35.9132	ENSG00000173588	CEP83
ENSG00000173597	15.7163	31.6645	29.3854	66.611	ENSG00000173597	SULT1B1
ENSG00000173598	21.429	21.6279	30.5523	16.8225	ENSG00000173598	NUDT4
ENSG00000173599	25.8354	42.2439	15.5224	23.0304	ENSG00000173599	PC
ENSG00000173610	0.869708	4.95911	4.41631	8.96273	ENSG00000173610	UGT2A1
ENSG00000173611	7.58504	9.02876	9.4395	13.1826	ENSG00000173611	SCAI
ENSG00000173612	0	0.0464976	0.0630551	0.0794651	ENSG00000173612	GPRC6A
ENSG00000173614	13.4756	21.3202	23.6154	31.9276	ENSG00000173614	NMNAT1
ENSG00000173621	7.67881	17.7913	32.1364	14.3747	ENSG00000173621	LRFN4

ENSG00000173626	9.10104	21.7429	18.6751	36.6796	ENSG00000173626	TRAPPC3L
ENSG00000173627	0.0433419	0.381776	0.423892	0.755912	ENSG00000173627	APOBEC4
ENSG00000173638	4.72385	10.6247	6.94605	8.74451	ENSG00000173638	SLC19A1
ENSG00000173641	0.166986	0.624519	0.748689	1.12135	ENSG00000173641	HSPB7
ENSG00000173653	19.4842	28.3162	21.2186	12.1501	ENSG00000173653	RCE1
ENSG00000173660	116.456	102.935	59.4893	66.4072	ENSG00000173660	UQCRH
ENSG00000173662	0.0314083	0.151326	0.0598314	0.373254	ENSG00000173662	TAS1R1
ENSG00000173673	0	0	0	0.104287	ENSG00000173673	HES3
ENSG00000173674	28.0458	19.1519	28.0542	24.6367	ENSG00000173674	EIF1AX
ENSG00000173678	0.358802	4.42831	1.49864	3.73114	ENSG00000173678	SPDYE2B
ENSG00000173679	0.112371	0.0540741	0.147983	0.61267	ENSG00000173679	OR1L1
ENSG00000173681	4.64504	9.52911	9.3818	13.7593	ENSG00000173681	BCLAF3
ENSG00000173692	60.3381	59.1402	41.1627	54.157	ENSG00000173692	PSMD1
ENSG00000173698	3.42923	2.45538	2.03349	3.21202	ENSG00000173698	ADGRG2
ENSG00000173699	1.70399	1.66495	2.71254	4.75919	ENSG00000173699	SPATA3
ENSG00000173702	0.0954582	0.585182	0.173115	0.482779	ENSG00000173702	MUC13
ENSG00000173705	0.44807	0.7312	0.52176	1.33678	ENSG00000173705	SUSD5
ENSG00000173706	18.2774	17.9555	14.4399	26.7363	ENSG00000173706	HEG1
ENSG00000173714	0.256012	0.551247	0.619035	0.492685	ENSG00000173714	WFIKKN2
ENSG00000173715	20.8076	28.8524	29.5624	20.4784	ENSG00000173715	C11orf80
ENSG00000173726	73.8971	45.3468	49.0807	41.188	ENSG00000173726	TOMM20
ENSG00000173727	0.698097	0.466947	0.590561	3.21108	ENSG00000173727	AP000769.1
ENSG00000173728	0.900766	1.93457	2.53163	2.26302	ENSG00000173728	C1orf100
ENSG00000173744	41.7357	35.3941	35.29	29.3464	ENSG00000173744	AGFG1
ENSG00000173757	10.9889	20.119	15.3971	25.1814	ENSG00000173757	STAT5B
ENSG00000173762	0.778434	0.539834	0.404906	0.928665	ENSG00000173762	CD7
ENSG00000173769	0.040086	0.118767	0.0961501	0.298196	ENSG00000173769	TOPAZ1
ENSG00000173786	6.227	12.2258	13.2816	14.0958	ENSG00000173786	CNP
ENSG00000173801	390.32	217.022	229.306	116.669	ENSG00000173801	JUP
ENSG00000173805	3.04175	1.4761	2.29767	1.73578	ENSG00000173805	HAP1
ENSG00000173809	0.540124	1.94696	0.990413	1.79404	ENSG00000173809	TDRD12
ENSG00000173810	0	0	0	0	ENSG00000173810	PPIAP7
ENSG00000173812	61.9575	111.583	103.322	84.4336	ENSG00000173812	EIF1
ENSG00000173818	18.5974	33.585	37.2342	32.6196	ENSG00000173818	ENDOV
ENSG00000173821	52.7482	105.173	108.598	136.571	ENSG00000173821	RNF213
ENSG00000173825	0.280229	0.242864	0.195576	0.36869	ENSG00000173825	TIGD3
ENSG00000173826	0.481036	0.995718	0.689063	0.940744	ENSG00000173826	KCNH6
ENSG00000173838	0.669404	2.05127	2.00271	2.10675	ENSG00000173838	MARCH10
ENSG00000173846	46.0533	55.3034	60.6049	39.2621	ENSG00000173846	PLK3
ENSG00000173848	258.106	178.183	52.8969	117.254	ENSG00000173848	NET1
ENSG00000173852	13.374	23.0252	9.41759	19.0863	ENSG00000173852	DPY19L1
ENSG00000173862	0.231001	0.783458	0.553503	1.01676	ENSG00000173862	RP11-89N17.1
ENSG00000173868	0.0363391	0.164142	0.32042	0.419962	ENSG00000173868	PHOSPHO1
ENSG00000173875	14.7228	22.8381	20.1707	27.0136	ENSG00000173875	ZNF791
ENSG00000173876	0.0785741	0	0	0.0965328	ENSG00000173876	TUBB7P
ENSG00000173889	21.6953	36.387	32.7374	47.1648	ENSG00000173889	PHC3
ENSG00000173890	3.479	6.59917	5.72262	8.33741	ENSG00000173890	GPR160
ENSG00000173894	0.635402	0.898348	1.10603	0.813902	ENSG00000173894	CBX2
ENSG00000173898	55.0409	26.148	38.8015	11.884	ENSG00000173898	SPTBN2
ENSG00000173905	15.1111	23.38	20.2095	24.6243	ENSG00000173905	GOLIM4
ENSG00000173908	0	0	0	0.186314	ENSG00000173908	KRT28
ENSG00000173914	6.2246	9.68349	8.12895	15.3461	ENSG00000173914	RBM4B
ENSG00000173915	181.932	94.7578	97.8509	61.3788	ENSG00000173915	USMG5
ENSG00000173917	0.40139	0.427624	3.44568	15.443	ENSG00000173917	HOXB2

ENSG00000173918	9.28346	23.0881	26.1064	33.4276	ENSG00000173918	C1QTNF1
ENSG00000173926	3.458	2.86934	3.50967	7.19362	ENSG00000173926	MARCH3
ENSG00000173928	3.7523	5.81245	3.98775	4.4736	ENSG00000173928	SWSAP1
ENSG00000173930	0.579551	1.23757	1.00845	2.16081	ENSG00000173930	SLCO4C1
ENSG00000173933	48.8649	47.1208	54.8815	44.095	ENSG00000173933	RBM4
ENSG00000173947	1.2931	0.752046	0.724871	0.986352	ENSG00000173947	PIFO
ENSG00000173950	14.1202	16.8543	22.0651	16.4636	ENSG00000173950	XXYLT1
ENSG00000173954	0	0	0	0	ENSG00000173954	SNURFL
ENSG00000173960	11.3111	11.2752	11.2124	16.3562	ENSG00000173960	UBXN2A
ENSG00000173966	0.31136	0.0966159	0	0	ENSG00000173966	RP11-18M17.1
ENSG00000173976	0.728583	1.42283	1.1809	1.98584	ENSG00000173976	RAX2
ENSG00000173988	0.0528026	0.37452	0.190551	0.216786	ENSG00000173988	LRRC63
ENSG00000173991	0.489439	0.469725	0.424175	0.92089	ENSG00000173991	TCAP
ENSG00000173992	22.5895	29.1786	26.1659	25.4613	ENSG00000173992	CCS
ENSG00000174004	1.0953	0.818043	2.03842	2.85656	ENSG00000174004	NRROS
ENSG00000174007	1.6973	1.92575	2.50507	4.40135	ENSG00000174007	CEP19
ENSG00000174010	1.39129	2.42927	2.00924	2.23318	ENSG00000174010	KLHL15
ENSG00000174013	7.95389	5.08112	6.24626	5.13556	ENSG00000174013	FBXO45
ENSG00000174015	0.0356888	0.240679	0.404047	0.273664	ENSG00000174015	SPERT
ENSG00000174016	0.0363751	0.0350745	0.122816	0.12001	ENSG00000174016	FAM46D
ENSG00000174021	32.2055	31.9737	30.6772	28.6931	ENSG00000174021	GNG5
ENSG00000174028	41.4099	3.34568	7.1628	12.9866	ENSG00000174028	FAM3C2
ENSG00000174032	8.45542	10.3173	10.5971	14.1667	ENSG00000174032	SLC25A30
ENSG00000174038	10.9263	26.0663	26.693	37.0414	ENSG00000174038	C9orf131
ENSG00000174059	0.592526	1.18442	0.676333	2.15838	ENSG00000174059	CD34
ENSG00000174080	4.02904	2.76616	4.90819	10.2959	ENSG00000174080	CTSF
ENSG00000174083	0	0	0.0644318	0	ENSG00000174083	PIK3RS
ENSG00000174093	4.71554	6.97962	7.62795	7.17838	ENSG00000174093	PRP11-1407O15.2
ENSG00000174099	9.35002	12.8639	18.5882	29.7918	ENSG00000174099	MSRB3
ENSG00000174100	5.93699	6.44374	7.03219	3.03978	ENSG00000174100	MRPL45
ENSG00000174106	24.8211	26.6486	18.6341	20.1405	ENSG00000174106	LEMD3
ENSG00000174109	8.23691	7.64915	8.3113	3.78162	ENSG00000174109	C16orf91
ENSG00000174111	3.72961	4.87688	4.92106	3.66006	ENSG00000174111	SOCS7
ENSG00000174123	0.198606	0.499818	0.655802	1.07022	ENSG00000174123	TLR10
ENSG00000174125	3.07454	1.91407	2.12098	2.68673	ENSG00000174125	TLR1
ENSG00000174130	0.879345	2.66933	3.51337	2.36074	ENSG00000174130	TLR6
ENSG00000174132	17.5819	18.9614	14.2033	9.1181	ENSG00000174132	FAM174A
ENSG00000174136	15.6776	27.435	13.8241	111.773	ENSG00000174136	RGMB
ENSG00000174137	0.929957	0.498189	2.58004	2.65004	ENSG00000174137	FAM53A
ENSG00000174145	0.33029	0.104158	0.245681	0.224076	ENSG00000174145	NWD2
ENSG00000174151	5.47501	4.85351	5.72557	3.1403	ENSG00000174151	CYB561D1
ENSG00000174156	0.0698875	0.162019	0.303628	0.45666	ENSG00000174156	GSTA3
ENSG00000174165	16.6904	14.7345	10.0025	6.86564	ENSG00000174165	ZDHHC24
ENSG00000174173	14.9255	11.5384	10.3747	8.6607	ENSG00000174173	TRMT10C
ENSG00000174175	0.126775	0.705164	0.0797401	0.416912	ENSG00000174175	SELP
ENSG00000174177	13.0179	11.8164	19.8714	11.0737	ENSG00000174177	CTU2
ENSG00000174194	6.62229	20.0239	27.2488	22.3686	ENSG00000174194	AGAP8
ENSG00000174196	0	0	0	0	ENSG00000174196	FAM121D
ENSG00000174197	15.7928	20.1437	18.9641	25.0051	ENSG00000174197	MGA
ENSG00000174206	3.30283	4.64893	5.49977	2.91673	ENSG00000174206	C12orf66
ENSG00000174225	0.412119	0.613331	0.937682	0.377487	ENSG00000174225	ARL13A
ENSG00000174226	0.50551	1.47887	0.847765	2.89557	ENSG00000174226	SNX31
ENSG00000174227	25.922	33.7518	43.7219	31.5658	ENSG00000174227	PIGG
ENSG00000174231	49.3663	89.5383	79.9251	105.929	ENSG00000174231	PRPF8

ENSG00000174233	20.7954	16.8636	20.8659	18.2328	ENSG00000174233	ADCY6
ENSG00000174236	1.43022	2.32877	1.66585	4.17785	ENSG00000174236	REP15
ENSG00000174238	16.3659	14.4493	21.9678	21.1263	ENSG00000174238	PITPNA
ENSG00000174243	45.8805	45.2861	46.0277	42.0666	ENSG00000174243	DDX23
ENSG00000174255	0.64209	1.37475	0.937065	1.6502	ENSG00000174255	ZNF80
ENSG00000174276	6.5978	4.64634	6.24677	2.44484	ENSG00000174276	ZNHIT2
ENSG00000174279	0.209278	0.237507	0.250986	0.344658	ENSG00000174279	EVX2
ENSG00000174282	19.7025	16.575	18.0759	15.8399	ENSG00000174282	ZBTB4
ENSG00000174292	10.5196	12.1456	19.2575	8.84599	ENSG00000174292	TNK1
ENSG00000174306	22.2271	18.9592	19.5168	37.717	ENSG00000174306	ZHX3
ENSG00000174307	111.142	52.8546	79.0365	30.6353	ENSG00000174307	PHLDA3
ENSG00000174325	0	0.113805	0.0545369	0.128878	ENSG00000174325	DIRC1
ENSG00000174326	0.682526	0.840905	1.00846	0.974259	ENSG00000174326	SLC16A11
ENSG00000174327	2.0276	3.79077	3.95218	2.64807	ENSG00000174327	SLC16A13
ENSG00000174332	0.0391048	0.169668	0.0538966	4.52568	ENSG00000174332	GLIS1
ENSG00000174339	0.346501	0.500179	0.401816	0.566559	ENSG00000174339	OR2Y1
ENSG00000174343	1.12131	1.03201	0.968447	2.54083	ENSG00000174343	CHRNA9
ENSG00000174348	0.459353	1.9312	1.09949	2.0251	ENSG00000174348	PODN
ENSG00000174353	3.59638	0	0	0	ENSG00000174353	STAG3L3
ENSG00000174358	0.0652847	0.157391	0.243017	0.216051	ENSG00000174358	SLC6A19
ENSG00000174368	2.43279	8.18622	6.19175	6.21329	ENSG00000174368	PMS2P2
ENSG00000174370	2.94104	4.25439	5.94344	2.67827	ENSG00000174370	C11orf45
ENSG00000174371	2.24063	8.51304	2.93142	7.27256	ENSG00000174371	EXO1
ENSG00000174373	34.6724	56.9964	44.1988	50.027	ENSG00000174373	RALGAPA1
ENSG00000174374	7.03704	14.3459	10.8925	13.3296	ENSG00000174374	WBSCR16
ENSG00000174384	0.905796	4.86266	7.57799	1.82638	ENSG00000174384	RP11-313P13.4
ENSG00000174405	10.1617	7.37392	9.96633	6.64782	ENSG00000174405	LIG4
ENSG00000174407	0.193451	0.370202	0.501342	0.308013	ENSG00000174407	C20orf166
ENSG00000174408	0	0	0	0	ENSG00000174408	PPIAP24
ENSG00000174417	0.0413202	0.278577	0.0359726	0.151517	ENSG00000174417	TRHR
ENSG00000174418	0	0	0	0	ENSG00000174418	RPL35P9
ENSG00000174428	12.2952	24.536	22.4932	29.0598	ENSG00000174428	GTF2IRD2B
ENSG00000174429	0.061439	0.695671	0.294226	0.77902	ENSG00000174429	ABRA
ENSG00000174437	195.159	213.953	154.678	155.74	ENSG00000174437	ATP2A2
ENSG00000174442	10.5044	20.8585	15.2334	17.9001	ENSG00000174442	ZWILCH
ENSG00000174444	1257.05	959.795	860.21	599.708	ENSG00000174444	RPL4
ENSG00000174446	8.51049	7.66174	7.26441	5.5225	ENSG00000174446	SNAPC5
ENSG00000174448	2.71266	3.08259	4.7968	4.6603	ENSG00000174448	STARD6
ENSG00000174450	0	0.0768347	0.131587	0.116889	ENSG00000174450	GOLGA6L2
ENSG00000174453	0.0944046	0.309859	0.310005	0.370604	ENSG00000174453	VWC2L
ENSG00000174456	18.6064	38.1909	37.0249	48.2228	ENSG00000174456	C12orf76
ENSG00000174460	0.0509329	0	0	0.0837181	ENSG00000174460	ZCCHC12
ENSG00000174469	0.77212	1.43019	1.07641	1.93022	ENSG00000174469	CNTNAP2
ENSG00000174473	0.414038	0.653308	0.385262	1.03567	ENSG00000174473	GALNTL6
ENSG00000174482	1.87615	1.94972	1.31088	2.50286	ENSG00000174482	LINGO2
ENSG00000174483	15.6682	24.6086	24.8437	22.0164	ENSG00000174483	BBS1
ENSG00000174485	9.4272	12.5914	13.2968	19.2171	ENSG00000174485	DENND4A
ENSG00000174495	0	0	0	0	ENSG00000174495	AC005017.2
ENSG00000174498	1.15762	2.82815	2.69472	5.00272	ENSG00000174498	IGDCC3
ENSG00000174500	4.21856	6.70966	5.50766	3.80951	ENSG00000174500	GCSAM
ENSG00000174501	19.9006	49.0158	26.1077	61.0251	ENSG00000174501	ANKRD36C
ENSG00000174502	1.14269	0.307767	0.834268	0.759541	ENSG00000174502	SLC26A9
ENSG00000174514	1.08193	3.0054	1.73904	2.34406	ENSG00000174514	MFSD4A
ENSG00000174516	6.7134	6.67334	6.10199	7.26482	ENSG00000174516	PELI3

ENSG00000174521	0.265797	0.312913	0.154155	0.417686	ENSG00000174521	TTC9B
ENSG00000174527	1.12627	2.22363	2.82897	2.30565	ENSG00000174527	MYO1H
ENSG00000174529	0.71789	1.17943	1.01537	1.10859	ENSG00000174529	TMEM81
ENSG00000174547	14.875	18.039	11.2754	8.75504	ENSG00000174547	MRPL11
ENSG00000174562	0.697942	1.65518	1.24129	1.61908	ENSG00000174562	KLK15
ENSG00000174564	86.3558	148.346	106.671	20.2838	ENSG00000174564	IL20RB
ENSG00000174567	0.728421	0.21621	0.249258	0.311665	ENSG00000174567	GOLT1A
ENSG00000174572	0	0	0	0.113277	ENSG00000174572	RP11-209A2.1
ENSG00000174574	34.5698	20.103	29.5973	22.6447	ENSG00000174574	AKIRIN1
ENSG00000174576	0.0690906	0.0809012	0.116753	0.315854	ENSG00000174576	NPAS4
ENSG00000174579	7.81943	12.4782	12.3575	10.7561	ENSG00000174579	MSL2
ENSG00000174586	2.35804	4.46718	7.10319	4.55522	ENSG00000174586	ZNF497
ENSG00000174595	0.0784229	0.0376742	0	0	ENSG00000174595	KLF14
ENSG00000174599	1.67362	1.9088	1.74985	0.892348	ENSG00000174599	TRAM1L1
ENSG00000174600	0.329091	0.709793	0.600027	5.81106	ENSG00000174600	CMKLR1
ENSG00000174606	18.9932	39.1713	35.5479	35.9782	ENSG00000174606	ANGEL2
ENSG00000174607	0.719812	4.04116	1.94498	4.07767	ENSG00000174607	UGT8
ENSG00000174611	0.071882	0.181994	0.706809	0.450572	ENSG00000174611	KY
ENSG00000174628	14.0635	21.4003	22.3607	27.7174	ENSG00000174628	IQCK
ENSG00000174640	1.7146	3.67024	1.4474	14.4489	ENSG00000174640	SLCO2A1
ENSG00000174652	14.7857	18.7254	25.3074	12.6329	ENSG00000174652	ZNF266
ENSG00000174667	0	0	0	0	ENSG00000174667	OR7D4
ENSG00000174669	2.61542	6.9816	5.08438	2.2457	ENSG00000174669	SLC29A2
ENSG00000174672	0.589348	0.513879	1.46708	1.15439	ENSG00000174672	BRSK2
ENSG00000174677	0	0	0	0	ENSG00000174677	VN1R6P
ENSG00000174678	0	0	0	0.0227979	ENSG00000174678	FAM47DP
ENSG00000174684	6.0391	11.4594	4.88282	7.32539	ENSG00000174684	B4GAT1
ENSG00000174695	29.4852	20.4614	20.6973	23.8833	ENSG00000174695	TMEM167A
ENSG00000174697	0.294677	0.795524	0.704409	1.07378	ENSG00000174697	LEP
ENSG00000174705	16.0681	13.1807	12.4124	21.863	ENSG00000174705	SH3PXD2B
ENSG00000174715	0.492752	1.61172	0.911591	1.1258	ENSG00000174715	RP11-79L9.2
ENSG00000174718	43.682	27.5231	22.5062	19.4242	ENSG00000174718	KIAA1551
ENSG00000174720	24.3284	31.561	26.2525	22.1378	ENSG00000174720	LARP7
ENSG00000174721	0.491277	1.31049	0.904121	1.50452	ENSG00000174721	FGFBP3
ENSG00000174738	11.4701	7.51272	5.90529	5.4065	ENSG00000174738	NR1D2
ENSG00000174740	0.0508192	0.181505	0.209875	0.728465	ENSG00000174740	PABPC5
ENSG00000174744	30.0725	26.7884	35.5534	22.6597	ENSG00000174744	BRMS1
ENSG00000174748	390.661	324.678	272.164	168.138	ENSG00000174748	RPL15
ENSG00000174749	16.2242	38.4162	38.6919	71.9509	ENSG00000174749	C4orf32
ENSG00000174775	85.9966	121.561	123.208	37.4249	ENSG00000174775	HRAS
ENSG00000174776	0.1736	0.395549	0.739053	0.519527	ENSG00000174776	WDR49
ENSG00000174780	41.9551	42.9449	51.7838	26.0766	ENSG00000174780	SRP72
ENSG00000174788	0.673176	1.04042	1.35132	0.273557	ENSG00000174788	PCP2
ENSG00000174791	18.0108	43.3275	38.6179	21.9457	ENSG00000174791	RIN1
ENSG00000174792	4.14493	8.57463	11.0056	17.4194	ENSG00000174792	C4orf26
ENSG00000174796	15.0256	25.1135	26.2984	29.567	ENSG00000174796	THAP6
ENSG00000174799	6.75091	13.0982	8.57614	20.5847	ENSG00000174799	CEP135
ENSG00000174804	0.616659	1.05167	1.1435	1.88883	ENSG00000174804	FZD4
ENSG00000174807	0.109516	0.152336	1.10562	21.121	ENSG00000174807	CD248
ENSG00000174808	1.0238	0.301353	0.456471	0.485207	ENSG00000174808	BTC
ENSG00000174827	1.12063	2.33757	1.52193	2.31764	ENSG00000174827	PDZK1
ENSG00000174837	2.91372	5.98714	5.78811	7.06269	ENSG00000174837	ADGRE1
ENSG00000174839	14.1591	23.2198	17.3724	22.2582	ENSG00000174839	DENND6A
ENSG00000174840	11.7022	9.34632	10.7466	11.7837	ENSG00000174840	PDE12

ENSG00000174842	7.15415	10.3015	10.0959	11.0446	ENSG00000174842	GLMN
ENSG00000174844	1.68065	3.25693	3.08007	6.80721	ENSG00000174844	DNAH12
ENSG00000174851	79.9977	57.6057	52.3933	32.6568	ENSG00000174851	YIF1A
ENSG00000174871	1.09773	0.631603	2.07633	1.51626	ENSG00000174871	CNIH2
ENSG00000174876	0.0388844	0.122453	0.0489813	0.182038	ENSG00000174876	AMY1B
ENSG00000174885	0	0.0396929	0.0183164	0	ENSG00000174885	NLRP6
ENSG00000174886	79.9729	65.4351	60.4256	44.1565	ENSG00000174886	NDUFA11
ENSG00000174891	18.957	26.5923	17.9606	29.1757	ENSG00000174891	RSRC1
ENSG00000174898	1.07881	2.05157	1.7066	2.90852	ENSG00000174898	CATSPERD
ENSG00000174899	1.09456	2.20551	1.59015	3.36172	ENSG00000174899	PQLC2L
ENSG00000174903	61.0367	31.5612	21.9633	24.3096	ENSG00000174903	RAB1B
ENSG00000174912	2.79826	6.32734	4.05005	8.78578	ENSG00000174912	METTL15P1
ENSG00000174914	0	0	0	0	ENSG00000174914	OR9G1
ENSG00000174915	27.831	31.2467	31.9324	23.3945	ENSG00000174915	PTDSS2
ENSG00000174917	33.3502	37.001	30.52	37.413	ENSG00000174917	C19orf70
ENSG00000174928	5.37998	5.73655	5.99835	5.56409	ENSG00000174928	C3orf33
ENSG00000174930	0	0	0.0285328	0	ENSG00000174930	VN2R1P
ENSG00000174937	0	0	0	0	ENSG00000174937	OR5M3
ENSG00000174938	9.05291	13.5607	19.1217	14.9232	ENSG00000174938	SEZ6L2
ENSG00000174939	1.14167	3.30441	2.92762	6.40216	ENSG00000174939	ASPHD1
ENSG00000174942	0	0.12316	0.110998	0.41723	ENSG00000174942	POR5R1
ENSG00000174943	11.9429	12.2309	15.9803	13.6246	ENSG00000174943	KCTD13
ENSG00000174944	0.330557	0.193943	0.116017	0.21995	ENSG00000174944	P2RY14
ENSG00000174945	1.35188	2.13003	3.97767	7.81877	ENSG00000174945	AMZ1
ENSG00000174946	0.128046	0.308742	1.3698	0.494129	ENSG00000174946	GPR171
ENSG00000174948	0.119865	0.138655	0.0627218	0.07899	ENSG00000174948	GPR149
ENSG00000174950	2.24105	6.51248	2.04685	2.37249	ENSG00000174950	CD164L2
ENSG00000174951	6.96547	15.8398	16.4501	8.51933	ENSG00000174951	FUT1
ENSG00000174953	25.0974	38.7838	38.0491	40.9986	ENSG00000174953	DHX36
ENSG00000174957	0	0	0	0	ENSG00000174957	OR5J2
ENSG00000174963	0.103818	0.272398	0.485821	2.57801	ENSG00000174963	ZIC4
ENSG00000174970	0	0.0582946	0.052683	0	ENSG00000174970	OR10AG1
ENSG00000174977	0	0	0	0	ENSG00000174977	AC026271.5
ENSG00000174982	0	0	0	0	ENSG00000174982	OR4S2
ENSG00000174989	4.65085	8.32818	8.66512	10.1964	ENSG00000174989	FBXW8
ENSG00000174990	0.597412	0.859081	1.42006	0.956475	ENSG00000174990	CA5A
ENSG00000174992	0.241761	0.780641	0.358244	0.982732	ENSG00000174992	ZG16
ENSG00000174996	24.4016	23.4869	23.6879	23.8424	ENSG00000174996	KLC2
ENSG00000175003	1.50186	2.29027	5.14041	2.35455	ENSG00000175003	SLC22A1
ENSG00000175018	0.580858	2.31409	1.6469	2.51843	ENSG00000175018	TEX36
ENSG00000175029	59.399	120.562	102.666	120.591	ENSG00000175029	CTBP2
ENSG00000175040	3.98857	4.25063	8.21972	13.1061	ENSG00000175040	CHST2
ENSG00000175048	3.1205	5.67707	5.44755	3.95751	ENSG00000175048	ZDHHC14
ENSG00000175054	15.1643	21.8925	20.1849	26.5622	ENSG00000175054	ATR
ENSG00000175063	7.63116	40.0533	4.61006	15.8671	ENSG00000175063	UBE2C
ENSG00000175065	10.7144	0.343656	0.317489	1.12245	ENSG00000175065	DSG4
ENSG00000175066	22.0572	34.1775	23.5239	36.6414	ENSG00000175066	GK5
ENSG00000175073	5.49035	5.69843	6.81337	7.92872	ENSG00000175073	VCPIP1
ENSG00000175077	0.151806	0.388642	0.366216	0.400268	ENSG00000175077	RTP1
ENSG00000175084	0.170828	0	0.147696	0	ENSG00000175084	DES
ENSG00000175087	3.5906	3.29401	2.69042	1.70131	ENSG00000175087	PDIK1L
ENSG00000175093	1.15749	0.760576	0.301964	1.00523	ENSG00000175093	SPSB4
ENSG00000175097	1.31281	0.912515	1.70846	1.08371	ENSG00000175097	RAG2
ENSG00000175104	14.9806	12.552	10.5022	13.9777	ENSG00000175104	TRAF6

ENSG00000175105	5.23248	6.12506	5.73827	6.02119	ENSG00000175105	ZNF654
ENSG00000175106	21.272	45.7999	45.4073	47.6569	ENSG00000175106	TVP23C
ENSG00000175110	23.0511	31.7193	23.2379	21.0926	ENSG00000175110	MRPS22
ENSG00000175115	29.4626	55.7908	46.3548	64.4125	ENSG00000175115	PACS1
ENSG00000175121	29.4086	1.91925	3.53607	4.60928	ENSG00000175121	WFDC5
ENSG00000175130	22.7014	4.50859	9.63942	13.5842	ENSG00000175130	MARCKSL1
ENSG00000175137	18.0015	11.276	12.5641	15.4125	ENSG00000175137	SH3BP5L
ENSG00000175143	0	0.0525412	0.189945	0.238186	ENSG00000175143	OR2T1
ENSG00000175155	5.05958	2.3219	2.66448	4.98398	ENSG00000175155	YPEL2
ENSG00000175161	0.70301	1.20574	1.38197	1.99502	ENSG00000175161	CADM2
ENSG00000175166	201.166	193.787	120.306	165.195	ENSG00000175166	PSMD2
ENSG00000175170	0.679936	3.34147	3.67213	4.07167	ENSG00000175170	FAM182B
ENSG00000175175	0.036671	0.353596	0.159845	0.403273	ENSG00000175175	PPM1E
ENSG00000175182	16.8718	16.8722	13.334	13.1055	ENSG00000175182	FAM131A
ENSG00000175183	6.99122	14.945	6.29145	11.6307	ENSG00000175183	CSRP2
ENSG00000175189	0.0283049	0.0545581	0.197287	0.0310575	ENSG00000175189	INHBC
ENSG00000175193	17.7252	14.8362	24.5475	16.2929	ENSG00000175193	PARL
ENSG00000175197	29.3103	48.9658	52.1102	12.4064	ENSG00000175197	DDIT3
ENSG00000175198	6.62117	17.2683	17.6601	22.666	ENSG00000175198	PCCA
ENSG00000175202	0.0586082	0.0543097	0.0943782	0.118355	ENSG00000175202	HIGD2B
ENSG00000175203	92.2712	62.019	73.313	70.8144	ENSG00000175203	DCTN2
ENSG00000175206	0.992668	1.53564	0.842577	1.64145	ENSG00000175206	NPPA
ENSG00000175213	6.97512	10.5384	10.0025	5.02092	ENSG00000175213	ZNF408
ENSG00000175215	27.1643	39.2879	37.5732	41.0764	ENSG00000175215	CTDSP2
ENSG00000175216	40.461	86.3377	41.4244	59.5519	ENSG00000175216	CKAP5
ENSG00000175220	22.4971	23.6859	29.0312	24.2049	ENSG00000175220	ARHGAP1
ENSG00000175221	9.69242	9.05751	8.77744	8.3057	ENSG00000175221	MED16
ENSG00000175224	28.05	37.7109	37.2453	50.0956	ENSG00000175224	ATG13
ENSG00000175229	0.0999867	0	0.178337	0.297435	ENSG00000175229	GAL3ST3
ENSG00000175262	0.348238	0.97282	0.719768	1.42558	ENSG00000175262	C1orf127
ENSG00000175264	0.451563	0.737844	0.651567	2.31379	ENSG00000175264	CHST1
ENSG00000175265	25.0013	38.8968	60.7366	61.6975	ENSG00000175265	GOLGA8A
ENSG00000175267	0.161196	0.328206	0.423779	0.450987	ENSG00000175267	VWA3A
ENSG00000175274	17.4822	13.64	11.7559	28.6112	ENSG00000175274	TP53I11
ENSG00000175279	4.55733	4.2149	3.68959	4.19119	ENSG00000175279	CENPS
ENSG00000175283	14.1608	13.3103	9.97761	7.23921	ENSG00000175283	DOLK
ENSG00000175287	4.27555	8.06879	5.17568	14.6238	ENSG00000175287	PHYHD1
ENSG00000175294	0	0.0889178	0.0368223	0.627752	ENSG00000175294	CATSPER1
ENSG00000175302	0.0615147	0.13471	0.0811729	0.187281	ENSG00000175302	ANKRD30BP1
ENSG00000175305	3.7781	3.17589	1.10236	5.89895	ENSG00000175305	CCNE2
ENSG00000175309	22.5008	41.889	53.6691	45.6866	ENSG00000175309	PHYKPL
ENSG00000175311	1.17805	2.41863	2.65672	3.3735	ENSG00000175311	ANKS4B
ENSG00000175315	87.9782	1.8296	4.73314	9.46508	ENSG00000175315	CST6
ENSG00000175318	7.07656	20.7527	18.6924	18.8972	ENSG00000175318	GRAMD2A
ENSG00000175319	0	0	0	5.20109	ENSG00000175319	NF1P5
ENSG00000175322	8.55252	29.0437	16.6701	32.832	ENSG00000175322	ZNF519
ENSG00000175324	17.9756	12.8417	13.5118	8.97468	ENSG00000175324	LSM1
ENSG00000175325	0.159069	0.114912	0.0346239	0.0870457	ENSG00000175325	PROP1
ENSG00000175329	0.157329	0.477413	0.402374	0.511558	ENSG00000175329	ISX
ENSG00000175334	11.2565	19.0194	16.8704	26.7601	ENSG00000175334	BANF1
ENSG00000175336	0.834344	1.4682	1.46426	2.27942	ENSG00000175336	APOF
ENSG00000175344	0.254694	0.500321	0.302041	0.559378	ENSG00000175344	CHRNA7
ENSG00000175348	37.8893	24.9577	24.7056	13.9864	ENSG00000175348	TMEM9B
ENSG00000175352	1.84865	2.88201	1.50527	3.3702	ENSG00000175352	NRIP3

ENSG00000175354	23.0521	43.1207	42.7221	50.3396	ENSG00000175354	PTPN2
ENSG00000175356	1.31691	2.09736	2.75953	3.41567	ENSG00000175356	SCUBE2
ENSG00000175376	27.0146	15.8798	15.1557	17.692	ENSG00000175376	EIF1AD
ENSG00000175387	46.7764	50.9941	43.2912	42.1824	ENSG00000175387	SMAD2
ENSG00000175390	108.738	82.2386	62.7397	60.2427	ENSG00000175390	EIF3F
ENSG00000175393	1.07297	0.630951	0.311029	0.584555	ENSG00000175393	OR10A6
ENSG00000175395	1.88615	4.1591	4.03925	4.46592	ENSG00000175395	ZNF25
ENSG00000175398	0	0	0	0	ENSG00000175398	OR10P1
ENSG00000175414	9.92853	8.12588	11.9978	14.7516	ENSG00000175414	ARL10
ENSG00000175416	396.87	119.984	81.5067	101.556	ENSG00000175416	CLTB
ENSG00000175426	0.670043	4.02157	5.53572	4.52434	ENSG00000175426	PCSK1
ENSG00000175445	0.129369	0.250113	0.162948	0.746583	ENSG00000175445	LPL
ENSG00000175449	1.6123	2.79679	1.95043	1.83665	ENSG00000175449	RFESD
ENSG00000175455	16.2311	38.5861	26.0809	43.4658	ENSG00000175455	CCDC14
ENSG00000175463	1.24989	0.838822	0.883275	1.4881	ENSG00000175463	TBC1D10C
ENSG00000175467	21.5898	14.9202	26.7293	25.8859	ENSG00000175467	SART1
ENSG00000175470	13.5228	15.2972	14.5026	13.4985	ENSG00000175470	PPP2R2D
ENSG00000175471	1.66337	2.71493	2.67092	2.58261	ENSG00000175471	MCTP1
ENSG00000175482	55.0129	43.3295	28.834	33.6397	ENSG00000175482	POLD4
ENSG00000175485	0.0543596	0.156964	0.189151	0.237199	ENSG00000175485	OR52W1
ENSG00000175489	0.626107	1.91005	1.53166	2.18416	ENSG00000175489	LRRC25
ENSG00000175497	1.27738	2.99416	2.98612	5.1481	ENSG00000175497	DPP10
ENSG00000175505	7.80522	2.79665	2.71045	6.51892	ENSG00000175505	CLCF1
ENSG00000175509	0.129843	0.103125	0.461857	0.343212	ENSG00000175509	RP11-395L14.13
ENSG00000175513	0.0362883	0.088603	0.240115	0.498724	ENSG00000175513	TSGA10IP
ENSG00000175514	0.0458586	0.0393585	0.0355767	0.0447124	ENSG00000175514	GPR152
ENSG00000175518	0	0.186027	0.314837	0.396775	ENSG00000175518	UBQLNL
ENSG00000175520	0.236714	0.151704	0.160898	0.433203	ENSG00000175520	UBQLN3
ENSG00000175535	0.0783922	0	0	0.155831	ENSG00000175535	PNLIP
ENSG00000175536	0.918872	2.87579	2.57706	0.917849	ENSG00000175536	LIPT2
ENSG00000175538	0.560593	1.23788	1.03879	1.64828	ENSG00000175538	KCNE3
ENSG00000175544	2.66047	6.86897	6.61263	7.58815	ENSG00000175544	CABP4
ENSG00000175548	4.19031	10.9526	7.55322	6.31129	ENSG00000175548	ALG10B
ENSG00000175550	104.86	106.131	57.7236	63.3664	ENSG00000175550	DRAP1
ENSG00000175556	0.181628	0.0627497	0.185037	0.199204	ENSG00000175556	LONRF3
ENSG00000175564	0.847329	1.82883	1.47451	2.31152	ENSG00000175564	UCP3
ENSG00000175567	1.62414	2.33192	4.1498	2.54706	ENSG00000175567	UCP2
ENSG00000175573	15.3357	22.9468	8.08511	11.3047	ENSG00000175573	C11orf68
ENSG00000175575	8.61506	14.2899	15.9171	21.8797	ENSG00000175575	PAAF1
ENSG00000175581	14.3082	18.5334	15.9203	21.2711	ENSG00000175581	MRPL48
ENSG00000175582	61.0594	46.1703	78.6628	42.0829	ENSG00000175582	RAB6A
ENSG00000175591	13.452	7.98813	3.17891	2.85364	ENSG00000175591	P2RY2
ENSG00000175592	36.1223	51.746	12.7117	47.0784	ENSG00000175592	FOSL1
ENSG00000175595	12.5707	15.4519	15.6482	21.0276	ENSG00000175595	ERCC4
ENSG00000175600	18.8604	17.3917	18.2747	14.9178	ENSG00000175600	SUGCT
ENSG00000175602	12.6047	22.9499	8.64033	28.5429	ENSG00000175602	CCDC85B
ENSG00000175604	0.976735	1.62293	1.46389	3.88201	ENSG00000175604	RP11-276H1.3
ENSG00000175606	13.4596	11.136	11.6881	5.58257	ENSG00000175606	TMEM70
ENSG00000175619	0	0	0	0.0696024	ENSG00000175619	OR4B1
ENSG00000175634	34.0333	24.9145	28.065	15.0145	ENSG00000175634	RPS6KB2
ENSG00000175643	2.65432	5.21627	1.82517	2.80572	ENSG00000175643	RMI2
ENSG00000175646	0	0	0	0.206805	ENSG00000175646	PRM1
ENSG00000175658	0.0839975	0.19792	0.219555	0.727277	ENSG00000175658	DRD5P2
ENSG00000175662	72.1487	41.2636	32.452	34.8321	ENSG00000175662	TOM1L2

ENSG00000175664	0.274194	0.351302	0.396685	0.779477	ENSG00000175664	TEX26
ENSG00000175676	0	0.0292172	0.0295309	0	ENSG00000175676	GOLGA8EP
ENSG00000175691	3.13314	2.77882	3.66519	2.63678	ENSG00000175691	ZNF77
ENSG00000175697	1.24886	0.937758	1.18045	1.76942	ENSG00000175697	GPR156
ENSG00000175707	11.0188	9.94185	8.47423	3.50179	ENSG00000175707	KDF1
ENSG00000175711	2.05999	4.45203	4.03573	7.09878	ENSG00000175711	B3GNTL1
ENSG00000175718	0	0.00755585	0.00683153	0.0172428	ENSG00000175718	RBMXL3
ENSG00000175727	23.3969	27.1804	23.2636	46.1421	ENSG00000175727	MLXIP
ENSG00000175728	0.956758	1.19389	0.725345	1.3565	ENSG00000175728	C11orf44
ENSG00000175730	0.406846	0.540679	0.74903	0.347998	ENSG00000175730	BAK1P1
ENSG00000175741	0	0	0	0.470125	ENSG00000175741	RWDD4P2
ENSG00000175745	0.363429	0.819329	0.698636	6.06246	ENSG00000175745	NR2F1
ENSG00000175746	0.669532	2.23674	2.15251	3.52541	ENSG00000175746	C15orf54
ENSG00000175749	0.104417	0.701995	0.634052	0.338041	ENSG00000175749	EIF3KP1
ENSG00000175756	49.9525	33.1213	31.386	26.1579	ENSG00000175756	AURKAIP1
ENSG00000175764	2.8705	6.48679	5.53529	6.26794	ENSG00000175764	TTLL11
ENSG00000175766	0.142929	0.44057	0.473933	1.42823	ENSG00000175766	EIF4E1B
ENSG00000175768	52.1928	33.2085	33.8019	22.9995	ENSG00000175768	TOMM5
ENSG00000175779	0	0.0538124	0.0487508	0.0612659	ENSG00000175779	C15orf53
ENSG00000175782	12.4685	19.4573	19.8967	26.5504	ENSG00000175782	SLC35E3
ENSG00000175785	0.225766	0.162776	0.294161	0.799247	ENSG00000175785	PRIMA1
ENSG00000175787	6.72909	12.3973	11.0247	21.6671	ENSG00000175787	ZNF169
ENSG00000175792	29.9238	36.4379	38.1184	34.1256	ENSG00000175792	RUVBL1
ENSG00000175793	706.411	531.059	467.057	362.126	ENSG00000175793	SFN
ENSG00000175800	0	0.130115	0.0587388	0.0734341	ENSG00000175800	OR52B3P
ENSG00000175806	4.46157	10.1359	8.5925	8.64069	ENSG00000175806	MSRA
ENSG00000175809	0	0.0370013	0.168822	0.294367	ENSG00000175809	ZNF645
ENSG00000175820	0.0216075	0.0764367	0.0565836	0.0794049	ENSG00000175820	CCDC168
ENSG00000175826	19.697	26.3678	28.6093	21.5192	ENSG00000175826	CTDNEP1
ENSG00000175827	0	0	0	0	ENSG00000175827	AP001266.1
ENSG00000175832	23.7369	38.1837	16.7493	30.9213	ENSG00000175832	ETV4
ENSG00000175841	0.87945	1.13214	1.23182	2.62081	ENSG00000175841	FAM172BP
ENSG00000175854	10.2853	8.70137	8.26252	6.46218	ENSG00000175854	SWI5
ENSG00000175857	1.17644	2.63955	2.95864	6.50049	ENSG00000175857	GAPT
ENSG00000175866	148.611	121.485	96.7658	69.9127	ENSG00000175866	BAIAP2
ENSG00000175868	3.00344	5.38056	4.90918	7.96477	ENSG00000175868	CALCB
ENSG00000175874	6.86502	8.35164	6.12547	10.4392	ENSG00000175874	CREG2
ENSG00000175877	0.103582	0.23349	0.21	0.409097	ENSG00000175877	TMEM270
ENSG00000175879	4.529	1.17283	0.0814652	3.5816	ENSG00000175879	HOXD8
ENSG00000175886	0	0.439058	0.153462	0.305962	ENSG00000175886	RPL7AP66
ENSG00000175893	13.861	19.3708	20.613	30.0848	ENSG00000175893	ZDHHC21
ENSG00000175894	0.0612907	0.0525447	0.0595143	0.0917732	ENSG00000175894	TSPEAR
ENSG00000175895	11.2423	10.2729	10.5524	6.39655	ENSG00000175895	PLEKHF2
ENSG00000175899	1.50268	1.09589	1.68453	3.76581	ENSG00000175899	A2M
ENSG00000175906	14.8661	22.2818	27.2171	7.42086	ENSG00000175906	ARL4D
ENSG00000175911	4.42337	4.44528	5.2645	5.87038	ENSG00000175911	AC127496.1
ENSG00000175920	1.45083	4.19861	1.41224	1.19363	ENSG00000175920	DOK7
ENSG00000175928	0.143031	0.795384	0.892113	0.94672	ENSG00000175928	LRRN1
ENSG00000175931	12.8993	13.0617	13.0774	18.8105	ENSG00000175931	UBE2O
ENSG00000175938	9.70191	18.921	11.9753	7.26106	ENSG00000175938	ORAI3
ENSG00000175946	0.0284602	0.0274286	0	0.0936807	ENSG00000175946	KLHL38
ENSG00000175970	5.94716	6.40454	8.56662	6.54792	ENSG00000175970	UNC119B
ENSG00000175984	31.6829	18.3918	20.2305	17.4799	ENSG00000175984	DENND2C
ENSG00000175985	0.653345	0.864813	0.55567	1.20958	ENSG00000175985	PLEKHD1

ENSG00000176007	0	0.220345	0.729923	0	ENSG00000176007	FAM220BP
ENSG00000176009	0.105694	0	0	0.354032	ENSG00000176009	ASCL3
ENSG00000176014	332.175	196.459	117.331	149.54	ENSG00000176014	TUBB6
ENSG00000176018	7.46858	5.63394	8.61127	7.1202	ENSG00000176018	LYSMD3
ENSG00000176020	1.94771	0.546892	1.57832	3.17862	ENSG00000176020	AMIGO3
ENSG00000176022	8.92722	7.14266	9.1672	6.43019	ENSG00000176022	B3GALT6
ENSG00000176024	4.84026	7.0217	7.16115	7.45218	ENSG00000176024	ZNF613
ENSG00000176029	0.617112	1.3279	1.68459	2.08986	ENSG00000176029	C11orf16
ENSG00000176034	0.202386	0.629789	0.578552	0.797164	ENSG00000176034	CHDC2
ENSG00000176040	0.199324	0.355385	0.387198	0.606487	ENSG00000176040	TMPRSS7
ENSG00000176043	0	1.82897	0.880052	1.00392	ENSG00000176043	RP11-146I3.1
ENSG00000176046	14.4528	34.295	61.4448	6.03907	ENSG00000176046	NUPR1
ENSG00000176049	0.23249	0.459154	0.40425	0.941885	ENSG00000176049	JAKMIP2
ENSG00000176054	0.789048	1.40457	2.62544	0.628006	ENSG00000176054	RPL23P2
ENSG00000176055	2.03737	3.75655	4.87569	3.24141	ENSG00000176055	MBLAC2
ENSG00000176058	4.22933	4.17491	5.2262	4.95437	ENSG00000176058	TPRN
ENSG00000176076	0.278158	0.231787	0.13839	0.435002	ENSG00000176076	KCNE5
ENSG00000176082	0.348953	0.419476	0.808989	0.76403	ENSG00000176082	AL357153.1
ENSG00000176083	1.32997	1.08184	2.37627	1.92826	ENSG00000176083	ZNF683
ENSG00000176087	10.3429	6.51639	12.5708	6.49699	ENSG00000176087	SLC35A4
ENSG00000176092	108.798	45.4637	54.8575	23.3031	ENSG00000176092	CRYBG2
ENSG00000176095	13.7334	13.1698	17.8653	15.8528	ENSG00000176095	IP6K1
ENSG00000176101	25.4702	22.4116	16.3988	10.2246	ENSG00000176101	SSNA1
ENSG00000176102	29.585	36.8882	43.1698	51.6676	ENSG00000176102	CSTF3
ENSG00000176105	49.8029	50.3223	49.2218	49.7842	ENSG00000176105	YES1
ENSG00000176108	11.7861	10.9209	8.774	8.43621	ENSG00000176108	CHMP6
ENSG00000176115	0	0	0	0	ENSG00000176115	AQP7P4
ENSG00000176124	15.6638	26.8975	29.6572	45.7889	ENSG00000176124	DLEU1
ENSG00000176125	1.49239	1.67931	2.18329	1.08586	ENSG00000176125	UFSP1
ENSG00000176134	0	2.78326	2.92587	5.65525	ENSG00000176134	AL445665.1
ENSG00000176136	0.0736286	0.112797	0.174148	0.413829	ENSG00000176136	MC5R
ENSG00000176142	36.2509	44.6807	34.0144	32.5128	ENSG00000176142	TMEM39A
ENSG00000176148	15.0475	20.5797	19.0999	30.2502	ENSG00000176148	TCP11L1
ENSG00000176153	2.30967	5.69032	4.13289	5.59071	ENSG00000176153	GPX2
ENSG00000176155	58.7343	134.454	127.757	177.066	ENSG00000176155	CCDC57
ENSG00000176160	0.0131995	0.114841	0.05747	0.190113	ENSG00000176160	HSF5
ENSG00000176165	0.0430237	0.0416458	0.0749333	0.0410463	ENSG00000176165	FOXG1
ENSG00000176170	91.2994	55.0166	26.0196	77.7338	ENSG00000176170	SPHK1
ENSG00000176171	19.8068	18.7821	12.8961	25.0432	ENSG00000176171	BNIP3
ENSG00000176177	0.0203443	0.918792	0.338731	0.253729	ENSG00000176177	ENTHD1
ENSG00000176182	1.50024	1.96419	1.67461	2.56781	ENSG00000176182	MYPOP
ENSG00000176183	0	0.0550971	0	0	ENSG00000176183	CH17-12M21.1
ENSG00000176194	4.43206	3.28489	1.14162	3.09645	ENSG00000176194	CIDEA
ENSG00000176198	0	0.0541326	0	0.0617407	ENSG00000176198	OR11H4
ENSG00000176200	0	0.128544	0.116152	0.0726955	ENSG00000176200	OR4D11
ENSG00000176204	5.80336	24.401	17.8604	40.7082	ENSG00000176204	LRRTM4
ENSG00000176208	2.00642	5.2296	2.01077	6.19751	ENSG00000176208	ATAD5
ENSG00000176209	8.02792	14.8565	10.3774	7.65676	ENSG00000176209	SMIM19
ENSG00000176219	0.531226	0.572941	0.444977	0.451556	ENSG00000176219	OR11H6
ENSG00000176222	6.41161	6.91081	8.34342	10.2319	ENSG00000176222	ZNF404
ENSG00000176225	47.5321	67.8971	47.5988	53.7669	ENSG00000176225	RTTN
ENSG00000176227	2.37129	0.966291	1.9431	1.16601	ENSG00000176227	CTAGE15
ENSG00000176230	0	0	0.0517196	0.194411	ENSG00000176230	OR4K17
ENSG00000176231	0	0	0	0	ENSG00000176231	OR10H4

ENSG00000176232	0	0	0	0	ENSG00000176232	RP5-1193P9.4
ENSG00000176236	1.21861	1.71746	2.08033	2.88576	ENSG00000176236	C10orf111
ENSG00000176239	0	0.192077	0.173559	0.217259	ENSG00000176239	OR51B6
ENSG00000176243	0	0	0	0	ENSG00000176243	CDV3P1
ENSG00000176244	6.71215	18.9069	17.0942	34.7823	ENSG00000176244	ACBD7
ENSG00000176246	0	0	0.0578531	0.0724196	ENSG00000176246	OR4L1
ENSG00000176248	16.1027	21.0991	25.5384	18.6231	ENSG00000176248	ANAPC2
ENSG00000176253	0	0	0	0	ENSG00000176253	OR4K13
ENSG00000176256	0.0469945	0.13914	0.118931	0.621482	ENSG00000176256	HMGB4
ENSG00000176261	33.5619	39.9137	45.0432	54.1287	ENSG00000176261	ZBTB8OS
ENSG00000176268	0.342559	0.649316	0.895689	0.910387	ENSG00000176268	CYCSP34
ENSG00000176269	0	0	0.792049	0	ENSG00000176269	OR4F21
ENSG00000176273	4.21114	6.09258	5.29487	8.02981	ENSG00000176273	SLC35G1
ENSG00000176274	3.04081	2.71157	3.6956	4.61268	ENSG00000176274	SLC25A53
ENSG00000176281	0	0.652414	0.540498	1.10874	ENSG00000176281	OR4K5
ENSG00000176289	0.198633	1.86385	2.18357	0.803712	ENSG00000176289	IDSP1
ENSG00000176290	0	0	0	0	ENSG00000176290	OR4K3
ENSG00000176293	3.41217	5.37061	4.51651	3.22767	ENSG00000176293	ZNF135
ENSG00000176294	0	0.276017	0.853886	0.443386	ENSG00000176294	OR4N2
ENSG00000176299	0.162738	0.0522122	0	0	ENSG00000176299	OR4M1
ENSG00000176302	0.0300533	0.197155	0.0505073	0.0949485	ENSG00000176302	FOXR1
ENSG00000176305	0	0	0	0	ENSG00000176305	AC087269.1
ENSG00000176312	0.157302	0.208048	0.187979	0.71708	ENSG00000176312	OR4H12P
ENSG00000176318	0	0	0	0	ENSG00000176318	FOXN3P1
ENSG00000176340	163.644	165.09	62.1358	65.9437	ENSG00000176340	COX8A
ENSG00000176343	0.821203	0	1.04965	1.34196	ENSG00000176343	RPL37AP8
ENSG00000176349	0.604413	1.19379	1.54022	1.9495	ENSG00000176349	AC104129.3
ENSG00000176354	4.21639	5.80589	7.00029	5.9338	ENSG00000176354	AC097359.1
ENSG00000176358	4.74159	13.235	8.11246	13.8565	ENSG00000176358	TAC4
ENSG00000176371	8.24317	19.7339	15.2127	23.8689	ENSG00000176371	ZSCAN2
ENSG00000176378	0.72917	0.401022	0.736577	1.05002	ENSG00000176378	PFN1P10
ENSG00000176381	0.98895	0.636793	0.378221	1.10604	ENSG00000176381	PRR18
ENSG00000176383	2.97048	4.30708	3.81474	4.00975	ENSG00000176383	B3GNT4
ENSG00000176386	13.8473	15.1138	12.141	14.0957	ENSG00000176386	CDC26
ENSG00000176387	3.6832	0.652987	3.29544	2.22252	ENSG00000176387	HSD11B2
ENSG00000176390	30.7926	46.5073	38.1718	67.8574	ENSG00000176390	CRLF3
ENSG00000176393	22.9948	28.8427	21.8696	20.5476	ENSG00000176393	RNPEP
ENSG00000176396	4.61309	3.27151	3.34968	2.74947	ENSG00000176396	EID2
ENSG00000176399	0.910679	0.649324	0.852255	0.74012	ENSG00000176399	DMRTA1
ENSG00000176401	2.94844	7.16023	6.57027	12.0621	ENSG00000176401	EID2B
ENSG00000176402	0.596705	0.261061	1.20832	1.00601	ENSG00000176402	GJC3
ENSG00000176406	12.3816	41.9042	25.0631	73.1071	ENSG00000176406	RIMS2
ENSG00000176407	31.2901	26.8838	23.1646	20.6655	ENSG00000176407	KCMF1
ENSG00000176410	0.702783	0.801356	1.2141	1.0776	ENSG00000176410	DNAJC30
ENSG00000176422	3.94158	4.22257	6.11142	4.32293	ENSG00000176422	SPRYD4
ENSG00000176428	0.366135	0.409532	0.494426	0.423368	ENSG00000176428	VPS37D
ENSG00000176435	0	0.0719605	0.0215275	0.218545	ENSG00000176435	CLEC14A
ENSG00000176438	3.59749	17.318	5.27173	10.6836	ENSG00000176438	SYNE3
ENSG00000176444	10.6053	8.94191	11.7293	12.89	ENSG00000176444	CLK2
ENSG00000176454	68.3469	52.881	22.1341	28.1288	ENSG00000176454	LPCAT4
ENSG00000176463	8.01346	24.0349	17.0044	14.4964	ENSG00000176463	SLCO3A1
ENSG00000176472	2.46441	2.00235	2.16971	2.26643	ENSG00000176472	ZNF575
ENSG00000176473	5.96484	8.7569	10.5335	10.5938	ENSG00000176473	WDR25
ENSG00000176476	5.93638	12.8808	8.98359	6.17079	ENSG00000176476	SGF29

ENSG00000176485	12.7527	10.7025	18.3028	33.6665	ENSG00000176485	PLA2G16
ENSG00000176490	0.337684	0.277015	0.710338	0.867076	ENSG00000176490	DIRAS1
ENSG00000176495	0	0	0.0514257	0.0644389	ENSG00000176495	OR5AN1
ENSG00000176510	0.063322	0.4264	0.165164	0.206796	ENSG00000176510	OR10AC1
ENSG00000176515	0.079179	0.106879	0.0828434	0.0892426	ENSG00000176515	AL033381.1
ENSG00000176531	25.7373	13.6676	18.034	14.1081	ENSG00000176531	PHLDB3
ENSG00000176532	2.50265	1.8122	0.576358	0.90089	ENSG00000176532	PRR15
ENSG00000176533	0.394697	0.511034	0.696971	1.57103	ENSG00000176533	GNG7
ENSG00000176540	0	0.182299	0.274605	0.0687665	ENSG00000176540	OR4C5
ENSG00000176542	4.00728	3.75012	3.3835	4.81557	ENSG00000176542	USF3
ENSG00000176547	0	0	0	0	ENSG00000176547	OR4C3
ENSG00000176555	0.0673525	0.129543	0	0	ENSG00000176555	OR4S1
ENSG00000176563	0.502187	0.401428	1.1493	0.805301	ENSG00000176563	CNTD1
ENSG00000176566	0.263066	0.331832	0.413641	0.488346	ENSG00000176566	DCAF4L2
ENSG00000176567	0	0	0.0594492	0.0743882	ENSG00000176567	OR4X1
ENSG00000176571	0.402992	1.71289	2.18751	1.62596	ENSG00000176571	CNBD1
ENSG00000176584	0.283283	0.556104	0.43912	0.798542	ENSG00000176584	DMBT1P1
ENSG00000176593	10.283	19.4053	19.1525	26.1367	ENSG00000176593	AC008969.1
ENSG00000176595	0.530383	0.0382728	0.200259	0.235599	ENSG00000176595	KBTBD11
ENSG00000176597	47.7331	43.2205	34.5378	33.572	ENSG00000176597	B3GNT5
ENSG00000176601	0.246085	0.551054	0.56069	1.13648	ENSG00000176601	MAP3K19
ENSG00000176605	0.0922734	0.044425	0	0.106624	ENSG00000176605	C14orf177
ENSG00000176619	27.027	40.0858	22.4064	27.4386	ENSG00000176619	LMNB2
ENSG00000176623	36.6752	49.122	44.6587	38.7576	ENSG00000176623	RMDN1
ENSG00000176624	28.9674	34.0757	37.0966	16.7776	ENSG00000176624	MEX3C
ENSG00000176635	0.212191	0.230084	0.161782	0.286973	ENSG00000176635	HORMAD2
ENSG00000176641	19.1414	12.6396	29.203	23.1316	ENSG00000176641	RNF152
ENSG00000176654	1.0095	1.50039	1.21855	1.97395	ENSG00000176654	NANOGP1
ENSG00000176658	34.3953	56.1419	33.2665	60.1991	ENSG00000176658	MYO1D
ENSG00000176659	1.29684	3.07118	4.72862	4.53549	ENSG00000176659	C20orf197
ENSG00000176678	0.359493	1.15249	0.862513	1.2889	ENSG00000176678	FOXL1
ENSG00000176679	0	0.0669374	0	0	ENSG00000176679	TGIF2LY
ENSG00000176681	1.48631	3.11138	4.18876	4.86628	ENSG00000176681	LRRC37A
ENSG00000176692	0.170241	0.0328049	0.118728	0.335803	ENSG00000176692	FOXC2
ENSG00000176695	0	0	0	0	ENSG00000176695	OR4F17
ENSG00000176697	0.65823	1.06097	1.54252	2.68245	ENSG00000176697	BDNF
ENSG00000176700	7.92335	7.3566	10.0453	8.73437	ENSG00000176700	SCAND2P
ENSG00000176714	1.47784	0.640102	1.08039	1.24818	ENSG00000176714	CCDC121
ENSG00000176715	17.2489	29.5613	30.6089	31.3379	ENSG00000176715	ACSF3
ENSG00000176716	0.361815	0.368188	0.868711	0.477246	ENSG00000176716	OR10AB1P
ENSG00000176720	17.7691	15.3886	19.2232	7.44089	ENSG00000176720	BOK
ENSG00000176723	1.07628	1.76889	2.13822	3.7943	ENSG00000176723	ZNF843
ENSG00000176731	61.9783	56.232	43.476	28.4734	ENSG00000176731	C8orf59
ENSG00000176732	6.46638	0.868068	2.72439	2.30625	ENSG00000176732	PFN4
ENSG00000176742	0.0643435	0	0.0559337	0	ENSG00000176742	OR51V1
ENSG00000176746	0.0869558	0.0838015	0.0252527	0.190795	ENSG00000176746	MAGEB6
ENSG00000176748	0.0658136	0.126593	0	0	ENSG00000176748	OR52Z1
ENSG00000176749	18.3273	4.76182	3.96133	5.877	ENSG00000176749	CDK5R1
ENSG00000176752	0	0	0	0	ENSG00000176752	OR51A1P
ENSG00000176753	0.351072	0.948143	0.986162	0.398052	ENSG00000176753	C15orf56
ENSG00000176761	0.0716196	0.0357978	0.12744	0.238693	ENSG00000176761	ZNF285B
ENSG00000176769	0.318013	0.470005	0.457526	0.69702	ENSG00000176769	TCERG1L
ENSG00000176771	7.18917	5.76747	15.2008	10.3586	ENSG00000176771	NCKAP5
ENSG00000176774	0.0314083	0	0.173301	0.222305	ENSG00000176774	MAGEB18

ENSG00000176782	0	0	0	0	ENSG00000176782	DEFB104A
ENSG00000176783	22.5091	31.0822	37.0565	30.5042	ENSG00000176783	RUFY1
ENSG00000176787	0	0	0	0.0690151	ENSG00000176787	OR52E2
ENSG00000176788	35.9791	28.344	39.549	36.4892	ENSG00000176788	BASP1
ENSG00000176797	0.577623	0.0692408	0.187548	3.86423	ENSG00000176797	DEFB103A
ENSG00000176798	0	0	0	0	ENSG00000176798	OR51L1
ENSG00000176809	5.57815	14.4337	18.4792	19.0049	ENSG00000176809	LRRC37A3
ENSG00000176812	0	0.0802858	0.135015	0	ENSG00000176812	RP11-629O4.1
ENSG00000176824	0.902288	1.77087	1.99007	5.7757	ENSG00000176824	AC009951.1
ENSG00000176826	3.93896	9.28892	14.0469	4.44952	ENSG00000176826	FKBP9P1
ENSG00000176834	46.0948	22.428	16.5171	29.5886	ENSG00000176834	VSIG10
ENSG00000176842	6.05384	2.76337	3.82076	2.0263	ENSG00000176842	IRX5
ENSG00000176845	51.0866	8.04684	16.2604	24.6611	ENSG00000176845	METRNL
ENSG00000176853	23.3848	23.1914	28.2098	33.6631	ENSG00000176853	FAM91A1
ENSG00000176855	0.044574	0.0442591	0.0389445	0	ENSG00000176855	KRT18P28
ENSG00000176857	1.03487	2.34822	2.37681	3.12462	ENSG00000176857	GJA1P1
ENSG00000176868	0	1.29724	0	0	ENSG00000176868	AL358781.1
ENSG00000176871	37.168	19.5734	13.9153	16.5208	ENSG00000176871	WSB2
ENSG00000176879	0	0	0	0	ENSG00000176879	OR51G1
ENSG00000176882	0	0	0	0	ENSG00000176882	RP11-432M24.4
ENSG00000176884	0.729719	0.145754	0.343123	0.265682	ENSG00000176884	GRIN1
ENSG00000176887	0.201866	0.952608	2.1393	3.84447	ENSG00000176887	SOX11
ENSG00000176890	2.6958	14.3017	6.8426	12.9198	ENSG00000176890	TYMS
ENSG00000176893	0	0	0	0	ENSG00000176893	OR51G2
ENSG00000176894	5.61954	7.09628	3.93022	7.49945	ENSG00000176894	PXMP2
ENSG00000176895	0	0	0	0	ENSG00000176895	OR51A7
ENSG00000176896	2.50456	4.32771	4.90283	8.41797	ENSG00000176896	TCEANC
ENSG00000176900	0	0.0551468	0.0498398	0	ENSG00000176900	OR51T1
ENSG00000176903	7.45517	9.38803	12.2453	9.98228	ENSG00000176903	PNMA1
ENSG00000176904	0	0	0	0	ENSG00000176904	OR51H1
ENSG00000176907	0.0628933	0.125809	0.113519	0.78989	ENSG00000176907	C8orf4
ENSG00000176909	1.56075	1.40965	1.06172	0.915529	ENSG00000176909	MAMSTR
ENSG00000176912	0.234383	2.48063	0.888628	1.13963	ENSG00000176912	C18orf56
ENSG00000176915	124.001	106.433	110.848	107.328	ENSG00000176915	ANKLE2
ENSG00000176919	2.01948	0.966067	0.961341	1.06098	ENSG00000176919	C8G
ENSG00000176920	12.1638	4.96184	4.79563	7.0142	ENSG00000176920	FUT2
ENSG00000176922	0	0.107567	0	0.0609409	ENSG00000176922	OR51S1
ENSG00000176923	0	0	0	0	ENSG00000176923	OR7A15P
ENSG00000176925	0	0.10229	0.046225	0.115958	ENSG00000176925	OR51F2
ENSG00000176927	4.00552	13.5786	10.2675	17.5553	ENSG00000176927	EFCAB5
ENSG00000176928	9.78419	3.86899	2.4703	2.21222	ENSG00000176928	GCNT4
ENSG00000176933	0.962215	0.849143	0.784061	0.175672	ENSG00000176933	TOB2P1
ENSG00000176937	0.0505936	0.0632967	0.0440215	0.165714	ENSG00000176937	OR52R1
ENSG00000176945	53.5259	35.5511	39.545	56.179	ENSG00000176945	MUC20
ENSG00000176946	17.1135	18.2529	19.1001	15.216	ENSG00000176946	THAP4
ENSG00000176951	0	0	0	0	ENSG00000176951	OR51N1P
ENSG00000176953	24.3131	29.5577	27.4476	27.8306	ENSG00000176953	NFATC2IP
ENSG00000176956	0.0772495	0.191856	0.242677	0.520092	ENSG00000176956	LY6H
ENSG00000176970	0.0481153	0.0524747	0.197778	1.13452	ENSG00000176970	RPL7L1P11
ENSG00000176971	0.3795	0.712501	2.16674	3.84563	ENSG00000176971	FIBIN
ENSG00000176973	12.9813	11.7704	10.0985	6.73303	ENSG00000176973	FAM89B
ENSG00000176974	8.11922	30.9276	13.1585	17.4902	ENSG00000176974	SHMT1
ENSG00000176978	75.3061	92.1413	73.6895	46.402	ENSG00000176978	DPP7
ENSG00000176979	0.0600171	0.0875546	0.0522853	0	ENSG00000176979	TRIM60

ENSG00000176984	1.10669	2.60385	2.06539	4.42796	ENSG00000176984	AP000679.2
ENSG00000176986	36.9846	23.1277	29.7995	29.9716	ENSG00000176986	SEC24C
ENSG00000176988	0.321816	0.371323	0.225015	1.04596	ENSG00000176988	FMR1NB
ENSG00000176994	8.29545	5.54071	7.57152	5.44245	ENSG00000176994	SMCR8
ENSG00000176998	1.86909	1.3845	0.332359	0.329597	ENSG00000176998	HCG4
ENSG00000177000	15.6441	17.0231	24.4646	17.4797	ENSG00000177000	MTHFR
ENSG00000177023	0	0	0	0	ENSG00000177023	DEFB104B
ENSG00000177025	2.37362	1.94078	2.62489	1.71762	ENSG00000177025	C19orf18
ENSG00000177030	20.459	26.5448	29.4852	18.9125	ENSG00000177030	DEAF1
ENSG00000177034	8.57284	12.3365	12.5312	8.36376	ENSG00000177034	MTX3
ENSG00000177042	31.9167	32.0651	31.5912	19.4338	ENSG00000177042	TMEM80
ENSG00000177045	3.12106	4.01497	4.74615	4.16928	ENSG00000177045	SIX5
ENSG00000177047	0.118431	0.184461	0.169484	0.239513	ENSG00000177047	IFNW1
ENSG00000177051	12.3227	9.91904	10.4292	14.3846	ENSG00000177051	FBXO46
ENSG00000177054	21.636	31.2271	19.0314	18.3177	ENSG00000177054	ZDHHC13
ENSG00000177058	45.0362	57.6561	51.4224	53.9525	ENSG00000177058	SLC38A9
ENSG00000177076	5.52496	6.64541	3.52113	2.03114	ENSG00000177076	ACER2
ENSG00000177082	16.9788	23.4409	31.9882	30.3625	ENSG00000177082	WDR73
ENSG00000177084	21.6667	44.4829	25.3277	49.65	ENSG00000177084	POLE
ENSG00000177096	2.04277	0.779898	0.971565	1.54972	ENSG00000177096	FAM109B
ENSG00000177098	1.13672	7.9231	7.84129	1.56833	ENSG00000177098	SCN4B
ENSG00000177103	0.981724	0.234863	0.138113	0.378573	ENSG00000177103	DSCAML1
ENSG00000177105	13.8465	11.53	11.5004	10.9785	ENSG00000177105	RHOG
ENSG00000177106	91.8125	104.504	120.641	32.3324	ENSG00000177106	EPS8L2
ENSG00000177108	0.0825375	0.350835	0.553918	0.130204	ENSG00000177108	ZDHHC22
ENSG00000177119	80.2795	70.5336	45.0733	51.8313	ENSG00000177119	ANO6
ENSG00000177125	3.70424	3.1048	3.7807	3.99568	ENSG00000177125	ZBTB34
ENSG00000177138	1.77973	3.56548	3.31424	5.16737	ENSG00000177138	FAM9B
ENSG00000177143	0	0	0	0	ENSG00000177143	CETN1
ENSG00000177144	4.14307	4.23672	10.6739	6.31023	ENSG00000177144	NUDT4P1
ENSG00000177150	14.4008	8.58028	13.1744	12.0304	ENSG00000177150	FAM210A
ENSG00000177151	0	0	0	0	ENSG00000177151	OR2T35
ENSG00000177156	108.49	70.4073	52.3983	59.1335	ENSG00000177156	TALDO1
ENSG00000177169	15.1728	15.5974	27.3941	18.9883	ENSG00000177169	ULK1
ENSG00000177173	0.891618	3.20786	2.4864	4.10496	ENSG00000177173	NAP1L4P1
ENSG00000177174	0	0	0	0	ENSG00000177174	OR14C36
ENSG00000177181	0.231348	0.429716	0.328073	0.431323	ENSG00000177181	RIMKLA
ENSG00000177182	2.08944	5.8294	4.77782	5.94751	ENSG00000177182	CLVS1
ENSG00000177186	1.16703	0.708757	1.92185	2.33837	ENSG00000177186	OR2M7
ENSG00000177189	18.867	20.5204	22.6583	19.1234	ENSG00000177189	RPS6KA3
ENSG00000177191	10.8468	5.36646	4.05789	2.97282	ENSG00000177191	B3GNT8
ENSG00000177192	15.751	22.5152	27.2424	21.4472	ENSG00000177192	PUS1
ENSG00000177197	0.490105	0.318025	0.291274	0.888214	ENSG00000177197	PCNPP5
ENSG00000177200	25.7784	50.0587	44.5877	55.9714	ENSG00000177200	CHD9
ENSG00000177201	0	0	0	0	ENSG00000177201	OR2T12
ENSG00000177202	0.511574	0.18454	0.16677	0.0696024	ENSG00000177202	SPACA4
ENSG00000177212	0	0	0	0	ENSG00000177212	OR2T33
ENSG00000177225	60.6435	47.1625	58.5292	43.2967	ENSG00000177225	GATD1
ENSG00000177233	0	0	0	0	ENSG00000177233	OR2M1P
ENSG00000177234	0.17851	0.457149	0.645732	0.585391	ENSG00000177234	LINC01561
ENSG00000177236	8.63098	7.07516	6.93154	9.46396	ENSG00000177236	AP006621.1
ENSG00000177238	0.262044	0.578046	0.563269	1.22213	ENSG00000177238	TRIM72
ENSG00000177239	39.7143	52.69	54.1743	35.8391	ENSG00000177239	MAN1B1
ENSG00000177243	0.577623	0.0692408	0.187548	3.86423	ENSG00000177243	DEFB103B

ENSG00000177257	0.292572	0	0.251303	0	ENSG00000177257	DEFB4B
ENSG00000177261	0	0	0	0	ENSG00000177261	ENSAP3
ENSG00000177272	0.146849	0.364413	0.383429	0.591297	ENSG00000177272	KCNA3
ENSG00000177275	0	0	0	0	ENSG00000177275	OR2AJ1
ENSG00000177283	4.1799	6.64366	3.66586	6.52084	ENSG00000177283	FZD8
ENSG00000177291	0.341134	0.49573	1.19868	1.85483	ENSG00000177291	GJD4
ENSG00000177294	0.340628	1.35647	1.49169	0.853846	ENSG00000177294	FBXO39
ENSG00000177300	0	0.16524	0.064082	0.0645664	ENSG00000177300	CLDN22
ENSG00000177301	0.0696038	0.0990133	0.0953584	0.232428	ENSG00000177301	KCNA2
ENSG00000177302	19.5654	36.1961	38.9461	43.8962	ENSG00000177302	TOP3A
ENSG00000177303	11.7036	11.4065	10.1786	7.69516	ENSG00000177303	CASKIN2
ENSG00000177306	1.54E-09	7.35E-10	2.12E-09	0	ENSG00000177306	OR7E125P
ENSG00000177311	58.1671	51.6632	40.649	73.9151	ENSG00000177311	ZBTB38
ENSG00000177324	0.346357	0.840453	0.825041	1.4885	ENSG00000177324	BEND2
ENSG00000177335	2.42396	3.68177	3.22664	5.10535	ENSG00000177335	C8orf31
ENSG00000177340	0.885691	1.72117	1.95056	2.09736	ENSG00000177340	FLJ13224
ENSG00000177350	0.403937	0.326176	0.484627	0.576476	ENSG00000177350	RPL13AP3
ENSG00000177352	5.9048	8.72335	8.54009	5.04614	ENSG00000177352	CCDC71
ENSG00000177354	0.0585749	0.275887	0.116523	0.451761	ENSG00000177354	C10orf71
ENSG00000177359	1.39001	3.05556	3.20123	3.8604	ENSG00000177359	AC024940.1
ENSG00000177363	1.97831	3.25432	3.09966	5.76668	ENSG00000177363	LRRN4CL
ENSG00000177370	6.52688	4.82906	5.92489	3.4246	ENSG00000177370	TIMM22
ENSG00000177374	1.63111	1.91217	1.49519	5.78139	ENSG00000177374	HIC1
ENSG00000177380	4.18791	4.04727	6.73589	5.1972	ENSG00000177380	PPFIA3
ENSG00000177383	8.38413	7.35912	10.4819	7.54674	ENSG00000177383	MAGEF1
ENSG00000177398	0.0505308	0.196761	0.165771	0.514035	ENSG00000177398	UMODL1
ENSG00000177400	0	0	0	0	ENSG00000177400	OR7E8P
ENSG00000177409	8.15551	3.68365	5.77336	9.50852	ENSG00000177409	SAMD9L
ENSG00000177414	0	0	0.297533	0.267171	ENSG00000177414	UBE2U
ENSG00000177418	0.145215	0.629627	0.7248	1.64452	ENSG00000177418	AC006001.1
ENSG00000177425	56.9948	90.3771	126.374	69.5606	ENSG00000177425	PAWR
ENSG00000177426	63.0302	99.4895	73.0281	60.2727	ENSG00000177426	TGIF1
ENSG00000177427	25.4393	12.6833	11.3634	6.68053	ENSG00000177427	MIEF2
ENSG00000177432	0.624417	0.970155	1.2355	2.00292	ENSG00000177432	NAP1L5
ENSG00000177447	0	0	0	0.284599	ENSG00000177447	CBX3P1
ENSG00000177452	0.366344	0.35147	0.529115	1.18193	ENSG00000177452	RP4-597J3.1
ENSG00000177453	4.26666	7.51441	6.96755	17.5578	ENSG00000177453	NIM1K
ENSG00000177455	0.120395	0.361835	0.249846	0.698636	ENSG00000177455	CD19
ENSG00000177459	0.194338	0	0.225701	0.177533	ENSG00000177459	C8orf47
ENSG00000177462	0	0	0	0	ENSG00000177462	OR2T8
ENSG00000177463	16.4984	25.0907	26.5727	29.4162	ENSG00000177463	NR2C2
ENSG00000177464	0.272788	0.680442	0.678057	1.05141	ENSG00000177464	GPR4
ENSG00000177465	0.558729	0.952384	0.861845	1.03076	ENSG00000177465	ACOT4
ENSG00000177468	0.206235	0.281907	0.291472	0.59771	ENSG00000177468	OLIG3
ENSG00000177469	93.3045	96.6092	70.6702	116.86	ENSG00000177469	CAVIN1
ENSG00000177476	0	0	0	0	ENSG00000177476	OR2G3
ENSG00000177479	91.9842	133.292	146.545	160.35	ENSG00000177479	ARIH2
ENSG00000177483	0.526745	1.57068	1.93365	1.47067	ENSG00000177483	RBM44
ENSG00000177485	4.61046	3.7082	4.27974	2.73654	ENSG00000177485	ZBTB33
ENSG00000177489	0	0	0	0	ENSG00000177489	OR2G2
ENSG00000177494	68.0104	30.37	8.49573	22.69	ENSG00000177494	ZBED2
ENSG00000177504	0	0.204024	0.0796976	0	ENSG00000177504	VCX2
ENSG00000177508	8.78673	5.44625	8.55573	10.115	ENSG00000177508	IRX3
ENSG00000177511	0.0675595	0.161012	0.222288	1.25394	ENSG00000177511	ST8SIA3

ENSG00000177519	0.0791098	0.0402652	0.0692648	0.265276	ENSG00000177519	RPRM
ENSG00000177535	0	0	0	0	ENSG00000177535	OR2B11
ENSG00000177542	11.7191	14.7849	18.5845	9.84762	ENSG00000177542	SLC25A22
ENSG00000177548	14.5058	20.2561	17.0453	21.3639	ENSG00000177548	RABEP2
ENSG00000177551	0.750121	0.870124	0.855355	0.970959	ENSG00000177551	NHLH2
ENSG00000177556	62.3989	28.325	18.9438	26.7122	ENSG00000177556	ATOX1
ENSG00000177558	0.101286	0	0	0	ENSG00000177558	FAM187B
ENSG00000177565	70.3069	77.9124	73.4048	64.1623	ENSG00000177565	TBL1XR1
ENSG00000177570	6.96294	5.5969	5.44116	3.7193	ENSG00000177570	SAMD12
ENSG00000177575	23.6995	60.5395	47.8139	107.277	ENSG00000177575	CD163
ENSG00000177576	33.5785	14.997	16.2367	12.6384	ENSG00000177576	C18orf32
ENSG00000177586	0	0	0	0	ENSG00000177586	OR7E149P
ENSG00000177590	0.145658	0.0822178	0.0885892	0.313876	ENSG00000177590	RP5-1051J4.6
ENSG00000177595	10.4247	17.0046	19.7329	23.4096	ENSG00000177595	PIDD1
ENSG00000177596	1.67301	4.61264	4.0725	4.93834	ENSG00000177596	AL355390.1
ENSG00000177599	4.34478	5.40524	4.97083	7.07811	ENSG00000177599	ZNF491
ENSG00000177600	434.765	360.487	320.013	255.577	ENSG00000177600	RPLP2
ENSG00000177602	1.20635	3.28023	1.02671	1.75112	ENSG00000177602	HASPIN
ENSG00000177606	32.1774	17.3627	40.6801	36.9664	ENSG00000177606	JUN
ENSG00000177613	6.36792	5.77492	6.24316	6.3814	ENSG00000177613	CSTF2T
ENSG00000177614	3.66457	0.0609252	0.724868	1.20495	ENSG00000177614	PGBD5
ENSG00000177627	1.42493	3.1086	4.50679	1.16251	ENSG00000177627	C12orf54
ENSG00000177628	50.4206	24.4747	30.3093	18.936	ENSG00000177628	GBA
ENSG00000177646	20.3692	26.8237	26.2056	24.9737	ENSG00000177646	ACAD9
ENSG00000177663	14.4538	15.2947	16.2127	9.01457	ENSG00000177663	IL17RA
ENSG00000177666	22.8175	16.1146	28.9786	13.1583	ENSG00000177666	PNPLA2
ENSG00000177669	0.153421	0.0369466	0.267179	0.207432	ENSG00000177669	MBOAT4
ENSG00000177673	0	0.0396391	0.0358302	0	ENSG00000177673	TEX44
ENSG00000177674	76.6621	73.6025	49.7275	29.6481	ENSG00000177674	AGTRAP
ENSG00000177675	0.246953	1.00094	0.916057	1.82627	ENSG00000177675	CD163L1
ENSG00000177679	3.36204	0.828816	1.42784	1.79429	ENSG00000177679	SRRM3
ENSG00000177683	13.5774	16.4558	17.2051	18.8566	ENSG00000177683	THAP5
ENSG00000177684	0	0	0	0	ENSG00000177684	DEFB114
ENSG00000177685	1.26085	1.74163	1.17713	1.88184	ENSG00000177685	CRACR2B
ENSG00000177688	1.39296	2.60554	1.22537	3.32641	ENSG00000177688	SUMO4
ENSG00000177689	0.348111	1.1577	1.11571	1.74091	ENSG00000177689	MAGEB10
ENSG00000177692	0.538707	0.284838	0.330181	0.16623	ENSG00000177692	DNAJC28
ENSG00000177693	0	0	0.050451	0.0632291	ENSG00000177693	OR4F4
ENSG00000177694	4.78328	5.5517	4.62015	10.0075	ENSG00000177694	NAALADL2
ENSG00000177697	345.482	350.63	239.042	156.798	ENSG00000177697	CD151
ENSG00000177700	57.9315	38.5916	22.7114	33.1424	ENSG00000177700	POLR2L
ENSG00000177706	7.14684	63.1034	18.1538	81.1395	ENSG00000177706	FAM20C
ENSG00000177707	2.9377	11.7839	4.32292	31.7479	ENSG00000177707	NECTIN3
ENSG00000177710	0.653716	0.603252	0.916129	1.38425	ENSG00000177710	SLC35G5
ENSG00000177721	0.550042	1.01236	0.904273	1.75914	ENSG00000177721	ANXA2R
ENSG00000177725	0.904756	1.56533	2.30405	1.93243	ENSG00000177725	AC105206.1
ENSG00000177728	21.8191	38.7281	40.6235	26.2644	ENSG00000177728	TMEM94
ENSG00000177731	132.832	144.087	128.534	103.66	ENSG00000177731	FLII
ENSG00000177732	2.09149	4.25933	7.36388	6.0311	ENSG00000177732	SOX12
ENSG00000177733	11.2566	9.65534	16.6547	12.4333	ENSG00000177733	HNRNPA0
ENSG00000177736	0.133692	0.818364	0.451286	0.360236	ENSG00000177736	RP11-474P12.3
ENSG00000177752	0.0667455	0.0484655	0.152025	0.164602	ENSG00000177752	YIPF7
ENSG00000177764	2.05142	2.41463	2.87629	2.28499	ENSG00000177764	ZCCHC3
ENSG00000177770	0	0	0	0	ENSG00000177770	CDKN2AIPNLP1

ENSG00000177776	0	0	0	0	ENSG00000177776	RPS2P2
ENSG00000177791	0.0750994	0.0361721	0.13079	0.123349	ENSG00000177791	MYOZ1
ENSG00000177800	1.10415	2.91012	2.8951	6.09682	ENSG00000177800	TMEM78
ENSG00000177803	0	0.100708	0	0.113674	ENSG00000177803	RP11-606P2.1
ENSG00000177807	0.276141	0.352406	0.444569	0.499016	ENSG00000177807	KCNJ10
ENSG00000177820	6.4336	3.21071	2.90943	0.713065	ENSG00000177820	AC004917.1
ENSG00000177830	35.615	39.876	40.3409	41.7434	ENSG00000177830	CHID1
ENSG00000177839	0.512024	0.340825	0.780877	1.97223	ENSG00000177839	PCDHB9
ENSG00000177842	1.71951	4.01342	3.90426	4.13598	ENSG00000177842	ZNF620
ENSG00000177854	3.1042	2.99353	2.24227	1.27141	ENSG00000177854	TMEM187
ENSG00000177855	0	0.160281	0.115191	0	ENSG00000177855	CACYBPP2
ENSG00000177868	10.8012	10.0408	10.9854	6.00549	ENSG00000177868	SVBP
ENSG00000177873	3.13404	5.05331	6.13331	4.48744	ENSG00000177873	ZNF619
ENSG00000177875	0.0712276	0.0915491	0.227608	0.625876	ENSG00000177875	CCDC184
ENSG00000177879	33.5218	39.5307	32.6883	31.6205	ENSG00000177879	AP3S1
ENSG00000177885	44.7053	40.2856	35.5311	44.3564	ENSG00000177885	GRB2
ENSG00000177888	7.45122	8.29478	6.77286	6.29517	ENSG00000177888	ZBTB41
ENSG00000177889	48.5525	31.074	22.5745	25.0164	ENSG00000177889	UBE2N
ENSG00000177910	0.0719966	0.0975699	0.0627801	0.0794315	ENSG00000177910	SPATA31C2
ENSG00000177917	13.4262	24.7667	18.3119	14.6657	ENSG00000177917	ARL6IP6
ENSG00000177932	2.44838	3.59023	3.9781	4.42318	ENSG00000177932	ZNF354C
ENSG00000177938	0	0.108854	0.295138	0.369977	ENSG00000177938	CAPZA3
ENSG00000177943	6.03738	13.1506	15.2599	9.50634	ENSG00000177943	MAMDC4
ENSG00000177946	2.41679	2.65299	3.86902	3.20071	ENSG00000177946	CENPBD1
ENSG00000177947	0.197158	0.484037	0.583412	0.573367	ENSG00000177947	ODF3
ENSG00000177951	17.644	41.8587	45.75	34.514	ENSG00000177951	BET1L
ENSG00000177954	1072.65	815.242	554.001	377.299	ENSG00000177954	RPS27
ENSG00000177963	58.051	40.2045	41.1968	32.3511	ENSG00000177963	RIC8A
ENSG00000177971	25.155	17.0885	20.2907	14.0032	ENSG00000177971	IMP3
ENSG00000177981	11.4805	10.7736	13.9717	9.65701	ENSG00000177981	ASB8
ENSG00000177984	1.00096	1.91283	2.4148	3.77019	ENSG00000177984	LCN15
ENSG00000177989	6.75829	17.7846	22.5214	11.4804	ENSG00000177989	ODF3B
ENSG00000177990	2.01675	3.82289	4.95929	5.51015	ENSG00000177990	DPY19L2
ENSG00000177992	0.0240165	0.0347474	0.0733078	0.185141	ENSG00000177992	SPATA31E1
ENSG00000177994	0.854403	2.57856	1.16827	3.05119	ENSG00000177994	C2orf73
ENSG00000178015	0.60033	0.524805	0.239011	0.477992	ENSG00000178015	GPR150
ENSG00000178021	0.070668	0.238501	0.415895	0.40806	ENSG00000178021	TSPYL6
ENSG00000178026	8.62429	18.103	16.365	6.93453	ENSG00000178026	LRRC75B
ENSG00000178028	8.02695	10.9326	15.3295	12.4604	ENSG00000178028	DMAP1
ENSG00000178031	1.0565	6.75852	2.82118	16.9069	ENSG00000178031	ADAMTSL1
ENSG00000178033	2.45847	1.95648	2.05365	3.51104	ENSG00000178033	FAM26E
ENSG00000178035	70.1613	84.8626	96.788	50.0958	ENSG00000178035	IMPDH2
ENSG00000178038	140.301	125.191	112.889	54.8933	ENSG00000178038	ALS2CL
ENSG00000178053	11.1704	7.68239	7.29403	10.1701	ENSG00000178053	MLF1
ENSG00000178055	0.0463015	0.178333	0.312003	0.1012	ENSG00000178055	PRSS42
ENSG00000178057	31.6571	20.3906	16.4505	15.151	ENSG00000178057	NDUFAF3
ENSG00000178074	6.10904	6.2484	6.15786	5.80113	ENSG00000178074	C2orf69
ENSG00000178075	3.88281	6.99841	4.42437	10.4937	ENSG00000178075	GRAMD1C
ENSG00000178078	43.6341	40.5272	44.1517	34.58	ENSG00000178078	STAP2
ENSG00000178081	0.413858	0.461239	0.770255	0.435651	ENSG00000178081	ULK4P3
ENSG00000178082	0	0.293252	0.0938762	0.226674	ENSG00000178082	TWF1P1
ENSG00000178084	0.340795	0	0.0293851	0.147896	ENSG00000178084	HTR3C
ENSG00000178093	0.722093	0.953779	1.2436	0.784501	ENSG00000178093	TSSK6

ENSG00000178096	3.87037	4.83459	4.31827	3.17405	ENSG00000178096	BOLA1
ENSG00000178104	51.9455	109.265	116.893	286.608	ENSG00000178104	PDE4DIP
ENSG00000178105	14.1724	25.1031	21.2075	26.759	ENSG00000178105	DDX10
ENSG00000178115	0.5237	1.25342	0.473051	0	ENSG00000178115	GOLGA8Q
ENSG00000178125	1.40828	6.7607	6.32991	8.05837	ENSG00000178125	PPP1R42
ENSG00000178127	59.24	72.0802	52.9785	61.5176	ENSG00000178127	NDUFV2
ENSG00000178146	0	0	0	0	ENSG00000178146	RP1-232L22
ENSG00000178149	8.7349	14.9296	10.5816	7.67699	ENSG00000178149	DALRD3
ENSG00000178150	2.70721	6.87031	6.69209	8.82069	ENSG00000178150	ZNF114
ENSG00000178162	2.91097	7.66955	5.69959	12.0743	ENSG00000178162	FAR2P2
ENSG00000178163	20.2281	16.2249	20.2541	11.219	ENSG00000178163	ZNF518B
ENSG00000178171	0.496509	0.864095	0.819396	1.31289	ENSG00000178171	AMER3
ENSG00000178172	44.7772	1.63785	2.13682	2.66047	ENSG00000178172	SPINK6
ENSG00000178175	0.897927	0.97027	1.59787	2.6596	ENSG00000178175	ZNF366
ENSG00000178177	4.36933	11.4101	5.85753	11.8454	ENSG00000178177	LCORL
ENSG00000178184	10.637	14.6279	25.6619	11.1623	ENSG00000178184	PARD6G
ENSG00000178187	1.80681	1.62492	1.83238	2.57263	ENSG00000178187	ZNF454
ENSG00000178188	23.9572	30.6758	29.8517	35.2251	ENSG00000178188	SH2B1
ENSG00000178199	1.00501	2.58098	1.85429	3.24436	ENSG00000178199	ZC3H12D
ENSG00000178201	0.957991	0.721848	1.51514	1.18313	ENSG00000178201	VN1R1
ENSG00000178202	7.2576	25.6289	18.2574	36.9846	ENSG00000178202	KDELC2
ENSG00000178206	0.109983	0.0939202	0.171718	0.381969	ENSG00000178206	CYP4F31P
ENSG00000178209	326.852	453.756	251.497	346.562	ENSG00000178209	PLEC
ENSG00000178217	0.365518	0.106525	0.180553	0.474325	ENSG00000178217	SH2D4B
ENSG00000178222	3.66084	8.70163	7.91928	15.0762	ENSG00000178222	RNF212
ENSG00000178226	1.42412	1.15533	0.84016	0.819967	ENSG00000178226	PRSS36
ENSG00000178229	6.12124	5.70812	7.92385	5.76677	ENSG00000178229	ZNF543
ENSG00000178233	0.732273	0.909984	1.44885	2.32758	ENSG00000178233	TMEM151B
ENSG00000178234	33.5922	31.7965	21.3926	27.8442	ENSG00000178234	GALNT11
ENSG00000178235	0.0621004	0.0800922	0.153597	0.277331	ENSG00000178235	SLITRK1
ENSG00000178243	0.118346	0.0854566	0.313199	0.162522	ENSG00000178243	C9orf62
ENSG00000178252	31.2401	61.7575	57.1994	59.0195	ENSG00000178252	WDR6
ENSG00000178257	0	0	0.697271	0	ENSG00000178257	PRM3
ENSG00000178279	0.127565	0.368759	0.225838	0.176078	ENSG00000178279	TNP2
ENSG00000178287	2.70707	3.31541	1.95727	6.38464	ENSG00000178287	SPAG11A
ENSG00000178295	8.26358	24.8774	12.8863	12.951	ENSG00000178295	GEN1
ENSG00000178297	0.921178	1.58808	1.68834	2.09693	ENSG00000178297	TMPRSS9
ENSG00000178301	1.21702	1.50116	2.54116	2.23393	ENSG00000178301	AQP11
ENSG00000178307	8.95245	7.10657	7.33754	5.5592	ENSG00000178307	TMEM11
ENSG00000178338	81.5211	217.393	144.738	65.0733	ENSG00000178338	ZNF354B
ENSG00000178342	0.791834	0.99034	0.484557	0.756322	ENSG00000178342	KCNG2
ENSG00000178343	0	0.0551899	0	0.0314154	ENSG00000178343	SHISA3
ENSG00000178358	0.0576219	0.443618	0.35081	0.942222	ENSG00000178358	OR2D3
ENSG00000178363	23.068	38.6455	12.4895	4.02045	ENSG00000178363	CALML3
ENSG00000178372	133.632	7.31904	27.42	29.5783	ENSG00000178372	CALML5
ENSG00000178381	13.4053	11.0978	15.107	9.65926	ENSG00000178381	ZFAND2A
ENSG00000178385	4.24542	4.54312	5.33517	4.30834	ENSG00000178385	PLEKHM3
ENSG00000178386	5.82623	6.02228	8.41232	4.77429	ENSG00000178386	ZNF223
ENSG00000178394	0.131655	0	0.114039	0	ENSG00000178394	HTR1A
ENSG00000178395	0	0	0	0	ENSG00000178395	CCDC185
ENSG00000178397	6.03536	6.34453	10.0282	4.41635	ENSG00000178397	FAM220A
ENSG00000178401	1.20784	1.31434	1.70033	3.10439	ENSG00000178401	DNAJC22
ENSG00000178403	0	0.0943838	0.0849814	0.160639	ENSG00000178403	NEUROG2
ENSG00000178404	0.684402	0.423151	0.280927	6.3077	ENSG00000178404	CEP295NL

ENSG00000178409	1.4174	1.30568	1.91125	3.07241	ENSG00000178409	BEND3
ENSG00000178425	7.29544	16.0114	8.41989	8.82914	ENSG00000178425	NT5DC1
ENSG00000178429	0.0997564	0	0.25866	0	ENSG00000178429	RPS3AP5
ENSG00000178430	2.35392	4.43069	5.06722	10.3132	ENSG00000178430	AC006111.1
ENSG00000178445	0.937311	27.9056	4.97772	3.19226	ENSG00000178445	GLDC
ENSG00000178449	9.22205	11.128	11.5191	7.7845	ENSG00000178449	COX14
ENSG00000178458	0.463777	0.412491	0.378665	0	ENSG00000178458	H3F3AP6
ENSG00000178460	1.68402	2.3115	2.28668	2.56758	ENSG00000178460	MCMDC2
ENSG00000178462	0.15422	0.247701	0.289553	0.190906	ENSG00000178462	TUBAL3
ENSG00000178464	0.803953	0	0.433671	0	ENSG00000178464	CTD-2129J16.15
ENSG00000178467	4.88583	8.00843	6.88963	11.2037	ENSG00000178467	P4HTM
ENSG00000178473	0	0	0	0	ENSG00000178473	UCN3
ENSG00000178498	6.16938	7.67812	6.81252	6.80206	ENSG00000178498	DTX3
ENSG00000178502	4.10769	3.5345	4.04916	2.29361	ENSG00000178502	KLHL11
ENSG00000178503	0	0	0	0	ENSG00000178503	NECAP1P1
ENSG00000178522	0	0.0369466	0.0244874	0.0421463	ENSG00000178522	AMBN
ENSG00000178531	1.7255	0.719249	1.50506	1.27401	ENSG00000178531	CTXN1
ENSG00000178537	4.64552	3.98294	4.70958	3.22329	ENSG00000178537	SLC25A20
ENSG00000178538	0.346775	0.31393	0.52305	0.671947	ENSG00000178538	CA8
ENSG00000178550	0.371587	0.559474	0.242314	0.624439	ENSG00000178550	AC010170.1
ENSG00000178556	0	0	0	0	ENSG00000178556	CKS1BP6
ENSG00000178562	0.255878	0.452205	0.490989	1.02909	ENSG00000178562	CD28
ENSG00000178567	4.83445	5.39646	7.12975	5.85999	ENSG00000178567	EPM2AIP1
ENSG00000178568	0.233492	1.15643	1.57511	1.94496	ENSG00000178568	ERBB4
ENSG00000178573	6.80285	4.04172	13.1815	5.46615	ENSG00000178573	MAF
ENSG00000178585	57.1796	45.3399	22.7295	31.2955	ENSG00000178585	CTNNBIP1
ENSG00000178586	0.0633197	0	0	0.0675562	ENSG00000178586	OR6B3
ENSG00000178591	0.0498638	0	0.0438686	0.260715	ENSG00000178591	DEFB125
ENSG00000178596	0.0628679	0	0.0546556	0	ENSG00000178596	GAPDHP29
ENSG00000178597	0.407973	0.268122	0.540212	0.4739	ENSG00000178597	PSAPL1
ENSG00000178602	0	0	0.110444	0	ENSG00000178602	OTOS
ENSG00000178605	10.4809	15.803	10.9299	9.06974	ENSG00000178605	GTPBP6
ENSG00000178607	15.9901	40.3653	45.9756	35.3743	ENSG00000178607	ERN1
ENSG00000178623	0.294974	0.144816	0.17778	0.662876	ENSG00000178623	GPR35
ENSG00000178631	0.451292	0.412502	0.70619	0.548196	ENSG00000178631	ACTG1P1
ENSG00000178636	3.88928	8.40178	7.33466	14.3274	ENSG00000178636	RP11-455G16.1
ENSG00000178642	0.494726	0.279913	0.987566	0.56677	ENSG00000178642	AL513477.1
ENSG00000178645	0.249772	0.579684	0.40184	0.890481	ENSG00000178645	C10orf53
ENSG00000178654	0.352465	0	0.822777	0	ENSG00000178654	RP11-366I21.1
ENSG00000178660	0	0	0	0	ENSG00000178660	ARMC10P1
ENSG00000178662	1.76662	1.62399	1.31564	1.04308	ENSG00000178662	CSRNP3
ENSG00000178665	3.58196	5.34848	7.93726	8.42283	ENSG00000178665	ZNF713
ENSG00000178685	7.04336	13.4035	10.368	11.0559	ENSG00000178685	PARP10
ENSG00000178690	3.08593	6.38027	6.13013	11.5485	ENSG00000178690	DYNAP
ENSG00000178691	10.2599	16.2047	15.0338	20.1788	ENSG00000178691	SUZ12
ENSG00000178694	6.55623	11.7347	9.31139	11.4689	ENSG00000178694	NSUN3
ENSG00000178695	19.8147	11.5233	7.83529	11.4411	ENSG00000178695	KCTD12
ENSG00000178700	3.02417	7.39321	7.32851	8.99681	ENSG00000178700	DHFR2
ENSG00000178715	0	0.774699	0.811129	0.434625	ENSG00000178715	RP11-169K16.8
ENSG00000178718	1.67122	1.17008	1.27787	2.27923	ENSG00000178718	RPP25
ENSG00000178719	55.1035	55.6147	51.0557	28.2007	ENSG00000178719	GRINA
ENSG00000178722	4.83425	10.4456	9.84687	15.6589	ENSG00000178722	C5orf64
ENSG00000178723	0	0.213222	0.0490582	0.121658	ENSG00000178723	GLULP4
ENSG00000178726	14.2668	13.6167	16.2922	4.32541	ENSG00000178726	THBD

ENSG00000178732	0.655816	1.07833	1.15811	1.23367	ENSG00000178732	GP5
ENSG00000178734	0.464835	0.321697	0.392662	0.666418	ENSG00000178734	LMO7DN
ENSG00000178741	51.3919	51.3656	31.783	28.367	ENSG00000178741	COX5A
ENSG00000178750	1.61084	1.20049	1.67273	1.19102	ENSG00000178750	STX19
ENSG00000178752	0.868304	5.6815	8.30074	4.97098	ENSG00000178752	ERFE
ENSG00000178761	29.6104	43.6182	39.1128	20.6349	ENSG00000178761	FAM219B
ENSG00000178762	0	0	0	0	ENSG00000178762	HIST1H2BPS1
ENSG00000178764	2.5316	2.4747	4.83037	2.38602	ENSG00000178764	ZHX2
ENSG00000178772	0.897675	2.33955	2.35809	3.58095	ENSG00000178772	CPN2
ENSG00000178773	16.6125	23.5943	15.1826	34.9973	ENSG00000178773	CPNE7
ENSG00000178776	2.60059	0.97689	1.14611	2.68181	ENSG00000178776	C5orf46
ENSG00000178789	0.0777716	0.0942501	0.128108	0.0677962	ENSG00000178789	CD300LB
ENSG00000178795	1.5592	2.65768	1.83611	3.04574	ENSG00000178795	GDPD4
ENSG00000178796	2.90E-09	9.21E-09	5.08E-09	1.16378	ENSG00000178796	RIIAD1
ENSG00000178802	20.3058	16.1512	12.8769	13.5047	ENSG00000178802	MPI
ENSG00000178804	0	0.348567	0.125412	0.455937	ENSG00000178804	H1FOO
ENSG00000178809	1.27724	4.1033	2.32509	3.67452	ENSG00000178809	TRIM73
ENSG00000178814	9.19886	24.3784	18.4892	9.32143	ENSG00000178814	OPLAH
ENSG00000178821	0.274529	0.344236	0.378287	0.177166	ENSG00000178821	TMEM52
ENSG00000178826	7.94083	7.40912	7.07399	2.69608	ENSG00000178826	TMEM139
ENSG00000178828	0	0.0458497	0.0414413	0	ENSG00000178828	RNF186
ENSG00000178836	0.352437	0.403967	1.66348	0	ENSG00000178836	AC114812.1
ENSG00000178852	1.68046	4.65343	2.4514	8.65937	ENSG00000178852	EFCAB13
ENSG00000178860	0.25193	0.0268257	3.7537	4.22039	ENSG00000178860	MSC
ENSG00000178863	0.648621	0.920952	1.30824	0.523725	ENSG00000178863	CEBPA-AS1
ENSG00000178878	1.89676	3.65271	2.57709	5.00522	ENSG00000178878	APOLD1
ENSG00000178882	0.210529	4.04299	0.55044	14.045	ENSG00000178882	RFLNA
ENSG00000178894	0	0	0	0	ENSG00000178894	AC073416.1
ENSG00000178896	11.3871	5.30588	6.36341	4.23728	ENSG00000178896	EXOSC4
ENSG00000178904	7.47342	13.7412	13.3154	19.9269	ENSG00000178904	DPY19L3
ENSG00000178913	26.774	18.7315	29.5828	18.8737	ENSG00000178913	TAF7
ENSG00000178917	1.48273	1.53667	2.22763	2.09916	ENSG00000178917	ZNF852
ENSG00000178919	0.37261	1.06433	0.843946	0.452702	ENSG00000178919	FOXE1
ENSG00000178921	12.4426	23.7397	19.2667	21.6739	ENSG00000178921	PFAS
ENSG00000178922	15.2029	19.9521	16.2373	19.2248	ENSG00000178922	HYI
ENSG00000178927	29.0192	40.7445	34.9508	41.0707	ENSG00000178927	C17orf62
ENSG00000178928	0.0623207	0.0862451	0.353667	0.238005	ENSG00000178928	TPRX1
ENSG00000178934	257.234	193.084	271.365	87.5501	ENSG00000178934	LGALS7B
ENSG00000178935	11.2062	12.8909	15.7266	17.7337	ENSG00000178935	ZNF552
ENSG00000178950	49.7162	50.8987	57.1303	56.5976	ENSG00000178950	GAK
ENSG00000178951	19.7209	16.8527	20.9427	17.5	ENSG00000178951	ZBTB7A
ENSG00000178952	86.299	88.2263	77.6067	61.9144	ENSG00000178952	TUFM
ENSG00000178965	0.111681	0.231307	0.208374	0.306457	ENSG00000178965	ERICH3
ENSG00000178966	1.21164	2.87953	1.60806	2.97174	ENSG00000178966	RMI1
ENSG00000178971	13.9527	18.8631	19.5031	14.2324	ENSG00000178971	CTC1
ENSG00000178972	1.39609	2.32899	1.91215	2.45567	ENSG00000178972	AC097658.1
ENSG00000178974	14.3951	16.8012	15.2484	10.5661	ENSG00000178974	FBXO34
ENSG00000178980	156.78	97.9861	58.2591	65.28	ENSG00000178980	SELENOW
ENSG00000178982	91.5686	72.0536	73.2249	65.5371	ENSG00000178982	EIF3K
ENSG00000178988	19.3004	12.9622	18.467	13.8201	ENSG00000178988	MRFAP1L1
ENSG00000178996	5.75641	7.51397	9.53055	6.74333	ENSG00000178996	SNX18
ENSG00000178997	0.820295	2.16265	2.1016	3.52809	ENSG00000178997	EXD1
ENSG00000178999	5.85705	42.8317	3.11999	17.2909	ENSG00000178999	AURKB
ENSG00000179002	0	0	0	0	ENSG00000179002	TAS1R2

ENSG00000179008	0.116357	0.224162	0.182394	0.127373	ENSG00000179008	C14orf39
ENSG00000179010	30.8012	21.6099	37.2022	36.8647	ENSG00000179010	MRFAP1
ENSG00000179021	11.6208	12.7038	11.5108	9.54011	ENSG00000179021	C3orf38
ENSG00000179023	0.0423709	0.124043	0.0833533	0.0585279	ENSG00000179023	KLHDC7A
ENSG00000179028	0.164181	0.310268	0.284169	0.267981	ENSG00000179028	RP11-363G10.2
ENSG00000179029	15.8533	28.1304	9.37601	9.81954	ENSG00000179029	TMEM107
ENSG00000179031	0.75858	0.161765	0.406062	0.184418	ENSG00000179031	LL0XNC01-131B10.2
ENSG00000179038	3.22793	7.31217	7.07651	12.0343	ENSG00000179038	AP001885.1
ENSG00000179041	6.5158	4.72667	8.83416	7.77264	ENSG00000179041	RRS1
ENSG00000179044	1.44084	0.710369	1.44291	0.593862	ENSG00000179044	EXOC3L1
ENSG00000179046	23.7038	19.0198	69.2487	68.1949	ENSG00000179046	TRIML2
ENSG00000179051	59.9203	52.6611	70.9481	37.5489	ENSG00000179051	RCC2
ENSG00000179055	0.109523	0.316243	0.190545	0.41813	ENSG00000179055	OR13D1
ENSG00000179057	5.31927	0.153203	2.59997	3.02088	ENSG00000179057	IGSF22
ENSG00000179058	0.142071	0.273745	0.309318	0.466906	ENSG00000179058	C9orf50
ENSG00000179059	1.94043	3.25605	16.957	10.2464	ENSG00000179059	ZFP42
ENSG00000179061	0.494501	0	0	0.260334	ENSG00000179061	AC012074.1
ENSG00000179066	0.0467608	0.0900492	0.0406959	0.102194	ENSG00000179066	AC020907.1
ENSG00000179071	0.322545	0.154284	0.179336	0.631391	ENSG00000179071	CCDC89
ENSG00000179073	0	0.119646	0	0.0653211	ENSG00000179073	TAAR3P
ENSG00000179083	0.19038	0.456855	0.371474	0.631582	ENSG00000179083	FAM133A
ENSG00000179085	9.26898	18.0932	6.6172	7.80495	ENSG00000179085	DPM3
ENSG00000179088	1.82319	3.30366	2.04411	6.58065	ENSG00000179088	C12orf42
ENSG00000179091	51.8469	59.2646	44.644	24.8811	ENSG00000179091	CYC1
ENSG00000179094	47.6425	46.2093	56.427	39.1666	ENSG00000179094	PER1
ENSG00000179097	0.0711773	0.104321	0.170646	0.313135	ENSG00000179097	HTR1F
ENSG00000179101	0.332584	0	0.291599	0.311625	ENSG00000179101	RP11-349N19.2
ENSG00000179104	6.26067	4.28206	3.82073	2.9361	ENSG00000179104	TMTC2
ENSG00000179111	0.89988	3.74067	1.9973	1.35544	ENSG00000179111	HES7
ENSG00000179115	28.4889	23.0607	25.1671	20.2843	ENSG00000179115	FARSA
ENSG00000179119	15.8152	6.22839	9.50451	7.85284	ENSG00000179119	SPTY2D1
ENSG00000179131	0	0	0.261945	0.727927	ENSG00000179131	RP11-458F8.3
ENSG00000179133	1.73699	3.87618	2.95949	5.4966	ENSG00000179133	C10orf67
ENSG00000179134	50.6741	62.1681	57.7892	82.2659	ENSG00000179134	SAMD4B
ENSG00000179142	0.0373579	0.180229	0.0651811	0.0830824	ENSG00000179142	CYP11B2
ENSG00000179144	0.199193	0.231101	0.250037	0.740414	ENSG00000179144	GIMAP7
ENSG00000179148	1.92952	4.06442	3.31295	1.70923	ENSG00000179148	ALOXE3
ENSG00000179151	11.853	17.4411	18.2265	23.4442	ENSG00000179151	EDC3
ENSG00000179152	16.047	17.7	14.7844	12.7814	ENSG00000179152	TCAIM
ENSG00000179157	0.360918	0.514782	0.0774569	0.483277	ENSG00000179157	RPS2P28
ENSG00000179163	13.3236	9.13731	3.71121	3.13641	ENSG00000179163	FUCA1
ENSG00000179165	0.106568	0.0513674	0.162362	0.116876	ENSG00000179165	PXT1
ENSG00000179168	1.08073	2.02615	1.89512	1.28454	ENSG00000179168	GGN
ENSG00000179170	0	0	0	0	ENSG00000179170	OR7E97P
ENSG00000179172	0	0	0	0	ENSG00000179172	HNRNPCL1
ENSG00000179178	7.32893	3.58696	3.50469	1.04991	ENSG00000179178	TMEM125
ENSG00000179195	20.6029	26.0348	34.9792	18.0779	ENSG00000179195	ZNF664
ENSG00000179213	1.68132	4.19141	2.01944	4.90899	ENSG00000179213	SIGLECL1
ENSG00000179218	847.706	1153.84	206.128	355.535	ENSG00000179218	CALR
ENSG00000179222	21.5974	19.8542	11.9194	33.7149	ENSG00000179222	MAGED1
ENSG00000179240	2.22023	4.63609	4.81122	7.9047	ENSG00000179240	AP002360.1
ENSG00000179241	5.48349	10.2319	11.3618	10.7893	ENSG00000179241	LDLRAD3
ENSG00000179242	8.07087	12.5852	1.80234	4.40732	ENSG00000179242	CDH4
ENSG00000179253	0.364934	1.12339	0.833491	1.65136	ENSG00000179253	AL162457.1

ENSG00000179256	0.294095	0.719862	0.488088	0.527017	ENSG00000179256	SMCO3
ENSG00000179262	47.3666	57.6486	54.0529	40.6437	ENSG00000179262	RAD23A
ENSG00000179270	0.0602566	0.123604	0.137982	0.157761	ENSG00000179270	C2orf71
ENSG00000179271	33.3417	23.2475	18.1219	14.82	ENSG00000179271	GADD45GIP1
ENSG00000179277	4.05647	1.33198	2.70035	1.01099	ENSG00000179277	MEIS3P1
ENSG00000179284	1.07589	3.0693	2.85833	5.08506	ENSG00000179284	DAND5
ENSG00000179292	0.0433162	0	0.112896	0.166059	ENSG00000179292	TMEM151A
ENSG00000179294	2.85721	2.16832	3.84458	1.67384	ENSG00000179294	C17orf96
ENSG00000179295	57.6373	91.8264	104.76	124.129	ENSG00000179295	PTPN11
ENSG00000179296	0.0196204	0.424134	1.71481	1.88953	ENSG00000179296	CTGLF12P
ENSG00000179299	3.51558	7.83617	6.16753	11.8289	ENSG00000179299	NSUN7
ENSG00000179300	0.209246	0.140654	0.0908317	0.458129	ENSG00000179300	RTL3
ENSG00000179304	4.08688	11.665	10.9188	20.728	ENSG00000179304	FAM156B
ENSG00000179314	4.88932	8.58969	7.14587	11.1817	ENSG00000179314	WSCD1
ENSG00000179331	0.559089	0.75518	1.085	1.48808	ENSG00000179331	RAB39A
ENSG00000179335	39.4541	42.8681	46.2094	40.6886	ENSG00000179335	CLK3
ENSG00000179342	0.0571587	0	0.0994011	0	ENSG00000179342	GS1-124K5.9
ENSG00000179344	0.0819964	0	0.23303	0.160451	ENSG00000179344	HLA-DQB1
ENSG00000179348	0.163108	0.109144	0.182166	0.137878	ENSG00000179348	GATA2
ENSG00000179361	6.36848	11.9269	8.25436	11.3313	ENSG00000179361	ARID3B
ENSG00000179362	3.27334	8.7467	6.21965	8.89702	ENSG00000179362	HMGN2P46
ENSG00000179363	0	0.0876716	0.158396	0.0987129	ENSG00000179363	TMEM31
ENSG00000179364	11.8685	18.0217	17.1114	14.4571	ENSG00000179364	PACS2
ENSG00000179381	0	0.0670271	0	0.0757663	ENSG00000179381	OR4K11P
ENSG00000179387	31.6112	36.2603	25.41	20.2727	ENSG00000179387	ELMOD2
ENSG00000179388	11.034	4.46564	2.37851	4.83051	ENSG00000179388	EGR3
ENSG00000179397	2.03873	2.98282	1.95857	3.29724	ENSG00000179397	CATSPERE
ENSG00000179399	0	0.018345	0.0331276	0	ENSG00000179399	GPC5
ENSG00000179403	44.0189	46.703	6.58051	14.6368	ENSG00000179403	VWA1
ENSG00000179407	0.093528	0.124038	0.191965	0.43736	ENSG00000179407	DNAJB8
ENSG00000179409	8.47962	9.22391	11.0983	9.09676	ENSG00000179409	GEMIN4
ENSG00000179412	0	0.207967	0.187877	0.0782357	ENSG00000179412	HNRNPCL4
ENSG00000179420	0.0703617	0.0676615	0.0611358	0.240343	ENSG00000179420	OR6W1P
ENSG00000179431	34.0345	38.4724	24.8967	20.5892	ENSG00000179431	FJX1
ENSG00000179443	0	0	0	0	ENSG00000179443	OR13C6P
ENSG00000179449	0	0	0.0425506	0	ENSG00000179449	AC124309.1
ENSG00000179454	11.4963	12.8934	11.2168	10.9037	ENSG00000179454	KLHL28
ENSG00000179455	2.23482	6.34693	9.09804	7.91147	ENSG00000179455	MKRN3
ENSG00000179456	3.4792	3.33491	2.65133	3.05021	ENSG00000179456	ZBTB18
ENSG00000179460	0	0	0	0	ENSG00000179460	EEF1A1P27
ENSG00000179467	1.81866	3.33424	4.91737	6.4177	ENSG00000179467	AL109806.1
ENSG00000179468	0	0.0852569	0	0.0321832	ENSG00000179468	OR9A2
ENSG00000179476	2.56026	2.85294	4.09658	2.27672	ENSG00000179476	C14orf28
ENSG00000179477	1.03432	3.21182	1.6867	1.97587	ENSG00000179477	ALOX12B
ENSG00000179520	0.250584	0.34904	0.681419	0.767383	ENSG00000179520	SLC17A8
ENSG00000179526	37.0676	32.0945	36.234	21.7096	ENSG00000179526	SHARPIN
ENSG00000179528	1.47928	1.09193	0.882599	1.52571	ENSG00000179528	LBX2
ENSG00000179532	5.80715	12.3688	14.7157	15.8206	ENSG00000179532	DNHD1
ENSG00000179542	0.289149	0.62801	0.520953	0.884141	ENSG00000179542	SLITRK4
ENSG00000179546	0.980871	0.893638	1.44297	2.12924	ENSG00000179546	HTR1D
ENSG00000179562	8.79712	11.194	14.9726	8.04024	ENSG00000179562	GCC1
ENSG00000179564	0.4043	0.774892	0.897828	0.75131	ENSG00000179564	LSMEM2
ENSG00000179571	0.078099	0.149422	0	0.0145338	ENSG00000179571	NBPF23
ENSG00000179577	0	0.205288	0.556694	1.80537	ENSG00000179577	AP003471.1

ENSG00000179580	0.248831	0.159438	0.288081	0.265112	ENSG00000179580	RNF151
ENSG00000179583	4.05235	5.73262	5.535	8.79478	ENSG00000179583	CIITA
ENSG00000179588	2.8028	7.78218	6.63121	7.34992	ENSG00000179588	ZFPM1
ENSG00000179593	32.2894	33.0392	14.4355	11.7137	ENSG00000179593	ALOX15B
ENSG00000179598	2.01688	1.52151	2.45296	1.97679	ENSG00000179598	PLD6
ENSG00000179603	0.222283	1.16854	0.207634	0.763728	ENSG00000179603	GRM8
ENSG00000179604	9.19146	16.7658	20.0644	7.93899	ENSG00000179604	CDC42EP4
ENSG00000179611	0.0376696	0.0375291	0.243331	0	ENSG00000179611	DGKZP1
ENSG00000179615	0	0	0.0585265	0.439521	ENSG00000179615	OR2AP1
ENSG00000179626	0	0	0	0	ENSG00000179626	OR6C4
ENSG00000179627	1.39088	1.65176	1.70948	1.32236	ENSG00000179627	ZBTB42
ENSG00000179630	2.94243	5.63511	5.66954	3.69753	ENSG00000179630	LACC1
ENSG00000179632	26.7109	22.8352	26.6482	16.2402	ENSG00000179632	MAF1
ENSG00000179636	0.157456	0.168285	0.423482	0.298739	ENSG00000179636	TPPP2
ENSG00000179639	0	0.247027	0.224475	0.112649	ENSG00000179639	FCER1A
ENSG00000179673	0.241372	0.456832	0.472474	0.471435	ENSG00000179673	RPRML
ENSG00000179674	0.691049	0.733917	0.702794	0.857563	ENSG00000179674	ARL14
ENSG00000179695	0.0665741	0.0652815	0.75209	0.579357	ENSG00000179695	OR6C2
ENSG00000179698	0.807456	1.02192	1.37696	1.22988	ENSG00000179698	WDR97
ENSG00000179709	0.147084	0.41437	0.477973	0.556772	ENSG00000179709	NLRP8
ENSG00000179715	1.61614	8.45307	8.39097	4.28327	ENSG00000179715	PCED1B
ENSG00000179750	2.00907	1.32013	0.236321	1.42939	ENSG00000179750	APOBEC3B
ENSG00000179751	0.375951	0.240507	0.325766	0.13465	ENSG00000179751	SYCN
ENSG00000179755	0.0846968	0.0814047	0.147084	0.0917702	ENSG00000179755	CTD-2144E22.5
ENSG00000179761	1.02217	2.74216	3.21717	4.7326	ENSG00000179761	PIPOX
ENSG00000179766	0.197471	0.287802	0.154389	0.279758	ENSG00000179766	ATP8B5P
ENSG00000179772	0	0	0.0389783	0.146868	ENSG00000179772	FOXS1
ENSG00000179774	0	0.0754974	0.238355	0.684911	ENSG00000179774	ATOH7
ENSG00000179776	1.48946	0.98054	1.03461	1.84853	ENSG00000179776	CDH5
ENSG00000179796	0.156995	0.150454	0.176264	0.413235	ENSG00000179796	LRRC3B
ENSG00000179799	0	0	0	0	ENSG00000179799	OR7E22P
ENSG00000179813	0.170599	0.210512	0.228888	0.468994	ENSG00000179813	FAM216B
ENSG00000179817	0.0403868	0	0.107549	0.0441947	ENSG00000179817	MRGPRX4
ENSG00000179820	35.9127	41.6833	15.2091	33.1084	ENSG00000179820	MYADM
ENSG00000179826	1.2312	1.11163	1.72514	1.76292	ENSG00000179826	MRGPRX3
ENSG00000179832	19.1986	20.4055	19.1234	18.6519	ENSG00000179832	MROH1
ENSG00000179833	11.9463	8.59841	11.8873	10.6411	ENSG00000179833	SERTAD2
ENSG00000179837	7.43893	4.02027	7.45923	4.62357	ENSG00000179837	RMB15B
ENSG00000179840	0.125854	0.18748	0.277259	0.546177	ENSG00000179840	PIK3CD-AS1
ENSG00000179841	0.655806	1.64435	1.62875	2.26993	ENSG00000179841	AKAP5
ENSG00000179846	3.89367	1.75349	1.92532	0.875598	ENSG00000179846	NKPD1
ENSG00000179855	0	0.0239579	0.043324	0.191465	ENSG00000179855	GIPC3
ENSG00000179862	55.329	61.0535	17.5277	29.4911	ENSG00000179862	CITED4
ENSG00000179869	2.46133	1.86956	1.76955	2.85237	ENSG00000179869	ABCA13
ENSG00000179873	0.22159	0.960174	0.440423	0.552788	ENSG00000179873	NLRP11
ENSG00000179886	5.37048	6.35178	8.65384	5.13486	ENSG00000179886	TIGD5
ENSG00000179889	45.3005	54.3193	60.2503	58.8216	ENSG00000179889	PDXDC1
ENSG00000179899	0.773167	0.568119	0.511145	1.04976	ENSG00000179899	PHC1P1
ENSG00000179902	0.065152	0.421505	0.688595	0.182055	ENSG00000179902	C1orf194
ENSG00000179909	1.96632	4.35629	6.29193	6.31445	ENSG00000179909	ZNF154
ENSG00000179912	19.0947	35.4541	37.746	42.8787	ENSG00000179912	R3HDM2
ENSG00000179913	23.5413	26.0207	3.81225	4.7978	ENSG00000179913	B3GNT3
ENSG00000179914	0.119839	0	0	0.12889	ENSG00000179914	ITLN1

ENSG00000179915	1.01307	2.65584	1.24842	2.55416	ENSG00000179915	NRXN1
ENSG00000179918	2.34218	3.28195	5.40056	2.88679	ENSG00000179918	SEPHS2
ENSG00000179919	0	0.126115	0	0.142674	ENSG00000179919	OR10A7
ENSG00000179921	0.534582	0.673388	0.666112	0.449895	ENSG00000179921	GPBAR1
ENSG00000179922	2.25696	3.16162	2.04092	1.68513	ENSG00000179922	ZNF784
ENSG00000179930	0.0746414	0.171991	0.130297	0.163605	ENSG00000179930	ZNF648
ENSG00000179933	35.2816	23.2701	20.6268	9.79851	ENSG00000179933	C14orf119
ENSG00000179934	0.238537	0.505272	0.622761	0.416962	ENSG00000179934	CCR8
ENSG00000179938	0.330243	1.29056	1.78576	1.15024	ENSG00000179938	GOLGA8J
ENSG00000179941	5.76643	5.75042	5.27223	3.65736	ENSG00000179941	BBS10
ENSG00000179943	3.15804	4.07761	4.08363	3.93812	ENSG00000179943	FIZ1
ENSG00000179950	39.2336	38.4673	38.9004	23.288	ENSG00000179950	PUF60
ENSG00000179954	0.549507	0.552325	0.410418	5.11095	ENSG00000179954	SSC5D
ENSG00000179958	7.45325	6.16647	6.25064	5.12418	ENSG00000179958	DCTPP1
ENSG00000179965	3.71317	6.11056	4.35219	7.05038	ENSG00000179965	ZNF771
ENSG00000179967	1.03718	1.70731	0	2.97847	ENSG00000179967	PPP1R14BP3
ENSG00000179978	0	0	0	0	ENSG00000179978	RP11-1319K7.1
ENSG00000179979	1.17689	2.68407	2.69733	4.60564	ENSG00000179979	CRIPAK
ENSG00000179981	2.32809	4.97822	3.63517	4.33178	ENSG00000179981	TSHZ1
ENSG00000179988	3.66865	5.21829	4.90531	4.83498	ENSG00000179988	PSTK
ENSG00000179994	0.0770734	0.12531	0.0903788	0.19504	ENSG00000179994	SPDYE7P
ENSG00000179997	0.564089	0.872149	0.726716	0.922512	ENSG00000179997	AC010894.4
ENSG00000180008	13.5361	10.1605	15.5295	8.35356	ENSG00000180008	SOCS4
ENSG00000180011	6.20878	8.44769	7.99389	6.59346	ENSG00000180011	ZADH2
ENSG00000180015	1.71251	0	1.13887	1.10577	ENSG00000180015	RP11-756P10.3
ENSG00000180016	0	0.131338	0.197764	0.233506	ENSG00000180016	OR1E1
ENSG00000180019	0.688584	1.93382	0.574285	1.92133	ENSG00000180019	AC079741.2
ENSG00000180035	3.4916	3.99335	5.52184	3.24932	ENSG00000180035	ZNF48
ENSG00000180042	0	0	0.121284	0.303457	ENSG00000180042	OR1R1P
ENSG00000180043	0	0	0.0517646	0.0780083	ENSG00000180043	FAM71E2
ENSG00000180044	0.0643658	0.103791	0.0681349	0.189095	ENSG00000180044	C3orf80
ENSG00000180053	0	0	0	0	ENSG00000180053	NKX2-6
ENSG00000180061	1.08376	1.17516	1.30598	2.13865	ENSG00000180061	TMEM150B
ENSG00000180066	0.512484	0.961574	1.03387	0.206601	ENSG00000180066	C10orf91
ENSG00000180068	0	0.0694455	0.130165	0	ENSG00000180068	OR3A4P
ENSG00000180071	5.71112	19.145	11.6813	14.425	ENSG00000180071	ANKRD18A
ENSG00000180083	3.62585	7.23945	5.68864	12.6379	ENSG00000180083	WFDC11
ENSG00000180089	1.41341	3.35715	2.73449	1.30795	ENSG00000180089	TMEM86B
ENSG00000180090	0.131627	0	0.171602	0.0716045	ENSG00000180090	OR3A1
ENSG00000180096	3.50372	6.38607	3.05735	5.83161	ENSG00000180096	SEPT1
ENSG00000180098	18.6997	27.5818	23.6245	42.0559	ENSG00000180098	TRNAU1AP
ENSG00000180104	13.3018	18.8429	22.9578	18.3247	ENSG00000180104	EXOC3
ENSG00000180105	0	0	0	0	ENSG00000180105	AC017081.2
ENSG00000180113	1.67284	0.996735	1.01442	1.15181	ENSG00000180113	TDRD6
ENSG00000180116	0.326594	1.03571	0.796028	1.72095	ENSG00000180116	C12orf40
ENSG00000180138	0.0230962	0	0.0201319	0.0253837	ENSG00000180138	CSNK1A1L
ENSG00000180150	0	0	0	0	ENSG00000180150	HMGN2P9
ENSG00000180152	1.38022	2.79218	2.1547	5.86968	ENSG00000180152	AC079753.4
ENSG00000180155	8.26586	4.83676	7.68149	11.2666	ENSG00000180155	LYNX1
ENSG00000180172	0	0	0	0	ENSG00000180172	RPS12P23
ENSG00000180176	0.528096	0.876434	0.659043	2.15499	ENSG00000180176	TH
ENSG00000180178	0.954522	1.77531	1.54318	2.33716	ENSG00000180178	FAR2P1
ENSG00000180182	15.341	24.966	18.7087	28.5561	ENSG00000180182	MED14
ENSG00000180185	11.8593	8.81582	14.4053	6.79389	ENSG00000180185	FAHD1

ENSG00000180189	1.08494	3.0081	2.21642	4.00085	ENSG00000180189	HMGB1P14
ENSG00000180190	12.8263	14.2995	14.6611	17.513	ENSG00000180190	TDRP
ENSG00000180198	25.4713	48.1433	35.7487	32.1093	ENSG00000180198	RCC1
ENSG00000180205	0	0	0	0	ENSG00000180205	WFDC9
ENSG00000180209	0.573095	0.111916	0.24594	0.1255	ENSG00000180209	MYLPF
ENSG00000180210	0.139169	0.351865	0.0970049	0.202015	ENSG00000180210	F2
ENSG00000180211	0.200742	0	0	0	ENSG00000180211	RP1-278E11.3
ENSG00000180219	0.0633925	0	0.0276101	0.0695046	ENSG00000180219	FAM71C
ENSG00000180221	0.307503	1.05105	1.9405	1.38186	ENSG00000180221	TPT1P10
ENSG00000180228	18.6555	27.7957	27.0736	22.0339	ENSG00000180228	PRKRA
ENSG00000180229	11.0911	11.816	24.3286	15.4314	ENSG00000180229	HERC2P3
ENSG00000180230	0	0	0	0	ENSG00000180230	NACAP2
ENSG00000180233	9.61859	21.3626	30.1487	16.4034	ENSG00000180233	ZNRF2
ENSG00000180245	0.200218	0.501407	0.418368	0.219113	ENSG00000180245	RRH
ENSG00000180251	1.127	3.33369	2.47614	4.83092	ENSG00000180251	SLC9A4
ENSG00000180257	7.43681	12.2317	15.1784	13.4151	ENSG00000180257	ZNF816
ENSG00000180259	0.121486	0.320886	0.158426	0.368925	ENSG00000180259	PRNT
ENSG00000180263	35.0144	52.0346	38.0482	41.425	ENSG00000180263	FGD6
ENSG00000180264	0.113879	0.953179	0.26473	0.661794	ENSG00000180264	ADGRD2
ENSG00000180269	0	0	0	0	ENSG00000180269	GPR139
ENSG00000180284	0	0	0	0	ENSG00000180284	RP5-1055C14.6
ENSG00000180287	34.7303	9.0963	2.72731	8.72839	ENSG00000180287	PLD5
ENSG00000180304	77.9726	37.9899	50.8206	116.649	ENSG00000180304	OAZ2
ENSG00000180305	0	0.0911862	0	0.102605	ENSG00000180305	WFDC10A
ENSG00000180316	0.957333	1.50766	1.71554	2.70438	ENSG00000180316	PNPLA1
ENSG00000180318	0.204541	0.274009	0.107392	0.536	ENSG00000180318	ALX1
ENSG00000180329	15.2721	12.155	10.9799	11.1311	ENSG00000180329	CCDC43
ENSG00000180332	0.769203	2.44598	1.27114	4.03768	ENSG00000180332	KCTD4
ENSG00000180336	2.54046	3.67977	2.99707	5.00714	ENSG00000180336	MEIOC
ENSG00000180340	0.648219	4.5651	1.78893	7.41004	ENSG00000180340	FZD2
ENSG00000180344	0	0.387001	0	0.857783	ENSG00000180344	AL035460.1
ENSG00000180346	4.31445	4.70421	7.26033	3.49239	ENSG00000180346	TIGD2
ENSG00000180347	0.477245	1.47592	1.00418	1.76259	ENSG00000180347	CCDC129
ENSG00000180353	1.3656	2.54295	2.55846	4.27515	ENSG00000180353	HCLS1
ENSG00000180354	9.03524	7.81038	12.3931	9.16434	ENSG00000180354	MTURN
ENSG00000180357	11.9681	17.0503	18.3217	23.7504	ENSG00000180357	ZNF609
ENSG00000180370	18.0927	19.1922	20.8041	22.3257	ENSG00000180370	PAK2
ENSG00000180376	28.2885	42.6551	41.96	48.8284	ENSG00000180376	CCDC66
ENSG00000180383	3.40269	3.24654	4.17137	7.97222	ENSG00000180383	DEFB124
ENSG00000180385	9.44084	20.0484	15.1093	27.5795	ENSG00000180385	EMC3-AS1
ENSG00000180386	0	0	0	0	ENSG00000180386	KRTAP9-7
ENSG00000180389	0.313661	0	0	0	ENSG00000180389	ATP5EP2
ENSG00000180398	73.0178	114.512	77.2199	112.887	ENSG00000180398	MCFD2
ENSG00000180409	0.0735854	0	0.138995	0.263383	ENSG00000180409	OR10AA1P
ENSG00000180423	2.41485	2.31406	4.34908	3.42288	ENSG00000180423	HARBI1
ENSG00000180424	0	0	0	0	ENSG00000180424	DEFB123
ENSG00000180425	0.946001	1.29112	1.35957	1.02695	ENSG00000180425	C11orf71
ENSG00000180432	0.536426	0.791651	0.641782	1.32773	ENSG00000180432	CYP8B1
ENSG00000180433	0	0	0	0.111879	ENSG00000180433	OR6K6
ENSG00000180437	0	0	0.0578531	0	ENSG00000180437	OR6K4P
ENSG00000180438	13.8715	18.9065	18.8245	35.1107	ENSG00000180438	TPRXL
ENSG00000180440	0.121556	0.454028	0.470555	0.672227	ENSG00000180440	SERTM1
ENSG00000180447	0.428893	0.357194	0.85096	10.3353	ENSG00000180447	GAS1
ENSG00000180448	2.36304	4.42738	5.18849	2.57977	ENSG00000180448	ARHGAP45

ENSG00000180475	0.591333	0.171841	0.517741	0.522112	ENSG00000180475	OR10Q1
ENSG00000180479	9.6615	13.3127	12.2202	11.2498	ENSG00000180479	ZNF571
ENSG00000180481	4.11377	8.45086	8.27463	15.6032	ENSG00000180481	GLIPR1L2
ENSG00000180483	0	0	0.526088	0.162447	ENSG00000180483	DEFB119
ENSG00000180488	16.7501	17.672	15.0503	17.3553	ENSG00000180488	MIGA1
ENSG00000180509	2.61732	6.06707	5.20152	8.20271	ENSG00000180509	KCNE1
ENSG00000180525	1.21068	1.85486	1.60885	7.51055	ENSG00000180525	PRR26
ENSG00000180530	69.7605	39.7625	40.7844	31.3131	ENSG00000180530	NRIP1
ENSG00000180532	0.586075	0.405724	0.696158	0.681136	ENSG00000180532	ZSCAN4
ENSG00000180535	0.190244	0.705113	0.58468	0.820838	ENSG00000180535	BHLHA15
ENSG00000180537	0.422178	0.420402	0.221157	1.40915	ENSG00000180537	RNF182
ENSG00000180539	0.207917	0.507177	0.603214	0.871634	ENSG00000180539	C9orf139
ENSG00000180543	3.93246	1.48556	4.6325	2.29045	ENSG00000180543	TSPYL5
ENSG00000180549	0.0331618	0.0428538	0.0630781	0.152866	ENSG00000180549	FUT7
ENSG00000180573	88.3435	118.857	82.9788	34.6115	ENSG00000180573	HIST1H2AC
ENSG00000180574	0.0745686	0.19764	0.183174	0.758664	ENSG00000180574	EIF2S3L
ENSG00000180581	9.41981	8.02632	8.7084	7.95304	ENSG00000180581	SRP9P1
ENSG00000180592	0.415168	1.24409	1.11173	3.92594	ENSG00000180592	SKIDA1
ENSG00000180596	41.0459	54.3238	28.6465	16.285	ENSG00000180596	HIST1H2BC
ENSG00000180610	0.618991	1.75349	1.89134	2.97639	ENSG00000180610	ZBTB12BP
ENSG00000180611	3.20091	2.6231	2.62319	2.26182	ENSG00000180611	MB21D2
ENSG00000180613	0.0649904	0.181684	0.0856895	0.221808	ENSG00000180613	GSX2
ENSG00000180616	0.0267842	0.273922	0.291575	0.248256	ENSG00000180616	SSTR2
ENSG00000180626	4.41337	4.72566	6.99038	5.15643	ENSG00000180626	ZNF594
ENSG00000180628	5.2655	5.97929	3.38363	4.66806	ENSG00000180628	PCGF5
ENSG00000180636	0	0	0	0.229424	ENSG00000180636	OR4E1
ENSG00000180638	0.68792	3.67044	5.95382	1.76809	ENSG00000180638	SLC47A2
ENSG00000180644	0.528681	0.879122	1.01401	1.10309	ENSG00000180644	PRF1
ENSG00000180658	0	0	0	0	ENSG00000180658	OR2A4
ENSG00000180660	0.0566512	0.182148	0.247247	0.373877	ENSG00000180660	MAB21L1
ENSG00000180662	0.138129	1.45674	0.23928	2.01588	ENSG00000180662	RPL21P8
ENSG00000180663	0	0	0	0	ENSG00000180663	VN1R3
ENSG00000180667	12.8928	6.09305	5.00163	4.92268	ENSG00000180667	YOD1
ENSG00000180672	3.3341	7.96163	8.61572	5.5163	ENSG00000180672	AC007362.1
ENSG00000180673	0	0.0300989	0.0276795	0.0339694	ENSG00000180673	EXOC5P1
ENSG00000180694	24.8361	19.1953	15.859	17.2357	ENSG00000180694	TMEM64
ENSG00000180697	0.123477	0.0308246	0.0278652	0.10231	ENSG00000180697	C3orf22
ENSG00000180708	0.133148	0.0640255	0	0.0724196	ENSG00000180708	OR10K2
ENSG00000180714	0.066234	0.191099	0	0	ENSG00000180714	OR5AZ1P
ENSG00000180720	0.237874	0	0.0345183	0.0433909	ENSG00000180720	CHRM4
ENSG00000180723	0	0	0	0	ENSG00000180723	OR51A9P
ENSG00000180725	0	0.0920247	0.249378	0.320531	ENSG00000180725	AC015871.1
ENSG00000180730	0.449564	1.0249	1.01461	1.99764	ENSG00000180730	SHISA2
ENSG00000180739	11.4982	11.329	10.2402	3.01566	ENSG00000180739	S1PR5
ENSG00000180745	0.052277	0	0	0.171518	ENSG00000180745	CLRN3
ENSG00000180747	100.28	239.864	155.988	103.258	ENSG00000180747	CTD-2547E10.2
ENSG00000180758	13.2838	7.03018	6.7622	8.08163	ENSG00000180758	GPR157
ENSG00000180764	0.8283	0.553699	0.762854	0.791216	ENSG00000180764	PIPSL
ENSG00000180767	0	0	0.138978	0	ENSG00000180767	CHST13
ENSG00000180770	0	0	0	0	ENSG00000180770	OR7E129P
ENSG00000180771	4.54098	4.21919	7.67165	4.66542	ENSG00000180771	SRSF8
ENSG00000180772	0.0190495	0.0459191	0.0332956	0.0418911	ENSG00000180772	AGTR2
ENSG00000180773	3.86211	5.031	6.74385	7.30694	ENSG00000180773	SLC36A4
ENSG00000180776	50.3069	43.5	23.5624	21.5313	ENSG00000180776	ZDHHC20

ENSG00000180777	0.609573	2.23806	3.53012	4.09995	ENSG00000180777	ANKRD30B
ENSG00000180785	0.0600836	0.159383	0.144073	0.232907	ENSG00000180785	OR51E1
ENSG00000180787	2.50426	2.01267	2.89608	2.01706	ENSG00000180787	ZFP3
ENSG00000180801	10.0859	19.0104	18.1848	22.8741	ENSG00000180801	ARSJ
ENSG00000180803	0.398478	0	0.344298	0.211343	ENSG00000180803	RP11-467D10.2
ENSG00000180806	4.97751	6.34499	7.96957	9.39495	ENSG00000180806	HOXC9
ENSG00000180815	0.470969	1.02422	0.98064	1.48553	ENSG00000180815	MAP3K15
ENSG00000180817	132.859	67.0762	50.6024	45.5011	ENSG00000180817	PPA1
ENSG00000180818	6.22838	8.01542	8.98331	7.41541	ENSG00000180818	HOXC10
ENSG00000180822	21.6214	49.8947	51.8574	81.3204	ENSG00000180822	PSMG4
ENSG00000180828	0.991407	0.219351	0.239838	0.948959	ENSG00000180828	BHLHE22
ENSG00000180834	1.27942	1.15031	1.44129	1.165	ENSG00000180834	MAP6D1
ENSG00000180855	2.06103	3.39582	1.64837	2.25633	ENSG00000180855	ZNF443
ENSG00000180861	3.51177	2.7635	1.91534	4.10619	ENSG00000180861	C12ORF36
ENSG00000180867	0.319163	0.768089	1.33424	0.932541	ENSG00000180867	PDIA3P1
ENSG00000180869	0.491941	0.610237	0.657451	1.66281	ENSG00000180869	LINC01555
ENSG00000180871	1.41747	2.26821	1.5025	2.87633	ENSG00000180871	CXCR2
ENSG00000180872	0	0	0	0	ENSG00000180872	DEFB112
ENSG00000180875	0.435815	1.13731	0.845917	1.64611	ENSG00000180875	GREM2
ENSG00000180878	0.264047	0.613352	1.01196	0.523264	ENSG00000180878	C11orf42
ENSG00000180879	73.5109	65.3757	34.0657	21.8015	ENSG00000180879	SSR4
ENSG00000180881	18.9316	42.3225	50.2999	61.5859	ENSG00000180881	CAPS2
ENSG00000180884	1.59971	2.68442	1.73527	1.96195	ENSG00000180884	ZNF792
ENSG00000180891	9.35613	14.2958	9.71541	9.96359	ENSG00000180891	CUEDC1
ENSG00000180900	28.5508	36.0346	47.128	19.253	ENSG00000180900	SCRIB
ENSG00000180901	11.1369	6.05146	6.95536	5.22104	ENSG00000180901	KCTD2
ENSG00000180902	12.16	30.3803	37.1667	34.1201	ENSG00000180902	D2HGDH
ENSG00000180909	0	0	0	0	ENSG00000180909	OR52B1P
ENSG00000180913	0.146651	0.423257	0.255011	0.238952	ENSG00000180913	OR56B3P
ENSG00000180914	4.15531	8.09804	7.13163	16.98	ENSG00000180914	OXTR
ENSG00000180917	25.1032	19.1616	20.9211	11.7022	ENSG00000180917	CMTR2
ENSG00000180919	0	0.0503221	0.0909632	0.114109	ENSG00000180919	OR56B4
ENSG00000180921	30.9635	25.8261	33.1248	17.361	ENSG00000180921	FAM83H
ENSG00000180926	0	0	0	0	ENSG00000180926	OR7E18P
ENSG00000180929	0.128352	0.197946	0.290798	0.226268	ENSG00000180929	GPR62
ENSG00000180934	0.056926	0	0	0	ENSG00000180934	OR56A1
ENSG00000180938	0.909157	1.36666	1.3657	0.88154	ENSG00000180938	ZNF572
ENSG00000180953	3.65367	8.2898	8.86203	8.86804	ENSG00000180953	ST20
ENSG00000180957	16.4134	21.574	25.4926	34.5383	ENSG00000180957	PITPNB
ENSG00000180964	27.8084	22.5075	16.8653	19.1645	ENSG00000180964	TCEAL8
ENSG00000180974	0	0	0	0	ENSG00000180974	OR52E4
ENSG00000180979	13.1394	11.6832	13.8961	11.367	ENSG00000180979	LRRC57
ENSG00000180987	2.0266	5.70683	3.08859	5.01566	ENSG00000180987	AC123768.1
ENSG00000180988	0.0592685	0	0	0	ENSG00000180988	OR52N2
ENSG00000180992	32.1651	22.9972	17.2149	13.9665	ENSG00000180992	MRPL14
ENSG00000180998	2.28895	7.6153	7.12183	13.9453	ENSG00000180998	GPR137C
ENSG00000180999	5.63474	15.5135	11.5928	17.0376	ENSG00000180999	C1orf105
ENSG00000181001	0.0645839	0.0621181	0.0561363	0.281144	ENSG00000181001	OR52N1
ENSG00000181004	3.08849	2.23517	2.79612	1.82573	ENSG00000181004	BBS12
ENSG00000181007	3.27241	3.93139	3.5164	7.25232	ENSG00000181007	ZFP82
ENSG00000181009	0	0	0	0	ENSG00000181009	OR52N5
ENSG00000181013	0	0.127304	0.299229	0.405958	ENSG00000181013	C17orf47
ENSG00000181016	1.46333	0.877796	3.10562	2.62077	ENSG00000181016	LSMEM1
ENSG00000181017	0	0	0	0	ENSG00000181017	OR56B2P

ENSG00000181019	26.2035	61.7541	18.5503	44.4314	ENSG00000181019	NQO1
ENSG00000181023	0	0	0.0486084	0	ENSG00000181023	OR56B1
ENSG00000181026	19.497	19.4332	16.8543	16.8992	ENSG00000181026	AEN
ENSG00000181027	23.1764	34.9295	37.7153	29.3603	ENSG00000181027	FKRP
ENSG00000181029	55.6731	37.1703	37.302	19.9383	ENSG00000181029	TRAPPC5
ENSG00000181031	1.39758	2.36404	2.29808	3.74647	ENSG00000181031	RPH3AL
ENSG00000181035	3.78852	4.76573	5.22331	5.74707	ENSG00000181035	SLC25A42
ENSG00000181036	1.56465	5.08271	3.79684	4.13839	ENSG00000181036	FCRL6
ENSG00000181038	15.2457	23.9946	17.6938	14.1987	ENSG00000181038	METTL23
ENSG00000181039	1.76846	7.03641	3.31853	10.3031	ENSG00000181039	ANKRD334A
ENSG00000181045	8.31134	9.97221	11.2053	10.5071	ENSG00000181045	SLC26A11
ENSG00000181061	182.205	45.8979	50.0486	46.958	ENSG00000181061	HIGD1A
ENSG00000181072	0.369111	0.843155	0.643188	1.95143	ENSG00000181072	CHRM2
ENSG00000181074	0.0591333	0.0569026	0.102851	0	ENSG00000181074	OR52N4
ENSG00000181085	4.56931	11.5464	24.496	5.18596	ENSG00000181085	MAPK15
ENSG00000181090	24.238	39.8921	44.5797	53.6789	ENSG00000181090	EHMT1
ENSG00000181092	1.47995	2.54422	2.94801	5.17088	ENSG00000181092	ADIPOQ
ENSG00000181101	0	0	0	0	ENSG00000181101	SDCCAG3P2
ENSG00000181104	22.9411	32.8134	22.5806	40.8814	ENSG00000181104	F2R
ENSG00000181109	0.0645839	0.0621181	0.168409	0.140572	ENSG00000181109	OR52P1P
ENSG00000181126	2.20364	1.74113	0.484491	1.24003	ENSG00000181126	HLA-V
ENSG00000181135	6.44288	6.16879	10.1896	6.02043	ENSG00000181135	ZNF707
ENSG00000181143	1.87241	0.251751	0.235883	1.15078	ENSG00000181143	MUC16
ENSG00000181163	595.748	668.235	607.065	412.105	ENSG00000181163	NPM1
ENSG00000181191	15.9543	13.9444	11.7245	8.44996	ENSG00000181191	PJA1
ENSG00000181192	10.7291	16.9444	8.90492	13.5841	ENSG00000181192	DHTKD1
ENSG00000181195	1.04292	2.40457	1.06383	3.10029	ENSG00000181195	PENK
ENSG00000181201	0	0	0	0	ENSG00000181201	HIST3H2BA
ENSG00000181214	0	0	0	0	ENSG00000181214	OR8G2P
ENSG00000181215	0.797962	1.3718	1.13246	2.28222	ENSG00000181215	C4orf50
ENSG00000181218	23.6408	10.3737	5.14067	1.9737	ENSG00000181218	HIST3H2A
ENSG00000181220	11.2657	13.7735	14.7943	13.3205	ENSG00000181220	ZNF746
ENSG00000181222	58.7724	77.5732	85.2154	95.4846	ENSG00000181222	POLR2A
ENSG00000181227	0.589377	2.12022	1.51241	1.82207	ENSG00000181227	RP4-682C21.2
ENSG00000181234	0	0	0.0377886	0.0357961	ENSG00000181234	TMEM132C
ENSG00000181240	0.479159	0.778889	0.648215	1.26243	ENSG00000181240	SLC25A41
ENSG00000181260	0	0	0	0.069897	ENSG00000181260	MTHFD2P7
ENSG00000181264	2.27555	4.0516	3.582	5.38471	ENSG00000181264	TMEM136
ENSG00000181273	0	0.0596852	0.053939	0.270225	ENSG00000181273	OR5AK2
ENSG00000181274	3.4248	2.68725	2.12656	1.92195	ENSG00000181274	FRAT2
ENSG00000181282	0.0456091	0.221729	0.119089	0.847471	ENSG00000181282	OR5AK3P
ENSG00000181284	11.0268	6.69537	7.93607	4.00671	ENSG00000181284	TMEM102
ENSG00000181291	0.0370086	0.0118823	0.0216383	0.135751	ENSG00000181291	TMEM132E
ENSG00000181296	0	0	0	0	ENSG00000181296	OR5G1P
ENSG00000181315	5.45037	5.7627	6.80589	7.88436	ENSG00000181315	ZNF322
ENSG00000181322	2.70836	4.34978	3.98884	4.0259	ENSG00000181322	NME9
ENSG00000181323	0	0	0.0548544	0.068684	ENSG00000181323	SPEM1
ENSG00000181325	0	0	0.0298422	0.112019	ENSG00000181325	OR9G3P
ENSG00000181333	55.9803	60.4692	82.618	55.4013	ENSG00000181333	HEPHL1
ENSG00000181350	24.9942	25.5083	40.4126	15.789	ENSG00000181350	LRRC75A
ENSG00000181355	3.94263	6.40705	5.42959	10.8505	ENSG00000181355	OFCC1
ENSG00000181358	0.0230973	0.0223031	0.031985	0.200986	ENSG00000181358	CTAGE10P
ENSG00000181359	1.08836	4.15738	3.98296	3.58161	ENSG00000181359	HSP90AA6P
ENSG00000181371	0.0584665	0	0	0.0637217	ENSG00000181371	OR5M8

ENSG00000181374	0	0	0	0	ENSG00000181374	CCL13
ENSG00000181378	0.948725	2.49382	2.3399	4.45694	ENSG00000181378	CFAP65
ENSG00000181381	23.0973	48.2984	31.3888	57.7505	ENSG00000181381	DDX60L
ENSG00000181392	2.77606	2.45409	3.33949	3.01794	ENSG00000181392	SYNE4
ENSG00000181395	0	0	0	0	ENSG00000181395	OR5AL1
ENSG00000181396	13.7813	15.7019	12.1273	10.2173	ENSG00000181396	OGFOD3
ENSG00000181404	14.5877	19.9931	10.2523	12.6938	ENSG00000181404	WASHC1
ENSG00000181408	0.450935	0.825255	0.864015	0.492933	ENSG00000181408	UTS2R
ENSG00000181409	3.10165	2.23222	3.03794	2.05538	ENSG00000181409	AATK
ENSG00000181418	0.588996	0.651319	0.551427	0.698953	ENSG00000181418	DDN
ENSG00000181433	0.0089866	0.0346615	0.0705107	0.108718	ENSG00000181433	SAGE1
ENSG00000181444	1.08344	0.821652	2.71338	2.34385	ENSG00000181444	ZNF467
ENSG00000181449	0.441098	0.996678	0.341714	0.854703	ENSG00000181449	SOX2
ENSG00000181450	4.35021	8.32693	9.16014	10.0319	ENSG00000181450	ZNF678
ENSG00000181458	122.404	122.904	134.266	250.242	ENSG00000181458	TMEM45A
ENSG00000181464	0	0	0	0	ENSG00000181464	CDRT1
ENSG00000181467	36.7087	22.6224	24.6782	20.1052	ENSG00000181467	RAP2B
ENSG00000181472	5.62486	5.33034	6.58707	3.32866	ENSG00000181472	ZBTB2
ENSG00000181481	20.2996	24.1431	25.7194	42.5461	ENSG00000181481	RNF135
ENSG00000181495	0	0	0	0	ENSG00000181495	AC026703.1
ENSG00000181499	0	0.107452	0.0971125	0	ENSG00000181499	OR6T1
ENSG00000181511	0	0	0	0	ENSG00000181511	RP4-655L22.4
ENSG00000181513	5.81476	8.2122	6.6004	11.3459	ENSG00000181513	ACBD4
ENSG00000181514	0.151929	0.292519	0.0881288	0.443183	ENSG00000181514	RP3-474G15.1
ENSG00000181518	0	0.109091	0.246484	0.185388	ENSG00000181518	OR8D4
ENSG00000181523	17.2273	25.4667	42.2483	23.4905	ENSG00000181523	SGSH
ENSG00000181524	0.523486	0	0.227061	0.790406	ENSG00000181524	RPL24P4
ENSG00000181541	0.774746	2.53752	1.83206	2.29984	ENSG00000181541	MAB21L2
ENSG00000181544	1.11483	4.45511	1.39682	3.69286	ENSG00000181544	FANCB
ENSG00000181552	0.211372	0.343721	0.127234	0.248327	ENSG00000181552	EDDM3B
ENSG00000181555	19.4879	24.3202	25.0706	32.5766	ENSG00000181555	SETD2
ENSG00000181562	0.067616	0.0650239	0.235957	0.220585	ENSG00000181562	EDDM3A
ENSG00000181577	0.294346	0.787113	0.710563	2.16718	ENSG00000181577	C6orf223
ENSG00000181585	0.280844	0.212347	0.273889	0.416694	ENSG00000181585	TMIE
ENSG00000181588	16.1848	9.70323	12.2735	11.9939	ENSG00000181588	MEX3D
ENSG00000181609	0	0.0551468	0	0.374821	ENSG00000181609	OR52D1
ENSG00000181610	27.6833	18.6135	21.603	14.1251	ENSG00000181610	MRPS23
ENSG00000181616	0	0.110782	0.150181	0.501952	ENSG00000181616	OR52H1
ENSG00000181617	0	0.244622	0.22173	0.273779	ENSG00000181617	FDCSP
ENSG00000181619	1.08578	4.07825	3.45697	8.58506	ENSG00000181619	GPR135
ENSG00000181625	7.12669	14.3098	16.6811	9.64563	ENSG00000181625	SLX1B
ENSG00000181626	0.674075	0.961523	0.671516	1.48144	ENSG00000181626	ANKRD62
ENSG00000181631	0.145763	0.31946	0.184898	0.380542	ENSG00000181631	P2RY13
ENSG00000181634	0.967085	2.8641	2.21077	1.9619	ENSG00000181634	TNFSF15
ENSG00000181638	7.04554	10.0931	17.3662	12.2162	ENSG00000181638	ZFP41
ENSG00000181649	14.0973	14.2422	9.26418	11.9346	ENSG00000181649	PHLDA2
ENSG00000181652	25.8489	6.52202	8.79601	19.3539	ENSG00000181652	ATG9B
ENSG00000181656	0.0155747	0.120096	0.0544331	0.119964	ENSG00000181656	GPR88
ENSG00000181666	44.0684	66.4018	73.6709	74.0854	ENSG00000181666	HKR1
ENSG00000181689	0	0.0640255	0	0.0362098	ENSG00000181689	OR8K3
ENSG00000181690	5.2205	8.04654	8.02191	8.88475	ENSG00000181690	PLAG1
ENSG00000181693	0	0	0	0	ENSG00000181693	OR8H1
ENSG00000181698	0	0	0.034396	0.101493	ENSG00000181698	OR5T1
ENSG00000181704	37.422	30.6153	26.2914	22.6996	ENSG00000181704	YIPF6

ENSG00000181705	0	0	0	0	ENSG00000181705	RP11-11L12.2
ENSG00000181718	0	0.137675	0.11488	0.0677138	ENSG00000181718	OR5T2
ENSG00000181722	10.7358	24.7547	23.9281	38.4578	ENSG00000181722	ZBTB20
ENSG00000181733	0	0	0	0.0630897	ENSG00000181733	OR2Z1
ENSG00000181741	1.39028	2.69622	1.10065	3.3644	ENSG00000181741	FDX1P1
ENSG00000181744	6.25923	14.3097	6.91579	7.93602	ENSG00000181744	C3orf58
ENSG00000181751	2.29942	1.66902	1.76019	1.57679	ENSG00000181751	C5orf30
ENSG00000181752	0.0678815	0.198435	0.176953	0.147626	ENSG00000181752	OR8K5
ENSG00000181754	0.348471	0.43823	0.238646	0.233022	ENSG00000181754	AMIGO1
ENSG00000181761	0	0	0	0	ENSG00000181761	OR8H3
ENSG00000181767	0	0.0640255	0.231412	0	ENSG00000181767	OR8H2
ENSG00000181773	0.877202	0.97426	0.48601	0.989908	ENSG00000181773	GPR3
ENSG00000181778	0	0.0460183	0	0	ENSG00000181778	TMEM252
ENSG00000181780	0	0	0	0	ENSG00000181780	OR5J1P
ENSG00000181781	0.420004	0.628656	0.490683	0.866349	ENSG00000181781	ODF3L2
ENSG00000181785	0.127266	0.183637	0.0553238	0	ENSG00000181785	OR5AS1
ENSG00000181786	0	0	0	0	ENSG00000181786	ACTL9
ENSG00000181788	19.94	18.2276	20.7713	9.37485	ENSG00000181788	SIAH2
ENSG00000181789	68.9606	60.5097	48.8937	84.9383	ENSG00000181789	COPG1
ENSG00000181790	0.196498	0.67981	0.480124	0.501881	ENSG00000181790	ADGRB1
ENSG00000181791	0	0.0562628	0.101696	0	ENSG00000181791	AC009041.1
ENSG00000181803	0	0	0	0.135112	ENSG00000181803	OR6S1
ENSG00000181804	1.24941	6.31366	6.68515	1.72601	ENSG00000181804	SLC9A9
ENSG00000181817	3.3744	4.00056	5.02403	5.03563	ENSG00000181817	LSM10
ENSG00000181819	0	0.0758172	0	0	ENSG00000181819	KCTD9P2
ENSG00000181826	16.8455	19.071	11.7959	10.1384	ENSG00000181826	RELL1
ENSG00000181827	10.2309	13.7398	17.6888	15.4912	ENSG00000181827	RFX7
ENSG00000181830	13.128	8.03099	6.89399	5.94779	ENSG00000181830	SLC35C1
ENSG00000181837	0.067091	0.129042	0.116601	0.510814	ENSG00000181837	OR5D17P
ENSG00000181847	0.885866	1.05985	1.94522	4.69424	ENSG00000181847	TIGIT
ENSG00000181852	17.7918	23.7664	31.261	10.0291	ENSG00000181852	RNF41
ENSG00000181856	9.26702	18.6877	48.008	94.1878	ENSG00000181856	SLC2A4
ENSG00000181867	0.0730155	0	0.0634504	0.0794291	ENSG00000181867	FTMT
ENSG00000181873	2.56038	4.20185	4.54011	5.54498	ENSG00000181873	IBA57
ENSG00000181885	255.622	98.0548	21.2548	13.3463	ENSG00000181885	CLDN7
ENSG00000181894	7.26556	7.94599	9.47951	7.34685	ENSG00000181894	ZNF329
ENSG00000181896	8.59108	9.96791	9.39129	12.9796	ENSG00000181896	ZNF101
ENSG00000181903	0.0577502	0.0555755	0.050227	0	ENSG00000181903	OR4C6
ENSG00000181904	13.572	9.3271	13.2542	12.2069	ENSG00000181904	C5orf24
ENSG00000181908	0.342503	0.833605	0.667328	1.05675	ENSG00000181908	AP003774.1
ENSG00000181915	7.84555	6.14739	6.94081	4.87752	ENSG00000181915	ADO
ENSG00000181924	26.8419	25.6128	32.2448	21.0541	ENSG00000181924	COA4
ENSG00000181927	0.0670216	0	0.0578531	0.0748171	ENSG00000181927	OR4P4
ENSG00000181929	41.9219	48.7218	51.2811	52.106	ENSG00000181929	PRKAG1
ENSG00000181935	0.134182	0	0.0583003	0.0729734	ENSG00000181935	OR4C16
ENSG00000181938	42.9304	56.6922	50.3205	112.734	ENSG00000181938	GINS3
ENSG00000181939	0.108833	0.366633	0.33136	0.298494	ENSG00000181939	OR4C15
ENSG00000181943	0	0	0	0	ENSG00000181943	OR4A21P
ENSG00000181950	0	0.0637807	0.057632	0.144292	ENSG00000181950	OR4A13P
ENSG00000181958	0	0	0	0	ENSG00000181958	OR4A15
ENSG00000181961	0	0	0	0	ENSG00000181961	OR4A16
ENSG00000181963	0	0	0	0	ENSG00000181963	OR52K2
ENSG00000181965	0.104477	0.134211	0.0606611	0	ENSG00000181965	NEUROG1
ENSG00000181977	0	0	0	0	ENSG00000181977	PYY3

ENSG00000181982	2.46	2.32061	3.91981	4.27712	ENSG00000181982	CCDC149
ENSG00000181984	0	0	0	0	ENSG00000181984	GOLGA8CP
ENSG00000181991	14.0391	15.7516	12.9445	15.6274	ENSG00000181991	MRPS11
ENSG00000181997	0	0	0	0	ENSG00000181997	AQP7P2
ENSG00000182000	0.42237	0.403611	0	0.223592	ENSG00000182000	RP11-651P23.2
ENSG00000182004	43.6859	47.6374	26.6335	34.0761	ENSG00000182004	SNRPE
ENSG00000182010	7.61124	5.41792	4.4108	8.43126	ENSG00000182010	RTKN2
ENSG00000182013	0.674973	1.12556	1.0389	1.65127	ENSG00000182013	PNMA8A
ENSG00000182022	45.692	22.7602	24.1186	28.6916	ENSG00000182022	CHST15
ENSG00000182035	0.190662	0.18242	0.32946	0	ENSG00000182035	ADIG
ENSG00000182040	0.491597	1.02727	2.78307	1.2427	ENSG00000182040	USH1G
ENSG00000182048	0.119235	0.206049	0.186729	0.265024	ENSG00000182048	TRPC2
ENSG00000182050	0.903102	0.973031	0.998888	1.27366	ENSG00000182050	MGAT4C
ENSG00000182053	0.0600726	0.0288539	0	0	ENSG00000182053	TRIM49B
ENSG00000182054	19.1278	31.5249	9.83709	16.5242	ENSG00000182054	IDH2
ENSG00000182070	0	0.0617252	0.139498	0	ENSG00000182070	OR52A1
ENSG00000182077	0.0362719	0.088256	0.0617732	0.087484	ENSG00000182077	PTCHD3
ENSG00000182083	0	0	0	0	ENSG00000182083	OR6B2
ENSG00000182087	118.993	141.992	141.07	79.5277	ENSG00000182087	TMEM259
ENSG00000182093	19.2771	18.8233	12.21	11.7232	ENSG00000182093	WRB
ENSG00000182095	42.9465	102.862	103.326	129.322	ENSG00000182095	TNRC18
ENSG00000182103	0.597702	0.715656	0.747614	2.79085	ENSG00000182103	FAM181B
ENSG00000182107	20.4854	19.0619	6.80586	4.13407	ENSG00000182107	TMEM30B
ENSG00000182108	21.4566	15.1187	16.8238	11.3466	ENSG00000182108	DEXI
ENSG00000182111	0.407924	0.842651	0.932962	1.81875	ENSG00000182111	ZNF716
ENSG00000182117	122.927	64.8213	46.175	39.4668	ENSG00000182117	NOP10
ENSG00000182118	7.70624	5.4915	6.34609	4.35402	ENSG00000182118	FAM89A
ENSG00000182132	0.0307744	0.143962	0.177389	0.430748	ENSG00000182132	KCNIP1
ENSG00000182134	6.14118	7.38662	3.70772	5.52113	ENSG00000182134	TDRKH
ENSG00000182141	6.31218	8.55473	7.2739	11.482	ENSG00000182141	ZNF708
ENSG00000182149	101.734	86.3693	92.969	76.195	ENSG00000182149	IST1
ENSG00000182150	18.1077	24.5715	27.7566	27.4549	ENSG00000182150	ERCC6L2
ENSG00000182154	19.0587	14.907	12.2861	9.71767	ENSG00000182154	MRPL41
ENSG00000182156	0.0281512	0.080285	0.0730803	0.184337	ENSG00000182156	ENPP7
ENSG00000182158	16.4152	28.862	23.4192	39.7494	ENSG00000182158	CREB3L2
ENSG00000182162	0.709572	1.34179	1.53814	1.55313	ENSG00000182162	P2RY8
ENSG00000182168	0.158812	0.384029	0.254822	0.805284	ENSG00000182168	UNC5C
ENSG00000182170	0	0	0	0	ENSG00000182170	MRGPRG
ENSG00000182173	18.7062	28.575	25.7639	21.2404	ENSG00000182173	TSEN54
ENSG00000182175	5.49588	5.47848	4.7889	4.25993	ENSG00000182175	RGMA
ENSG00000182177	1.46276	3.55254	3.87433	5.95999	ENSG00000182177	ASB18
ENSG00000182179	3.28643	17.7809	4.77067	15.5539	ENSG00000182179	UBA7
ENSG00000182180	33.6716	35.0677	33.081	22.9078	ENSG00000182180	MRPS16
ENSG00000182183	4.21069	7.81151	6.71371	9.687	ENSG00000182183	FAM159A
ENSG00000182185	15.1788	49.1763	41.8955	57.0972	ENSG00000182185	RAD51B
ENSG00000182187	4.559	0.83433	1.31496	0.348324	ENSG00000182187	CRYGB
ENSG00000182195	0	0	0	0.596505	ENSG00000182195	LDOC1
ENSG00000182196	68.8782	57.6307	42.5629	36.4065	ENSG00000182196	ARL6IP4
ENSG00000182197	38.9052	87.901	43.2323	69.9395	ENSG00000182197	EXT1
ENSG00000182199	34.2805	97.2075	90.4432	31.7846	ENSG00000182199	SHMT2
ENSG00000182208	18.7931	21.8798	18.799	11.9267	ENSG00000182208	MOB2
ENSG00000182217	2.38902	2.37222	6.12148	1.18967	ENSG00000182217	HIST2H4B
ENSG00000182218	1.15304	2.17118	2.17393	3.26137	ENSG00000182218	HHIPL1
ENSG00000182220	81.652	87.8823	66.5385	64.1741	ENSG00000182220	ATP6AP2

ENSG00000182223	0.0797793	0.115265	0.138921	0.174622	ENSG00000182223	ZAR1
ENSG00000182224	4.18698	5.28559	7.63101	7.14482	ENSG00000182224	CYB5D1
ENSG00000182230	3.60468	6.15059	7.32809	9.44879	ENSG00000182230	FAM153B
ENSG00000182240	48.3462	68.5672	28.1863	33.6035	ENSG00000182240	BACE2
ENSG00000182242	0.0395549	0.2667	0.137758	0.155192	ENSG00000182242	TEX28P1
ENSG00000182247	20.686	13.8509	21.3547	20.0028	ENSG00000182247	UBE2E2
ENSG00000182253	1.96082	0.347902	0.453386	3.5568	ENSG00000182253	SYNM
ENSG00000182255	0.112454	0.272124	0.227154	0.358925	ENSG00000182255	KCNA4
ENSG00000182256	0.0577196	1.28806	1.14763	1.5393	ENSG00000182256	GABRG3
ENSG00000182257	0.828293	1.38062	1.97216	1.96863	ENSG00000182257	PRR34
ENSG00000182261	81.213	4.94394	1.82685	8.21014	ENSG00000182261	NLRP10
ENSG00000182263	2.02994	3.15507	1.9799	2.16041	ENSG00000182263	FIGN
ENSG00000182264	1.71376	5.61374	9.43807	4.5335	ENSG00000182264	IZUMO1
ENSG00000182271	0	0.0525964	0.0433468	0.0596085	ENSG00000182271	TMIGD1
ENSG00000182272	30.3143	26.1891	34.6481	33.4548	ENSG00000182272	B4GALNT4
ENSG00000182287	3.56041	5.13985	3.43742	7.05885	ENSG00000182287	AP1S2
ENSG00000182307	12.7361	14.5582	19.7244	14.5911	ENSG00000182307	C8orf33
ENSG00000182308	0.629535	1.17308	1.38605	1.95827	ENSG00000182308	DCAF4L1
ENSG00000182315	0.0421418	0	0	0	ENSG00000182315	MBD3L3
ENSG00000182318	1.79263	1.51891	2.1952	2.71144	ENSG00000182318	ZSCAN22
ENSG00000182319	6.91555	6.61556	9.62183	7.11177	ENSG00000182319	SGK223
ENSG00000182324	0.5821	1.58862	2.25911	2.04586	ENSG00000182324	KCNJ14
ENSG00000182325	17.2177	19.9434	25.0652	14.3277	ENSG00000182325	FBXL6
ENSG00000182326	4.04478	8.26972	11.8516	32.3488	ENSG00000182326	C1S
ENSG00000182327	1.86288	1.78496	2.76963	0.909034	ENSG00000182327	GLTPD2
ENSG00000182329	1.48515	2.48237	2.37867	4.31592	ENSG00000182329	KIAA2012
ENSG00000182330	0.0269268	0.0299899	0.0268323	0.0675634	ENSG00000182330	PRAMEF8
ENSG00000182333	0.0433226	0.132569	0.570205	0.351099	ENSG00000182333	LIPF
ENSG00000182334	0.868811	1.02836	0.754986	0.290782	ENSG00000182334	OR5P3
ENSG00000182346	0.201129	1.11982	1.1613	0.787559	ENSG00000182346	DAOA
ENSG00000182347	0.230999	0.943097	0.817317	0.81598	ENSG00000182347	RP11-39K24.9
ENSG00000182348	0	0	0.0402205	0.0253873	ENSG00000182348	ZNF804B
ENSG00000182351	0	0	0	0	ENSG00000182351	CRIP1P4
ENSG00000182352	2.16611	6.15805	4.61844	8.84669	ENSG00000182352	C17orf77
ENSG00000182359	3.22029	4.12444	3.20153	2.66465	ENSG00000182359	KBTBD3
ENSG00000182362	7.82418	9.00465	8.26119	8.43192	ENSG00000182362	YBEY
ENSG00000182365	0	0	0	0	ENSG00000182365	OR5F2P
ENSG00000182368	0	1.18198	1.12078	0.801095	ENSG00000182368	FAM27A
ENSG00000182372	21.1892	18.0355	13.1251	9.27935	ENSG00000182372	CLN8
ENSG00000182378	10.7832	11.5752	11.1587	16.0496	ENSG00000182378	PLCXD1
ENSG00000182379	0.891572	3.73069	1.8703	1.7104	ENSG00000182379	NXPH4
ENSG00000182383	0	0.341875	0	0	ENSG00000182383	RPL27AP5
ENSG00000182389	0.790048	0.765406	1.47398	1.09725	ENSG00000182389	CACNB4
ENSG00000182393	0.0743771	0	0	0	ENSG00000182393	IFNL1
ENSG00000182397	0.687205	1.90347	1.58113	2.48222	ENSG00000182397	DNM1P46
ENSG00000182400	12.2674	8.06253	14.1741	8.60905	ENSG00000182400	TRAPPC6B
ENSG00000182405	1.93334	2.78216	2.5572	1.81431	ENSG00000182405	PGBD4
ENSG00000182415	4.69E-06	2.47E-05	1.32E-05	9.75E-06	ENSG00000182415	CDY2A
ENSG00000182446	56.8394	62.1698	67.1811	70.1353	ENSG00000182446	NPLOC4
ENSG00000182447	0.122112	0.235226	0.248062	0.267231	ENSG00000182447	OTOL1
ENSG00000182450	0.101189	0.336761	0.11118	0.14894	ENSG00000182450	KCNK4
ENSG00000182459	0.0878807	0.0614953	0.0509744	0.0644032	ENSG00000182459	TEX19
ENSG00000182463	0.427361	1.54507	4.16331	2.77308	ENSG00000182463	TSHZ2

ENSG00000182472	3.86835	9.11717	5.76813	5.5788	ENSG00000182472	CAPN12
ENSG00000182473	48.4934	38.4208	47.6581	29.9336	ENSG00000182473	EXOC7
ENSG00000182477	0.133319	0	0.0579271	0.145023	ENSG00000182477	OR2B8P
ENSG00000182481	25.1017	53.1423	15.1033	27.331	ENSG00000182481	KPNA2
ENSG00000182484	32.7021	27.5304	21.0377	26.5934	ENSG00000182484	WASH6P
ENSG00000182487	0.0618943	0.0873047	0.0457377	0	ENSG00000182487	NCF1B
ENSG00000182489	2.14715	0.758985	0.946632	0.44643	ENSG00000182489	XKRX
ENSG00000182492	0.0263198	0.0946319	1.63545	13.297	ENSG00000182492	BGN
ENSG00000182500	5.39888	6.77075	5.05227	3.7659	ENSG00000182500	ORAI1
ENSG00000182502	0.0788374	0	0	0	ENSG00000182502	ABHD17AP5
ENSG00000182504	7.00069	10.7036	10.7194	7.01286	ENSG00000182504	CEP97
ENSG00000182508	0.110398	0.0673102	0.186865	0.163926	ENSG00000182508	LHFPL1
ENSG00000182511	2.45518	2.98123	1.20803	3.60766	ENSG00000182511	FES
ENSG00000182512	89.3144	117.576	87.7631	34.979	ENSG00000182512	GLRX5
ENSG00000182518	4.50556	6.81396	6.44837	7.29133	ENSG00000182518	FAM104B
ENSG00000182521	1.68987	1.01135	1.57527	3.90178	ENSG00000182521	TBPL2
ENSG00000182531	0.18007	0.113606	0	0	ENSG00000182531	OR7E115P
ENSG00000182533	0.199205	0.952099	0.473248	2.03441	ENSG00000182533	CAV3
ENSG00000182534	47.4935	33.6042	35.4698	40.6719	ENSG00000182534	MXRA7
ENSG00000182541	83.8088	56.3781	124.895	39.0528	ENSG00000182541	LIMK2
ENSG00000182544	27.1869	19.2919	17.0664	9.78293	ENSG00000182544	MFSD5
ENSG00000182545	3.69049	5.27974	6.09575	7.26983	ENSG00000182545	RNASE10
ENSG00000182551	16.8657	15.0454	13.3689	19.8155	ENSG00000182551	ADI1
ENSG00000182552	27.4475	17.1296	13.2959	12.3278	ENSG00000182552	RWDD4
ENSG00000182557	0.220191	0.542646	0	0.309934	ENSG00000182557	SPNS3
ENSG00000182565	0	0	0	0	ENSG00000182565	OR4C2P
ENSG00000182566	1.10332	3.04783	1.69065	4.41732	ENSG00000182566	CLEC4G
ENSG00000182568	7.06278	6.29791	9.00304	9.16513	ENSG00000182568	SATB1
ENSG00000182572	12.7054	60.4717	16.3394	18.4159	ENSG00000182572	HIST1H3I
ENSG00000182574	0.067376	0	1.17656	0.147482	ENSG00000182574	RP3-341D10.1
ENSG00000182575	0.263643	0.224922	0.333445	0.313328	ENSG00000182575	NXPH3
ENSG00000182578	1.40016	3.69766	2.64753	5.41271	ENSG00000182578	CSF1R
ENSG00000182580	27.0408	11.8341	16.6137	7.48077	ENSG00000182580	EPHB3
ENSG00000182583	0	0	0	0.362434	ENSG00000182583	VCX
ENSG00000182584	1.47124	1.85413	2.08003	2.10068	ENSG00000182584	ACTL10
ENSG00000182585	16.5534	16.148	29.5701	10.6816	ENSG00000182585	EPGN
ENSG00000182591	0	0	0	0	ENSG00000182591	KRTAP11-1
ENSG00000182600	2.9492	3.69897	6.13201	3.70969	ENSG00000182600	C2orf82
ENSG00000182601	0	0.104797	0.0757239	0.441079	ENSG00000182601	HS3ST4
ENSG00000182606	30.4661	24.1176	30.7508	27.7672	ENSG00000182606	TRAK1
ENSG00000182611	13.0354	52.9998	11.3235	15.3646	ENSG00000182611	HIST1H2AJ
ENSG00000182612	9.11247	11.3815	13.244	21.3491	ENSG00000182612	TSPAN10
ENSG00000182613	0.0658136	0.094945	0.143002	0.250616	ENSG00000182613	OR2V2
ENSG00000182621	1.04672	2.29252	3.09159	4.25846	ENSG00000182621	PLCB1
ENSG00000182625	0.764251	2.10055	0	1.5782	ENSG00000182625	RP11-123C21.1
ENSG00000182628	24.7975	27.8031	12.9925	19.9542	ENSG00000182628	SKA2
ENSG00000182631	0.0874056	0.0631988	0.0761825	0.0480223	ENSG00000182631	RXFP3
ENSG00000182632	0.780249	1.07657	1.17798	1.81691	ENSG00000182632	CCNYL2
ENSG00000182634	0	0	0	0	ENSG00000182634	OR10G7
ENSG00000182636	2.70515	1.27389	0.314075	3.82246	ENSG00000182636	NDN
ENSG00000182645	0.966459	1.26149	1.62983	2.78243	ENSG00000182645	CCDC172
ENSG00000182646	5.88632	9.42287	14.0562	13.0222	ENSG00000182646	FAM156A
ENSG00000182652	0	0	0	0.141971	ENSG00000182652	OR4Q3
ENSG00000182667	18.3842	62.2679	39.1846	86.2988	ENSG00000182667	NTM

ENSG00000182670	40.9522	47.5616	56.0822	101.757	ENSG00000182670	TTC3
ENSG00000182674	0.107835	0.25109	0.133621	0.239412	ENSG00000182674	KCNB2
ENSG00000182676	1.87424	2.22472	1.80469	1.02956	ENSG00000182676	PPP1R27
ENSG00000182685	6.59223	6.78827	8.6216	6.2342	ENSG00000182685	BRICD5
ENSG00000182687	0.387636	0	0.0749854	0.0475274	ENSG00000182687	GALR2
ENSG00000182698	0	0	0	0	ENSG00000182698	RESP18
ENSG00000182700	1.87672	2.29031	2.61776	5.01326	ENSG00000182700	IGIP
ENSG00000182704	31.5782	51.4665	38.8765	31.2534	ENSG00000182704	TSKU
ENSG00000182707	0	0	0	0	ENSG00000182707	FXYD6P3
ENSG00000182712	1.35063	1.63402	1.06592	1.47094	ENSG00000182712	CMC4
ENSG00000182718	5508.06	2975.43	852.42	1938.14	ENSG00000182718	ANXA2
ENSG00000182722	0.0649887	0.502986	0.48599	0.28288	ENSG00000182722	SEPHS1P1
ENSG00000182732	1.91076	3.3284	3.04196	4.90625	ENSG00000182732	RGS6
ENSG00000182742	0.207499	0.307557	0.750295	4.17807	ENSG00000182742	HOXB4
ENSG00000182747	0.330128	0.250045	0.0822026	0.259012	ENSG00000182747	SLC35D3
ENSG00000182749	24.8529	20.4135	15.2242	11.0558	ENSG00000182749	PAQR7
ENSG00000182752	2.49614	2.35294	6.0732	91.9582	ENSG00000182752	PAPPA
ENSG00000182759	0.871821	1.04581	1.52035	13.051	ENSG00000182759	MAFA
ENSG00000182768	31.2535	21.7703	31.2153	16.2722	ENSG00000182768	NGRN
ENSG00000182771	0.466431	0.257561	0.401321	0.29496	ENSG00000182771	GRID1
ENSG00000182774	640.169	381.636	433.678	257.555	ENSG00000182774	RPS17
ENSG00000182776	0.164181	0.310268	0.284169	0.267981	ENSG00000182776	RP11-114H20.1
ENSG00000182782	8.76751	5.16949	2.89479	2.46695	ENSG00000182782	HCAR2
ENSG00000182783	0.0303631	0.10551	0.052806	0	ENSG00000182783	OR2T29
ENSG00000182791	0.225856	0.217774	0.0984458	0.103867	ENSG00000182791	CCDC87
ENSG00000182793	0	0	0	0.0937137	ENSG00000182793	GSTA5
ENSG00000182795	100.564	30.6666	35.4541	20.6371	ENSG00000182795	C1orf116
ENSG00000182796	6.56842	10.5156	11.2708	13.1085	ENSG00000182796	TMEM198B
ENSG00000182798	0.0814077	0.0784087	0.0708748	0.178154	ENSG00000182798	MAGEB17
ENSG00000182809	0.58451	10.2779	6.43028	3.79823	ENSG00000182809	CRIP2
ENSG00000182810	4.54317	3.74878	4.34366	2.85642	ENSG00000182810	DDX28
ENSG00000182814	0	0	0.0872253	0	ENSG00000182814	FUNDC2P2
ENSG00000182816	0	0	0	0	ENSG00000182816	KRTAP13-2
ENSG00000182824	0.0915625	0.0294114	0.0531762	0.134364	ENSG00000182824	LINC01662
ENSG00000182827	30.0225	14.1109	15.7855	21.5467	ENSG00000182827	ACBD3
ENSG00000182831	16.7639	19.7762	20.684	13.5052	ENSG00000182831	C16orf72
ENSG00000182836	0.255267	0.807735	0.579823	1.02555	ENSG00000182836	PLCXD3
ENSG00000182841	14.9157	21.2641	20.8018	17.2974	ENSG00000182841	RRP7BP
ENSG00000182851	0.0488956	0.212097	0.256377	0.107407	ENSG00000182851	GPIHBP1
ENSG00000182853	0.397418	0.268361	0.733317	0.511891	ENSG00000182853	VMO1
ENSG00000182854	0	0	0	0.0684377	ENSG00000182854	OR4F15
ENSG00000182858	16.9524	18.6902	8.71462	7.41628	ENSG00000182858	ALG12
ENSG00000182866	1.86062	2.47849	2.4645	3.31268	ENSG00000182866	LCK
ENSG00000182870	0.222817	0.343072	0.222921	0.778003	ENSG00000182870	GALNT9
ENSG00000182871	15.3115	60.6445	44.6133	98.0302	ENSG00000182871	COL18A1
ENSG00000182872	9.32348	8.94532	9.53297	6.48352	ENSG00000182872	RBM10
ENSG00000182885	0.236892	0.556641	0.284442	0.571195	ENSG00000182885	ADGRG3
ENSG00000182888	0	0	0	0	ENSG00000182888	RP11-558O12.1
ENSG00000182890	0.028262	0.0279295	0.0761006	0.0647794	ENSG00000182890	GLUD2
ENSG00000182896	0.259591	0.0989525	0.376653	0.0561039	ENSG00000182896	TMEM95
ENSG00000182898	0.275572	0.103161	0.249503	0.813723	ENSG00000182898	TCHHL1
ENSG00000182899	419.14	313.099	240.206	179.628	ENSG00000182899	RPL35A
ENSG00000182901	14.2901	41.5495	34.0498	71.8064	ENSG00000182901	RGS7
ENSG00000182902	0.716965	0.700216	0.56469	0.801113	ENSG00000182902	SLC25A18

ENSG00000182903	7.46909	9.86603	10.0577	9.57384	ENSG00000182903	ZNF721
ENSG00000182909	1.05696	1.31648	0.914794	1.33797	ENSG00000182909	LENG9
ENSG00000182912	0.171398	0.244924	0.249708	0.719514	ENSG00000182912	C21orf90
ENSG00000182916	0.67423	2.05812	1.51721	5.37925	ENSG00000182916	TCEAL7
ENSG00000182919	14.8925	11.9013	13.5357	19.9204	ENSG00000182919	C11orf54
ENSG00000182921	0	0	0	0	ENSG00000182921	CCDC75P1
ENSG00000182923	8.4783	12.0155	9.88423	13.7238	ENSG00000182923	CEP63
ENSG00000182931	0.220326	0.105787	0	0	ENSG00000182931	WFDC10B
ENSG00000182934	59.2296	61.6928	57.8993	39.597	ENSG00000182934	SRPRA
ENSG00000182938	0.110045	0.0453802	0	0	ENSG00000182938	OTOP3
ENSG00000182944	106.91	96.3498	117.563	100.014	ENSG00000182944	EWSR1
ENSG00000182950	0.150169	0.674657	0.174222	0.273289	ENSG00000182950	ODF3L1
ENSG00000182952	31.135	80.0712	53.5317	33.625	ENSG00000182952	HMGN4
ENSG00000182957	1.14844	0.934205	0.95935	8.96311	ENSG00000182957	SPATA13
ENSG00000182963	14.0041	16.7827	10.4281	24.8687	ENSG00000182963	GJC1
ENSG00000182965	0.243485	0.50814	0.44877	1.07738	ENSG00000182965	NPM1P14
ENSG00000182968	0.185421	0.298466	0.242799	0.451313	ENSG00000182968	SOX1
ENSG00000182973	19.9954	35.014	30.3031	39.563	ENSG00000182973	CNOT10
ENSG00000182974	0	0	0	0	ENSG00000182974	OR4M2
ENSG00000182979	25.3951	35.6953	43.1827	34.9721	ENSG00000182979	MTA1
ENSG00000182983	5.07264	6.48366	7.05858	8.47525	ENSG00000182983	ZNF662
ENSG00000182985	9.22067	17.7643	18.5803	5.79931	ENSG00000182985	CADM1
ENSG00000182986	36.9251	45.4738	52.4531	64.1899	ENSG00000182986	ZNF320
ENSG00000182993	6.45742	15.4841	16.2766	26.3624	ENSG00000182993	C12orf60
ENSG00000183010	11.5417	21.2401	34.6529	13.9458	ENSG00000183010	PYCR1
ENSG00000183011	37.9321	44.3362	20.1151	20.6561	ENSG00000183011	NAA38
ENSG00000183016	0.359296	0.0943842	0.315167	0.291643	ENSG00000183016	IQCA1P1
ENSG00000183018	10.4221	2.89036	6.02537	6.63368	ENSG00000183018	SPNS2
ENSG00000183019	0.657442	0.591877	0.601022	1.73237	ENSG00000183019	MCEMP1
ENSG00000183020	42.9554	57.0034	66.0549	77.2589	ENSG00000183020	AP2A2
ENSG00000183022	0.431025	0.103761	0	0.11608	ENSG00000183022	TPM3P8
ENSG00000183023	2.33434	12.0299	1.01841	10.305	ENSG00000183023	SLC8A1
ENSG00000183024	0	0.0595432	0.161432	0.0673971	ENSG00000183024	OR1G1
ENSG00000183032	2.41284	6.42953	5.45774	10.3081	ENSG00000183032	SLC25A21
ENSG00000183034	0.0972314	0.0259493	0.181849	0.0595373	ENSG00000183034	OTOP2
ENSG00000183035	0	0.025683	0.0232304	0.0877464	ENSG00000183035	CYLC1
ENSG00000183036	0	0	0	0	ENSG00000183036	PCP4
ENSG00000183038	0	0	0	0	ENSG00000183038	GGTLC3
ENSG00000183044	20.4875	15.5547	19.5654	28.6652	ENSG00000183044	ABAT
ENSG00000183048	13.1464	8.81914	10.7002	7.88846	ENSG00000183048	SLC25A10
ENSG00000183049	4.17876	17.5257	8.20969	16.8963	ENSG00000183049	CAMK1D
ENSG00000183054	13.6955	16.2988	17.5733	13.1644	ENSG00000183054	RGPD6
ENSG00000183055	0.349389	0.960324	1.12853	5.45299	ENSG00000183055	FAM133CP
ENSG00000183060	9.47252	9.27202	12.1448	6.23226	ENSG00000183060	LYSMD4
ENSG00000183066	1.32422	3.15716	2.23323	4.21342	ENSG00000183066	WBP2NL
ENSG00000183067	0.645093	3.84552	2.88683	3.11955	ENSG00000183067	IGSF5
ENSG00000183072	0.418509	0.502431	0.635323	1.01612	ENSG00000183072	NKX2-5
ENSG00000183077	12.7344	21.8419	28.2231	24.9858	ENSG00000183077	AFMID
ENSG00000183086	0	0.147884	0	0	ENSG00000183086	GATSL1
ENSG00000183087	105.782	181.885	61.8338	334.64	ENSG00000183087	GAS6
ENSG00000183090	0.2095	0.0533048	1.2231	0.334968	ENSG00000183090	FREM3
ENSG00000183091	3.45907	4.25359	3.74335	7.65093	ENSG00000183091	NEB
ENSG00000183092	1.47182	2.44974	3.19605	3.35851	ENSG00000183092	BEGAIN
ENSG00000183098	0.782198	0.927642	5.23301	1.81404	ENSG00000183098	GPC6

ENSG00000183103	0.0950759	0.109191	1.12E-08	0	ENSG00000183103	LYPD4
ENSG00000183111	22.9786	7.85867	21.475	4.46492	ENSG00000183111	ARHGEF37
ENSG00000183114	0.0214181	0.061947	0.112011	0.564897	ENSG00000183114	FAM43B
ENSG00000183117	0.474551	1.11563	0.927574	1.61277	ENSG00000183117	CSMD1
ENSG00000183122	0.392431	0.314494	0.284207	0.85876	ENSG00000183122	OR2A3P
ENSG00000183128	0.105608	0.134345	0.060631	0.114491	ENSG00000183128	CALHM3
ENSG00000183130	0	0	0	0	ENSG00000183130	OR2T11
ENSG00000183134	0.363753	0.295226	0.487084	0.364754	ENSG00000183134	PTGDR2
ENSG00000183137	16.0955	29.8574	24.4182	40.4674	ENSG00000183137	CEP57L1
ENSG00000183145	1.3879	4.12938	3.46789	5.80664	ENSG00000183145	RIPPLY3
ENSG00000183146	0.794059	1.78387	1.05197	3.17502	ENSG00000183146	PRORY
ENSG00000183148	0.516856	0.215211	0.179622	1.12467	ENSG00000183148	ANKRD20A2
ENSG00000183150	0.127659	1.42257	0.0851689	0.282561	ENSG00000183150	GPR19
ENSG00000183153	1.24821	0.224354	0.184561	0.375586	ENSG00000183153	GJD3
ENSG00000183154	0.714964	1.35879	1.32392	1.8022	ENSG00000183154	AC138356.1
ENSG00000183155	3.73427	2.47773	3.04639	3.30644	ENSG00000183155	RABIF
ENSG00000183160	4.05148	10.8325	9.92639	50.0705	ENSG00000183160	TMEM119
ENSG00000183161	3.25786	3.63665	5.4761	3.10901	ENSG00000183161	FANCF
ENSG00000183166	0.297557	0.631189	0.539897	0.828583	ENSG00000183166	CALN1
ENSG00000183169	0	0.0311419	0	0.0751812	ENSG00000183169	POM121L1P
ENSG00000183171	0.0266239	0.0128407	0.166083	0.0441429	ENSG00000183171	RP11-49C9.2
ENSG00000183172	1.13065	1.83608	1.49104	1.44355	ENSG00000183172	SMDT1
ENSG00000183185	0.509741	0.801154	1.05568	1.38274	ENSG00000183185	GABRR3
ENSG00000183186	12.2677	5.60569	1.7387	5.66155	ENSG00000183186	C2CD4C
ENSG00000183196	0.850614	1.93814	0.392258	1.21136	ENSG00000183196	CHST6
ENSG00000183199	0.163448	0.178485	0.221273	0.156374	ENSG00000183199	AC093768.1
ENSG00000183206	1.35637	2.78525	3.10988	5.92105	ENSG00000183206	POTEC
ENSG00000183207	57.5045	66.5364	53.4709	58.9675	ENSG00000183207	RUVBL2
ENSG00000183208	2.40994	3.0822	3.41912	5.44106	ENSG00000183208	GDPGP1
ENSG00000183214	10.6484	13.2144	3.75845	9.98349	ENSG00000183214	MICA
ENSG00000183230	1.25635	1.67165	0.922863	2.40297	ENSG00000183230	CTNNA3
ENSG00000183239	0.700155	0.334909	0.756965	0.438817	ENSG00000183239	RP5-1120P11.4
ENSG00000183246	157.633	164.99	149.722	76.4691	ENSG00000183246	RIMBP3C
ENSG00000183248	0.186721	0.400705	0.252744	0.556295	ENSG00000183248	PRR36
ENSG00000183249	0	0	0	0	ENSG00000183249	NF1P3
ENSG00000183250	2.21892	1.6578	2.21381	1.40608	ENSG00000183250	LINC01547
ENSG00000183251	0	0	0.054788	0.0686017	ENSG00000183251	OR51B4
ENSG00000183255	90.5401	74.7625	61.0975	46.4073	ENSG00000183255	PTTG1IP
ENSG00000183258	23.2028	17.5137	30.3086	21.2619	ENSG00000183258	DDX41
ENSG00000183260	7.3162	4.36136	5.63837	3.13096	ENSG00000183260	ABHD16B
ENSG00000183269	0	0	0	0	ENSG00000183269	OR52E8
ENSG00000183273	1.30324	1.48263	2.29517	4.15043	ENSG00000183273	CCDC60
ENSG00000183281	4.84476	6.99543	9.18108	12.474	ENSG00000183281	PLGLB1
ENSG00000183283	76.209	42.2783	31.6844	27.4894	ENSG00000183283	DAZAP2
ENSG00000183287	4.07236	10.0114	2.02559	26.196	ENSG00000183287	CCBE1
ENSG00000183291	74.8183	50.9603	47.1512	34.4343	ENSG00000183291	SELENOF
ENSG00000183292	1.7091	2.84186	4.17861	5.52537	ENSG00000183292	TISP43
ENSG00000183298	0.088181	0.0847832	0	0.477929	ENSG00000183298	RP11-556K13.1
ENSG00000183303	0.868783	0.988285	1.04204	0.373193	ENSG00000183303	OR5P2
ENSG00000183304	0.47944	0.532199	0.48325	0.615344	ENSG00000183304	FAM9A
ENSG00000183305	0.664877	0.490991	0.472323	0	ENSG00000183305	MAGEA2B
ENSG00000183307	0.136416	0.118412	0.114373	0.119144	ENSG00000183307	TMEM121B
ENSG00000183309	8.39288	8.86928	12.1218	7.37739	ENSG00000183309	ZNF623
ENSG00000183310	0	0	0	0	ENSG00000183310	OR2T34

ENSG00000183311	301.633	132.526	106.346	219.74	ENSG00000183311	TUBB
ENSG00000183313	0	0	0	0	ENSG00000183313	OR52L1
ENSG00000183317	1.10666	2.73518	1.81756	3.29418	ENSG00000183317	EPHA10
ENSG00000183318	0	0	0	0	ENSG00000183318	SPDYE4
ENSG00000183323	12.5837	26.1982	23.8914	35.3445	ENSG00000183323	CCDC125
ENSG00000183324	0.462853	1.35327	1.13745	1.25704	ENSG00000183324	REC114
ENSG00000183336	5.28994	3.65456	4.17977	2.11545	ENSG00000183336	BOLA2
ENSG00000183337	7.90553	9.42484	6.57448	14.3239	ENSG00000183337	BCOR
ENSG00000183340	4.2545	6.01964	7.32739	7.42999	ENSG00000183340	JRKL
ENSG00000183346	0.0365319	0.0695758	0.182348	0.112217	ENSG00000183346	C10orf107
ENSG00000183347	9.99696	13.5072	6.51533	1.76529	ENSG00000183347	GBP6
ENSG00000183354	12.9311	19.6662	20.8631	19.9764	ENSG00000183354	KIAA2026
ENSG00000183378	17.0322	7.76697	14.9962	8.66728	ENSG00000183378	OVCH2
ENSG00000183379	0.164094	1.10467	0.408742	0.383048	ENSG00000183379	SYNDIG1L
ENSG00000183386	7.88566	9.10772	10.2899	12.7009	ENSG00000183386	FHL3
ENSG00000183389	0.197744	0.285564	0.172485	0.269939	ENSG00000183389	OR56A4
ENSG00000183395	0.223651	0.903676	0.244303	0.79268	ENSG00000183395	PMCH
ENSG00000183396	0.30951	0.198187	0.179008	0.334096	ENSG00000183396	TMEM89
ENSG00000183397	7.30261	9.85583	10.7361	12.4642	ENSG00000183397	C19orf71
ENSG00000183401	15.1203	16.538	16.6376	25.0184	ENSG00000183401	CCDC159
ENSG00000183405	0.583448	0.113339	0.111145	0	ENSG00000183405	RPS7P1
ENSG00000183421	24.9771	14.1911	18.0388	8.15583	ENSG00000183421	RIPK4
ENSG00000183423	0.17755	0.294839	0.442985	0.29183	ENSG00000183423	LRIT3
ENSG00000183426	32.4264	69.536	109.865	67.0122	ENSG00000183426	NPIPA1
ENSG00000183431	29.4207	29.2693	35.0848	29.8195	ENSG00000183431	SF3A3
ENSG00000183432	0.61138	2.50926	0.798417	1.58515	ENSG00000183432	ZBTB8OSP1
ENSG00000183434	0.102346	0.198529	0.209223	0.225815	ENSG00000183434	TFDP3
ENSG00000183439	1.46142	2.4523	2.88713	2.38483	ENSG00000183439	TRIM61
ENSG00000183444	5.7568	7.64992	11.4756	2.67113	ENSG00000183444	OR7E38P
ENSG00000183454	0.181468	0.353375	0.147703	0.175925	ENSG00000183454	GRIN2A
ENSG00000183458	17.8728	33.6311	63.3685	27.0928	ENSG00000183458	RP11-958N24.1
ENSG00000183461	0	0.0443425	0	0	ENSG00000183461	XAGE1C
ENSG00000183463	0	0	0	0	ENSG00000183463	URAD
ENSG00000183470	0.328304	0.478181	0.589933	1.12357	ENSG00000183470	FLJ40288
ENSG00000183473	0.334288	0.252604	0.365488	0.419119	ENSG00000183473	SDTR3
ENSG00000183474	30.1428	33.0568	39.8585	54.7049	ENSG00000183474	GTF2H2C
ENSG00000183475	6.20632	7.18206	8.09239	4.95642	ENSG00000183475	ASB7
ENSG00000183476	0.0518023	0.0499309	0.0225699	0.170612	ENSG00000183476	SH2D7
ENSG00000183479	0.838466	0.45599	0.923033	0.490633	ENSG00000183479	TREX2
ENSG00000183484	4.55471	3.96987	2.83718	7.10476	ENSG00000183484	GPR132
ENSG00000183486	13.0838	24.9242	26.9414	40.8455	ENSG00000183486	MX2
ENSG00000183495	4.45421	8.64558	9.33805	12.6516	ENSG00000183495	EP400
ENSG00000183496	0.470071	0.446228	0.981539	1.8999	ENSG00000183496	MEX3B
ENSG00000183504	0.607798	4.741	3.06184	7.92622	ENSG00000183504	AL132868.1
ENSG00000183506	14.3221	21.1184	18.8181	21.2404	ENSG00000183506	PI4KAP2
ENSG00000183508	0.169775	0.394147	0.289235	0.718079	ENSG00000183508	FAM46C
ENSG00000183513	16.5436	24.7578	27.1204	29.9545	ENSG00000183513	COA5
ENSG00000183514	0	0	0	0	ENSG00000183514	TDGF1P2
ENSG00000183520	24.2794	22.6518	19.7114	23.0877	ENSG00000183520	UTP11
ENSG00000183527	17.2632	24.3688	26.1471	12.1364	ENSG00000183527	PSMG1
ENSG00000183530	18.3236	16.276	15.3298	20.2053	ENSG00000183530	PRR14L
ENSG00000183531	1.25743	0.564414	2.32115	0	ENSG00000183531	Z98256.1
ENSG00000183542	0.122056	0.37015	0.35207	0.425047	ENSG00000183542	KLRC4
ENSG00000183549	0.738172	1.22721	0.854515	1.75609	ENSG00000183549	ACSM5

ENSG00000183558	6.84812	4.15388	4.45246	2.15923	ENSG00000183558	HIST2H2AA3
ENSG00000183559	0.114734	0.0552076	0	0	ENSG00000183559	C10orf120
ENSG00000183560	0	0	0	0	ENSG00000183560	IZUMO1R
ENSG00000183562	3.71487	9.43962	8.49614	7.09013	ENSG00000183562	AC131971.1
ENSG00000183566	1.46183	2.50712	2.68959	4.41351	ENSG00000183566	BPIFA4P
ENSG00000183569	6.70247	5.47744	6.59448	5.10946	ENSG00000183569	SERHL2
ENSG00000183570	9.75319	35.2562	24.9145	61.4924	ENSG00000183570	PCBP3
ENSG00000183571	0.309834	0.355476	0.270657	0.618039	ENSG00000183571	PGPEP1L
ENSG00000183574	1.35259	0.556113	1.36117	0.483865	ENSG00000183574	RNF5
ENSG00000183576	24.9785	22.0438	21.9956	18.1161	ENSG00000183576	SETD3
ENSG00000183578	4.63203	2.91634	3.2773	4.32081	ENSG00000183578	TNFAIP8L3
ENSG00000183579	4.13695	6.38624	5.9065	3.51942	ENSG00000183579	ZNRF3
ENSG00000183580	0.503628	1.6756	1.14775	3.59542	ENSG00000183580	FBXL7
ENSG00000183586	0	0	0	0	ENSG00000183586	HMGN3P1
ENSG00000183597	30.9777	25.6525	31.3033	37.0947	ENSG00000183597	TANGO2
ENSG00000183598	7.49488	20.7567	4.23216	4.49128	ENSG00000183598	HIST2H3D
ENSG00000183604	10.5046	22.9565	36.761	34.4562	ENSG00000183604	SMG1P5
ENSG00000183605	12.4039	15.2534	21.4814	9.74572	ENSG00000183605	SFXN4
ENSG00000183607	0.162	0.335993	0.269968	0.509833	ENSG00000183607	GKN2
ENSG00000183615	0.133663	0.257089	0.175637	0.581564	ENSG00000183615	FAM167B
ENSG00000183617	14.0479	10.8393	10.887	6.5856	ENSG00000183617	MRPL54
ENSG00000183621	1.45557	2.77374	3.31938	3.47089	ENSG00000183621	ZNF438
ENSG00000183624	17.3696	17.7803	11.1873	9.45388	ENSG00000183624	HMCES
ENSG00000183625	0.972111	1.51754	1.55175	3.23099	ENSG00000183625	CCR3
ENSG00000183628	5.53443	6.53546	8.70153	5.82031	ENSG00000183628	DGCR6
ENSG00000183629	0.279823	0.436382	0.390758	0.476249	ENSG00000183629	GOLGA8G
ENSG00000183631	0	0	0.042254	0.318226	ENSG00000183631	PRR32
ENSG00000183632	0.255377	0.122311	0.220887	0.147858	ENSG00000183632	TP53TG3
ENSG00000183638	3.89167	5.87119	5.94022	11.6638	ENSG00000183638	RP1L1
ENSG00000183640	0	0	0	0	ENSG00000183640	KRTAP8-1
ENSG00000183643	0.0979017	0.559826	0.249562	0.681182	ENSG00000183643	C15orf32
ENSG00000183644	1.70081	1.35897	0.857951	2.2237	ENSG00000183644	C11orf88
ENSG00000183647	7.90229	9.62572	7.94389	12.4218	ENSG00000183647	ZNF530
ENSG00000183648	67.4678	64.7932	45.0481	41.8803	ENSG00000183648	NDUFB1
ENSG00000183653	0.0363522	0.130155	0.353851	0.61295	ENSG00000183653	GRIK1-AS2
ENSG00000183654	7.45522	2.88468	1.89766	12.1382	ENSG00000183654	MARCH11
ENSG00000183655	2.72129	3.41673	2.8612	2.18594	ENSG00000183655	KLHL25
ENSG00000183657	1.59713	3.06741	2.68071	5.67281	ENSG00000183657	PP13439
ENSG00000183662	0	0.165832	0.102892	0.48375	ENSG00000183662	FAM19A1
ENSG00000183663	0.0654021	0.125843	0.227366	0.142319	ENSG00000183663	RP11-44N17.1
ENSG00000183665	6.63016	9.6938	10.3916	7.4039	ENSG00000183665	TRMT12
ENSG00000183666	9.76186	24.3741	20.3495	18.936	ENSG00000183666	GUSBP1
ENSG00000183668	0.843754	0.751135	1.01954	2.76399	ENSG00000183668	PSG9
ENSG00000183671	4.13153	1.5592	4.48527	2.04784	ENSG00000183671	GPR1
ENSG00000183675	2.29677	2.99096	4.10869	6.78928	ENSG00000183675	PTPN20B
ENSG00000183678	0	0.833518	0	0	ENSG00000183678	CTAG1A
ENSG00000183682	0.179151	0.170065	0.585753	0.322169	ENSG00000183682	BMP8A
ENSG00000183684	53.4134	42.1351	38.2306	30.7636	ENSG00000183684	ALYREF
ENSG00000183688	1.59474	1.85776	1.72509	3.78579	ENSG00000183688	RFLNB
ENSG00000183690	1.07906	3.58521	1.56204	2.80968	ENSG00000183690	EFHC2
ENSG00000183691	1.90805	1.13865	0.617058	0.713628	ENSG00000183691	NOG
ENSG00000183695	0.0276409	0.0799202	0.103841	0.151668	ENSG00000183695	MRGPRX2
ENSG00000183696	304.781	536.641	297.217	188.411	ENSG00000183696	UPP1
ENSG00000183704	0.0693278	0.13334	0.120482	0.0753681	ENSG00000183704	SLC9B1P1

ENSG00000183706	0	0	0	0	ENSG00000183706	OR4N4
ENSG00000183709	0	0.0905886	0	0.0972143	ENSG00000183709	IFNL2
ENSG00000183715	0.380432	1.72386	1.23179	1.70037	ENSG00000183715	OPCML
ENSG00000183718	6.19936	14.0502	14.8791	26.2273	ENSG00000183718	TRIM52
ENSG00000183722	6.57053	10.901	6.78731	20.5336	ENSG00000183722	LHFPL6
ENSG00000183723	18.2345	16.6911	10.8785	10.7456	ENSG00000183723	CMTM4
ENSG00000183726	67.1407	47.886	34.4322	32.6682	ENSG00000183726	TMEM50A
ENSG00000183729	0.0205196	0.0197837	0.107318	0	ENSG00000183729	NPBWR1
ENSG00000183733	0.0461054	0.132904	0.240115	0.249362	ENSG00000183733	FIGLA
ENSG00000183734	0.0612942	0.443285	0.427166	0	ENSG00000183734	ASCL2
ENSG00000183735	13.9823	18.7135	16.807	20.4178	ENSG00000183735	TBK1
ENSG00000183741	22.0766	12.0105	20.6599	18.0929	ENSG00000183741	CBX6
ENSG00000183742	87.2785	35.6003	10.097	8.64103	ENSG00000183742	MACC1
ENSG00000183747	21.2706	39.8763	37.4483	59.8833	ENSG00000183747	ACSM2A
ENSG00000183748	0.138565	0.0638429	0.142784	0.239025	ENSG00000183748	MRC1L1
ENSG00000183751	26.8653	23.9364	23.132	16.3384	ENSG00000183751	TBL3
ENSG00000183753	0.0864617	0.209464	0.0777448	0.344863	ENSG00000183753	BPY2
ENSG00000183760	8.0339	5.9022	3.23705	6.09127	ENSG00000183760	ACP7
ENSG00000183762	8.07761	13.5677	7.55388	12.0178	ENSG00000183762	KREMEN1
ENSG00000183763	3.06168	11.2772	5.34697	5.83317	ENSG00000183763	TRAIP
ENSG00000183765	11.0467	31.3682	16.1328	26.5817	ENSG00000183765	CHEK2
ENSG00000183770	0.268574	0.259537	0.559934	0.60057	ENSG00000183770	FOXL2
ENSG00000183773	2.64344	6.30041	7.16221	1.23868	ENSG00000183773	AIFM3
ENSG00000183775	0.153023	0.233039	0.228822	0.40687	ENSG00000183775	KCTD16
ENSG00000183778	1.41667	2.90323	2.87872	3.96319	ENSG00000183778	B3GALT5
ENSG00000183779	2.77694	1.71006	2.67697	4.11866	ENSG00000183779	ZNF703
ENSG00000183780	18.3103	11.8904	11.9474	27.1277	ENSG00000183780	SLC35F3
ENSG00000183783	0.16971	0.162564	0.0931909	0.361664	ENSG00000183783	KCTD8
ENSG00000183784	0.860304	1.637	1.26071	2.68375	ENSG00000183784	C9orf66
ENSG00000183785	0.297233	1.05754	0.83178	0.990814	ENSG00000183785	TUBA8
ENSG00000183791	0.0906025	0	1.81949	3.70099	ENSG00000183791	ELOA3
ENSG00000183793	4.22369	14.7032	14.0105	1.03899	ENSG00000183793	NPIPA5
ENSG00000183795	0.0864617	0.241535	0.0777448	0.344863	ENSG00000183795	BPY2B
ENSG00000183798	0.175449	0.376436	0.297769	0.39314	ENSG00000183798	EMILIN3
ENSG00000183801	0.41099	1.37178	1.17653	1.24836	ENSG00000183801	OLFML1
ENSG00000183807	0.55478	0.937678	0.493905	1.19508	ENSG00000183807	FAM162B
ENSG00000183808	10.1431	16.4121	16.5448	16.9272	ENSG00000183808	RBM12B
ENSG00000183813	1.33859	2.69569	2.37328	4.7473	ENSG00000183813	CCR4
ENSG00000183814	2.2167	4.88403	2.30373	2.96533	ENSG00000183814	LIN9
ENSG00000183826	7.41695	10.3131	8.51469	10.0823	ENSG00000183826	BTBD9
ENSG00000183828	20.7996	39.242	27.811	12.0962	ENSG00000183828	NUDT14
ENSG00000183831	1.13983	3.16991	2.68796	4.49095	ENSG00000183831	ANKRD45
ENSG00000183833	0.700547	1.56084	1.8212	3.66543	ENSG00000183833	MAATS1
ENSG00000183837	0.0747336	0.333561	0.211107	0.214133	ENSG00000183837	PNMA3
ENSG00000183840	3.8975	12.2322	3.90205	3.55339	ENSG00000183840	GPR39
ENSG00000183844	1.43713	3.82464	4.44442	5.31593	ENSG00000183844	FAM3B
ENSG00000183850	2.14574	4.47168	2.657	4.94619	ENSG00000183850	ZNF730
ENSG00000183853	21.2002	79.3541	63.3766	46.1128	ENSG00000183853	KIRREL1
ENSG00000183856	4.46124	32.4659	4.00787	12.3032	ENSG00000183856	IQGAP3
ENSG00000183862	0.0193915	0.0186971	0	0	ENSG00000183862	CNGA2
ENSG00000183864	14.8071	11.984	14.5151	10.7256	ENSG00000183864	TOB2
ENSG00000183873	3.43694	7.38601	6.3005	11.659	ENSG00000183873	SCN5A
ENSG00000183876	2.61833	7.3411	6.35148	3.95745	ENSG00000183876	ARSI
ENSG00000183878	15.026	25.4915	19.4978	1.05862	ENSG00000183878	UTY

ENSG00000183888	0.744102	1.90845	1.32575	3.1376	ENSG00000183888	C1orf64
ENSG00000183889	27.7497	69.296	137.316	69.0365	ENSG00000183889	AC138969.1
ENSG00000183891	8.1564	13.4139	10.1609	6.55148	ENSG00000183891	TTC32
ENSG00000183900	23.2859	9.60488	1.96351	15.0205	ENSG00000183900	AC099522.1
ENSG00000183908	0.0747817	0.317375	0.302409	0.546898	ENSG00000183908	LRRC55
ENSG00000183909	0	0.134234	0.0606443	0.0758667	ENSG00000183909	OR4G2P
ENSG00000183911	0	0.17432	0.443495	0.363927	ENSG00000183911	RPL21P132
ENSG00000183914	0.804022	2.41252	1.81246	2.34788	ENSG00000183914	DNAH2
ENSG00000183918	0	0.065487	0.222026	0.199017	ENSG00000183918	SH2D1A
ENSG00000183921	0.169156	0.162037	0.210103	0.122951	ENSG00000183921	SDR42E2
ENSG00000183929	0.315219	0.734518	1.18313	1.71347	ENSG00000183929	DUSP5P1
ENSG00000183935	5.10707	2.4751	2.58788	2.21254	ENSG00000183935	HTR7P1
ENSG00000183938	0	0	0	0.259182	ENSG00000183938	TRBV21OR9-2
ENSG00000183941	5.35359	6.30104	9.70986	1.76418	ENSG00000183941	HIST2H4A
ENSG00000183943	21.4262	19.9491	25.5902	14.913	ENSG00000183943	PRKX
ENSG00000183955	35.035	47.0542	34.2634	29.4689	ENSG00000183955	KMT5A
ENSG00000183960	0.0421385	0.250273	0.0275645	0.150386	ENSG00000183960	KCNH8
ENSG00000183963	172.366	205.92	84.6522	174.572	ENSG00000183963	SMTN
ENSG00000183971	0.277851	2.604	1.51834	0.295817	ENSG00000183971	NPW
ENSG00000183977	0.518218	1.26258	1.22058	1.0078	ENSG00000183977	PP2D1
ENSG00000183978	23.8688	10.8281	8.02284	10.3162	ENSG00000183978	COA3
ENSG00000183979	0.765259	1.13753	1.88314	3.0405	ENSG00000183979	NPB
ENSG00000183981	0	0	0	0	ENSG00000183981	MAGEA13P
ENSG00000184005	0.737094	1.14884	1.70821	1.06479	ENSG00000184005	ST6GALNAC3
ENSG00000184007	100.205	84.0478	68.5337	67.877	ENSG00000184007	PTP4A2
ENSG00000184009	529.234	308.17	190.092	284.031	ENSG00000184009	ACTG1
ENSG00000184012	4.93112	8.73982	8.21688	15.4806	ENSG00000184012	TMPRSS2
ENSG00000184014	17.1202	36.0186	37.6909	63.9493	ENSG00000184014	DENND5A
ENSG00000184022	0.175005	0.134084	0.101468	0.254321	ENSG00000184022	OR2T10
ENSG00000184029	0.727439	1.15158	1.09174	1.27457	ENSG00000184029	DSCR4
ENSG00000184032	0	0	0	0	ENSG00000184032	KRTAP20-2
ENSG00000184033	0	0.0149304	0	0	ENSG00000184033	CTAG1B
ENSG00000184040	0.794965	2.6881	2.85533	2.0496	ENSG00000184040	TMEM236
ENSG00000184047	29.1666	27.782	26.8396	24.0175	ENSG00000184047	DIABLO
ENSG00000184055	0	0	0	0.620436	ENSG00000184055	OR7E87P
ENSG00000184056	19.3174	22.4613	16.7342	14.3116	ENSG00000184056	VPS33B
ENSG00000184058	4.51214	2.91698	9.14106	7.7004	ENSG00000184058	TBX1
ENSG00000184060	2.12687	0.806664	3.02935	1.06286	ENSG00000184060	ADAP2
ENSG00000184076	48.8589	32.133	20.361	16.8689	ENSG00000184076	UQCR10
ENSG00000184083	1.97912	4.47037	4.03457	5.64554	ENSG00000184083	FAM120C
ENSG00000184084	3.76815	10.9946	3.9167	22.1882	ENSG00000184084	CTD-2372A4.1
ENSG00000184100	0.0852252	0.0757272	0.0329001	0.12802	ENSG00000184100	BRD7P2
ENSG00000184106	0	0	0	0.329746	ENSG00000184106	TREML3P
ENSG00000184108	0	0.0463165	0.0418631	0.105562	ENSG00000184108	TRIML1
ENSG00000184110	188.336	167.446	190.251	112.378	ENSG00000184110	EIF3C
ENSG00000184111	0.373316	0.89293	0.161241	0.793244	ENSG00000184111	RP11-366I13.3
ENSG00000184113	0.326383	0.197579	0.362016	0.354777	ENSG00000184113	CLDN5
ENSG00000184117	37.5497	28.5565	20.6948	29.9817	ENSG00000184117	NIPSNAP1
ENSG00000184139	1.0073	0.725152	0.111419	0.729576	ENSG00000184139	RPL7AP28
ENSG00000184140	0.190898	0.329233	0.608562	0.415594	ENSG00000184140	OR4F6
ENSG00000184144	0.371749	0.863413	1.20576	0.560804	ENSG00000184144	CNTN2
ENSG00000184148	1.0853	0.521792	0.706668	1.176	ENSG00000184148	SPRR4
ENSG00000184154	7.81112	18.4178	14.5102	21.5555	ENSG00000184154	LRTOMT
ENSG00000184155	0	0	0	0	ENSG00000184155	OR10J5

ENSG00000184156	0.231399	0.385349	0.273259	0.875823	ENSG00000184156	KCNQ3
ENSG00000184160	0.108304	0.139101	0.0689412	0.15778	ENSG00000184160	ADRA2C
ENSG00000184162	9.19058	13.1223	9.48054	6.04206	ENSG00000184162	NR2C2AP
ENSG00000184163	2.13637	3.23825	5.53627	1.46613	ENSG00000184163	C1QTNF12
ENSG00000184164	48.4957	83.6569	18.0037	36.3652	ENSG00000184164	CRELD2
ENSG00000184166	0.0665741	0.256102	0.173559	0	ENSG00000184166	OR1D2
ENSG00000184178	7.07179	8.27437	8.46073	9.52713	ENSG00000184178	SCFD2
ENSG00000184182	33.3944	41.4161	34.0804	35.2624	ENSG00000184182	UBE2F
ENSG00000184185	0.0604731	0.0646573	0.16689	0.195077	ENSG00000184185	KCNJ12
ENSG00000184188	0.0551421	0	0	0	ENSG00000184188	CTC-512J14.7
ENSG00000184194	0.698747	1.35193	1.5594	4.06705	ENSG00000184194	GPR173
ENSG00000184203	25.1492	24.5322	19.3957	18.1403	ENSG00000184203	PPP1R2
ENSG00000184205	3.75734	4.7853	7.24067	5.804	ENSG00000184205	TSPYL2
ENSG00000184206	1.12114	3.99578	5.50215	7.29398	ENSG00000184206	GOLGA6L4
ENSG00000184207	8.50214	8.8495	6.07889	5.22517	ENSG00000184207	PGP
ENSG00000184208	3.53703	5.4101	7.39669	7.2436	ENSG00000184208	C22orf46
ENSG00000184209	19.5608	28.0604	26.6419	35.3769	ENSG00000184209	SNRNP35
ENSG00000184210	0.0372262	0.0358611	0.23257	0.0815298	ENSG00000184210	DGAT2L6
ENSG00000184216	21.2747	19.0568	21.0137	15.7978	ENSG00000184216	IRAK1
ENSG00000184220	10.5229	19.1337	15.1905	21.3451	ENSG00000184220	CMSS1
ENSG00000184221	0.0561857	0.0236242	0.0213664	0.026951	ENSG00000184221	OLIG1
ENSG00000184224	24.9846	33.0489	29.5123	37.707	ENSG00000184224	C11orf72
ENSG00000184226	0.379054	0.500837	0.977579	2.84511	ENSG00000184226	PCDH9
ENSG00000184227	0.935926	2.15243	0.0862693	0.560138	ENSG00000184227	ACOT1
ENSG00000184232	15.7141	26.6392	17.9714	27.5189	ENSG00000184232	OAF
ENSG00000184247	4.47199	5.81442	2.67117	14.2829	ENSG00000184247	AC100791.1
ENSG00000184254	1044.22	336.285	146.708	181.219	ENSG00000184254	ALDH1A3
ENSG00000184258	0.182116	0.131524	0.0396268	10.1022	ENSG00000184258	CDR1
ENSG00000184260	22.1752	39.7228	22.8871	12.7402	ENSG00000184260	HIST2H2AC
ENSG00000184261	0.226324	0.967793	0.42569	1.07951	ENSG00000184261	KCNK12
ENSG00000184270	5.57135	15.0148	3.41812	4.30573	ENSG00000184270	HIST2H2AB
ENSG00000184271	1.82988	4.01223	6.39645	6.96024	ENSG00000184271	POU6F1
ENSG00000184276	0.352564	0.332772	1.21903	0.622046	ENSG00000184276	DEFB108B
ENSG00000184277	20.4778	31.7901	26.5003	28.9858	ENSG00000184277	TM2D3
ENSG00000184281	33.9776	24.2503	34.5667	15.3246	ENSG00000184281	TSSC4
ENSG00000184292	604.345	283.942	165.254	80.7991	ENSG00000184292	TACSTD2
ENSG00000184293	0.0570512	0.587461	0.198485	0.315937	ENSG00000184293	CLECL1
ENSG00000184302	0.0592154	0.0380778	0.105102	0.0433994	ENSG00000184302	SIX6
ENSG00000184303	0.141658	0	0	0	ENSG00000184303	DRD5P1
ENSG00000184304	1.25217	2.69988	2.61821	10.1632	ENSG00000184304	PRKD1
ENSG00000184305	4.47046	9.6162	9.2646	15.6035	ENSG00000184305	CCSER1
ENSG00000184307	2.09281	2.18062	1.86253	0.949407	ENSG00000184307	ZDHHC23
ENSG00000184313	1.11233	2.77426	2.84234	4.24161	ENSG00000184313	MROH7
ENSG00000184319	6.94119	10.5268	12.0528	16.2516	ENSG00000184319	RPL23AP82
ENSG00000184321	0	0	0	0.0713369	ENSG00000184321	OR51J1
ENSG00000184330	0.403227	0.0493745	1.05764	0.703955	ENSG00000184330	S100A7A
ENSG00000184343	1.24042	1.22062	2.68037	1.22865	ENSG00000184343	SRPK3
ENSG00000184344	0	0	0	0	ENSG00000184344	GDF3
ENSG00000184345	0	0	0.107301	0.266169	ENSG00000184345	IQCF2
ENSG00000184347	2.84091	11.5842	23.086	20.0412	ENSG00000184347	SLIT3
ENSG00000184348	8.44412	15.9715	8.59045	3.84568	ENSG00000184348	HIST1H2AK
ENSG00000184349	5.04056	8.81073	13.3273	11.1005	ENSG00000184349	EFNA5
ENSG00000184350	0.0458852	0	0.0794624	0.0454219	ENSG00000184350	MRGPRE
ENSG00000184351	0	0	0.184821	0.689655	ENSG00000184351	KRTAP19-1

ENSG00000184357	24.8828	91.247	16.9837	42.3685	ENSG00000184357	HIST1H1B
ENSG00000184361	0.98773	2.15306	2.07001	2.80279	ENSG00000184361	SPATA32
ENSG00000184363	148.171	117.47	192.773	66.4941	ENSG00000184363	PKP3
ENSG00000184368	0.89015	0.739222	1.12435	1.43139	ENSG00000184368	MAP7D2
ENSG00000184371	0.947036	4.31422	2.8564	15.2781	ENSG00000184371	CSF1
ENSG00000184374	0.80955	2.58143	4.54348	7.23152	ENSG00000184374	COLEC10
ENSG00000184378	1.07222	1.03164	0.808636	0.868453	ENSG00000184378	ACTRT3
ENSG00000184381	12.2481	18.6882	21.3319	18.9896	ENSG00000184381	PLA2G6
ENSG00000184384	5.00767	4.37262	3.90276	11.871	ENSG00000184384	MAML2
ENSG00000184385	0.579849	1.2329	0.85961	1.95675	ENSG00000184385	UMODL1-AS1
ENSG00000184388	0.0491389	0.18201	0.223186	0.0929349	ENSG00000184388	PABPC1L2B
ENSG00000184389	0.0600928	0.405556	0.209029	0.392823	ENSG00000184389	A3GALT2
ENSG00000184394	0	0	0	0	ENSG00000184394	OR4N5
ENSG00000184402	8.22202	11.499	12.1955	13.5543	ENSG00000184402	SS18L1
ENSG00000184408	0.0300968	0.0484081	0.242062	0.563434	ENSG00000184408	KCND2
ENSG00000184414	0.825884	2.20182	1.45049	2.66371	ENSG00000184414	RP11-44M6.3
ENSG00000184423	0	0	0	0	ENSG00000184423	AC0900043.1
ENSG00000184428	6.12355	10.8777	11.9517	11.1827	ENSG00000184428	TOP1MT
ENSG00000184432	91.1788	83.311	69.995	109.231	ENSG00000184432	COPB2
ENSG00000184434	0.978407	1.59918	1.69853	2.32957	ENSG00000184434	LRRC19
ENSG00000184436	10.3385	9.66482	9.2377	5.01751	ENSG00000184436	THAP7
ENSG00000184445	20.9382	61.4423	20.4519	41.2576	ENSG00000184445	KNTC1
ENSG00000184451	0.0964449	1.08054	0.693164	0.947986	ENSG00000184451	CCR10
ENSG00000184454	1.15473	2.35576	1.68247	3.72417	ENSG00000184454	NCMAP
ENSG00000184459	1.66751	1.41309	1.94736	0.686822	ENSG00000184459	BPIFC
ENSG00000184465	26.3416	80.6286	62.9764	59.9077	ENSG00000184465	WDR27
ENSG00000184470	11.0835	18.9512	15.7094	23.1452	ENSG00000184470	TXNRD2
ENSG00000184471	0	0.0681102	0.0649676	0	ENSG00000184471	C1QTNF8
ENSG00000184478	0.120325	0.28945	0.261588	0.458818	ENSG00000184478	OR56A3
ENSG00000184481	3.47465	1.60135	1.55816	1.5639	ENSG00000184481	FOXO4
ENSG00000184486	0.260919	0.478716	0.441626	0.983293	ENSG00000184486	POU3F2
ENSG00000184489	1.28622	2.75401	4.45644	1.77834	ENSG00000184489	PTP4A3
ENSG00000184490	0	0	0	0	ENSG00000184490	AP000351.9
ENSG00000184492	0	0.1402	0.185151	0.160553	ENSG00000184492	FOXD4L1
ENSG00000184494	4.65105	3.54583	2.17492	1.03442	ENSG00000184494	NEU1
ENSG00000184497	1.85025	2.71349	2.45782	4.71286	ENSG00000184497	TMEM255B
ENSG00000184500	8.45525	3.43061	5.43514	3.87859	ENSG00000184500	PROS1
ENSG00000184502	2.09776	0.478463	0.503932	0.177469	ENSG00000184502	GAST
ENSG00000184507	0.185459	0.193383	0.124387	0.141347	ENSG00000184507	NUTM1
ENSG00000184508	6.99319	7.19044	7.04219	3.52757	ENSG00000184508	HDDC3
ENSG00000184515	0.169452	0.427512	0.336407	0.978949	ENSG00000184515	BEX5
ENSG00000184517	4.94776	4.35388	5.27152	4.91779	ENSG00000184517	ZFP1
ENSG00000184523	0	0.229841	0	0	ENSG00000184523	PTGER4P2
ENSG00000184524	0.626865	0.905924	1.10418	1.18286	ENSG00000184524	CEND1
ENSG00000184530	0.0997275	0.257486	0.49848	0.331849	ENSG00000184530	C6orf58
ENSG00000184544	0	0.121104	0	0.0685196	ENSG00000184544	DHRS7C
ENSG00000184545	2.54942	0.69708	5.34882	2.40756	ENSG00000184545	DUSP8
ENSG00000184551	1.99683	3.54525	3.41228	5.56358	ENSG00000184551	AC132872.1
ENSG00000184557	1.02165	1.65149	1.54058	3.1003	ENSG00000184557	SOCS3
ENSG00000184560	0	0	0	0.0383552	ENSG00000184560	C17orf74
ENSG00000184564	9.31847	9.23457	4.5709	6.19197	ENSG00000184564	SLITRK6
ENSG00000184566	0.0523826	0.0504235	0	0.0571683	ENSG00000184566	AC132216.1
ENSG00000184571	0.30727	0.480563	0.441042	0.733043	ENSG00000184571	PIWIL3
ENSG00000184574	7.93047	13.6478	9.63904	6.09022	ENSG00000184574	LPAR5

ENSG00000184575	34.5585	88.9254	99.4533	46.7563	ENSG00000184575	XPOT
ENSG00000184584	13.1362	31.2258	9.78244	15.2549	ENSG00000184584	TMEM173
ENSG00000184588	1.47007	1.31408	1.88476	9.92855	ENSG00000184588	PDE4B
ENSG00000184596	0.317552	0.992092	1.49826	1.29167	ENSG00000184596	AF207550.1
ENSG00000184599	0.115758	0.278496	0.160903	0.2028	ENSG00000184599	FAM19A3
ENSG00000184601	0.120131	0.192849	0.104592	0.0876453	ENSG00000184601	C14orf180
ENSG00000184602	5.80708	5.76078	6.28404	2.62558	ENSG00000184602	SNN
ENSG00000184608	0.358586	1.47086	1.56595	2.3544	ENSG00000184608	FAM167A-AS1
ENSG00000184611	0.0999627	0.277342	0.129149	0.535935	ENSG00000184611	KCNH7
ENSG00000184612	0	1.51411	0.836756	1.33329	ENSG00000184612	RPL7P26
ENSG00000184613	4.03788	7.32151	4.47986	7.15636	ENSG00000184613	NELL2
ENSG00000184616	1.19449	4.38713	3.82826	7.08745	ENSG00000184616	AC004166.6
ENSG00000184617	0.254613	0.334232	0.22489	0.0326914	ENSG00000184617	ZNF840P
ENSG00000184619	1.55148	2.00201	1.46397	2.02167	ENSG00000184619	KRBA2
ENSG00000184624	0	0	0	0	ENSG00000184624	ZNF72P
ENSG00000184634	8.84444	12.2735	17.7683	14.4718	ENSG00000184634	MED12
ENSG00000184635	11.5806	16.7052	14.824	18.9957	ENSG00000184635	ZNF93
ENSG00000184640	81.9118	94.2923	75.7421	92.2729	ENSG00000184640	SEPT9
ENSG00000184647	0.221416	0.545989	0.535733	1.17875	ENSG00000184647	PRSS55
ENSG00000184650	0.160994	0	0	0.0568278	ENSG00000184650	ODF4
ENSG00000184659	0.0371732	0.18091	0.351634	0.280432	ENSG00000184659	FOXD4L4
ENSG00000184661	3.78144	15.8924	2.80114	5.9071	ENSG00000184661	CDCA2
ENSG00000184669	0.333797	1.14317	0.655772	1.28917	ENSG00000184669	OR7E14P
ENSG00000184672	0.330951	1.32617	1.17302	3.19092	ENSG00000184672	RALYL
ENSG00000184674	13.0917	24.8061	22.3461	39.0689	ENSG00000184674	GSTT1
ENSG00000184675	1.21988	1.61456	2.52146	1.71102	ENSG00000184675	AMER1
ENSG00000184677	9.33474	8.42425	8.5053	7.65125	ENSG00000184677	ZBTB40
ENSG00000184678	8.40735	9.33412	4.15687	3.50123	ENSG00000184678	HIST2H2BE
ENSG00000184682	0.186206	0.257892	0.349746	0.219998	ENSG00000184682	C11orf89
ENSG00000184697	0.166442	0.65659	4.44958	0.0730597	ENSG00000184697	CLDN6
ENSG00000184698	0	0	0.050227	0.062951	ENSG00000184698	OR51M1
ENSG00000184702	14.7962	6.60816	10.3426	19.4764	ENSG00000184702	SEPT5
ENSG00000184708	12.4393	17.355	21.9958	21.9838	ENSG00000184708	EIF4ENIF1
ENSG00000184709	0.530565	0	0.0430665	0.0544517	ENSG00000184709	LRRC26
ENSG00000184716	0	0.0694262	0.139392	0	ENSG00000184716	SERINC4
ENSG00000184719	4.5372	5.26439	4.61255	7.46592	ENSG00000184719	RNLS
ENSG00000184724	0	0	0	0	ENSG00000184724	KRTAP6-1
ENSG00000184730	0.120545	0.369262	0.44559	0.846232	ENSG00000184730	APOBR
ENSG00000184731	27.5663	34.4718	11.2658	24.2578	ENSG00000184731	FAM110C
ENSG00000184735	0	0.0765773	0.0461527	0.0872118	ENSG00000184735	DDX53
ENSG00000184741	0	0	0	0	ENSG00000184741	OR5AQ1P
ENSG00000184743	57.9995	33.2939	31.7159	28.3641	ENSG00000184743	ATL3
ENSG00000184750	0.0340267	0	0	0	ENSG00000184750	MAGEA2
ENSG00000184752	63.9988	41.0127	25.9863	24.102	ENSG00000184752	NDUFA12
ENSG00000184761	0.0355497	0.066926	0	0.114166	ENSG00000184761	AC013269.1
ENSG00000184774	0.489975	0.852942	0.958786	1.86322	ENSG00000184774	MGAT4EP
ENSG00000184779	213.44	222.989	96.292	33.3233	ENSG00000184779	RPS17
ENSG00000184785	0.188705	0.145424	0.165448	0.495887	ENSG00000184785	SMIM10
ENSG00000184786	1.61716	2.13587	1.47805	1.29099	ENSG00000184786	TCTE3
ENSG00000184787	13.0309	20.8878	26.5074	26.4309	ENSG00000184787	UBE2G2
ENSG00000184788	1.55664	0.910123	1.06738	0.952608	ENSG00000184788	SATL1
ENSG00000184789	0	0	0	0	ENSG00000184789	OR4C10P
ENSG00000184792	20.5392	25.584	23.1426	45.1253	ENSG00000184792	OSBP2
ENSG00000184795	0	0	0	0	ENSG00000184795	UNC93B5

ENSG00000184809	4.02461	8.34696	8.61386	15.6044	ENSG00000184809	B3GALT5-AS1
ENSG00000184811	0.0883279	0.166186	0.10462	0.181568	ENSG00000184811	TUSC5
ENSG00000184814	0.0896108	0.17473	0.0790202	0.234312	ENSG00000184814	PRR23B
ENSG00000184825	17.1539	59.8152	14.847	14.9423	ENSG00000184825	HIST1H2AH
ENSG00000184828	4.60031	5.1185	8.18708	7.30771	ENSG00000184828	ZBTB7C
ENSG00000184831	6.28316	9.15367	4.47369	3.1614	ENSG00000184831	APOO
ENSG00000184838	0.186634	0.455408	0.681901	5.28891	ENSG00000184838	PRR16
ENSG00000184840	72.0434	78.6693	76.8493	65.1946	ENSG00000184840	TMED9
ENSG00000184844	0	0	0	0	ENSG00000184844	CYCSP45
ENSG00000184845	0.0266317	0.0513715	0.151485	0.190737	ENSG00000184845	DRD1
ENSG00000184857	6.89437	9.92461	13.9062	14.4619	ENSG00000184857	TMEM186
ENSG00000184860	10.9578	12.0136	12.0886	3.626	ENSG00000184860	SDR42E1
ENSG00000184863	14.5669	22.3228	24.1992	26.5068	ENSG00000184863	RBM33
ENSG00000184867	12.314	14.4121	9.92294	16.5884	ENSG00000184867	ARMCX2
ENSG00000184879	0	0	0	0	ENSG00000184879	RP11-7G23.8
ENSG00000184881	0	0	0.10227	0.128157	ENSG00000184881	OR51B2
ENSG00000184886	3.73927	0.39576	6.93085	2.35E-05	ENSG00000184886	PIGW
ENSG00000184887	21.6342	18.9226	16.5667	11.6322	ENSG00000184887	BTBD6
ENSG00000184895	1.58928	1.61156	3.57491	0	ENSG00000184895	SRY
ENSG00000184897	42.7273	69.5903	49.6547	27.1117	ENSG00000184897	H1FX
ENSG00000184898	1.76374	4.29178	3.52853	4.50279	ENSG00000184898	RBM43
ENSG00000184900	31.7838	37.5168	30.2886	39.2166	ENSG00000184900	SUMO3
ENSG00000184903	11.691	17.6746	17.5969	18.9418	ENSG00000184903	IMMP2L
ENSG00000184905	0	0.289989	0.129627	0.142467	ENSG00000184905	TCEAL2
ENSG00000184906	2.01504	2.36202	9.87018	4.43238	ENSG00000184906	AMYH02020865.1
ENSG00000184908	0.0646281	0.186921	0.625864	0.211023	ENSG00000184908	CLCNKB
ENSG00000184909	1.28662	3.86239	2.76963	4.95392	ENSG00000184909	C1ORF220
ENSG00000184911	0.0571456	0.3968	0.297264	0.184608	ENSG00000184911	DMRTC1B
ENSG00000184916	19.3353	61.9175	59.8335	26.3524	ENSG00000184916	JAG2
ENSG00000184922	5.48311	12.4864	12.9266	18.2419	ENSG00000184922	FMNL1
ENSG00000184923	1.79227	1.60961	5.40017	4.34324	ENSG00000184923	NUTM2A
ENSG00000184924	8.18352	5.17258	3.39427	5.14622	ENSG00000184924	PTRHD1
ENSG00000184925	4.50404	5.63469	3.89678	8.2169	ENSG00000184925	LCN12
ENSG00000184933	0.128253	0.164688	0.334937	1.03878	ENSG00000184933	OR6A2
ENSG00000184937	0.116382	0.619594	0.149533	0.602006	ENSG00000184937	WT1
ENSG00000184939	15.262	20.1231	26.955	28.9228	ENSG00000184939	ZFP90
ENSG00000184945	0	0	0	0	ENSG00000184945	AQP12A
ENSG00000184949	5.02638	3.61613	3.92176	5.62067	ENSG00000184949	FAM227A
ENSG00000184954	0	0	0	0	ENSG00000184954	OR6C70
ENSG00000184956	0.243579	1.05811	0.886188	1.33671	ENSG00000184956	MUC6
ENSG00000184961	0.899804	1.24901	0.630829	0	ENSG00000184961	AL772307.1
ENSG00000184967	10.8124	9.87583	12.2681	5.52259	ENSG00000184967	NOC4L
ENSG00000184979	2.10842	3.58623	2.57296	2.78068	ENSG00000184979	USP18
ENSG00000184983	6.85869	6.86074	6.16687	4.47528	ENSG00000184983	NDUFA6
ENSG00000184984	1.7135	3.37631	3.27995	5.039	ENSG00000184984	CHRM5
ENSG00000184985	3.0738	0.331003	3.1445	2.5703	ENSG00000184985	SORCS2
ENSG00000184986	0.647719	1.21463	0.66435	2.60377	ENSG00000184986	TMEM121
ENSG00000184988	3.56191	5.18578	3.56177	8.71368	ENSG00000184988	TMEM106A
ENSG00000184990	25.6965	38.167	22.3689	15.8502	ENSG00000184990	SIVA1
ENSG00000184992	14.0031	13.2257	6.07093	9.42926	ENSG00000184992	BRI3BP
ENSG00000184995	3.04341	7.19541	12.6473	17.65	ENSG00000184995	IFNE
ENSG00000184999	0.699358	0.711698	0.521051	0.757834	ENSG00000184999	SLC22A10
ENSG00000185000	19.912	25.2835	14.7983	16.8939	ENSG00000185000	DGAT1
ENSG00000185002	0.0945011	0.166959	0.109727	0.0864483	ENSG00000185002	RFX6

ENSG00000185008	1.16296	3.67051	2.1833	2.87935	ENSG00000185008	ROBO2
ENSG00000185009	14.9438	14.8253	16.3089	10.7885	ENSG00000185009	AP3M1
ENSG00000185010	0.436768	0.288924	0.845589	0.453418	ENSG00000185010	F8
ENSG00000185013	3.02904	2.99941	3.90447	4.45235	ENSG00000185013	NT5C1B
ENSG00000185015	4.73746	8.08921	6.62556	6.60823	ENSG00000185015	CA13
ENSG00000185019	3.84747	5.90034	5.47779	6.6967	ENSG00000185019	UBOX5
ENSG00000185020	1.10731	3.12135	1.09583	0.804113	ENSG00000185020	RP11-111G23.1
ENSG00000185022	22.5495	13.0214	7.16128	18.3505	ENSG00000185022	MAFF
ENSG00000185024	15.3102	21.2149	22.9085	22.1518	ENSG00000185024	BRF1
ENSG00000185028	0.0734987	0	0.128782	0.120578	ENSG00000185028	LRRC14B
ENSG00000185031	0	0.189401	0.103309	0.129	ENSG00000185031	SLC2A3P2
ENSG00000185033	41.5974	216.766	86.6291	98.011	ENSG00000185033	SEMA4B
ENSG00000185037	0	0.0375513	0	0	ENSG00000185037	ZNF733P
ENSG00000185038	0.009981	0.0506275	0.0261168	0.22959	ENSG00000185038	MROH2A
ENSG00000185040	0.212739	0.218391	0.115762	0.275397	ENSG00000185040	SPDYE16
ENSG00000185041	0.000585709	0	0	0.00075577	ENSG00000185041	RP11-321E2.6
ENSG00000185043	8.96825	22.812	9.97894	11.2118	ENSG00000185043	CIB1
ENSG00000185046	1.77778	3.12934	2.78727	4.20984	ENSG00000185046	ANKS1B
ENSG00000185049	21.105	24.037	23.6288	24.7306	ENSG00000185049	NELFA
ENSG00000185052	0.511824	0.481703	1.21646	0.856376	ENSG00000185052	SLC24A3
ENSG00000185053	0	0.174556	0.0439066	0.313812	ENSG00000185053	SGCZ
ENSG00000185055	1.40564	3.19566	4.75895	5.16367	ENSG00000185055	EFCAB10
ENSG00000185056	0.0999197	0.0212039	0.130415	0.096823	ENSG00000185056	C5orf47
ENSG00000185069	0	0	0.0578942	0	ENSG00000185069	KRT76
ENSG00000185070	73.8856	90.4715	103.275	105.624	ENSG00000185070	FLRT2
ENSG00000185074	0	0	0	0	ENSG00000185074	OR7E31P
ENSG00000185078	0	0.120834	0	0	ENSG00000185078	AC093698.1
ENSG00000185085	7.34358	5.78149	8.65547	4.58253	ENSG00000185085	INTS5
ENSG00000185087	1.24495	1.66416	1.84876	2.57556	ENSG00000185087	FAM169B
ENSG00000185088	63.7923	30.2101	31.6733	51.6123	ENSG00000185088	RPS27L
ENSG00000185090	1.45496	0.483374	0.440945	1.08851	ENSG00000185090	MANEAL
ENSG00000185097	0.124217	0.258945	0.132008	0.192383	ENSG00000185097	OR4F16
ENSG00000185100	4.99709	12.4703	12.2138	12.4668	ENSG00000185100	ADSSL1
ENSG00000185101	49.1563	57.5219	42.4562	26.7558	ENSG00000185101	ANO9
ENSG00000185104	17.2113	25.8443	25.1928	16.4964	ENSG00000185104	FAF1
ENSG00000185105	0.242665	0.0577476	0.309146	0.235434	ENSG00000185105	MYADML2
ENSG00000185112	8.60224	1.43997	2.24415	2.19831	ENSG00000185112	FAM43A
ENSG00000185115	11.3002	10.3882	11.2708	6.79375	ENSG00000185115	NSMCE3
ENSG00000185122	19.5931	26.4799	24.5292	21.1156	ENSG00000185122	HSF1
ENSG00000185127	13.7248	10.6058	10.2431	6.48265	ENSG00000185127	C6orf120
ENSG00000185128	12.0854	17.2787	22.3686	10.4563	ENSG00000185128	TBC1D3F
ENSG00000185129	38.8598	124.037	45.8085	32.1363	ENSG00000185129	PURA
ENSG00000185130	9.26137	41.7517	11.3718	9.55145	ENSG00000185130	HIST1H2BL
ENSG00000185133	1.21873	2.29323	2.7816	3.96948	ENSG00000185133	INPP5J
ENSG00000185149	0.0617656	0.134178	0.0807832	0.101952	ENSG00000185149	NPY2R
ENSG00000185155	0.488033	1.1422	0.871047	2.60046	ENSG00000185155	MIXL1
ENSG00000185156	0.275286	0.217107	0.19856	0.16488	ENSG00000185156	MFSD6L
ENSG00000185158	16.674	29.4744	35.8658	35.2495	ENSG00000185158	LRRC37B
ENSG00000185162	4.28534	8.34502	5.49237	11.6398	ENSG00000185162	AP001324.1
ENSG00000185163	9.2234	12.7932	15.1658	15.1826	ENSG00000185163	DDX51
ENSG00000185164	42.6634	67.3826	69.1123	59.025	ENSG00000185164	NOMO2
ENSG00000185176	0.109049	0.1402	0.110912	0.143537	ENSG00000185176	AQP12B
ENSG00000185177	0.0135725	0	0.0360173	0	ENSG00000185177	ZNF479
ENSG00000185182	0	0	0	0	ENSG00000185182	GOLGA8DP

ENSG00000185187	6.64358	16.4746	11.3057	13.8887	ENSG00000185187	SIGIRR
ENSG00000185189	18.0105	13.8419	24.9373	12.3168	ENSG00000185189	NRBP2
ENSG00000185198	0	0.054427	0.0983793	0	ENSG00000185198	PRSS57
ENSG00000185201	30.9435	78.556	24.9158	56.3975	ENSG00000185201	IFITM2
ENSG00000185215	14.9346	8.06576	10.4624	17.8554	ENSG00000185215	TNFAIP2
ENSG00000185219	4.93087	7.9045	8.38015	11.6775	ENSG00000185219	ZNF445
ENSG00000185220	8.46715	16.2455	14.2381	24.2117	ENSG00000185220	PGBD2
ENSG00000185221	0	0	0	0	ENSG00000185221	GAPDHP24
ENSG00000185222	31.0715	18.488	18.8358	28.6791	ENSG00000185222	TCEAL9
ENSG00000185231	0.270122	0.391034	0.413225	1.15888	ENSG00000185231	MC2R
ENSG00000185236	14.5864	22.3156	15.9756	20.126	ENSG00000185236	RAB11B
ENSG00000185238	12.025	18.9713	21.0929	14.9823	ENSG00000185238	PRMT3
ENSG00000185245	0.398702	0.854157	1.71836	0.862943	ENSG00000185245	GP1BA
ENSG00000185246	19.4273	22.1441	26.9785	23.6005	ENSG00000185246	PRPF39
ENSG00000185247	0.0403835	0.00784444	0.0720191	0.0558687	ENSG00000185247	MAGEA11
ENSG00000185250	1.23369	2.57752	2.95483	3.50076	ENSG00000185250	PPIL6
ENSG00000185252	4.88269	5.6151	6.11117	5.62238	ENSG00000185252	ZNF74
ENSG00000185254	0	0	0	0	ENSG00000185254	TEX28
ENSG00000185261	1.76845	4.20108	4.65582	5.04621	ENSG00000185261	KIAA0825
ENSG00000185262	23.8655	31.1866	11.8596	13.4462	ENSG00000185262	UBALD2
ENSG00000185264	0	0	0	0	ENSG00000185264	TEX33
ENSG00000185267	0.512484	0.995346	1.37962	1.09329	ENSG00000185267	CDNF
ENSG00000185269	0.111874	0.305259	0.206843	0.507472	ENSG00000185269	NOTUM
ENSG00000185271	0.0304491	0.0294688	0	0.0667885	ENSG00000185271	KLHL33
ENSG00000185272	0.5088	2.16599	0.540932	0.639713	ENSG00000185272	RBM11
ENSG00000185274	0.348502	0.61158	0.705419	1.13735	ENSG00000185274	GALNT17
ENSG00000185275	0.794028	2.18045	1.77694	0	ENSG00000185275	CD24P4
ENSG00000185278	3.19209	4.56429	3.75587	5.66448	ENSG00000185278	ZBTB37
ENSG00000185290	0.994777	1.66508	1.14629	0.798102	ENSG00000185290	NUPR2
ENSG00000185291	0.605375	1.6093	1.72274	1.07557	ENSG00000185291	IL3RA
ENSG00000185294	0.0256399	0	0.011168	0.0140709	ENSG00000185294	SPPL2C
ENSG00000185296	0.246464	0.473056	0.106795	0.935343	ENSG00000185296	AC026785.1
ENSG00000185298	16.2639	14.4719	19.1504	10.8702	ENSG00000185298	CCDC137
ENSG00000185303	0.0835983	0.0742127	0.0669987	0.397592	ENSG00000185303	SFTPA2
ENSG00000185304	0.898375	0.518489	3.92732	3.29532	ENSG00000185304	RGPD2
ENSG00000185305	9.69202	9.10716	10.1771	7.88498	ENSG00000185305	ARL15
ENSG00000185306	1.18892	1.12461	0.510493	0.920395	ENSG00000185306	C12orf56
ENSG00000185313	0.0556942	0.0799326	0.0795029	0.137085	ENSG00000185313	SCN10A
ENSG00000185319	0.20466	1.28459	0.39924	0.590279	ENSG00000185319	SSXP4
ENSG00000185324	46.217	97.7926	92.9524	79.3535	ENSG00000185324	CDK10
ENSG00000185332	10.713	15.5133	18.696	33.5084	ENSG00000185332	TMEM105
ENSG00000185338	2.82675	3.34571	1.74345	4.12312	ENSG00000185338	SOCS1
ENSG00000185339	3.04044	2.41927	1.73955	2.73735	ENSG00000185339	TCN2
ENSG00000185340	9.84356	13.4053	9.38011	8.8553	ENSG00000185340	GAS2L1
ENSG00000185344	23.8711	24.477	24.8874	19.481	ENSG00000185344	ATP6V0A2
ENSG00000185345	0.822181	0.62446	1.10507	1.72896	ENSG00000185345	PRKN
ENSG00000185347	2.92782	9.95851	3.45064	3.85475	ENSG00000185347	C14orf80
ENSG00000185352	0.138907	0.134686	0.0910191	0.15222	ENSG00000185352	HS6ST3
ENSG00000185359	111.758	111.307	109.487	100.53	ENSG00000185359	HGS
ENSG00000185361	4.63755	12.0105	5.87926	10.8229	ENSG00000185361	TNFAIP8L1
ENSG00000185372	0.0658136	0.094945	0.143002	0.250616	ENSG00000185372	OR2V1
ENSG00000185379	3.69923	5.80524	5.6988	7.65707	ENSG00000185379	RAD51D
ENSG00000185385	0	0.164506	0.351471	1.00753	ENSG00000185385	OR7A17

ENSG00000185386	3.56733	7.83418	14.3629	5.80188	ENSG00000185386	MAPK11
ENSG00000185390	0	0	0	0	ENSG00000185390	FGF7P2
ENSG00000185404	8.90953	16.1745	24.6477	23.7609	ENSG00000185404	SP140L
ENSG00000185414	2.68113	2.0107	1.55039	2.32428	ENSG00000185414	MRPL30
ENSG00000185418	20.3532	41.5623	31.2687	60.0856	ENSG00000185418	TARSL2
ENSG00000185420	7.56736	19.7781	10.4529	29.3893	ENSG00000185420	SMYD3
ENSG00000185432	1.27465	3.75702	2.58744	4.83967	ENSG00000185432	METTL7A
ENSG00000185436	9.73605	13.1205	12.678	6.45168	ENSG00000185436	IFNLR1
ENSG00000185437	3.54572	4.51512	3.65184	3.23861	ENSG00000185437	SH3BGR
ENSG00000185442	8.21011	15.9616	18.5055	33.9932	ENSG00000185442	FAM174B
ENSG00000185448	0	0	0.0186839	0	ENSG00000185448	FAM47A
ENSG00000185453	0.97347	2.75209	2.02967	2.03469	ENSG00000185453	C19orf68
ENSG00000185467	1.75839	0.478888	0.288604	0.653931	ENSG00000185467	KPNA7
ENSG00000185475	38.0193	30.3759	27.5831	10.1902	ENSG00000185475	TMEM179B
ENSG00000185477	0.235779	0.446114	0.374694	0.721038	ENSG00000185477	GPRIN3
ENSG00000185479	2180.79	150.27	486.196	300.703	ENSG00000185479	KRT6B
ENSG00000185480	4.72784	15.0198	7.26869	12.9665	ENSG00000185480	PARPBP
ENSG00000185482	1.67064	3.54205	5.31244	3.82753	ENSG00000185482	STAC3
ENSG00000185483	2.80535	2.76479	2.28512	3.97988	ENSG00000185483	ROR1
ENSG00000185485	34.2896	33.8839	44.0088	48.5071	ENSG00000185485	SDHAP1
ENSG00000185499	18.5252	8.40413	4.34531	6.62605	ENSG00000185499	MUC1
ENSG00000185504	15.3933	18.3565	21.5862	13.961	ENSG00000185504	FAAP100
ENSG00000185507	15.5173	33.9296	31.2953	24.87	ENSG00000185507	IRF7
ENSG00000185513	19.2141	27.2895	28.1529	26.2973	ENSG00000185513	L3MBTL1
ENSG00000185515	4.43629	5.69423	5.16923	8.01641	ENSG00000185515	BRCC3
ENSG00000185518	0.519977	1.38934	0.891536	1.24719	ENSG00000185518	SV2B
ENSG00000185519	1.10395	1.04868	1.17277	0.663034	ENSG00000185519	FAM131C
ENSG00000185522	4.91019	6.3433	4.8752	3.128	ENSG00000185522	LMNTD2
ENSG00000185523	0.597412	0.28636	0.77576	0.159728	ENSG00000185523	SPATA45
ENSG00000185527	0.385549	0.558937	1.00614	1.24138	ENSG00000185527	PDE6G
ENSG00000185532	0.363401	0.576974	0.76705	11.8202	ENSG00000185532	PRKG1
ENSG00000185551	18.414	8.2082	6.03229	18.4184	ENSG00000185551	NR2F2
ENSG00000185554	0.0161246	0.0143184	0.122351	0.0535702	ENSG00000185554	NXF2
ENSG00000185559	1.16221	0.354753	0.977003	1.26168	ENSG00000185559	DLK1
ENSG00000185561	1.93586	1.92139	4.02059	1.56301	ENSG00000185561	TLCD2
ENSG00000185565	3.15032	9.02892	7.53132	10.2143	ENSG00000185565	LSAMP
ENSG00000185567	290.166	263.02	222.251	187.939	ENSG00000185567	AHNAK2
ENSG00000185585	1.07007	5.98995	6.63208	17.513	ENSG00000185585	OLFML2A
ENSG00000185591	23.1908	23.1697	20.7227	14.7276	ENSG00000185591	SP1
ENSG00000185594	0	0	0	0	ENSG00000185594	SPATA8
ENSG00000185596	36.4861	38.5467	29.1164	24.5759	ENSG00000185596	WASH3P
ENSG00000185607	0.376623	0.362515	0.14854	1.42852	ENSG00000185607	ACTBP7
ENSG00000185608	13.4824	15.7209	15.3139	12.3715	ENSG00000185608	MRPL40
ENSG00000185610	0	0.0566842	0.102497	0.114378	ENSG00000185610	DBX2
ENSG00000185614	5.0092	8.0527	11.1882	3.28562	ENSG00000185614	FAM212A
ENSG00000185615	2.51124	1.98417	1.14723	1.45543	ENSG00000185615	PDIA2
ENSG00000185619	35.6116	34.2947	27.819	32.203	ENSG00000185619	PCGF3
ENSG00000185621	4.56849	7.47187	7.64481	7.40176	ENSG00000185621	LMLN
ENSG00000185624	461.864	602.024	331.329	312.636	ENSG00000185624	P4HB
ENSG00000185627	47.5669	42.3902	40.4295	36.2458	ENSG00000185627	PSMD13
ENSG00000185630	14.3902	32.5795	28.2308	60.9253	ENSG00000185630	PBX1
ENSG00000185631	0.201677	0.193062	0	0.427291	ENSG00000185631	AC017079.1
ENSG00000185633	4.8909	11.8097	12.4523	5.87236	ENSG00000185633	NDUFA4L2
ENSG00000185634	27.0842	57.824	51.8121	83.402	ENSG00000185634	SHC4

ENSG00000185638	0	0	0	0	ENSG00000185638	FTH1P14
ENSG00000185640	0.0862475	0.507389	0.307244	0.38783	ENSG00000185640	KRT79
ENSG00000185641	0	0.781305	0	0	ENSG00000185641	AC034236.1
ENSG00000185650	122.135	127.959	67.8623	132.156	ENSG00000185650	ZFP36L1
ENSG00000185651	43.2212	24.2361	17.4056	20.1426	ENSG00000185651	UBE2L3
ENSG00000185652	0.653363	0.218459	1.22906	0.625913	ENSG00000185652	NTF3
ENSG00000185658	34.6437	38.5761	41.0814	41.8644	ENSG00000185658	BRWD1
ENSG00000185662	0.167533	0.160495	0	0	ENSG00000185662	SMIM23
ENSG00000185664	24.8131	13.7091	10.7166	6.01055	ENSG00000185664	PMEL
ENSG00000185666	6.77767	17.7739	12.545	17.7849	ENSG00000185666	SYN3
ENSG00000185668	0.579687	1.70625	2.3419	1.24214	ENSG00000185668	POU3F1
ENSG00000185669	0.593763	0.667462	1.20999	2.53098	ENSG00000185669	SNAI3
ENSG00000185670	10.0732	11.3601	10.7779	9.37948	ENSG00000185670	ZBTB3
ENSG00000185674	0.671065	0.874501	0.450511	0.3138	ENSG00000185674	LYG2
ENSG00000185681	0.377392	0.686362	0.984178	0.981016	ENSG00000185681	MORN5
ENSG00000185684	4.30399	6.83384	9.6426	16.5852	ENSG00000185684	EP400NL
ENSG00000185686	0.0645768	0.0933361	0.199696	0.388286	ENSG00000185686	PRAME
ENSG00000185689	1.07667	3.18333	1.13932	1.59058	ENSG00000185689	C6orf201
ENSG00000185697	1.29988	3.04021	1.25156	5.91076	ENSG00000185697	MYBL1
ENSG00000185701	0	0	0	0	ENSG00000185701	OR5M5P
ENSG00000185710	22.5127	48.9144	32.5213	28.3123	ENSG00000185710	SMG1P4
ENSG00000185716	34.4307	25.2742	9.47868	18.0737	ENSG00000185716	C16orf52
ENSG00000185721	29.0584	23.5957	20.6498	17.1337	ENSG00000185721	DRG1
ENSG00000185722	20.911	43.0821	33.1013	48.525	ENSG00000185722	ANKFY1
ENSG00000185728	26.0703	33.0196	27.0075	40.3409	ENSG00000185728	YTHDF3
ENSG00000185730	8.80001	10.2148	9.96474	6.36466	ENSG00000185730	ZNF696
ENSG00000185736	0.447258	0.319767	0.304622	0.342345	ENSG00000185736	ADARB2
ENSG00000185737	0.12913	0.472415	0.387043	0.753196	ENSG00000185737	NRG3
ENSG00000185739	0.267708	0.551674	0.457404	0.785123	ENSG00000185739	SRL
ENSG00000185742	0.147442	0.149911	0.118868	0.311612	ENSG00000185742	C11orf87
ENSG00000185745	9.8696	14.5882	21.341	19.5292	ENSG00000185745	IFIT1
ENSG00000185751	0	0	0	0	ENSG00000185751	XAGE2
ENSG00000185753	8.7198	13.5652	9.04623	12.651	ENSG00000185753	CXorf38
ENSG00000185758	0.176364	0.351937	0.367209	0.721428	ENSG00000185758	CLDN24
ENSG00000185760	2.95132	12.349	6.53786	7.50292	ENSG00000185760	KCNQ5
ENSG00000185761	10.215	15.7622	12.715	12.1422	ENSG00000185761	ADAMTSL5
ENSG00000185774	1.03539	2.19269	2.95397	2.45827	ENSG00000185774	KCNIP4
ENSG00000185775	0	0	0	0	ENSG00000185775	SPATA31A6
ENSG00000185787	61.1313	58.5793	58.9962	106.526	ENSG00000185787	MORF4L1
ENSG00000185792	0.109811	0.180906	0.244826	0.188818	ENSG00000185792	NLRP9
ENSG00000185798	4.1666	4.89046	7.24474	5.46222	ENSG00000185798	WDR53
ENSG00000185800	33.9142	43.6019	46.8565	53.2604	ENSG00000185800	DMWD
ENSG00000185803	35.2741	33.3745	21.7124	16.788	ENSG00000185803	SLC52A2
ENSG00000185808	20.8155	7.97677	8.53784	6.82094	ENSG00000185808	PIGP
ENSG00000185811	0.147169	0.302541	0.243215	0.268706	ENSG00000185811	IKZF1
ENSG00000185813	24.4288	25.8446	14.9976	15.1053	ENSG00000185813	PCYT2
ENSG00000185818	0.182134	0.175727	0.288653	0.310244	ENSG00000185818	NAT8L
ENSG00000185821	0.0665741	0.128051	0	0.0724196	ENSG00000185821	OR6C76
ENSG00000185823	0.999707	1.90768	2.21406	3.15119	ENSG00000185823	NPAP1
ENSG00000185825	87.2938	86.0176	45.3177	30.1692	ENSG00000185825	BCAP31
ENSG00000185829	7.47236	12.4696	24.0395	11.8216	ENSG00000185829	ARL17A
ENSG00000185834	0	0.224991	0	0	ENSG00000185834	RPL12P4
ENSG00000185838	3.56287	6.85351	4.43188	4.67979	ENSG00000185838	GNB1L
ENSG00000185839	0.863182	1.31411	1.19651	1.46294	ENSG00000185839	AL035411.1

ENSG00000185842	15.0966	28.1113	32.5681	28.2254	ENSG00000185842	DNAH14
ENSG00000185860	2.67709	6.68137	6.98644	12.4355	ENSG00000185860	CCDC190
ENSG00000185862	1.04863	1.38219	1.20908	3.23298	ENSG00000185862	EVI2B
ENSG00000185863	0.643575	1.14099	0.837576	2.19485	ENSG00000185863	TMEM210
ENSG00000185864	89.5341	252.993	283.266	285.159	ENSG00000185864	NPIPB4
ENSG00000185869	5.19679	8.75412	9.79491	14.8272	ENSG00000185869	ZNF829
ENSG00000185873	7.85076	2.26589	2.17593	2.78618	ENSG00000185873	TMPRSS11B
ENSG00000185875	0.722898	2.55821	2.35048	1.95544	ENSG00000185875	THNSL1
ENSG00000185880	4.44538	10.2724	8.46971	11.8001	ENSG00000185880	TRIM69
ENSG00000185883	49.6213	31.3958	25.4896	21.194	ENSG00000185883	ATP6V0C
ENSG00000185885	43.4785	293.314	126.19	152.269	ENSG00000185885	IFITM1
ENSG00000185888	0.0468453	0	0.122308	0.153565	ENSG00000185888	PRSS38
ENSG00000185894	0.0864617	0.241535	0.0777448	0.344863	ENSG00000185894	BPY2C
ENSG00000185896	149.172	136.281	140.528	69.9675	ENSG00000185896	LAMP1
ENSG00000185897	0	0	0	0.00542596	ENSG00000185897	FFAR3
ENSG00000185899	0	0.688426	0.395901	0.920498	ENSG00000185899	TAS2R60
ENSG00000185900	29.5649	36.6474	23.8638	19.7034	ENSG00000185900	POMK
ENSG00000185903	0.0748064	0	0	0.324931	ENSG00000185903	AL590806.1
ENSG00000185905	1.21926	1.97772	1.99025	4.31266	ENSG00000185905	C16orf54
ENSG00000185909	21.1318	13.1927	26.4459	8.56291	ENSG00000185909	KLHDC8B
ENSG00000185915	0	0.111931	0.0337602	0.0638172	ENSG00000185915	KLHL34
ENSG00000185917	15.5285	21.5774	22.8878	16.8881	ENSG00000185917	SETD4
ENSG00000185920	3.69607	8.47812	6.09324	8.13406	ENSG00000185920	PTCH1
ENSG00000185924	0.897873	1.90472	0.718342	1.55141	ENSG00000185924	RTN4RL1
ENSG00000185926	0	0	0	0	ENSG00000185926	OR4C46
ENSG00000185928	3.94565	5.42521	4.93674	5.09243	ENSG00000185928	PAGR1
ENSG00000185933	0.269241	0.556407	0.707943	0.72187	ENSG00000185933	CALHM1
ENSG00000185940	0	0	0	0	ENSG00000185940	KRTAP5-5
ENSG00000185942	0.785017	1.34323	1.46377	3.13201	ENSG00000185942	NKAIN3
ENSG00000185945	0.00681164	0.00623529	0.0123619	0.0254563	ENSG00000185945	NXF2B
ENSG00000185946	11.4728	15.6425	21.7396	15.7105	ENSG00000185946	RNPC3
ENSG00000185947	20.0335	22.2061	15.8703	22.4735	ENSG00000185947	ZNF267
ENSG00000185950	4.75048	6.0495	9.00377	7.23812	ENSG00000185950	IRS2
ENSG00000185955	1.68551	1.21214	0.878638	1.32646	ENSG00000185955	C7orf61
ENSG00000185958	1.33887	2.18982	2.11703	3.3092	ENSG00000185958	FAM186A
ENSG00000185960	2.15521	4.95373	4.66042	7.7527	ENSG00000185960	SHOX
ENSG00000185962	0	1.61327	0	5.6031	ENSG00000185962	LCE3A
ENSG00000185963	75.6535	39.7	44.8292	29.1699	ENSG00000185963	BICD2
ENSG00000185966	12.996	2.23541	2.46113	16.0937	ENSG00000185966	LCE3E
ENSG00000185972	0.0582309	0	0	0.255529	ENSG00000185972	CCIN
ENSG00000185973	2.93119	4.73217	4.50395	4.39313	ENSG00000185973	TMLHE
ENSG00000185974	0.0706309	0.0765838	0.010933	0.082802	ENSG00000185974	GRK1
ENSG00000185978	0	0.0462886	0.0208964	0.103325	ENSG00000185978	H2AFB3
ENSG00000185982	0	0	0	0	ENSG00000185982	DEFB128
ENSG00000185985	0.115522	0.245276	0.265857	0.39995	ENSG00000185985	SLITRK2
ENSG00000185986	7.63683	10.9215	18.5713	13.6601	ENSG00000185986	SDHAP3
ENSG00000185988	0.321715	0.202164	0.0764406	0.642328	ENSG00000185988	PLK5
ENSG00000185989	2.51899	4.10157	2.70268	17.2711	ENSG00000185989	RASA3
ENSG00000185990	0	0	0.580008	0.104487	ENSG00000185990	F8A3
ENSG00000186001	25.2774	47.3752	40.1158	62.7243	ENSG00000186001	LRCH3
ENSG00000186007	9.98478	4.53321	2.32603	1.70848	ENSG00000186007	LEMD1
ENSG00000186008	0	0	0	0	ENSG00000186008	RPS4XP21
ENSG00000186009	0.0390485	0.112839	0.0339996	0.128229	ENSG00000186009	ATP4B
ENSG00000186010	109.584	72.5485	61.1499	48.3713	ENSG00000186010	NDUFA13

ENSG00000186017	5.53024	5.4912	5.95627	8.05875	ENSG00000186017	ZNF566
ENSG00000186020	14.387	25.2095	26.7319	36.7961	ENSG00000186020	ZNF529
ENSG00000186026	3.84885	4.96884	4.98331	7.24728	ENSG00000186026	ZNF284
ENSG00000186038	0.0262022	0.0512014	0.159823	0.230111	ENSG00000186038	HTR3E
ENSG00000186047	0.264296	0.277966	0.607609	0.502685	ENSG00000186047	DLEU7
ENSG00000186049	0.0447829	0.0276103	0.0453913	0.149005	ENSG00000186049	KRT73
ENSG00000186051	0	0	0	0	ENSG00000186051	TAL2
ENSG00000186063	9.82286	15.695	11.0359	18.931	ENSG00000186063	AIDA
ENSG00000186073	10.807	21.2092	19.158	20.7269	ENSG00000186073	C15orf41
ENSG00000186074	0.186265	0.743653	0.630936	0.707679	ENSG00000186074	CD300LF
ENSG00000186075	1.50291	3.35891	3.20321	5.92771	ENSG00000186075	ZPBP2
ENSG00000186076	0	0	0	0	ENSG00000186076	AC012085.1
ENSG00000186081	5705.47	5217.17	4343.66	2410.74	ENSG00000186081	KRT5
ENSG00000186082	0	0.0919563	0	0.1053	ENSG00000186082	KRT18P14
ENSG00000186086	0.104862	0.0697455	0.165549	0.316756	ENSG00000186086	NBPF6
ENSG00000186088	17.5149	20.4257	20.83	17.615	ENSG00000186088	GSAP
ENSG00000186090	0	0	0	0.0640066	ENSG00000186090	HTR3D
ENSG00000186092	0	0	0	0	ENSG00000186092	OR4F5
ENSG00000186094	0.352463	0.603469	0.893532	1.1789	ENSG00000186094	AGBL4
ENSG00000186103	0.0693066	0.596054	0.133342	0.40688	ENSG00000186103	ARGFX
ENSG00000186104	5.35415	9.17873	11.8382	3.63456	ENSG00000186104	CYP2R1
ENSG00000186105	0.241724	0.778023	0.640725	0.910447	ENSG00000186105	LRRC70
ENSG00000186106	7.03353	7.60144	11.457	13.956	ENSG00000186106	ANKRD46
ENSG00000186111	8.23265	6.97474	10.0206	15.7714	ENSG00000186111	PIP5K1C
ENSG00000186113	0	0.0635378	0	0.0718742	ENSG00000186113	OR5D14
ENSG00000186115	0.851988	0.477068	0.661413	0.721827	ENSG00000186115	CYP4F2
ENSG00000186117	0	0.307309	0	0	ENSG00000186117	OR5L1
ENSG00000186118	0.217097	0.511448	0.427941	1.09773	ENSG00000186118	TEX38
ENSG00000186119	0.322174	0.927928	0.291883	0.711824	ENSG00000186119	OR5D18
ENSG00000186124	0	0	0.0592158	0.0740994	ENSG00000186124	OR9M1P
ENSG00000186130	5.44641	4.27986	5.38828	3.36275	ENSG00000186130	ZBTB6
ENSG00000186132	3.78791	5.21537	5.50236	5.68432	ENSG00000186132	C2orf76
ENSG00000186136	0.0660652	0.317689	0.287063	0.215623	ENSG00000186136	TAS2R42
ENSG00000186141	12.5568	13.8395	13.5122	13.4901	ENSG00000186141	POLR3C
ENSG00000186143	0	0	0	0	ENSG00000186143	PRR30
ENSG00000186146	0	0	0	0	ENSG00000186146	DEFB131A
ENSG00000186150	0.03852	0.222336	0.100489	0	ENSG00000186150	UBL4B
ENSG00000186152	0	0	0	0	ENSG00000186152	LILRP1
ENSG00000186153	14.4363	31.4594	27.4503	35.2554	ENSG00000186153	WWOX
ENSG00000186160	0.412493	1.15741	0.709286	1.20737	ENSG00000186160	CYP4Z1
ENSG00000186162	8.64547	10.0527	12.919	11.9763	ENSG00000186162	CIDECP
ENSG00000186163	0	0	0	0.0453801	ENSG00000186163	TRY2P
ENSG00000186166	10.5878	13.5382	14.1643	17.1859	ENSG00000186166	CCDC84
ENSG00000186174	58.3111	52.5516	69.5185	54.8171	ENSG00000186174	BCL9L
ENSG00000186184	58.8547	57.0706	42.3048	30.8603	ENSG00000186184	POLR1D
ENSG00000186185	2.54626	12.155	2.13102	9.14669	ENSG00000186185	KIF18B
ENSG00000186187	26.9771	20.9047	18.6241	22.8473	ENSG00000186187	ZNRF1
ENSG00000186188	0.69802	1.29105	0.672053	1.70678	ENSG00000186188	FFAR4
ENSG00000186190	0.0400746	0	0.104889	0	ENSG00000186190	BPIFB3
ENSG00000186191	0.131322	0.503976	0.113753	0.845597	ENSG00000186191	BPIFB4
ENSG00000186193	1.91458	7.83593	1.92085	1.71459	ENSG00000186193	SAPCD2
ENSG00000186197	0.519894	2.56884	3.44791	2.1196	ENSG00000186197	EDARADD
ENSG00000186198	0.197737	0.0744618	0.259082	0.159582	ENSG00000186198	SLC51B
ENSG00000186204	12.319	4.05248	1.93913	3.51144	ENSG00000186204	CYP4F12

ENSG00000186205	1.26503	3.45678	0.79247	1.67865	ENSG00000186205	MARC1
ENSG00000186207	0	0.0756875	0.137363	0.35593	ENSG00000186207	LCE5A
ENSG00000186212	4.32249	0.308451	1.85004	0.351066	ENSG00000186212	SOWAHB
ENSG00000186222	6.76917	5.31971	6.68887	4.00372	ENSG00000186222	BLOC1S4
ENSG00000186223	0	0	0	0	ENSG00000186223	SSU72P4
ENSG00000186226	0.46253	0.587327	0.49213	1.34977	ENSG00000186226	LCE1E
ENSG00000186230	5.78708	8.73387	6.95961	6.23507	ENSG00000186230	ZNF749
ENSG00000186231	0.0899383	0.434129	0.182245	0.409666	ENSG00000186231	KLHL32
ENSG00000186232	0	0	0	0	ENSG00000186232	SSU72P3
ENSG00000186234	1.19162	2.04942	2.21678	2.23374	ENSG00000186234	FAM86MP
ENSG00000186235	0.494016	1.20411	1.07097	2.58456	ENSG00000186235	AC016757.1
ENSG00000186244	0	0.544402	0	0.599519	ENSG00000186244	AC091180.1
ENSG00000186260	14.381	23.8484	24.2955	30.1996	ENSG00000186260	MKL2
ENSG00000186265	0.169303	0.267296	0.188397	0.466445	ENSG00000186265	BTLA
ENSG00000186268	0	0.0630574	0	0	ENSG00000186268	OR10D4P
ENSG00000186272	4.20737	5.12007	7.38812	4.44474	ENSG00000186272	ZNF17
ENSG00000186275	63.405	72.5756	106.118	149.371	ENSG00000186275	NBPF12
ENSG00000186280	0.0117292	0.01691	0.865654	0.014409	ENSG00000186280	KDM4D
ENSG00000186281	0.35538	2.6365	0.347394	0.822044	ENSG00000186281	GPAT2
ENSG00000186283	20.2582	26.6716	28.8568	25.6968	ENSG00000186283	TOR3A
ENSG00000186288	0.049494	0.178033	0.103193	0.419403	ENSG00000186288	PABPC1L2A
ENSG00000186297	0	0	0	0.271507	ENSG00000186297	GABRA5
ENSG00000186298	46.3399	36.1754	30.166	29.0613	ENSG00000186298	PPP1CC
ENSG00000186300	4.15154	3.35243	2.97434	3.5907	ENSG00000186300	ZNF555
ENSG00000186301	1.77314	2.11475	3.2991	1.66182	ENSG00000186301	MST1P2
ENSG00000186306	0	0	0	0	ENSG00000186306	OR10T2
ENSG00000186310	0.194927	0.147974	0.191278	0.505763	ENSG00000186310	NAP1L3
ENSG00000186312	12.6993	12.0882	17.0873	18.1229	ENSG00000186312	CA5BP1
ENSG00000186314	9.81021	19.4788	13.8513	15.4472	ENSG00000186314	PRELID2
ENSG00000186318	10.3065	14.6435	18.0061	18.8278	ENSG00000186318	BACE1
ENSG00000186322	0	0	0.32863	0.130888	ENSG00000186322	GOLGA6L17P
ENSG00000186326	0.340684	0.110234	0.134575	0.357229	ENSG00000186326	RGS9BP
ENSG00000186328	0.597792	0.283962	0	0.31241	ENSG00000186328	AL451165.1
ENSG00000186329	23.027	55.4064	55.0448	133.38	ENSG00000186329	TMEM212
ENSG00000186334	0.427038	1.13892	1.10232	1.35781	ENSG00000186334	SLC36A3
ENSG00000186335	1.59726	3.72322	3.51226	6.15607	ENSG00000186335	SLC36A2
ENSG00000186340	93.2475	179.403	257.257	200.746	ENSG00000186340	THBS2
ENSG00000186350	9.52417	9.17476	16.9612	6.65343	ENSG00000186350	RXRA
ENSG00000186352	4.54119	4.96678	4.50597	3.96882	ENSG00000186352	ANKRD37
ENSG00000186354	0.331998	0.313793	0.247544	0.902717	ENSG00000186354	C9orf47
ENSG00000186364	0	0	0	0	ENSG00000186364	NUDT17
ENSG00000186367	0.745075	1.37013	1.62722	3.34957	ENSG00000186367	KIAA1024L
ENSG00000186376	1.76473	2.60636	2.77675	2.66002	ENSG00000186376	ZNF75D
ENSG00000186377	0.143905	0.250272	0.209738	0.307077	ENSG00000186377	CYP4X1
ENSG00000186393	0.102311	0.263682	0.218679	0.40992	ENSG00000186393	KRT26
ENSG00000186395	2.0594	1.67095	8.1858	1.59043	ENSG00000186395	KRT10
ENSG00000186399	0.760975	1.39117	1.93209	0.897712	ENSG00000186399	GOLGA8R
ENSG00000186400	0	0	0	0	ENSG00000186400	OR10X1
ENSG00000186407	1.92026	3.75917	2.99095	5.97738	ENSG00000186407	CD300E
ENSG00000186409	7.47598	16.6058	15.8867	24.6075	ENSG00000186409	CCDC30
ENSG00000186416	4.37711	5.49521	5.66578	5.01812	ENSG00000186416	NKRF
ENSG00000186417	1.48713	2.85923	2.95468	3.56449	ENSG00000186417	GLDN
ENSG00000186431	0.508036	0.828791	1.10703	2.11598	ENSG00000186431	FCAR
ENSG00000186432	35.5705	28.496	30.0897	26.1395	ENSG00000186432	KPNA4

ENSG00000186439	0.598746	1.49961	1.59904	1.49086	ENSG00000186439	TRDN
ENSG00000186440	0	0	0	0	ENSG00000186440	OR6P1
ENSG00000186442	0.0723135	0.0539313	0.0210165	0.0264804	ENSG00000186442	KRT3
ENSG00000186446	4.68388	5.77223	6.70631	3.61188	ENSG00000186446	ZNF501
ENSG00000186448	9.78752	15.7465	14.9941	19.3719	ENSG00000186448	ZNF197
ENSG00000186451	0.391261	0.617098	0.417156	0.693523	ENSG00000186451	SPATA12
ENSG00000186452	1.05092	2.07063	2.13769	3.64014	ENSG00000186452	TMPRSS12
ENSG00000186453	0.183058	0.879639	0.754359	0.854598	ENSG00000186453	FAM228A
ENSG00000186458	0.24372	0.726556	0.587854	0.611455	ENSG00000186458	DEFB132
ENSG00000186462	1.34515	1.0284	0.661861	0.500665	ENSG00000186462	NAP1L2
ENSG00000186466	0.128042	0.204307	1.95026	0.795646	ENSG00000186466	AQP7P1
ENSG00000186468	567.808	509.594	474.176	234.094	ENSG00000186468	RPS23
ENSG00000186469	2.28901	4.25194	3.61027	7.76123	ENSG00000186469	GNG2
ENSG00000186470	5.09454	2.1878	6.2871	12.5158	ENSG00000186470	BTN3A2
ENSG00000186471	0.225137	0	0	0.759122	ENSG00000186471	AKAP14
ENSG00000186472	1.87527	5.7228	5.89648	5.53358	ENSG00000186472	PCLO
ENSG00000186474	2.67886	1.64077	0.868306	2.33316	ENSG00000186474	KLK12
ENSG00000186479	0.0259376	0.154744	0.125343	0.205561	ENSG00000186479	RGS7BP
ENSG00000186480	102.095	82.2147	8.64492	84.4599	ENSG00000186480	INSIG1
ENSG00000186481	0.838481	2.73545	1.63797	3.62013	ENSG00000186481	ANKRD20A5P
ENSG00000186487	1.076	2.52737	2.12942	4.445	ENSG00000186487	MYT1L
ENSG00000186493	3.90121	6.06348	9.3583	6.178	ENSG00000186493	C5orf38
ENSG00000186496	9.36291	10.2867	9.69191	16.9268	ENSG00000186496	ZNF396
ENSG00000186501	23.6824	12.8427	14.7851	10.5324	ENSG00000186501	TMEM222
ENSG00000186508	0.348967	0.268468	0.121289	0.303467	ENSG00000186508	OR9I2P
ENSG00000186509	0.246249	0.479585	0.459922	0.782273	ENSG00000186509	OR9Q1
ENSG00000186510	0.610305	0.847557	0.343076	1.75216	ENSG00000186510	CLCNKA
ENSG00000186513	0.0718373	0.0539575	0.0981124	0.305681	ENSG00000186513	OR9Q2
ENSG00000186517	3.0895	1.6135	2.07595	3.3365	ENSG00000186517	ARHGAP30
ENSG00000186522	21.6375	36.1257	25.4417	37.7839	ENSG00000186522	SEPT10
ENSG00000186523	7.48344	18.2904	28.2307	11.3581	ENSG00000186523	FAM86B1
ENSG00000186529	21.9016	6.77727	3.54979	7.43339	ENSG00000186529	CYP4F3
ENSG00000186532	9.94066	16.2113	14.6556	23.0466	ENSG00000186532	SMYD4
ENSG00000186543	1.00891	1.34575	0.913629	1.15805	ENSG00000186543	CROCCP5
ENSG00000186562	0	0	0	0	ENSG00000186562	DEFB105A
ENSG00000186564	0.646866	0.992275	0.701234	0.915549	ENSG00000186564	FOXD2
ENSG00000186566	20.2274	25.0125	23.8818	37.7922	ENSG00000186566	GPATCH8
ENSG00000186567	8.42891	8.19721	16.6936	10.4238	ENSG00000186567	CEACAM19
ENSG00000186572	0	0	0	0	ENSG00000186572	DEFB107A
ENSG00000186575	36.0045	23.1094	19.6663	30.4873	ENSG00000186575	NF2
ENSG00000186577	18.3624	25.6453	7.48775	12.756	ENSG00000186577	SMIM29
ENSG00000186579	0	0	0	0	ENSG00000186579	DEFB106A
ENSG00000186583	0.0158578	0.0696402	0.163712	0.0347734	ENSG00000186583	SPATC1
ENSG00000186591	67.6835	50.1442	70.4774	63.2913	ENSG00000186591	UBE2H
ENSG00000186599	0	0	0	0	ENSG00000186599	DEFB105B
ENSG00000186603	0.599663	0.881961	0.471311	0.915069	ENSG00000186603	HPDL
ENSG00000186625	12.5319	17.1559	14.3165	10.7036	ENSG00000186625	KATNA1
ENSG00000186628	1.23889	2.16364	2.61178	2.08558	ENSG00000186628	FSD2
ENSG00000186635	32.7262	64.0046	53.9081	41.8551	ENSG00000186635	ARAP1
ENSG00000186638	1.11108	3.25007	1.53826	1.82357	ENSG00000186638	KIF24
ENSG00000186642	3.88873	9.78451	7.47878	8.37831	ENSG00000186642	PDE2A
ENSG00000186645	0.351059	1.40658	1.81944	2.28394	ENSG00000186645	SPDYE17
ENSG00000186648	0.121946	0.454874	0.783129	0.583179	ENSG00000186648	CARMIL3
ENSG00000186652	0.123078	0.374713	0.223632	0.382204	ENSG00000186652	PRG2

ENSG00000186654	14.4194	15.539	17.9404	19.8506	ENSG00000186654	PRR5
ENSG00000186660	20.3746	19.4708	21.6987	19.0706	ENSG00000186660	ZFP91
ENSG00000186665	1.32275	1.51197	1.23361	1.55384	ENSG00000186665	C17orf58
ENSG00000186666	3.58444	4.41126	4.35653	3.39314	ENSG00000186666	BCDIN3D
ENSG00000186675	0.0247276	0	0	0.16902	ENSG00000186675	MAGEE2
ENSG00000186676	0.123582	0.222492	0.0402052	0.101291	ENSG00000186676	EEF1GP1
ENSG00000186678	0	0	0	0	ENSG00000186678	AL590240.1
ENSG00000186684	5.30969	5.41294	5.88104	9.47378	ENSG00000186684	CYP27C1
ENSG00000186687	7.02433	6.69383	10.3713	15.3069	ENSG00000186687	LYRM7
ENSG00000186704	4.09875	11.9663	15.7456	11.1347	ENSG00000186704	DTX2P1
ENSG00000186710	0.464587	0.491995	0.644542	1.07708	ENSG00000186710	CFAP73
ENSG00000186714	0.375967	1.12538	1.90373	2.86251	ENSG00000186714	CCDC73
ENSG00000186715	1.54486	3.4071	5.63634	2.13756	ENSG00000186715	MST1L
ENSG00000186716	31.0165	51.8182	55.0776	49.5352	ENSG00000186716	BCR
ENSG00000186723	0.0540198	0.0720033	0.068833	0	ENSG00000186723	OR10H1
ENSG00000186732	0.16148	0.229608	0.319954	0.26158	ENSG00000186732	MPPED1
ENSG00000186743	0.715442	1.20306	0.620945	0.774836	ENSG00000186743	TPI1P3
ENSG00000186765	0.480562	0.252654	0.33535	0.386047	ENSG00000186765	FSCN2
ENSG00000186766	0.325468	0.465532	0.184611	0.549983	ENSG00000186766	FOXI2
ENSG00000186767	1.3175	1.26968	1.01164	1.37033	ENSG00000186767	SPIN4
ENSG00000186777	0.483555	1.72463	0.490668	1.15399	ENSG00000186777	ZNF732
ENSG00000186787	3.90627	5.11576	6.76239	6.53405	ENSG00000186787	SPIN2B
ENSG00000186788	0	0	0	0	ENSG00000186788	SPATA31D3
ENSG00000186790	0.303085	0.392616	0.506139	0.484877	ENSG00000186790	FOXE3
ENSG00000186792	2.8669	2.96807	1.99521	0.835417	ENSG00000186792	HYAL3
ENSG00000186795	0.0521193	0.509092	0.453716	0.228196	ENSG00000186795	KCNK18
ENSG00000186803	0.193752	0	0.735478	1.28697	ENSG00000186803	IFNA10
ENSG00000186806	3.68228	2.68742	2.37385	2.59894	ENSG00000186806	VSIG10L
ENSG00000186807	109.226	31.8376	79.557	22.4559	ENSG00000186807	ANXA8L2
ENSG00000186810	0.158941	0.163702	0.556645	0.289938	ENSG00000186810	CXCR3
ENSG00000186812	9.15623	18.0004	17.5834	29.3207	ENSG00000186812	ZNF397
ENSG00000186814	16.1502	27.5115	33.9543	51.2706	ENSG00000186814	ZSCAN30
ENSG00000186815	21.7264	36.6425	32.6483	90.5612	ENSG00000186815	TPCN1
ENSG00000186818	0.745233	1.657	1.50797	2.75599	ENSG00000186818	LILRB4
ENSG00000186825	0.0517299	0	0.135447	0.0541444	ENSG00000186825	C2orf27B
ENSG00000186827	0.03352	0.265179	0.189682	0.232392	ENSG00000186827	TNFRSF4
ENSG00000186831	17.8455	18.358	89.709	6.56446	ENSG00000186831	KRT17P2
ENSG00000186832	1871.71	524.433	749.311	449.521	ENSG00000186832	KRT16
ENSG00000186834	5.49533	6.43793	7.35933	8.80818	ENSG00000186834	HEXIM1
ENSG00000186838	2.46451	2.85228	4.37798	1.34993	ENSG00000186838	SELENOV
ENSG00000186844	1.6051	0.427625	0.579305	7.37724	ENSG00000186844	LCE1A
ENSG00000186847	6135.15	6465.98	2440.37	3079.68	ENSG00000186847	KRT14
ENSG00000186854	7.09014	16.4237	14.2704	20.0501	ENSG00000186854	TRABD2A
ENSG00000186860	0	0	0	0	ENSG00000186860	KRTAP17-1
ENSG00000186862	3.3958	6.84612	6.0036	9.85291	ENSG00000186862	PDZD7
ENSG00000186866	20.7314	26.9503	23.8537	31.0702	ENSG00000186866	POFUT2
ENSG00000186867	0.0491547	0.157434	0.640194	0.183567	ENSG00000186867	QRFPR
ENSG00000186868	0.949078	1.77549	1.26105	2.07535	ENSG00000186868	MAPT
ENSG00000186871	1.45106	4.90853	0.97185	2.76774	ENSG00000186871	ERCC6L
ENSG00000186881	0	0.160488	0.0966975	0.30363	ENSG00000186881	OR13F1
ENSG00000186886	0	0.12404	0.336643	0.141949	ENSG00000186886	AP006437.1
ENSG00000186889	4.54293	6.85248	4.10038	6.42355	ENSG00000186889	TMEM17
ENSG00000186891	1.04583	2.30761	0.968137	0.40732	ENSG00000186891	TNFRSF18
ENSG00000186895	0.0354633	0	0	0.0384906	ENSG00000186895	FGF3

ENSG00000186897	0.0544402	0.10494	0	0.119498	ENSG00000186897	C1QL4
ENSG00000186907	0.0507626	0.566573	0.132825	1.56922	ENSG00000186907	RTN4RL2
ENSG00000186908	21.3024	29.506	20.2906	25.363	ENSG00000186908	ZDHHC17
ENSG00000186910	0.0394046	0.0759109	0.0343089	0	ENSG00000186910	SERPINA11
ENSG00000186912	0.105184	0.168896	0.305352	0.691432	ENSG00000186912	P2RY4
ENSG00000186918	14.8583	35.8726	22.2807	24.9976	ENSG00000186918	ZNF395
ENSG00000186919	1.39151	2.77146	4.94855	5.49774	ENSG00000186919	ZACN
ENSG00000186924	0	0	0	0	ENSG00000186924	KRTAP22-1
ENSG00000186925	0	0	0	0.321831	ENSG00000186925	KRTAP19-6
ENSG00000186930	0	0	0	0	ENSG00000186930	KRTAP6-2
ENSG00000186940	0.177418	0.169638	0.167803	0.48007	ENSG00000186940	CHCHD2P9
ENSG00000186943	0	0	0.112273	0.070286	ENSG00000186943	OR13C8
ENSG00000186951	13.5132	16.1717	14.0451	19.8847	ENSG00000186951	PPARA
ENSG00000186952	1.83047	3.96217	4.51392	5.12049	ENSG00000186952	TMEM232
ENSG00000186960	3.06184	9.62651	9.50166	25.1284	ENSG00000186960	LINC01551
ENSG00000186965	0.905629	1.49006	1.38912	2.38648	ENSG00000186965	KRTAP19-2
ENSG00000186967	0	0	0	0	ENSG00000186967	KRTAP19-4
ENSG00000186970	0.328792	0.157512	0.426555	0.175313	ENSG00000186970	KRTAP15-1
ENSG00000186971	0	0	0	0	ENSG00000186971	KRTAP13-4
ENSG00000186973	2.39661	4.52524	2.14007	3.38779	ENSG00000186973	FAM183A
ENSG00000186976	2.60114	4.81137	5.54569	6.51375	ENSG00000186976	EFCAB6
ENSG00000186977	0	0	0	0	ENSG00000186977	KRTAP19-5
ENSG00000186980	0	0	0	0	ENSG00000186980	KRTAP23-1
ENSG00000186994	1.64716	1.62089	1.06304	1.137	ENSG00000186994	KANK3
ENSG00000186998	0.849967	2.0206	1.21785	2.75171	ENSG00000186998	EMID1
ENSG00000187003	0.122207	0.196176	0.106395	0.267439	ENSG00000187003	ACTL7A
ENSG00000187005	0.334453	0	0	0	ENSG00000187005	KRTAP21-1
ENSG00000187010	1.23059	3.85527	3.41643	4.21448	ENSG00000187010	RHD
ENSG00000187013	0.264959	0.218772	0.065919	0.207218	ENSG00000187013	C17orf82
ENSG00000187017	14.0072	12.367	11.5871	4.52525	ENSG00000187017	ESPN
ENSG00000187021	1.41499	4.06549	3.71493	6.15602	ENSG00000187021	PNLIPRP1
ENSG00000187024	12.8688	14.0425	13.5245	16.9468	ENSG00000187024	PTRH1
ENSG00000187026	0	0	0	0	ENSG00000187026	KRTAP21-2
ENSG00000187033	0.176059	0.190927	0.150915	0.395639	ENSG00000187033	SAMD7
ENSG00000187037	3.87202	6.07528	7.01171	13.2979	ENSG00000187037	GPR141
ENSG00000187045	0.120268	0.400008	0.268788	0.341516	ENSG00000187045	TMPRSS6
ENSG00000187048	1.11026	1.16435	1.48254	0.655525	ENSG00000187048	CYP4A11
ENSG00000187049	4.07027	5.63319	5.09982	4.48808	ENSG00000187049	TMEM216
ENSG00000187051	40.1977	29.3108	27.6386	17.4638	ENSG00000187051	RPS19BP1
ENSG00000187054	0.24465	0.219108	0.185281	0.411832	ENSG00000187054	TMPRSS11A
ENSG00000187060	0	1.38778	0.833605	0	ENSG00000187060	RP11-187C18.3
ENSG00000187066	1.40021	2.44553	1.57952	1.32908	ENSG00000187066	TMEM262
ENSG00000187068	0.440258	0.535837	0.519476	1.20686	ENSG00000187068	C3orf70
ENSG00000187079	34.4283	33.9186	23.8461	54.0452	ENSG00000187079	TEAD1
ENSG00000187080	0.0547615	0	0	0.238932	ENSG00000187080	OR2AK2
ENSG00000187082	0	0	0	0	ENSG00000187082	DEFB106B
ENSG00000187091	57.8957	39.4763	30.6529	18.458	ENSG00000187091	PLCD1
ENSG00000187094	0.712057	0.687337	0.779553	0.678845	ENSG00000187094	CCK
ENSG00000187097	10.1795	17.4052	15.1054	20.2351	ENSG00000187097	ENTPD5
ENSG00000187098	15.5387	17.7883	19.4777	35.0392	ENSG00000187098	MITF
ENSG00000187103	0.138628	0.133028	0.240135	0	ENSG00000187103	FUNDC2P3
ENSG00000187105	3.53086	6.9559	8.04738	12.1589	ENSG00000187105	HEATR4
ENSG00000187109	86.9373	122.575	123.756	162.964	ENSG00000187109	NAP1L1
ENSG00000187116	0.243694	0.525942	0.442282	0.881757	ENSG00000187116	LILRA5

ENSG00000187118	10.2635	15.3649	13.5095	20.0073	ENSG00000187118	CMC1
ENSG00000187122	0.183744	0.684253	1.78073	3.42888	ENSG00000187122	SLIT1
ENSG00000187123	2.33279	3.01807	1.6104	3.51934	ENSG00000187123	LYPD6
ENSG00000187134	5.4914	12.9289	7.95818	5.46488	ENSG00000187134	AKR1C1
ENSG00000187135	0.156403	0.263292	0.136672	0.342506	ENSG00000187135	VSTM2B
ENSG00000187140	0.0543546	0.105323	0.239105	0.509882	ENSG00000187140	FOXD3
ENSG00000187144	1.39848	2.16107	2.08919	3.99196	ENSG00000187144	SPATA21
ENSG00000187145	22.2286	29.229	25.4387	25.1692	ENSG00000187145	MRPS21
ENSG00000187147	34.6916	36.9618	35.2247	36.3382	ENSG00000187147	RNF220
ENSG00000187151	0.0704533	0.226388	0.0823337	0.154777	ENSG00000187151	ANGPTL5
ENSG00000187164	6.19283	12.9087	14.1559	12.8435	ENSG00000187164	SHTN1
ENSG00000187166	0	0	0	0	ENSG00000187166	H1FNT
ENSG00000187170	0.224576	0	0.193664	0	ENSG00000187170	LCE4A
ENSG00000187172	0.291331	1.16698	0.76166	1.13376	ENSG00000187172	BAGE2
ENSG00000187173	0	0.115003	0.208661	1.54668	ENSG00000187173	LCE2A
ENSG00000187175	0	0	0	0	ENSG00000187175	KRTAP12-1
ENSG00000187180	0	0	0	0.245616	ENSG00000187180	LCE2C
ENSG00000187185	2.2951	5.59739	4.13533	7.51618	ENSG00000187185	AC092118.1
ENSG00000187186	1.82299	2.58652	2.55403	4.14789	ENSG00000187186	AL162231.1
ENSG00000187187	8.58233	17.1942	18.1021	32.8399	ENSG00000187187	ZNF546
ENSG00000187189	5.40463	4.23153	4.94105	4.5102	ENSG00000187189	TSPYL4
ENSG00000187191	0	0	0	0.0503139	ENSG00000187191	DAZ3
ENSG00000187193	78.3054	67.4777	27.913	41.8221	ENSG00000187193	MT1X
ENSG00000187210	8.09173	3.57336	2.8737	6.54771	ENSG00000187210	GCNT1
ENSG00000187223	0.115308	0.110679	0.100406	0.372419	ENSG00000187223	LCE2D
ENSG00000187231	21.8485	16.9766	9.2479	22.31	ENSG00000187231	SESTD1
ENSG00000187238	0	0	0	0.781618	ENSG00000187238	LCE3B
ENSG00000187239	13.881	15.5379	12.4942	15.2077	ENSG00000187239	FNBP1
ENSG00000187240	6.27657	22.7052	20.5985	17.4433	ENSG00000187240	DYNC2H1
ENSG00000187242	0	0	0.013232	0.0166583	ENSG00000187242	KRT12
ENSG00000187243	0.795036	0.407631	1.39869	9.40493	ENSG00000187243	MAGED4B
ENSG00000187244	20.9152	87.5661	157.936	44.5248	ENSG00000187244	BCAM
ENSG00000187257	7.23758	9.03884	6.59975	8.06957	ENSG00000187257	RSBN1L
ENSG00000187258	0.641749	0.837675	0.783963	1.34441	ENSG00000187258	NPSR1
ENSG00000187260	0.140994	0.66411	4.70883	0.727083	ENSG00000187260	WDR86
ENSG00000187266	1.87654	5.54832	1.36391	2.64768	ENSG00000187266	EPOR
ENSG00000187268	2.21954	2.98991	2.1759	3.20774	ENSG00000187268	FAM9C
ENSG00000187272	0	0	0	0	ENSG00000187272	KRTAP9-8
ENSG00000187288	0.191743	0.666467	0.339759	0.764789	ENSG00000187288	CIDEC
ENSG00000187323	2.92856	9.19309	6.38951	9.75826	ENSG00000187323	DCC
ENSG00000187325	3.9993	4.24855	3.38621	3.21723	ENSG00000187325	TAF9B
ENSG00000187372	0.315309	0.0828291	0.237716	0.364214	ENSG00000187372	PCDHB13
ENSG00000187391	3.71674	7.89651	7.17317	12.3222	ENSG00000187391	MAGI2
ENSG00000187398	0.591233	1.10564	1.35631	2.2315	ENSG00000187398	LUZP2
ENSG00000187416	0.491598	1.07123	0.788181	0.850745	ENSG00000187416	LHFPL3
ENSG00000187446	61.3845	28.926	27.5184	33.136	ENSG00000187446	CHP1
ENSG00000187456	0.278876	1.20186	0.775469	1.1073	ENSG00000187456	RDM1
ENSG00000187461	0.519284	0.775313	0.923646	1.67255	ENSG00000187461	AL583828.1
ENSG00000187472	0	0	0	0	ENSG00000187472	AL589826.1
ENSG00000187474	0.915853	2.57696	1.79648	3.77832	ENSG00000187474	FPR3
ENSG00000187475	0.275164	0	0.0798373	0.198452	ENSG00000187475	HIST1H1T
ENSG00000187479	0.754124	0.217491	0.118057	0.403279	ENSG00000187479	C11orf96
ENSG00000187481	0	0	0	0	ENSG00000187481	HSD3BP1
ENSG00000187483	0.0332833	0.192414	0.0869694	0.145918	ENSG00000187483	SERPINA13P

ENSG00000187486	0.805087	0.761869	0.618366	4.35985	ENSG00000187486	KCNJ11
ENSG00000187492	1.79577	4.78635	3.5995	9.98618	ENSG00000187492	CDHR4
ENSG00000187498	12.3515	29.6326	41.8872	141.156	ENSG00000187498	COL4A1
ENSG00000187504	0	0	0	0	ENSG00000187504	RPL7P48
ENSG00000187510	0.266176	1.20254	0.71236	1.09606	ENSG00000187510	PLEKHG7
ENSG00000187513	0.177345	0.573131	0.315458	2.09064	ENSG00000187513	GJA4
ENSG00000187514	179.09	316.47	135.98	195.546	ENSG00000187514	PTMA
ENSG00000187516	0	0	0	0	ENSG00000187516	HYPM
ENSG00000187522	23.5908	21.7693	23.5819	13.3534	ENSG00000187522	HSPA14
ENSG00000187527	0.892803	1.19104	0.944218	2.07628	ENSG00000187527	ATP13A5
ENSG00000187531	22.9217	14.8298	17.0409	13.018	ENSG00000187531	SIRT7
ENSG00000187533	0.492834	0.917132	1.29153	2.68841	ENSG00000187533	PRR27
ENSG00000187534	5.89487	1.92521	0.158035	0.570448	ENSG00000187534	PRR13P5
ENSG00000187535	7.43486	14.3407	14.1652	13.4675	ENSG00000187535	IFT140
ENSG00000187536	0.271987	0.267922	0.788814	1.60099	ENSG00000187536	TPM3P7
ENSG00000187537	0.498698	1.09884	1.0772	1.33783	ENSG00000187537	POTEG
ENSG00000187545	0.0379899	0	0.13232	0.0831883	ENSG00000187545	PRAMEF10
ENSG00000187546	0.601866	1.07013	0.727972	3.00177	ENSG00000187546	AGMO
ENSG00000187550	0	0.0562628	0	0	ENSG00000187550	SBK2
ENSG00000187553	0.0368034	0.0709091	0.0640982	0.0809662	ENSG00000187553	CYP26C1
ENSG00000187554	5.91534	6.95412	7.98761	7.55253	ENSG00000187554	TLR5
ENSG00000187555	51.1881	57.7379	68.9863	68.5962	ENSG00000187555	USP7
ENSG00000187556	0.619193	1.32573	1.25406	2.34798	ENSG00000187556	NANOS3
ENSG00000187559	0.0467111	0.216718	0.43344	0	ENSG00000187559	FOXD4L3
ENSG00000187566	2.27934	2.04635	2.11134	2.03366	ENSG00000187566	NHLRC1
ENSG00000187569	0.112861	0.597397	0.295758	0.184591	ENSG00000187569	DPPA3
ENSG00000187581	0.138628	0.665756	0	0	ENSG00000187581	COX8C
ENSG00000187583	15.1782	10.2635	11.3425	7.6093	ENSG00000187583	PLEKHN1
ENSG00000187589	0.0659845	0.124707	0.209175	0.0728238	ENSG00000187589	TERF1P2
ENSG00000187595	2.77241	4.95251	4.3016	6.89463	ENSG00000187595	ZNF385C
ENSG00000187600	0.536371	1.12153	0.999653	0.525939	ENSG00000187600	TMEM247
ENSG00000187601	5.85927	4.07453	1.70048	6.0635	ENSG00000187601	MAGEH1
ENSG00000187605	6.30643	6.1286	9.77344	4.86742	ENSG00000187605	TET3
ENSG00000187607	10.7693	15.2762	18.3973	16.4839	ENSG00000187607	ZNF286A
ENSG00000187608	22.8675	41.1004	37.5482	32.1235	ENSG00000187608	ISG15
ENSG00000187609	6.49204	10.74	13.9078	16.2085	ENSG00000187609	EXD3
ENSG00000187612	0	0	0	0	ENSG00000187612	OR5W2
ENSG00000187616	0.436316	2.21534	1.24681	0.89597	ENSG00000187616	MYMK
ENSG00000187624	2.00617	1.45494	2.62669	2.66212	ENSG00000187624	C17orf97
ENSG00000187626	2.37765	3.06759	2.97235	2.30417	ENSG00000187626	ZKSCAN4
ENSG00000187627	0.382113	0.0847183	0.620829	0	ENSG00000187627	RGPD1
ENSG00000187630	6.71635	9.19688	9.49541	7.77479	ENSG00000187630	DHRS4L2
ENSG00000187634	0.890401	0.784418	1.05923	0.792935	ENSG00000187634	SAMD11
ENSG00000187642	5.78269	3.20213	4.37403	2.18486	ENSG00000187642	PERM1
ENSG00000187650	3.60369	6.30102	6.35753	6.92771	ENSG00000187650	VMAC
ENSG00000187653	5.18854	1.84634	1.6079	3.53942	ENSG00000187653	TMSB4XP8
ENSG00000187657	0	0	0	0	ENSG00000187657	TSPY13P
ENSG00000187658	0	0.094616	0	0.106419	ENSG00000187658	C5orf52
ENSG00000187664	0.0315307	0.0456106	0.0275409	0.0693892	ENSG00000187664	HAPLN4
ENSG00000187667	5.90058	13.5254	13.1271	18.2599	ENSG00000187667	WHAMMP3
ENSG00000187672	0.403314	1.20913	1.54217	1.48093	ENSG00000187672	ERC2
ENSG00000187676	4.52707	5.88245	3.16667	4.57797	ENSG00000187676	B3GLCT
ENSG00000187678	20.6398	34.6225	16.8631	37.6597	ENSG00000187678	SPRY4
ENSG00000187682	0.0468877	0.114703	0.0612091	0.204937	ENSG00000187682	ERAS

ENSG00000187686	0.158347	0.395932	0.467257	0.83283	ENSG00000187686	KRT18P59
ENSG00000187688	0.494756	0.511362	0.844331	8.71025	ENSG00000187688	TRPV2
ENSG00000187689	0.0591333	0	0	0	ENSG00000187689	AMTN
ENSG00000187690	0	0.0141887	0.0384803	0.0323015	ENSG00000187690	CXorf67
ENSG00000187695	0.247729	0.873164	0.771641	0.917868	ENSG00000187695	AC112484.1
ENSG00000187699	3.64279	8.70904	10.4555	12.6004	ENSG00000187699	C2orf88
ENSG00000187701	0.0653162	0.0628199	0	0.142142	ENSG00000187701	OR2T27
ENSG00000187713	15.7718	12.3009	14.1275	7.2505	ENSG00000187713	TMEM203
ENSG00000187714	0.0688626	0	0.0400142	0	ENSG00000187714	SLC18A3
ENSG00000187715	0.332527	0.73657	0.701575	1.18959	ENSG00000187715	KBTBD12
ENSG00000187720	35.9239	67.3919	38.2486	43.8761	ENSG00000187720	THSD4
ENSG00000187721	0	0	0	0	ENSG00000187721	GTF2IP3
ENSG00000187726	3.38507	5.32692	6.04055	9.21802	ENSG00000187726	DNAJB13
ENSG00000187730	0	0	0.0257704	0.032448	ENSG00000187730	GABRD
ENSG00000187733	0	0	0	0	ENSG00000187733	AMY1C
ENSG00000187735	36.16	44.1772	43.6831	33.2141	ENSG00000187735	TCEA1
ENSG00000187736	4.31437	7.49486	6.02794	5.56088	ENSG00000187736	NHEJ1
ENSG00000187741	9.92368	28.3578	12.3614	33.9676	ENSG00000187741	FANCA
ENSG00000187742	25.176	46.9776	48.5457	61.1808	ENSG00000187742	SECISBP2
ENSG00000187747	0.061156	0.354984	0.159535	0.66613	ENSG00000187747	OR52B6
ENSG00000187753	1.07138	2.69222	2.20272	3.63915	ENSG00000187753	C9orf153
ENSG00000187754	0.298157	0.733311	0.374392	1.27785	ENSG00000187754	SSX7
ENSG00000187758	0.75403	3.65836	3.21316	1.06345	ENSG00000187758	ADH1A
ENSG00000187762	1.93465	5.67803	4.8121	6.71387	ENSG00000187762	HSPE1P11
ENSG00000187763	0	0.128876	0.407577	0.364403	ENSG00000187763	OR2B7P
ENSG00000187764	4.4582	8.76122	6.84628	8.19122	ENSG00000187764	SEMA4D
ENSG00000187766	0	0	0	0.0393328	ENSG00000187766	KRTAP10-8
ENSG00000187772	0.0582053	0.0936661	0.0257535	0.149655	ENSG00000187772	LIN28B
ENSG00000187773	0	0	0	0.0969999	ENSG00000187773	FAM69C
ENSG00000187775	1.58429	2.82619	4.5083	2.82157	ENSG00000187775	DNAH17
ENSG00000187778	27.8587	28.3426	26.608	15.5657	ENSG00000187778	MCRS1
ENSG00000187783	0	0.305728	0.158987	0.200218	ENSG00000187783	TMEM72
ENSG00000187786	0	0	0	0	ENSG00000187786	SCXB
ENSG00000187790	3.41415	10.3555	7.09584	6.62198	ENSG00000187790	FANCM
ENSG00000187791	0.0390059	0.516193	0.144859	0.535728	ENSG00000187791	FAM205C
ENSG00000187792	2.24261	2.8951	3.09822	4.18653	ENSG00000187792	ZNF70
ENSG00000187796	0.896354	2.97218	1.43421	1.86712	ENSG00000187796	CARD9
ENSG00000187800	5.13584	10.5217	7.25863	16.9007	ENSG00000187800	PEAR1
ENSG00000187801	1.32783	3.00199	3.57139	2.12658	ENSG00000187801	ZFP69B
ENSG00000187806	0.120957	0.232139	0.314447	0.130061	ENSG00000187806	TMEM202
ENSG00000187808	0.290319	0	0.126406	0.0397462	ENSG00000187808	SOWAHD
ENSG00000187811	1.4292	2.17775	2.02617	3.73828	ENSG00000187811	AP000867.1
ENSG00000187812	0.151929	0.0523456	0.106633	0.128471	ENSG00000187812	AC019294.1
ENSG00000187815	2.67986	3.28688	3.02366	3.10361	ENSG00000187815	ZFP69
ENSG00000187821	0	0.0531551	0.132266	0	ENSG00000187821	HELT
ENSG00000187823	0.0200593	0	0.0698877	0.0220337	ENSG00000187823	RTL4
ENSG00000187824	3.74998	5.96508	9.66262	12.3736	ENSG00000187824	TMEM220
ENSG00000187833	0	0.0173308	0.0157072	0.0395337	ENSG00000187833	C2orf78
ENSG00000187837	90.3403	211.049	99.5738	77.2489	ENSG00000187837	HIST1H1C
ENSG00000187838	29.9011	26.2006	39.5843	19.7125	ENSG00000187838	PLSCR3
ENSG00000187840	46.4718	54.9412	48.2429	22.1193	ENSG00000187840	EIF4EBP1
ENSG00000187847	0	0	0	0	ENSG00000187847	OR7E25P
ENSG00000187848	0.105834	0.28884	0.053207	0.234048	ENSG00000187848	P2RX2
ENSG00000187855	0.0741176	0.166696	0.107591	0.273026	ENSG00000187855	ASCL4

ENSG00000187857	0	0	0	0	ENSG00000187857	OR6C75
ENSG00000187860	3.29736	3.76215	5.18042	4.26092	ENSG00000187860	CCDC157
ENSG00000187862	1.26574	1.2156	0.914853	2.13418	ENSG00000187862	TTC24
ENSG00000187866	3.55498	1.91867	3.81815	2.28011	ENSG00000187866	FAM122A
ENSG00000187867	0.596729	0.436212	0.216147	0.516823	ENSG00000187867	PALM3
ENSG00000187870	0	0.060182	0.0616306	0	ENSG00000187870	RNFT1P3
ENSG00000187871	0.673755	1.29874	1.28859	3.03413	ENSG00000187871	GFRAL
ENSG00000187889	3.42628	6.47099	6.12725	13.2498	ENSG00000187889	FYB2
ENSG00000187893	1.08637	2.54878	1.42834	2.37734	ENSG00000187893	CXXC1P1
ENSG00000187900	0.0673525	0.0647714	0	0	ENSG00000187900	OR5H7P
ENSG00000187902	0.0531668	0.0231306	0.0308288	0.0972978	ENSG00000187902	SHISA7
ENSG00000187905	3.84399	7.0594	6.08415	11.3104	ENSG00000187905	LRRC74B
ENSG00000187908	0.042432	0.163693	0.104211	0.171258	ENSG00000187908	DMBT1
ENSG00000187912	0.833944	1.72371	1.8352	2.82042	ENSG00000187912	CLEC17A
ENSG00000187918	0	0	0.0495668	0.124263	ENSG00000187918	OR51I2
ENSG00000187922	0.0663846	0.217259	0.29675	0.631677	ENSG00000187922	LCN10
ENSG00000187942	1.81407	3.67749	3.76744	6.29424	ENSG00000187942	LDLRAD2
ENSG00000187944	0.55584	1.39966	3.21148	1.5157	ENSG00000187944	C2orf66
ENSG00000187950	0.795358	1.47811	2.15036	0.9312	ENSG00000187950	OVCH1
ENSG00000187951	10.4242	40.7693	17.3369	37.3957	ENSG00000187951	ARHGAP11B
ENSG00000187952	0	0	0	0	ENSG00000187952	HS6ST1P1
ENSG00000187953	15.8538	15.5229	19.8063	14.5437	ENSG00000187953	PMS2CL
ENSG00000187954	31.1942	23.8318	31.7513	18.1634	ENSG00000187954	CYHR1
ENSG00000187955	0.638026	0.849291	0.537659	1.17487	ENSG00000187955	COL14A1
ENSG00000187957	3.94056	3.06468	1.93275	2.5104	ENSG00000187957	DNER
ENSG00000187959	0	0.204254	0.283343	0.152474	ENSG00000187959	CPSF4L
ENSG00000187961	28.3579	32.6201	23.7042	25.6789	ENSG00000187961	KLHL17
ENSG00000187969	0.078537	0	0	0.0822834	ENSG00000187969	ZCCHC13
ENSG00000187980	0.531356	0.990326	1.20968	2.03802	ENSG00000187980	PLA2G2C
ENSG00000187984	2.85975	7.95855	6.72475	12.5439	ENSG00000187984	ANKRD19P
ENSG00000187987	3.23737	5.77187	6.37828	4.11848	ENSG00000187987	ZSCAN23
ENSG00000187988	0	0	0	0	ENSG00000187988	KCTD9P3
ENSG00000187990	90.5466	79.5143	32.8181	26.1582	ENSG00000187990	HIST1H2BG
ENSG00000187994	5.22935	7.01129	5.18541	6.5567	ENSG00000187994	RINL
ENSG00000187997	1.40693	2.26366	2.18262	3.24633	ENSG00000187997	C17orf99
ENSG00000187999	0	0.131073	0.0592797	0.0740619	ENSG00000187999	HNRNPA1P61
ENSG00000188000	3.09276	6.31944	6.04674	10.1388	ENSG00000188000	OR7D2
ENSG00000188001	3.63485	6.1733	6.09274	6.35849	ENSG00000188001	TPRG1
ENSG00000188002	6.26723	9.39677	14.0338	7.35672	ENSG00000188002	AC026412.1
ENSG00000188004	0.631506	1.13776	0.815913	0.851758	ENSG00000188004	SNHG28
ENSG00000188010	11.0409	4.54314	5.83628	4.71647	ENSG00000188010	MORN2
ENSG00000188011	0.0242761	0.046802	0.0423119	0.116679	ENSG00000188011	RTP5
ENSG00000188013	1.21408	0.539057	0.965609	0.572028	ENSG00000188013	AC087499.1
ENSG00000188015	12.8016	30.2713	33.671	15.2285	ENSG00000188015	S100A3
ENSG00000188021	11.682	7.59657	10.6805	12.7721	ENSG00000188021	UBQLN2
ENSG00000188026	10.8685	12.8632	12.2447	13.5848	ENSG00000188026	RILPL1
ENSG00000188029	0.311304	0.556282	0.368557	0.626389	ENSG00000188029	CTSL3P
ENSG00000188032	0.17541	0.275944	0.651017	0.569743	ENSG00000188032	C19orf67
ENSG00000188033	6.42202	8.72667	9.41231	11.5834	ENSG00000188033	ZNF490
ENSG00000188037	0.0173368	0.0997154	0.015009	0.0189366	ENSG00000188037	CLCN1
ENSG00000188038	1.21398	1.57875	2.30723	2.49441	ENSG00000188038	NRN1L
ENSG00000188039	0.975896	1.76058	1.41124	2.09773	ENSG00000188039	NWD1
ENSG00000188042	28.2678	40.2805	12.3949	31.1366	ENSG00000188042	ARL4C
ENSG00000188050	0.0807107	0.155478	0.0351347	0	ENSG00000188050	RNF133

ENSG00000188051	2.88775	5.58227	4.21065	6.39275	ENSG00000188051	TMEM221
ENSG00000188056	0.0250034	0.28617	0.152603	0.308718	ENSG00000188056	TREML4
ENSG00000188060	1.23924	2.97406	2.47949	3.55639	ENSG00000188060	RAB42
ENSG00000188064	4.28794	8.7805	3.51723	9.99573	ENSG00000188064	WNT7B
ENSG00000188069	0	0.0640255	0.0578531	0.144839	ENSG00000188069	OR51F1
ENSG00000188073	1.45387	1.4614	2.18368	1.10102	ENSG00000188073	PMS2P10
ENSG00000188076	0	0	0	0	ENSG00000188076	SCGB1C1
ENSG00000188078	0	0	0.16095	0	ENSG00000188078	AL022313.1
ENSG00000188086	0.0704433	0.187487	0.12185	0.0622592	ENSG00000188086	PRSS45
ENSG00000188089	6.59044	4.13998	6.2535	4.73912	ENSG00000188089	PLA2G4E
ENSG00000188092	8.69339	12.4114	8.02934	3.83062	ENSG00000188092	GPR89B
ENSG00000188095	0.991404	1.74943	1.20903	2.4262	ENSG00000188095	MESP2
ENSG00000188100	8.18264	8.00346	2.174	12.6225	ENSG00000188100	FAM25A
ENSG00000188101	0	0.0287689	0.0591649	0	ENSG00000188101	ALOX15P2
ENSG00000188107	3.10404	8.74423	8.9082	14.0183	ENSG00000188107	EYS
ENSG00000188112	57.6613	24.9184	26.6148	19.8541	ENSG00000188112	C6orf132
ENSG00000188120	0.074841	0.336722	0.416617	0.566554	ENSG00000188120	DAZ1
ENSG00000188124	0.171154	0.219619	0.148863	0.310994	ENSG00000188124	OR2AG2
ENSG00000188130	9.55779	17.0348	25.4769	23.0136	ENSG00000188130	MAPK12
ENSG00000188133	0.0303141	0.146173	0.105729	0.200162	ENSG00000188133	TMEM215
ENSG00000188152	2.05748	3.45984	3.32741	4.31392	ENSG00000188152	NUTM2G
ENSG00000188153	44.5588	99.5753	133.471	75.2371	ENSG00000188153	COL4A5
ENSG00000188155	0.114115	0.176745	0.253605	0.231801	ENSG00000188155	KRTAP10-6
ENSG00000188157	178.845	444.12	343.264	287.666	ENSG00000188157	AGRN
ENSG00000188158	3.53025	9.7039	8.67175	5.86667	ENSG00000188158	NHS
ENSG00000188162	0.103596	0.228186	0.125617	0.265481	ENSG00000188162	OTOG
ENSG00000188163	0.725257	1.39935	0.576792	0.777705	ENSG00000188163	FAM166A
ENSG00000188167	4.18949	5.49248	5.16844	4.12303	ENSG00000188167	TMPPE
ENSG00000188171	3.99141	5.32188	7.6393	4.90605	ENSG00000188171	ZNF626
ENSG00000188175	0.221111	0.157824	0.169994	0.218396	ENSG00000188175	HEPACAM2
ENSG00000188176	0.0489191	0.0284096	0.0213388	0	ENSG00000188176	SMTNL2
ENSG00000188177	1.80456	4.87033	4.55887	5.22198	ENSG00000188177	ZC3H6
ENSG00000188186	36.3767	44.81	37.6627	34.5912	ENSG00000188186	LAMTOR4
ENSG00000188191	7.40982	7.08946	7.37627	5.71795	ENSG00000188191	PRKAR1B
ENSG00000188199	2.11382	2.70367	4.45754	4.53096	ENSG00000188199	NUTM2B
ENSG00000188211	2.09784	3.8881	5.12319	4.08397	ENSG00000188211	NCR3LG1
ENSG00000188215	21.6654	7.15134	8.96502	10.9598	ENSG00000188215	DCUN1D3
ENSG00000188219	0	0	0	0.0185056	ENSG00000188219	POTEE
ENSG00000188223	2.14563	3.10667	1.42068	3.23655	ENSG00000188223	AD000671.1
ENSG00000188227	12.721	18.7839	21.2259	27.9749	ENSG00000188227	ZNF793
ENSG00000188229	188.799	162.349	59.0128	92.7136	ENSG00000188229	TUBB4B
ENSG00000188234	4.18593	3.67363	3.86587	5.65133	ENSG00000188234	AGAP4
ENSG00000188242	9.53819	10.3973	20.0528	6.26727	ENSG00000188242	PP7080
ENSG00000188243	44.0362	39.6286	36.2586	24.6395	ENSG00000188243	COMMD6
ENSG00000188257	0.273149	0.45491	0.155325	1.31191	ENSG00000188257	PLA2G2A
ENSG00000188263	0.20182	0.210627	0.191613	0.229435	ENSG00000188263	IL17REL
ENSG00000188266	3.60964	6.11088	5.57773	7.72832	ENSG00000188266	HYKK
ENSG00000188269	2.06098	6.12696	5.30577	9.89969	ENSG00000188269	OR7A5
ENSG00000188277	4.23052	2.8111	2.3529	2.47112	ENSG00000188277	C15orf62
ENSG00000188279	18.0404	15.4356	36.2667	26.7466	ENSG00000188279	FAM25C
ENSG00000188280	0.25799	0.368716	0.235409	1.01453	ENSG00000188280	AC007731.1
ENSG00000188282	0.614896	1.57064	2.55943	1.97393	ENSG00000188282	RUFY4
ENSG00000188283	13.4837	27.5641	29.5665	35.1198	ENSG00000188283	ZNF383
ENSG00000188290	31.0981	6.0302	18.8732	15.2178	ENSG00000188290	HES4

ENSG00000188293	6.38404	0.163608	9.23779	3.31969	ENSG00000188293	IGFL1
ENSG00000188295	8.43488	7.84784	8.94149	11.5593	ENSG00000188295	ZNF669
ENSG00000188305	0.81689	2.23062	0.883003	3.665	ENSG00000188305	C19orf35
ENSG00000188306	0.0311068	0.0299752	0	0.0341105	ENSG00000188306	LRRIQ4
ENSG00000188312	1.08543	2.42121	2.53403	1.86349	ENSG00000188312	CENPP
ENSG00000188313	59.7748	80.6026	47.8544	58.0973	ENSG00000188313	PLSCR1
ENSG00000188314	0	0	0	0	ENSG00000188314	OR7D1P
ENSG00000188315	2.83879	3.99827	5.30578	6.12079	ENSG00000188315	C3orf62
ENSG00000188316	0.930242	1.52513	1.33153	1.47097	ENSG00000188316	ENO4
ENSG00000188321	7.5641	10.3593	13.3097	14.6825	ENSG00000188321	ZNF559
ENSG00000188322	0.29476	0.757097	0.725215	0.962505	ENSG00000188322	SBK1
ENSG00000188324	0.0718181	0.127076	0.229651	0.215623	ENSG00000188324	OR6C6
ENSG00000188334	0	0	0	0	ENSG00000188334	BSPH1
ENSG00000188340	0	0	0	0.0733172	ENSG00000188340	OR6N2
ENSG00000188342	48.9138	32.4318	31.4143	25.9622	ENSG00000188342	GTF2F2
ENSG00000188343	8.32091	14.698	14.7238	16.7888	ENSG00000188343	FAM92A
ENSG00000188352	22.7514	40.1841	28.4833	54.6971	ENSG00000188352	FOCAD
ENSG00000188368	2.07721	3.08285	2.8868	4.91502	ENSG00000188368	PRR19
ENSG00000188372	6.81957	11.5543	19.1391	18.2729	ENSG00000188372	ZP3
ENSG00000188373	0.356123	1.8217	3.15268	0.507448	ENSG00000188373	C10orf99
ENSG00000188375	0.122831	0.118696	0.108353	0.335124	ENSG00000188375	H3F3C
ENSG00000188379	0.0527557	0.152345	0.413071	0.345424	ENSG00000188379	IFNA2
ENSG00000188383	0.0136574	0.468729	0.791606	0.691311	ENSG00000188383	GPAT2P2
ENSG00000188384	1.87731	1.83705	2.64131	1.74531	ENSG00000188384	CSPG4P8
ENSG00000188385	0.118372	0.0838612	0.106971	0.326347	ENSG00000188385	JAKMIP3
ENSG00000188386	0.113796	0.078941	0.127598	0.0887128	ENSG00000188386	PPP3R2
ENSG00000188388	0	0.364172	0.114941	0.174289	ENSG00000188388	GOLGA6L3
ENSG00000188389	0.309428	0.651899	0.426318	0.396376	ENSG00000188389	PDCD1
ENSG00000188393	0.994172	1.81074	1.96882	3.16859	ENSG00000188393	CLEC2A
ENSG00000188394	0.530504	1.89866	1.01116	2.08945	ENSG00000188394	GPR21
ENSG00000188396	6.15554	9.94497	13.1003	6.48865	ENSG00000188396	TCTEX1D4
ENSG00000188399	0	0.299057	0	0.113826	ENSG00000188399	ANKRD36P1
ENSG00000188403	0	0	0	0	ENSG00000188403	IGHV1OR15-9
ENSG00000188404	0.110232	0.356809	0.267186	0.249149	ENSG00000188404	SELL
ENSG00000188408	0	0	0.0439903	0.0549914	ENSG00000188408	MAGEB5
ENSG00000188419	14.9982	19.3194	20.7218	20.7161	ENSG00000188419	CHM
ENSG00000188425	0.0369872	0.178645	0.0644175	0.202527	ENSG00000188425	NANOS2
ENSG00000188428	3.74412	6.22976	7.11031	8.19233	ENSG00000188428	BLOC1S5
ENSG00000188438	0	0	0	0	ENSG00000188438	DEFB108F
ENSG00000188439	0.0531341	0.051145	0.09245	0	ENSG00000188439	OR4P1P
ENSG00000188451	0.400039	1.56395	2.7002	1.43952	ENSG00000188451	SRP72P2
ENSG00000188452	5.11676	14.998	13.7015	23.4722	ENSG00000188452	CERKL
ENSG00000188459	0	0	0	0	ENSG00000188459	WASF4P
ENSG00000188460	0	0	0	0	ENSG00000188460	ACTBP11
ENSG00000188467	1.34825	1.15319	0.458265	1.03899	ENSG00000188467	SLC24A5
ENSG00000188474	0.581548	2.13013	0.949371	1.27022	ENSG00000188474	ZNF788
ENSG00000188483	12.3883	7.82101	7.00105	7.10051	ENSG00000188483	IER5L
ENSG00000188486	6.2346	13.7033	4.44222	7.15298	ENSG00000188486	H2AFX
ENSG00000188487	0.417878	0.520518	0.507876	1.07985	ENSG00000188487	INSC
ENSG00000188488	0.764888	2.04563	1.34361	1.12031	ENSG00000188488	SERPINA5
ENSG00000188493	1.54017	3.67583	4.26792	3.67841	ENSG00000188493	C19orf54
ENSG00000188501	0.579229	1.98924	2.0432	3.63378	ENSG00000188501	LCTL
ENSG00000188505	63.588	4.74895	5.29426	11.6577	ENSG00000188505	NCCRP1
ENSG00000188508	234.676	27.4705	83.1286	45.353	ENSG00000188508	KRTDAP

ENSG00000188511	1.22779	3.00162	2.55155	6.64389	ENSG00000188511	C22orf34
ENSG00000188512	0	0	0	0	ENSG00000188512	AF279873.1
ENSG00000188517	0.146126	0.532268	0.314169	0.920853	ENSG00000188517	COL25A1
ENSG00000188522	32.7445	34.5191	32.8329	20.0572	ENSG00000188522	FAM83G
ENSG00000188523	0.105255	0.0864209	0.163467	0.294307	ENSG00000188523	CFAP77
ENSG00000188529	23.1092	36.0763	31.011	38.245	ENSG00000188529	SRSF10
ENSG00000188536	0.42237	0	0	0	ENSG00000188536	HBA2
ENSG00000188542	2.41329	3.2255	3.11573	3.71417	ENSG00000188542	DUSP28
ENSG00000188549	96.4905	54.3086	42.8807	69.0106	ENSG00000188549	C15orf52
ENSG00000188554	33.02	34.1565	33.5306	31.8868	ENSG00000188554	NBR1
ENSG00000188558	0	0	0	0	ENSG00000188558	OR2G6
ENSG00000188559	7.10536	5.86476	9.43947	7.30625	ENSG00000188559	RALGAPA2
ENSG00000188566	8.82927	9.5964	12.9654	8.19008	ENSG00000188566	NDOR1
ENSG00000188573	0.768722	0.663706	0.432144	1.39886	ENSG00000188573	FBLL1
ENSG00000188580	0.499152	0.977121	1.06092	0.901977	ENSG00000188580	NKAIN2
ENSG00000188581	0.0348967	0	0	0.0379334	ENSG00000188581	KRTAP1-1
ENSG00000188582	0.382993	1.24232	0.852316	2.91394	ENSG00000188582	PAQR9
ENSG00000188596	22.2945	52.1766	48.1803	99.2208	ENSG00000188596	CFAP54
ENSG00000188599	6.17014	34.9512	28.8935	19.2039	ENSG00000188599	NPIPP1
ENSG00000188603	29.0902	33.7131	32.8501	44.209	ENSG00000188603	CLN3
ENSG00000188610	0.461336	2.22864	0.622228	0.928109	ENSG00000188610	FAM72B
ENSG00000188611	1.26798	2.14009	3.05112	2.52317	ENSG00000188611	ASAH2
ENSG00000188612	84.771	64.5404	35.1894	53.8292	ENSG00000188612	SUMO2
ENSG00000188613	2.30501	2.93698	3.10696	3.40255	ENSG00000188613	NANOS1
ENSG00000188620	0.104668	0	0.0457297	0.115161	ENSG00000188620	HMX3
ENSG00000188624	62.588	4.57914	13.793	24.7695	ENSG00000188624	IGFL3
ENSG00000188626	1.98429	4.23105	3.27193	2.50389	ENSG00000188626	GOLGA8M
ENSG00000188629	2.10565	2.77595	3.91692	2.38923	ENSG00000188629	ZNF177
ENSG00000188636	5.16071	4.48158	7.0349	4.10397	ENSG00000188636	RTL6
ENSG00000188641	1.51258	4.86472	2.78543	9.87583	ENSG00000188641	DPYD
ENSG00000188643	670.456	331.449	259.287	156.855	ENSG00000188643	S100A16
ENSG00000188646	0	0	0	0	ENSG00000188646	AC123904.1
ENSG00000188647	24.1194	30.5464	23.3527	27.0819	ENSG00000188647	PTAR1
ENSG00000188649	0.25701	0.472167	1.02482	1.04859	ENSG00000188649	CC2D2B
ENSG00000188655	0	0.0598002	0.0724241	0.0683059	ENSG00000188655	RNASE9
ENSG00000188656	0	0.0523214	0	0	ENSG00000188656	TSPY7P
ENSG00000188659	3.90509	8.94382	4.25824	4.63772	ENSG00000188659	SAXO2
ENSG00000188662	0.331334	0.519788	0.287561	1.43603	ENSG00000188662	HILS1
ENSG00000188668	0	0	0	0	ENSG00000188668	OR7E90P
ENSG00000188672	0.522715	0.406651	0.491343	0.103378	ENSG00000188672	RHCE
ENSG00000188674	0.383581	0.24866	0.467263	0.817909	ENSG00000188674	C2orf80
ENSG00000188676	0.29894	1.0172	0.991939	1.70022	ENSG00000188676	IDO2
ENSG00000188677	10.0175	8.48888	14.4924	23.2947	ENSG00000188677	PARVB
ENSG00000188681	2.99747	3.00162	1.30564	0.322277	ENSG00000188681	TEKT4P2
ENSG00000188686	1.33576	0.962582	1.69852	1.73134	ENSG00000188686	SCXA
ENSG00000188687	4.879	11.8514	13.836	18.203	ENSG00000188687	SLC4A5
ENSG00000188690	27.5771	21.0606	23.875	17.4507	ENSG00000188690	UROS
ENSG00000188691	0.0896685	0.258486	0.347802	0.0970495	ENSG00000188691	OR56A5
ENSG00000188694	0	0.0335753	0.0910527	0.0381823	ENSG00000188694	KRTAP24-1
ENSG00000188706	23.8939	18.045	17.5354	15.5609	ENSG00000188706	ZDHHC9
ENSG00000188707	1.39593	1.65979	1.38391	0.609884	ENSG00000188707	ZBED6CL
ENSG00000188710	1.02332	1.56507	1.06072	3.03605	ENSG00000188710	QRFP
ENSG00000188712	0	0.320949	0.464011	0.290413	ENSG00000188712	OR13D3P
ENSG00000188716	0	0	0	0.11116	ENSG00000188716	DUPD1

ENSG00000188722	0.320872	0.617032	0.092701	0.345521	ENSG00000188722	AL391005.1
ENSG00000188725	18.9433	17.7052	19.7839	13.6504	ENSG00000188725	SMIM15
ENSG00000188729	0.143656	0.201898	0.304106	0.364374	ENSG00000188729	OSTN
ENSG00000188730	0.0808355	0.262626	0.284465	0.32491	ENSG00000188730	VWC2
ENSG00000188732	4.62476	8.66485	7.8218	13.3433	ENSG00000188732	FAM221A
ENSG00000188735	12.4027	17.3514	16.3029	25.4182	ENSG00000188735	TMEM120B
ENSG00000188738	15.3358	43.1071	41.0294	106.859	ENSG00000188738	FSIP2
ENSG00000188739	25.6856	22.4215	23.997	23.2305	ENSG00000188739	RBM34
ENSG00000188747	4.81501	4.08342	5.26804	1.4417	ENSG00000188747	NOXA1
ENSG00000188755	0	0	0.0663076	0	ENSG00000188755	TBC1D3P2
ENSG00000188760	2.46371	1.80293	1.80273	1.48064	ENSG00000188760	TMEM198
ENSG00000188761	1.68891	1.9133	3.80593	4.59982	ENSG00000188761	BCL2L15
ENSG00000188763	0.11898	0.0572962	0.113959	0.159035	ENSG00000188763	FZD9
ENSG00000188765	0	0	0	0	ENSG00000188765	TMSB4XP2
ENSG00000188766	6.79538	12.8867	11.2049	14.8072	ENSG00000188766	SPRED3
ENSG00000188770	0.0432503	0.124119	0.0376487	0	ENSG00000188770	OPTC
ENSG00000188771	0.123475	0.396802	0.411438	0.643688	ENSG00000188771	PLET1
ENSG00000188778	0.0579191	0.0588106	0.040237	0.174584	ENSG00000188778	ADRB3
ENSG00000188779	0.271487	0.185167	0.206056	0.348349	ENSG00000188779	SKOR1
ENSG00000188782	0	0.119614	0.10827	0.0680588	ENSG00000188782	CATSPER4
ENSG00000188783	0.51153	1.07481	1.37472	3.01718	ENSG00000188783	PRELP
ENSG00000188784	0	0.0797188	0.360102	0	ENSG00000188784	PLA2G2E
ENSG00000188785	10.0696	14.1728	16.0212	13.4427	ENSG00000188785	ZNF548
ENSG00000188786	7.92014	4.66156	9.96305	4.26171	ENSG00000188786	MTF1
ENSG00000188800	0.95586	1.60919	1.00868	2.49649	ENSG00000188800	TMCO2
ENSG00000188801	0.147531	0.769614	0.535332	0.534699	ENSG00000188801	ZNF322P1
ENSG00000188803	0.356868	0.336251	0.595964	0.788494	ENSG00000188803	SHISA6
ENSG00000188807	4.85634	6.26614	7.4914	5.45818	ENSG00000188807	TMEM201
ENSG00000188811	12.7583	19.9447	16.8309	15.3262	ENSG00000188811	NHLRC3
ENSG00000188816	0.106134	0.267757	0.0637155	0.365667	ENSG00000188816	HMX2
ENSG00000188817	1.51096	4.34966	4.12503	7.46491	ENSG00000188817	SNTN
ENSG00000188818	3.89274	4.50386	6.12932	1.63932	ENSG00000188818	ZDHHC11
ENSG00000188820	0.952852	0	0.235756	1.22447	ENSG00000188820	FAM26F
ENSG00000188822	1.1322	2.67021	2.21234	4.27424	ENSG00000188822	CNR2
ENSG00000188827	4.91194	8.93641	6.18985	8.37406	ENSG00000188827	SLX4
ENSG00000188828	7.29536	15.4616	18.0897	27.2058	ENSG00000188828	GLRA4
ENSG00000188831	0	0	0	0	ENSG00000188831	DPPA3P2
ENSG00000188833	0.155627	0.243764	0.209316	0.0291743	ENSG00000188833	ENTPD8
ENSG00000188846	311.422	267.127	242.581	153.643	ENSG00000188846	RPL14
ENSG00000188848	0.31008	0.265794	0.357602	0.256971	ENSG00000188848	BEND4
ENSG00000188850	3.52611	5.57489	6.17657	11.5075	ENSG00000188850	AC114947.1
ENSG00000188856	0	0.142754	0.0715729	0	ENSG00000188856	RPSAP47
ENSG00000188859	0.0422762	0.201148	0.117662	0.226713	ENSG00000188859	FAM78B
ENSG00000188868	3.68682	4.31094	3.54205	3.44933	ENSG00000188868	ZNF563
ENSG00000188869	0.905162	2.03293	1.75943	2.94557	ENSG00000188869	TMC3
ENSG00000188873	0	0	0.0968384	0	ENSG00000188873	AC120036.1
ENSG00000188877	0	0	0	0.0347312	ENSG00000188877	POTEA
ENSG00000188878	8.32336	15.3386	9.87779	11.972	ENSG00000188878	FBF1
ENSG00000188883	1.15475	1.66734	3.51386	0.916523	ENSG00000188883	KLRG2
ENSG00000188886	0.0456493	0.0879135	0.158925	0.0997894	ENSG00000188886	ASTL
ENSG00000188888	0.0364679	0.0735672	0.304897	0.224426	ENSG00000188888	GPR179
ENSG00000188895	42.7606	46.9171	53.062	51.7309	ENSG00000188895	MSL1
ENSG00000188897	2.12372	5.82779	4.57176	4.97702	ENSG00000188897	AC099489.1
ENSG00000188906	0.263487	1.02203	0.833092	0.871058	ENSG00000188906	LRRK2

ENSG00000188909	0	0	0	0	ENSG00000188909	BSX
ENSG00000188910	143.971	126.998	52.6828	36.3146	ENSG00000188910	GJB3
ENSG00000188916	0.97771	3.24472	2.79332	4.04447	ENSG00000188916	FAM196A
ENSG00000188917	12.9541	19.7726	19.0475	25.0968	ENSG00000188917	TRMT2B
ENSG00000188921	7.82951	11.5559	7.97474	9.87944	ENSG00000188921	HACD4
ENSG00000188931	4.32559	9.08776	7.47833	9.51361	ENSG00000188931	CFAP126
ENSG00000188933	10.2499	46.0663	34.033	61.1793	ENSG00000188933	USP32P1
ENSG00000188937	0.235866	0.328386	0.247861	0.674122	ENSG00000188937	NYX
ENSG00000188938	13.3183	10.879	12.1606	7.27504	ENSG00000188938	FAM120AOS
ENSG00000188958	4.24084	6.4414	7.41284	12.1755	ENSG00000188958	UTS2B
ENSG00000188959	0.165913	0.561107	0.227138	1.06683	ENSG00000188959	C9orf152
ENSG00000188976	58.7991	42.411	53.9408	43.5221	ENSG00000188976	NOC2L
ENSG00000188981	1.1471	1.55192	1.88457	1.62326	ENSG00000188981	MSANTD1
ENSG00000188984	0.741873	2.21243	1.42814	2.5819	ENSG00000188984	AADACL3
ENSG00000188985	0	0.0928248	0	0	ENSG00000188985	DHFRP1
ENSG00000188986	17.2155	20.7909	17.7391	12.6549	ENSG00000188986	NELFB
ENSG00000188987	24.1278	46.9594	19.3085	15.2917	ENSG00000188987	HIST1H4D
ENSG00000188991	0.0188406	0.181112	0.131282	0.165308	ENSG00000188991	SLC15A5
ENSG00000188992	0.147843	0.0712118	0.0967419	0.323814	ENSG00000188992	LIPI
ENSG00000188993	0.114793	0.426296	0.456804	0.666486	ENSG00000188993	LRRC66
ENSG00000188994	26.0577	37.2151	36.7092	60.5302	ENSG00000188994	ZNF292
ENSG00000188996	0.419733	0.692563	0.938461	1.4504	ENSG00000188996	HUS1B
ENSG00000188997	8.01154	9.50792	10.7732	16.7222	ENSG00000188997	KCTD21
ENSG00000189001	155.453	14.4898	29.6106	54.0274	ENSG00000189001	SBSN
ENSG00000189002	0.0301439	0.0577619	0	0	ENSG00000189002	PROS2P
ENSG00000189007	11.8923	21.7931	29.3514	16.4276	ENSG00000189007	ADAT2
ENSG00000189011	3.09252	1.36496	6.21978	6.08232	ENSG00000189011	AC138783.12
ENSG00000189013	0	0	0	0	ENSG00000189013	KIR2DL4
ENSG00000189014	0.278217	0.114766	0.537589	0.136803	ENSG00000189014	FAM35DP
ENSG00000189023	0.296504	0.285692	0.202116	0.109416	ENSG00000189023	MAGEB16
ENSG00000189030	1.29046	1.38187	1.85862	2.84057	ENSG00000189030	VHLL
ENSG00000189037	0	0	0	0	ENSG00000189037	DUSP21
ENSG00000189042	18.4937	41.3444	35.875	53.7779	ENSG00000189042	ZNF567
ENSG00000189043	47.3739	43.2536	31.653	28.0064	ENSG00000189043	NDUFA4
ENSG00000189045	2.09789	2.60757	2.38816	2.41624	ENSG00000189045	ANKDD1B
ENSG00000189046	6.90596	12.2768	16.7506	11.2118	ENSG00000189046	ALKBH2
ENSG00000189050	11.1128	9.67979	8.27366	8.17836	ENSG00000189050	RNFT1
ENSG00000189051	5.86016	2.05057	1.2828	2.80924	ENSG00000189051	RNF222
ENSG00000189052	0	0	0	0	ENSG00000189052	CGB5
ENSG00000189056	0.850234	0.576817	0.418052	2.94637	ENSG00000189056	RELN
ENSG00000189057	6.26854	14.1997	9.49529	21.8321	ENSG00000189057	FAM111B
ENSG00000189058	1.86581	3.11914	2.55253	9.0042	ENSG00000189058	APOD
ENSG00000189060	33.2431	35.5295	56.0108	23.3078	ENSG00000189060	H1F0
ENSG00000189064	0	0	0	0	ENSG00000189064	GAGE2A
ENSG00000189067	47.5751	46.1218	59.5721	37.1027	ENSG00000189067	LITAF
ENSG00000189068	0.11044	0.300606	0.169699	0.607346	ENSG00000189068	VSTM1
ENSG00000189077	10.8458	8.47816	6.12062	5.88644	ENSG00000189077	TMEM120A
ENSG00000189079	13.3543	22.2849	19.7053	26.6971	ENSG00000189079	ARID2
ENSG00000189089	0.667751	1.69161	1.01036	1.05845	ENSG00000189089	RIMKLBP1
ENSG00000189090	0.948937	0.56335	2.81855	2.47667	ENSG00000189090	FAM25G
ENSG00000189091	99.2012	119.07	116.528	105.529	ENSG00000189091	SF3B3
ENSG00000189099	1.42341	3.9718	3.25133	4.72198	ENSG00000189099	PRSS48
ENSG00000189108	0.16961	0.0788705	0.0623436	0.0807399	ENSG00000189108	IL1RAPL2
ENSG00000189114	6.52281	4.89232	8.76847	5.56167	ENSG00000189114	BLOC1S3

ENSG00000189120	2.73921	2.43637	2.26718	1.61199	ENSG00000189120	SP6
ENSG00000189127	0.0831507	0.345276	0.276896	0.347616	ENSG00000189127	ANKRD34B
ENSG00000189129	6.07971	1.29849	1.73767	1.76742	ENSG00000189129	PLAC9
ENSG00000189132	0	0	0.0230294	0.087035	ENSG00000189132	FAM47B
ENSG00000189134	1.53346	0.950673	0.981047	0.551122	ENSG00000189134	NKAPL
ENSG00000189136	11.4785	15.6542	16.9474	22.1732	ENSG00000189136	UBE2Q2P1
ENSG00000189139	0.0186655	0.0359954	0.0650877	0.0821003	ENSG00000189139	FSCB
ENSG00000189143	116.578	14.7248	6.20021	13.0608	ENSG00000189143	CLDN4
ENSG00000189144	20.4681	20.9399	28.7715	22.2516	ENSG00000189144	ZNF573
ENSG00000189145	0	0	0	0.221859	ENSG00000189145	AC092268.1
ENSG00000189152	0.226936	0.287161	0.384264	0.50781	ENSG00000189152	GRAPL
ENSG00000189157	14.1339	20.1055	22.5251	31.8924	ENSG00000189157	FAM47E
ENSG00000189159	200.158	117.027	75.2386	89.1467	ENSG00000189159	JPT1
ENSG00000189164	4.57059	8.31841	6.48909	12.7977	ENSG00000189164	ZNF527
ENSG00000189166	0	0	0	0.0121887	ENSG00000189166	TNRC18P3
ENSG00000189167	0.113338	0.273059	0.390332	0.17995	ENSG00000189167	ZAR1L
ENSG00000189169	0	0	0	0.0394956	ENSG00000189169	KRTAP10-12
ENSG00000189171	71.6254	58.5537	30.6867	45.5567	ENSG00000189171	S100A13
ENSG00000189180	10.7653	15.5395	14.7799	12.3968	ENSG00000189180	ZNF33A
ENSG00000189181	0	0	0	0	ENSG00000189181	OR14I1
ENSG00000189182	0.60604	0.959936	1.46139	1.36608	ENSG00000189182	KRT77
ENSG00000189184	0.101594	0.14699	0.343014	9.46405	ENSG00000189184	PCDH18
ENSG00000189186	0.0290502	0.643179	0.594312	0.837126	ENSG00000189186	DCAF8L2
ENSG00000189190	16.1703	15.542	14.2963	10.3841	ENSG00000189190	ZNF600
ENSG00000189195	3.26626	3.91128	1.40968	3.27291	ENSG00000189195	AC104836.1
ENSG00000189212	1.40067	3.80185	3.25295	5.61358	ENSG00000189212	DPY19L2P1
ENSG00000189221	44.0282	21.4411	13.6368	15.389	ENSG00000189221	MAOA
ENSG00000189227	4.31883	5.64278	6.64881	2.20422	ENSG00000189227	C15orf61
ENSG00000189233	1.80221	3.55968	3.10363	5.19349	ENSG00000189233	NUGGC
ENSG00000189241	48.6386	24.8949	32.8697	21.9176	ENSG00000189241	TSPYL1
ENSG00000189252	0	0	0	0	ENSG00000189252	SPANXN3
ENSG00000189253	0	0	0	0	ENSG00000189253	TRIM64B
ENSG00000189266	30.2206	20.208	17.8534	29.5389	ENSG00000189266	PNRC2
ENSG00000189269	0.599802	0.657043	0.48846	0.428861	ENSG00000189269	DRICH1
ENSG00000189275	0.0804162	0.156049	0.182298	0.268267	ENSG00000189275	LINC01164
ENSG00000189280	113.865	86.8812	32.0476	18.9819	ENSG00000189280	GJB5
ENSG00000189283	1.48062	3.06612	4.88805	4.86193	ENSG00000189283	FHIT
ENSG00000189292	0.567473	0.825124	0.910024	1.63362	ENSG00000189292	ALKAL2
ENSG00000189298	3.3588	5.4376	5.01382	6.36937	ENSG00000189298	ZKSCAN3
ENSG00000189299	0	0.0570646	0.0343948	0.173466	ENSG00000189299	FOXR2
ENSG00000189306	43.9909	27.816	29.3782	18.9699	ENSG00000189306	RRP7A
ENSG00000189308	4.2535	5.74983	4.54351	5.28815	ENSG00000189308	LIN54
ENSG00000189319	11.5112	16.2775	19.4382	9.38386	ENSG00000189319	FAM53B
ENSG00000189320	3.88621	2.51304	1.43183	5.53402	ENSG00000189320	FAM180A
ENSG00000189325	0.029	0	0.0758625	0.0478785	ENSG00000189325	C6orf222
ENSG00000189326	0	0	0	0	ENSG00000189326	SPANXN4
ENSG00000189332	5.97685	6.10426	6.69128	7.09549	ENSG00000189332	AC090099.1
ENSG00000189334	441.185	316.582	302.854	157.331	ENSG00000189334	S100A14
ENSG00000189337	7.46826	7.19042	8.75821	7.55365	ENSG00000189337	KAZN
ENSG00000189339	15.3017	14.879	22.4833	18.173	ENSG00000189339	SLC35E2B
ENSG00000189343	18.4931	0.198153	37.5855	20.8287	ENSG00000189343	AC004448.1
ENSG00000189348	0	0.0417942	0.157073	0.234334	ENSG00000189348	FAM90A27P
ENSG00000189350	2.34767	5.1299	4.97707	7.8152	ENSG00000189350	TOGARAM2
ENSG00000189357	0	0	0.0195577	0	ENSG00000189357	SPATA31D4

ENSG00000189362	5.1712	14.5971	15.7608	10.9803	ENSG00000189362	NEMP2
ENSG00000189366	0.376091	0.70933	0.491789	1.19206	ENSG00000189366	ALG1L
ENSG00000189367	1.28027	0.391328	0.463961	5.38296	ENSG00000189367	KIAA0408
ENSG00000189369	0.901168	0.8131	1.27164	1.04031	ENSG00000189369	GSPT2
ENSG00000189372	0.325694	1.85906	1.69029	1.73735	ENSG00000189372	AL034369.1
ENSG00000189375	0.460887	0.173159	0.604653	0	ENSG00000189375	TBC1D28
ENSG00000189376	11.976	16.177	12.996	14.9597	ENSG00000189376	C8orf76
ENSG00000189377	1.6749	0.741005	0.389384	0.929044	ENSG00000189377	CXCL17
ENSG00000189393	0.0383417	0.0557239	0	0	ENSG00000189393	FAM90A14P
ENSG00000189398	0	0.198091	0.170708	4.80371	ENSG00000189398	OR7E12P
ENSG00000189401	0.644582	1.57603	1.22369	2.02556	ENSG00000189401	OTUD6A
ENSG00000189403	95.7234	148.924	76.6026	93.1891	ENSG00000189403	HMGB1
ENSG00000189409	0.957897	0.523591	1.20976	1.53792	ENSG00000189409	MMP23B
ENSG00000189410	53.3756	74.6299	58.8387	58.1701	ENSG00000189410	SH2D5
ENSG00000189420	0.735405	0.388299	0.867092	0.596127	ENSG00000189420	ZFP92
ENSG00000189423	1.10776	0.88416	1.63356	0.741777	ENSG00000189423	USP32P3
ENSG00000189430	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000189430	NCR1
ENSG00000189431	1.8441	1.86246	1.60566	0.97364	ENSG00000189431	RASSF10
ENSG00000189433	31.6815	17.9096	2.39575	6.77131	ENSG00000189433	GJB4
ENSG00000196071	0.304634	0.457151	0.652214	0.778971	ENSG00000196071	OR2L13
ENSG00000196072	20.7148	19.631	26.5475	12.4233	ENSG00000196072	BLOC1S2
ENSG00000196074	0.612479	1.89745	2.90556	3.38925	ENSG00000196074	SYCP2
ENSG00000196081	6.68771	15.9845	12.7493	21.9597	ENSG00000196081	ZNF724
ENSG00000196082	44.3626	166.978	136.659	204.175	ENSG00000196082	AC140061.1
ENSG00000196083	75.0045	126.902	89.9978	115.487	ENSG00000196083	IL1RAP
ENSG00000196085	0	0	0	0	ENSG00000196085	AC013442.1
ENSG00000196090	0.0456939	0.112403	0.0948959	0.106109	ENSG00000196090	PTPRT
ENSG00000196091	0.129584	0.182727	0.713013	1.58891	ENSG00000196091	MYBPC1
ENSG00000196092	1.87093	3.58215	0.823422	5.69158	ENSG00000196092	PAX5
ENSG00000196095	0.219859	1.05056	0.190347	1.16475	ENSG00000196095	AC126182.1
ENSG00000196098	0	0	0	0.0700281	ENSG00000196098	OR5K4
ENSG00000196099	0.44985	1.49772	0.897391	2.14368	ENSG00000196099	OR6M1
ENSG00000196101	0	0	0	0	ENSG00000196101	HLA-DRB3
ENSG00000196104	0.705663	1.31366	1.04232	2.16825	ENSG00000196104	SPOCK3
ENSG00000196109	0.962608	0.675536	0.155513	0.340357	ENSG00000196109	ZNF676
ENSG00000196110	7.36512	9.22163	8.31017	5.89858	ENSG00000196110	ZNF699
ENSG00000196114	1.31643	2.25828	0.746065	1.13787	ENSG00000196114	AL031577.1
ENSG00000196115	0	0.238956	0.323386	0.48269	ENSG00000196115	ADAM5
ENSG00000196116	7.32756	7.64987	4.72402	5.74226	ENSG00000196116	TDRD7
ENSG00000196118	1.73492	3.46709	0.600472	1.02334	ENSG00000196118	CCDC189
ENSG00000196119	0.0526485	0	0	0.0574551	ENSG00000196119	OR8A1
ENSG00000196123	8.09245	14.6489	10.4205	15.2254	ENSG00000196123	KIAA0895L
ENSG00000196126	0	0.0934111	0.211073	0.121351	ENSG00000196126	HLA-DRB1
ENSG00000196131	2.37973	6.96321	6.40965	7.87894	ENSG00000196131	VN1R2
ENSG00000196132	0.0273062	0.0762815	0.0252981	0.0320479	ENSG00000196132	MYT1
ENSG00000196136	6.73008	0.276269	13.7962	4.24638	ENSG00000196136	SERPINA3
ENSG00000196138	15.4634	37.2329	37.5737	83.8552	ENSG00000196138	AC005831.1
ENSG00000196139	3.01647	2.16807	5.80675	0.97915	ENSG00000196139	AKR1C3
ENSG00000196141	39.9722	48.9054	37.8265	55.2217	ENSG00000196141	SPATS2L
ENSG00000196143	0	0	0	0	ENSG00000196143	OR11H13P
ENSG00000196150	9.49915	15.3212	19.9518	18.7026	ENSG00000196150	ZNF250
ENSG00000196151	2.68613	4.64871	4.90828	2.96798	ENSG00000196151	WDSUB1
ENSG00000196152	5.77206	4.98926	5.04411	3.79814	ENSG00000196152	ZNF79
ENSG00000196154	32.7341	13.5161	9.80127	61.2068	ENSG00000196154	S100A4

ENSG00000196155	5.14791	11.4157	19.5884	16.664	ENSG00000196155	PLEKHG4
ENSG00000196156	0	0.127724	0.115411	0.144474	ENSG00000196156	KRTAP4-3
ENSG00000196159	0.891901	0.52657	2.16847	6.06253	ENSG00000196159	FAT4
ENSG00000196166	0.926336	1.60193	1.24528	2.90906	ENSG00000196166	C8orf86
ENSG00000196167	0.278064	1.71448	0.645344	1.17147	ENSG00000196167	COLCA1
ENSG00000196169	0.96747	2.25367	2.45743	3.85614	ENSG00000196169	KIF19
ENSG00000196171	0	0	0	0	ENSG00000196171	OR6K2
ENSG00000196172	2.08683	2.43695	1.47117	1.94805	ENSG00000196172	ZNF681
ENSG00000196176	3.64348	12.1653	2.08337	6.8471	ENSG00000196176	HIST1H4A
ENSG00000196177	4.84946	7.23937	7.01926	12.0076	ENSG00000196177	ACADSB
ENSG00000196182	16.7399	14.5166	15.5178	9.72057	ENSG00000196182	STK40
ENSG00000196183	2.40451	1.32114	1.8861	4.8909	ENSG00000196183	RPS2P4
ENSG00000196184	0	0	0	0	ENSG00000196184	OR10J1
ENSG00000196187	21.2291	39.0717	22.0671	35.1301	ENSG00000196187	TMEM63A
ENSG00000196188	0.196419	0.475046	0.286472	0.459274	ENSG00000196188	CTSE
ENSG00000196189	8.98647	9.49159	10.3004	4.9256	ENSG00000196189	SEMA4A
ENSG00000196193	0.28503	0.812186	0.734056	0	ENSG00000196193	AC034229.1
ENSG00000196196	0.132348	1.01021	0.172731	0.714259	ENSG00000196196	HRCT1
ENSG00000196199	23.165	31.8149	34.4127	39.9162	ENSG00000196199	MPHOSPH8
ENSG00000196204	17.9669	25.6531	29.1744	29.8394	ENSG00000196204	RNF216P1
ENSG00000196205	7.70286	5.6828	5.73709	6.15596	ENSG00000196205	EEF1A1P5
ENSG00000196208	1.43688	4.11725	2.56179	5.03612	ENSG00000196208	GREB1
ENSG00000196209	2.64513	3.04006	2.25881	3.13196	ENSG00000196209	SIRPB2
ENSG00000196214	21.5028	35.152	33.3066	45.5684	ENSG00000196214	ZNF766
ENSG00000196218	1.37602	0.418739	1.58042	0.499535	ENSG00000196218	RYR1
ENSG00000196220	16.5128	37.0571	30.7491	32.581	ENSG00000196220	SRGAP3
ENSG00000196224	0	0.134958	0.243884	0.076271	ENSG00000196224	KRTAP5-3
ENSG00000196226	6.48139	11.8196	4.43158	7.06178	ENSG00000196226	HIST1H2BB
ENSG00000196227	4.37821	8.14377	3.7428	5.22417	ENSG00000196227	FAM217B
ENSG00000196228	0	0.264215	0.358106	0.298717	ENSG00000196228	SULT1C3
ENSG00000196230	18.3229	27.907	5.53428	0.464868	ENSG00000196230	TUBB
ENSG00000196231	0	0	0	0	ENSG00000196231	OR2J2
ENSG00000196233	16.2096	18.8012	17.8098	23.5075	ENSG00000196233	LCOR
ENSG00000196235	53.9469	43.9886	54.3617	52.5083	ENSG00000196235	SUPT5H
ENSG00000196236	9.49064	11.3771	12.824	13.9967	ENSG00000196236	XPNPEP3
ENSG00000196240	0	0	0	0	ENSG00000196240	OR2T2
ENSG00000196242	4.45499	3.94105	5.25855	4.05086	ENSG00000196242	OR2C3
ENSG00000196247	3.76084	8.02044	7.79968	9.16918	ENSG00000196247	ZNF107
ENSG00000196248	0	0.677021	0.281666	0	ENSG00000196248	OR10S1
ENSG00000196260	0.177216	0	0	0	ENSG00000196260	SFTA2
ENSG00000196262	781.971	588.936	303.285	333.134	ENSG00000196262	PPIA
ENSG00000196263	8.60069	16.828	17.2449	27.6065	ENSG00000196263	ZNF471
ENSG00000196266	0	0	0	0	ENSG00000196266	OR10J3
ENSG00000196267	17.2195	21.1752	18.5134	26.5958	ENSG00000196267	ZNF836
ENSG00000196268	20.5507	41.7772	37.3565	34.1181	ENSG00000196268	ZNF493
ENSG00000196274	9.09375	30.4849	19.6958	52.5673	ENSG00000196274	Metazoa_SRP
ENSG00000196275	6.78057	12.8087	12.5969	19.1266	ENSG00000196275	GTF2IRD2
ENSG00000196277	0.387002	1.31096	1.72781	3.08099	ENSG00000196277	GRM7
ENSG00000196284	6.13926	16.3263	16.3869	25.0225	ENSG00000196284	SUPT3H
ENSG00000196289	0	0.0860224	0.0777541	0	ENSG00000196289	BECN2
ENSG00000196290	12.5044	17.4244	11.2163	8.68824	ENSG00000196290	NIF3L1
ENSG00000196296	1.8689	2.05016	5.45253	5.04383	ENSG00000196296	ATP2A1
ENSG00000196301	0.0394657	0.0375419	0	0	ENSG00000196301	HLA-DRB9
ENSG00000196302	4.1439	0.10859	0.107448	6.55785	ENSG00000196302	AC146944.1

ENSG00000196305	75.406	196.215	241.125	116.783	ENSG00000196305	IARS
ENSG00000196312	19.0546	23.9362	29.3291	25.2775	ENSG00000196312	MFSD14C
ENSG00000196313	4.86844	6.55869	7.21696	5.40606	ENSG00000196313	POM121
ENSG00000196323	6.99296	12.9952	13.0796	11.8242	ENSG00000196323	ZBTB44
ENSG00000196326	0	0.548129	0	5.62889	ENSG00000196326	AKR1CL1
ENSG00000196329	0.0602719	0.226815	0.458995	0.466019	ENSG00000196329	GIMAP5
ENSG00000196331	20.4071	48.1807	7.18786	11.9075	ENSG00000196331	HIST1H2BO
ENSG00000196335	3.20332	7.47605	7.5793	12.6376	ENSG00000196335	STK31
ENSG00000196337	2.37704	3.94718	5.59289	2.24232	ENSG00000196337	CGB7
ENSG00000196338	0.197972	0.711238	0.689909	0.881685	ENSG00000196338	NLGN3
ENSG00000196341	0	0	0	0	ENSG00000196341	OR8D1
ENSG00000196344	7.60976	6.70884	8.84814	15.987	ENSG00000196344	ADH7
ENSG00000196345	2.71701	3.97007	5.57653	4.59774	ENSG00000196345	ZKSCAN7
ENSG00000196350	0	0.00734616	0.00674381	0.0166242	ENSG00000196350	ZNF729
ENSG00000196352	38.386	31.3177	28.417	28.0337	ENSG00000196352	CD55
ENSG00000196353	3.27915	1.73238	1.73512	3.52919	ENSG00000196353	CPNE4
ENSG00000196355	16.1529	34.2239	33.4893	47.9021	ENSG00000196355	AC021860.1
ENSG00000196357	2.41687	4.96461	4.96476	3.78468	ENSG00000196357	ZNF565
ENSG00000196358	1.31226	2.74433	2.33302	2.28343	ENSG00000196358	NTNG2
ENSG00000196361	0.514887	0.894403	0.737487	1.87721	ENSG00000196361	ELAVL3
ENSG00000196363	13.6757	15.7024	13.8541	11.8809	ENSG00000196363	WDR5
ENSG00000196365	30.6605	55.4428	73.2767	36.771	ENSG00000196365	LONP1
ENSG00000196366	0.759188	1.02205	1.51964	0.71363	ENSG00000196366	C9orf163
ENSG00000196367	4.76736	6.27002	6.2829	9.63515	ENSG00000196367	TRRAP
ENSG00000196368	0.933962	1.85294	2.52126	1.96102	ENSG00000196368	NUDT11
ENSG00000196369	4.69017	8.73537	6.46576	9.53551	ENSG00000196369	SRGAP2B
ENSG00000196371	0.438015	1.38192	0.775368	2.18676	ENSG00000196371	FUT4
ENSG00000196372	5.14397	6.19268	4.97423	2.92198	ENSG00000196372	ASB13
ENSG00000196374	13.0403	33.2072	8.20205	12.5287	ENSG00000196374	HIST1H2BM
ENSG00000196376	0.13409	0.275549	0.33076	0.954797	ENSG00000196376	SLC35F1
ENSG00000196378	1.49539	2.61135	1.93921	2.64778	ENSG00000196378	ZNF34
ENSG00000196381	4.20424	6.15282	6.25161	8.65794	ENSG00000196381	ZNF781
ENSG00000196383	0	0	0	0	ENSG00000196383	OR4Q2
ENSG00000196387	13.3987	13.4405	18.6699	11.9688	ENSG00000196387	ZNF140
ENSG00000196388	3.24985	4.02434	5.02237	2.99381	ENSG00000196388	INCA1
ENSG00000196390	0.114209	0.096271	0.1933	0.349453	ENSG00000196390	AC116337.1
ENSG00000196391	3.0751	7.04361	5.32174	6.61911	ENSG00000196391	ZNF774
ENSG00000196395	0	0	0	0	ENSG00000196395	AC244505.1
ENSG00000196396	45.3	43.7407	24.5104	31.9739	ENSG00000196396	PTPN1
ENSG00000196400	4.90279	14.3322	13.8923	16.0568	ENSG00000196400	BX255923.1
ENSG00000196403	0.200495	0.0648168	0	0.0726955	ENSG00000196403	OR10D1P
ENSG00000196405	10.0128	15.8181	19.4943	27.003	ENSG00000196405	EVL
ENSG00000196406	0	0	0	0	ENSG00000196406	SPANXD
ENSG00000196407	3.67781	6.20106	5.0132	4.73756	ENSG00000196407	THEM5
ENSG00000196408	0.197275	0.535213	1.03247	0	ENSG00000196408	NOXO1
ENSG00000196409	2.90328	4.5646	4.10501	2.73905	ENSG00000196409	ZNF658
ENSG00000196411	107.845	107.29	109.902	58.9695	ENSG00000196411	EPHB4
ENSG00000196415	0	0	0	0	ENSG00000196415	PRTN3
ENSG00000196417	10.135	12.2614	10.381	12.0476	ENSG00000196417	ZNF765
ENSG00000196418	11.1662	20.71	20.0775	35.7669	ENSG00000196418	ZNF124
ENSG00000196419	142.261	183.76	120.957	163.964	ENSG00000196419	XRCC6
ENSG00000196420	0	0.429541	0	0.846856	ENSG00000196420	S100A5
ENSG00000196422	14.2712	15.2243	12.598	7.44642	ENSG00000196422	PPP1R26
ENSG00000196427	0	0	0	0	ENSG00000196427	NBPF4

ENSG00000196428	58.2353	24.7096	26.2029	44.2362	ENSG00000196428	TSC22D2
ENSG00000196431	0.107435	0.10318	0.0931713	0	ENSG00000196431	CRYBA4
ENSG00000196433	0.291215	0.396738	0.379768	0.548238	ENSG00000196433	ASMT
ENSG00000196436	0.216884	6.4623	6.681	2.51066	ENSG00000196436	NPIPB15
ENSG00000196437	6.99413	12.5535	10.912	15.3324	ENSG00000196437	ZNF569
ENSG00000196440	4.11793	6.84835	6.09008	9.8316	ENSG00000196440	ARMCX4
ENSG00000196449	13.1015	11.3423	10.8486	7.17709	ENSG00000196449	YRDC
ENSG00000196453	5.24769	5.0334	7.15345	3.75888	ENSG00000196453	ZNF777
ENSG00000196455	16.817	20.1644	12.8741	15.2061	ENSG00000196455	PIK3R4
ENSG00000196456	3.5831	7.01221	5.65754	7.1584	ENSG00000196456	ZNF775
ENSG00000196458	5.70172	8.38315	11.2191	13.9267	ENSG00000196458	ZNF605
ENSG00000196459	9.77483	13.0889	15.6745	16.8609	ENSG00000196459	TRAPPC2
ENSG00000196460	0.101944	0.134084	0.280174	29.2691	ENSG00000196460	RFX8
ENSG00000196465	18.1505	23.0743	20.5884	20.0275	ENSG00000196465	MYL6B
ENSG00000196466	4.75329	5.97022	2.6316	5.06522	ENSG00000196466	ZNF799
ENSG00000196468	0.0522752	0.0617862	0	0.0899141	ENSG00000196468	FGF16
ENSG00000196470	14.5824	21.2164	31.5646	30.7523	ENSG00000196470	SIAH1
ENSG00000196472	0	0	0	0	ENSG00000196472	AC111000.1
ENSG00000196475	0	0	0	0.0667107	ENSG00000196475	GK2
ENSG00000196476	1.48565	2.52382	2.21874	2.43068	ENSG00000196476	C20orf96
ENSG00000196482	1.22692	3.33308	2.65269	4.40162	ENSG00000196482	ESRRG
ENSG00000196497	16.3484	21.2678	27.6217	16.4845	ENSG00000196497	IPO4
ENSG00000196498	33.2205	58.1596	49.5658	116.048	ENSG00000196498	NCOR2
ENSG00000196502	2.2528	5.92003	2.80252	3.3839	ENSG00000196502	SULT1A1
ENSG00000196503	1.57866	2.25369	2.27216	3.45803	ENSG00000196503	ARL9
ENSG00000196504	86.5433	76.1029	89.7581	73.9786	ENSG00000196504	PRPF40A
ENSG00000196505	11.6124	12.7147	14.8885	11.1149	ENSG00000196505	GDAP2
ENSG00000196507	8.54155	6.4687	5.9648	9.5757	ENSG00000196507	TCEAL3
ENSG00000196510	36.4332	39.5847	48.943	36.9028	ENSG00000196510	ANAPC7
ENSG00000196511	3.95494	7.76499	7.62811	10.6423	ENSG00000196511	TPK1
ENSG00000196517	3.25704	26.398	42.016	6.85444	ENSG00000196517	SLC6A9
ENSG00000196526	22.2318	30.4454	29.8157	59.5591	ENSG00000196526	AFAP1
ENSG00000196531	381.111	244.146	223.706	171.817	ENSG00000196531	NACA
ENSG00000196532	23.2927	115.079	17.8642	30.7553	ENSG00000196532	HIST1H3C
ENSG00000196533	6.6927	6.70715	8.91443	13.3178	ENSG00000196533	C1orf186
ENSG00000196534	0	0	0	0	ENSG00000196534	OR9K1P
ENSG00000196535	61.7512	121.246	74.7343	85.4344	ENSG00000196535	MYO18A
ENSG00000196539	0	0	0	0	ENSG00000196539	OR2T3
ENSG00000196542	1.02736	0.346266	0.748415	0.437262	ENSG00000196542	SPTSSB
ENSG00000196544	6.33478	3.02171	2.9636	2.79053	ENSG00000196544	BORCS6
ENSG00000196547	7.9575	10.0932	9.42631	11.2885	ENSG00000196547	MAN2A2
ENSG00000196549	11.8108	22.6904	14.1591	274.745	ENSG00000196549	MME
ENSG00000196550	4.28371	3.90097	2.37362	4.81781	ENSG00000196550	FAM72A
ENSG00000196557	0.210293	0.181685	0.122437	2.40384	ENSG00000196557	CACNA1H
ENSG00000196562	146.4	230.223	203.028	80.1016	ENSG00000196562	SULF2
ENSG00000196564	5.00397	8.14287	7.39034	14.1518	ENSG00000196564	AL096700.1
ENSG00000196565	0.906166	1.95323	2.19105	4.13366	ENSG00000196565	HBG2
ENSG00000196569	1.21689	3.26841	1.63911	13.4585	ENSG00000196569	LAMA2
ENSG00000196570	0	0	0	0	ENSG00000196570	PFN3
ENSG00000196576	91.2258	140.353	175.742	105.6	ENSG00000196576	PLXNB2
ENSG00000196578	0	0	0	0.0732535	ENSG00000196578	OR5AC2
ENSG00000196581	4.12747	5.15508	4.15171	4.18139	ENSG00000196581	AJAP1
ENSG00000196584	7.10906	16.3661	13.9804	28.3165	ENSG00000196584	XRCC2
ENSG00000196586	26.9936	17.9237	17.2419	21.717	ENSG00000196586	MYO6

ENSG00000196588	22.4158	21.3613	30.7349	42.977	ENSG00000196588	MKL1
ENSG00000196591	42.9364	42.753	43.1498	52.5998	ENSG00000196591	HDAC2
ENSG00000196593	2.46064	4.14088	4.2936	6.25394	ENSG00000196593	ANKRD20A19P
ENSG00000196597	4.88557	8.26328	7.75045	7.67549	ENSG00000196597	ZNF782
ENSG00000196600	2.95438	7.41514	7.069	11.1484	ENSG00000196600	SLC22A25
ENSG00000196604	0	0.0695773	0.0277258	0.0639678	ENSG00000196604	POTEF
ENSG00000196605	10.6704	12.3617	15.7955	10.2791	ENSG00000196605	ZNF846
ENSG00000196610	0.0166366	0	0	0.0350395	ENSG00000196610	HLA-DQB2
ENSG00000196611	82.5079	63.8294	8.05544	171.618	ENSG00000196611	MMP1
ENSG00000196616	0.758915	1.38787	1.21773	2.49664	ENSG00000196616	ADH1B
ENSG00000196620	0.128951	0.0551545	0.180785	0	ENSG00000196620	UGT2B15
ENSG00000196622	0.0276799	0.00890841	0	0.0203596	ENSG00000196622	RIMBP3
ENSG00000196628	11.0376	20.1074	34.818	51.6465	ENSG00000196628	TCF4
ENSG00000196632	0.310939	0.432468	0.447169	0.548703	ENSG00000196632	WNK3
ENSG00000196636	5.81678	7.03551	6.70717	4.12496	ENSG00000196636	SDHAF3
ENSG00000196639	11.0508	13.1285	5.58984	10.0356	ENSG00000196639	HRH1
ENSG00000196642	35.4056	35.2741	34.0939	32.6276	ENSG00000196642	RABL6
ENSG00000196644	2.19825	6.19675	3.55396	5.63656	ENSG00000196644	GPR89C
ENSG00000196646	7.76989	5.4932	7.03619	8.75305	ENSG00000196646	ZNF136
ENSG00000196648	3.62707	8.26533	5.94966	6.58615	ENSG00000196648	GOLGA6L20
ENSG00000196652	5.05708	5.82198	7.29553	4.73469	ENSG00000196652	ZKSCAN5
ENSG00000196653	5.94734	5.13288	6.59311	3.98662	ENSG00000196653	ZNF502
ENSG00000196655	17.7891	20.9984	17.1669	20.8237	ENSG00000196655	TRAPPC4
ENSG00000196656	265.363	268.909	212.315	152.126	ENSG00000196656	AC004057.1
ENSG00000196659	2.08295	1.70868	1.65691	1.23663	ENSG00000196659	TTC30B
ENSG00000196660	0.549287	0.765891	0.560255	0.837895	ENSG00000196660	SLC30A10
ENSG00000196661	0	0.0603329	0.0545239	0.0682813	ENSG00000196661	OR8B3
ENSG00000196663	6.21718	7.86434	10.8696	9.51878	ENSG00000196663	TECPR2
ENSG00000196664	0.223604	0.565069	1.37172	0.87164	ENSG00000196664	TLR7
ENSG00000196666	0.336628	0.831746	0.584997	1.37174	ENSG00000196666	FAM180B
ENSG00000196670	12.3012	14.9765	20.3276	10.7613	ENSG00000196670	ZFP62
ENSG00000196674	0.808405	1.88418	3.71016	3.10979	ENSG00000196674	Z98881.1
ENSG00000196678	17.9012	25.5453	28.5966	19.1549	ENSG00000196678	ERI2
ENSG00000196683	64.3844	66.1152	61.261	57.3953	ENSG00000196683	TOMM7
ENSG00000196684	2.72232	6.16272	4.0668	5.48446	ENSG00000196684	HSH2D
ENSG00000196689	2.19866	3.87529	2.74945	5.43693	ENSG00000196689	TRPV1
ENSG00000196693	3.30376	4.75091	5.21569	4.06851	ENSG00000196693	ZNF33B
ENSG00000196700	16.7187	13.7544	18.7344	9.47589	ENSG00000196700	ZNF512B
ENSG00000196704	12.0258	15.8879	14.0958	9.68859	ENSG00000196704	AMZ2
ENSG00000196705	56.6964	46.67	54.6783	74.8427	ENSG00000196705	ZNF431
ENSG00000196711	0.0490617	0.141704	0.238239	0.161777	ENSG00000196711	ALKAL1
ENSG00000196712	27.0535	52.5436	53.176	72.8322	ENSG00000196712	NF1
ENSG00000196715	8.24967	7.41161	6.8121	6.92947	ENSG00000196715	VKORC1L1
ENSG00000196724	6.00572	8.1858	9.51831	12.5802	ENSG00000196724	ZNF418
ENSG00000196730	13.5489	1.44796	3.4013	8.61862	ENSG00000196730	DAPK1
ENSG00000196734	0.211885	0	0.184386	0.465842	ENSG00000196734	LCE1B
ENSG00000196735	1.02249	1.96654	1.39482	2.64972	ENSG00000196735	HLA-DQA1
ENSG00000196737	2.55718	6.3612	5.48257	11.1542	ENSG00000196737	AC087392.1
ENSG00000196739	16.6268	37.0652	41.497	49.2045	ENSG00000196739	COL27A1
ENSG00000196741	1.25039	2.3687	2.13313	2.03947	ENSG00000196741	LINC01560
ENSG00000196743	107.46	67.6692	68.3332	33.4042	ENSG00000196743	GM2A
ENSG00000196747	23.5809	95.2016	22.9402	13.3345	ENSG00000196747	HIST1H2AI
ENSG00000196748	0	0	0	0	ENSG00000196748	CLPSL2
ENSG00000196754	2422.12	4937.72	1229.58	1716.25	ENSG00000196754	S100A2

ENSG00000196757	6.51247	9.91217	5.99182	7.55437	ENSG00000196757	ZNF700
ENSG00000196758	0.0442219	0.171285	0.155117	0.301946	ENSG00000196758	AC079612.1
ENSG00000196767	0.441243	0.781587	1.2797	2.50074	ENSG00000196767	POU3F4
ENSG00000196772	0	0	0	0	ENSG00000196772	OR14A16
ENSG00000196774	0.0732655	0.201787	0	0.200234	ENSG00000196774	ANKRD20A1
ENSG00000196776	55.2396	139.843	50.6429	55.9409	ENSG00000196776	CD47
ENSG00000196777	0.351814	1.23246	4.88311	1.77713	ENSG00000196777	AL162574.1
ENSG00000196778	0	0	0.0518381	0	ENSG00000196778	OR52K1
ENSG00000196781	19.3971	14.6272	17.6071	9.86251	ENSG00000196781	TLE1
ENSG00000196782	1.54576	1.51483	1.95918	2.05176	ENSG00000196782	MAML3
ENSG00000196787	4.77305	17.8892	4.36126	5.5221	ENSG00000196787	HIST1H2AG
ENSG00000196792	38.1653	49.1596	52.3118	58.3382	ENSG00000196792	STRN3
ENSG00000196793	0.553509	1.19632	1.27256	1.82978	ENSG00000196793	ZNF239
ENSG00000196796	0	0	0.0652474	0	ENSG00000196796	NPIPB10P
ENSG00000196800	1.35562	0	0	0.37733	ENSG00000196800	SPINK14
ENSG00000196805	0	0.233123	0	0.294331	ENSG00000196805	SPRR2B
ENSG00000196811	1.28216	3.28668	3.74259	2.6771	ENSG00000196811	CHRNG
ENSG00000196812	2.97469	1.7102	1.85498	1.21353	ENSG00000196812	ZSCAN16
ENSG00000196814	54.7428	261.421	104.082	351.927	ENSG00000196814	MVB12B
ENSG00000196821	36.2723	19.2911	19.4358	17.3018	ENSG00000196821	C6orf106
ENSG00000196826	0.0259625	0.971716	0.758038	0.703405	ENSG00000196826	AC008758.1
ENSG00000196832	0	0	0.0961986	0	ENSG00000196832	OR11G2
ENSG00000196834	0.323564	0.629303	0.473268	1.12776	ENSG00000196834	POTEI
ENSG00000196839	5.45704	8.17629	3.99728	6.7959	ENSG00000196839	ADA
ENSG00000196843	2.39021	3.63181	3.90365	4.367	ENSG00000196843	ARID5A
ENSG00000196844	0.786727	1.74442	1.98594	3.32385	ENSG00000196844	PATE2
ENSG00000196850	7.73245	8.42258	5.43421	9.70926	ENSG00000196850	PPTC7
ENSG00000196859	0.0420095	0.040374	0.0364746	0.0455203	ENSG00000196859	KRT39
ENSG00000196860	0.417658	1.24137	2.4872	0.59084	ENSG00000196860	TOMM20L
ENSG00000196861	0	0	0	0	ENSG00000196861	AC002994.1
ENSG00000196862	0.0496741	0.033338	0.0289229	0	ENSG00000196862	RGPD4
ENSG00000196865	7.25581	10.8544	10.5077	9.59573	ENSG00000196865	NHLRC2
ENSG00000196866	29.6381	66.7299	37.871	12.6916	ENSG00000196866	HIST1H2AD
ENSG00000196867	7.5614	15.4837	9.82595	12.1365	ENSG00000196867	ZFP28
ENSG00000196872	5.88278	4.58827	0.50298	0.892691	ENSG00000196872	KIAA1211L
ENSG00000196873	1.87642	4.94388	9.30817	4.84416	ENSG00000196873	CBWD3
ENSG00000196876	0.726886	1.55383	4.71666	12.3426	ENSG00000196876	SCN8A
ENSG00000196878	2091.88	3129.76	1373.42	1747.24	ENSG00000196878	LAMB3
ENSG00000196890	18.2878	18.6643	3.28721	1.34557	ENSG00000196890	HIST3H2BB
ENSG00000196900	0.877715	0.833821	1.25651	0	ENSG00000196900	TEX43
ENSG00000196911	3.63384	4.04713	5.80625	5.10265	ENSG00000196911	KPNA5
ENSG00000196912	23.6407	51.0075	35.4493	57.0149	ENSG00000196912	ANKRD36B
ENSG00000196914	44.341	62.501	62.575	77.1857	ENSG00000196914	ARHGEF12
ENSG00000196917	3.11167	4.332	3.32975	4.80287	ENSG00000196917	HCAR1
ENSG00000196922	12.1573	13.308	19.6712	17.3738	ENSG00000196922	ZNF252P
ENSG00000196923	31.5558	65.3068	96.5565	117.241	ENSG00000196923	PDLIM7
ENSG00000196924	185.134	352.86	244.884	293.602	ENSG00000196924	FLNA
ENSG00000196927	0.854161	2.6395	2.23899	4.66694	ENSG00000196927	AC009093.1
ENSG00000196932	0.0751104	0.114795	0.204786	0.66771	ENSG00000196932	TMEM26
ENSG00000196933	0	0.564585	0	0.317493	ENSG00000196933	RPS26P11
ENSG00000196934	0	0	0	0	ENSG00000196934	RIMBP3B
ENSG00000196935	5.95669	16.2836	15.5149	24.2282	ENSG00000196935	SRGAP1
ENSG00000196936	0	0.192322	0.289265	0.483272	ENSG00000196936	OR2L8
ENSG00000196937	94.1452	44.4134	26.6346	45.3082	ENSG00000196937	FAM3C

ENSG00000196943	15.9021	16.5514	22.1081	10.0468	ENSG00000196943	NOP9
ENSG00000196944	0	0	0	0	ENSG00000196944	OR2T4
ENSG00000196946	0.633978	1.44886	1.95164	1.29297	ENSG00000196946	ZNF705A
ENSG00000196950	38.3365	45.1484	24.8985	18.7117	ENSG00000196950	SLC39A10
ENSG00000196954	53.6972	41.7901	54.9875	28.1769	ENSG00000196954	CASP4
ENSG00000196961	37.6384	43.8718	42.1269	39.8663	ENSG00000196961	AP2A1
ENSG00000196963	0	0.395984	0.182722	1.00232	ENSG00000196963	PCDHB16
ENSG00000196966	12.1288	30.7619	13.1159	12.1915	ENSG00000196966	HIST1H23E
ENSG00000196967	15.1796	16.8212	18.3512	19.5662	ENSG00000196967	ZNF585A
ENSG00000196968	13.7154	16.554	13.287	23.5827	ENSG00000196968	FUT11
ENSG00000196970	0.256482	0.275249	0.328743	0.486884	ENSG00000196970	NXF4
ENSG00000196975	32.7257	19.3969	34.1246	27.7957	ENSG00000196975	ANXA4
ENSG00000196976	3.09281	2.31908	1.34923	0.90519	ENSG00000196976	LAGE3
ENSG00000196979	0.292789	0.477686	0.446509	0.701287	ENSG00000196979	AL360004.1
ENSG00000196981	4.26672	6.76646	7.48279	9.67089	ENSG00000196981	WDR5B
ENSG00000196987	1.05322	1.7626	1.82098	2.3989	ENSG00000196987	LCA10
ENSG00000196990	0	0	0.0522867	0.129767	ENSG00000196990	FAM163B
ENSG00000196993	1.69964	1.94353	3.32653	6.82403	ENSG00000196993	NPIPB9
ENSG00000196998	20.1219	13.979	17.0049	11.687	ENSG00000196998	WDR45
ENSG00000197006	61.6462	38.5706	23.1211	26.3056	ENSG00000197006	METTL9
ENSG00000197008	5.03392	7.92763	6.8283	6.96449	ENSG00000197008	ZNF138
ENSG00000197013	16.704	29.9416	29.678	37.1166	ENSG00000197013	ZNF429
ENSG00000197015	15.0286	37.6537	39.5244	67.6769	ENSG00000197015	AL353898.1
ENSG00000197016	7.202	15.4931	18.0566	24.1414	ENSG00000197016	ZNF470
ENSG00000197019	9.3108	10.1147	10.7798	7.34561	ENSG00000197019	SERTAD1
ENSG00000197020	10.017	19.6378	16.9457	23.0404	ENSG00000197020	ZNF100
ENSG00000197021	5.62304	0.116325	7.82064	5.10415	ENSG00000197021	CXorf40B
ENSG00000197023	0	0	0	0	ENSG00000197023	OR51A6P
ENSG00000197024	10.9393	9.49424	10.6698	7.71258	ENSG00000197024	ZNF398
ENSG00000197037	9.55295	13.6882	12.8495	10.7147	ENSG00000197037	ZSCAN25
ENSG00000197038	0	1.10651	0	0.613825	ENSG00000197038	RBMY1A3P
ENSG00000197043	6.74818	46.9057	13.8746	79.234	ENSG00000197043	ANXA6
ENSG00000197044	7.18056	12.2457	12.1277	12.6788	ENSG00000197044	ZNF441
ENSG00000197045	38.9747	31.1068	28.7603	22.4416	ENSG00000197045	GMFB
ENSG00000197046	3.18975	8.32523	6.74122	12.2495	ENSG00000197046	SIGLEC15
ENSG00000197047	22.9078	49.7756	43.2811	100.544	ENSG00000197047	Z73979.1
ENSG00000197050	10.3925	12.0187	11.4107	10.7138	ENSG00000197050	ZNF420
ENSG00000197054	3.87398	6.91196	8.04461	5.27432	ENSG00000197054	ZNF763
ENSG00000197056	20.4561	25.9692	25.7954	24.7158	ENSG00000197056	ZMYM1
ENSG00000197057	0.27867	0.519807	0.379577	1.03961	ENSG00000197057	DTHD1
ENSG00000197061	21.4798	41.6378	20.7027	10.1273	ENSG00000197061	HIST1H4C
ENSG00000197062	4.36351	5.80784	3.91556	4.93271	ENSG00000197062	ZSCAN26
ENSG00000197063	13.0789	10.5568	11.9321	10.1371	ENSG00000197063	MAFG
ENSG00000197067	0	0	0	0.146507	ENSG00000197067	OR2T32P
ENSG00000197070	80.3824	90.1445	56.8941	25.0066	ENSG00000197070	ARRDC1
ENSG00000197071	0.731728	1.16286	2.52251	3.3398	ENSG00000197071	AC010243.1
ENSG00000197077	12.1323	19.491	21.7867	13.0287	ENSG00000197077	KIAA1671
ENSG00000197079	0.0700608	0	0	0	ENSG00000197079	KRT35
ENSG00000197081	44.2988	75.6493	136.182	61.2515	ENSG00000197081	IGF2R
ENSG00000197083	2.54375	4.29579	6.17879	2.68605	ENSG00000197083	ZNF300P1
ENSG00000197084	0.906344	1.02346	0.548623	1.60349	ENSG00000197084	LCE1C
ENSG00000197092	0	0	0	0.00423412	ENSG00000197092	GOLGA6L16P
ENSG00000197093	2.34958	6.61541	6.24296	5.76294	ENSG00000197093	GAL3ST4
ENSG00000197102	165.019	208.586	160.072	199.996	ENSG00000197102	DYNC1H1

ENSG00000197106	0.381502	0.610541	0.326984	0.592146	ENSG00000197106	SLC6A17
ENSG00000197110	0	0	0	0.122254	ENSG00000197110	IFNL3
ENSG00000197111	65.0187	111.338	115.182	116.724	ENSG00000197111	PCBP2
ENSG00000197114	18.7353	11.9116	13.7871	11.6281	ENSG00000197114	ZGPAT
ENSG00000197119	19.808	35.7776	34.3383	22.6662	ENSG00000197119	SLC25A29
ENSG00000197121	5.18637	19.757	17.029	16.1412	ENSG00000197121	PGAP1
ENSG00000197122	28.7955	45.1398	41.0307	34.4314	ENSG00000197122	SRC
ENSG00000197123	0	0.0356913	0.06449	0.0404148	ENSG00000197123	ZNF679
ENSG00000197124	6.12734	14.2599	16.1775	9.60865	ENSG00000197124	ZNF682
ENSG00000197125	0	0.0571626	0.0516605	0	ENSG00000197125	OR8B8
ENSG00000197128	10.8456	11.5953	15.6754	10.9061	ENSG00000197128	ZNF772
ENSG00000197134	6.3209	11.3529	7.55065	9.84869	ENSG00000197134	ZNF257
ENSG00000197136	22.1245	27.3897	32.9911	29.0297	ENSG00000197136	PCNX3
ENSG00000197140	13.6164	30.1517	28.9529	60.0658	ENSG00000197140	ADAM32
ENSG00000197142	0.516356	1.04907	0.625277	0.625353	ENSG00000197142	ACSL5
ENSG00000197146	0.672612	1.10471	1.20411	3.46002	ENSG00000197146	AL133458.1
ENSG00000197147	4.66528	3.52539	6.76926	2.56274	ENSG00000197147	LRRC8B
ENSG00000197149	0.39869	0.377632	0.388734	0.346741	ENSG00000197149	AC107956.1
ENSG00000197150	32.5723	40.489	29.4544	29.676	ENSG00000197150	ABCB8
ENSG00000197153	7.77717	25.7813	10.9099	8.59512	ENSG00000197153	HIST1H3J
ENSG00000197157	91.1498	143.518	117.022	131.751	ENSG00000197157	SND1
ENSG00000197161	0.0672649	0.260874	0.293208	0.221183	ENSG00000197161	AC023080.1
ENSG00000197162	5.9998	7.05361	9.42191	11.297	ENSG00000197162	ZNF785
ENSG00000197165	0.694886	1.21335	1.81717	1.31872	ENSG00000197165	SULT1A2
ENSG00000197168	0.651491	1.6579	1.53986	2.35859	ENSG00000197168	NEK5
ENSG00000197170	17.5073	18.9132	24.7586	25.5934	ENSG00000197170	PSMD12
ENSG00000197171	0.009462	0.0181999	0.0164453	0.0102936	ENSG00000197171	AL672167.1
ENSG00000197172	0	0	0	0	ENSG00000197172	MAGEA6
ENSG00000197177	0.191418	0.479025	0.504138	0.734339	ENSG00000197177	ADGRA1
ENSG00000197180	4.38934	3.6115	2.84304	3.46927	ENSG00000197180	CH17-340M24.3
ENSG00000197181	0.784424	1.90707	1.09101	3.90097	ENSG00000197181	PIWIL2
ENSG00000197182	42.4161	76.9321	97.3521	87.4356	ENSG00000197182	MIRLET7BHG
ENSG00000197183	8.22761	5.59114	6.90352	10.8781	ENSG00000197183	NOL4L
ENSG00000197185	0	0	0	0	ENSG00000197185	SSXP1
ENSG00000197191	29.4131	1.46224	3.69431	2.93187	ENSG00000197191	CYSRT1
ENSG00000197208	2.2812	6.03143	5.94442	4.08127	ENSG00000197208	SLC22A4
ENSG00000197213	0	0.0703176	0	0.519323	ENSG00000197213	ZSCAN5B
ENSG00000197214	0.0720087	0	0	0.0782357	ENSG00000197214	TCEA1P1
ENSG00000197217	140.12	107.731	83.4997	76.2749	ENSG00000197217	ENTPD4
ENSG00000197223	37.6175	49.9041	100.98	78.7609	ENSG00000197223	C1D
ENSG00000197226	59.8344	67.48	73.2987	69.1174	ENSG00000197226	TBC1D9B
ENSG00000197233	0.0663187	0	0	0.0721459	ENSG00000197233	OR1J2
ENSG00000197238	70.0877	216.917	92.0259	46.4407	ENSG00000197238	HIST1H4J
ENSG00000197241	0	0	0.0654897	0.0411753	ENSG00000197241	SLC2A7
ENSG00000197245	0.152071	0.111199	0.266959	0.166497	ENSG00000197245	FAM110D
ENSG00000197249	0.931803	2.8766	2.1327	1.42351	ENSG00000197249	SERPINA1
ENSG00000197253	0.261817	0.701289	0.961988	1.34632	ENSG00000197253	TPSB2
ENSG00000197254	0.797819	0	0	0	ENSG00000197254	AP000445.1
ENSG00000197256	13.0944	21.2408	14.3166	59.8157	ENSG00000197256	KANK2
ENSG00000197258	0.129569	0.0423894	0	0.0987157	ENSG00000197258	EIF4BP6
ENSG00000197261	28.3822	55.4118	46.7215	27.906	ENSG00000197261	C6orf141
ENSG00000197262	0	0	0	0	ENSG00000197262	CCL4L2
ENSG00000197263	0.058204	0	0	0	ENSG00000197263	OR8D2
ENSG00000197265	25.3687	23.7621	23.023	22.2132	ENSG00000197265	GTF2E2

ENSG00000197272	0.397532	0.721489	0.499365	0.882406	ENSG00000197272	IL27
ENSG00000197273	0	0	0.109641	0	ENSG00000197273	GUCA2A
ENSG00000197275	3.01248	8.60562	4.26494	6.70161	ENSG00000197275	RAD54B
ENSG00000197279	3.48179	5.33869	1.69408	1.34476	ENSG00000197279	ZNF165
ENSG00000197283	3.21955	8.46418	5.066	10.1855	ENSG00000197283	SYNGAP1
ENSG00000197284	0.506584	0.326722	1.70994	2.81608	ENSG00000197284	RP11-589F5.3
ENSG00000197296	5.84516	6.31695	4.98464	6.8418	ENSG00000197296	FITM2
ENSG00000197299	3.16128	8.749	2.14338	5.61473	ENSG00000197299	BLM
ENSG00000197301	20.9148	107.276	19.9797	117.835	ENSG00000197301	AC090673.1
ENSG00000197302	9.89922	11.309	13.4742	10.8585	ENSG00000197302	ZNF720
ENSG00000197309	0.0596092	0.115313	0.207352	0.259802	ENSG00000197309	OR10D3
ENSG00000197312	10.5807	17.344	16.9963	15.4741	ENSG00000197312	DDI2
ENSG00000197320	0.0576396	0	0.015561	0	ENSG00000197320	AC060834.1
ENSG00000197321	105.842	88.0372	115.314	106.181	ENSG00000197321	SVIL
ENSG00000197322	0.907446	2.22052	1.48355	2.83203	ENSG00000197322	C17orf102
ENSG00000197323	19.7282	22.9421	20.2976	21.4808	ENSG00000197323	TRIM33
ENSG00000197324	106.955	81.7629	66.8161	47.622	ENSG00000197324	LRP10
ENSG00000197329	22.598	22.203	19.2222	18.5122	ENSG00000197329	PELI1
ENSG00000197334	12.7502	21.7145	27.7511	38.7642	ENSG00000197334	Metazoa_SRP
ENSG00000197343	29.5613	52.8623	51.1893	45.5243	ENSG00000197343	ZNF655
ENSG00000197345	19.0074	17.1742	20.2057	12.7152	ENSG00000197345	MRPL21
ENSG00000197353	0	0	0.103379	0	ENSG00000197353	LYPD2
ENSG00000197355	3.39563	9.17344	4.74021	6.9132	ENSG00000197355	UAP1L1
ENSG00000197358	4.74097	5.14301	4.12352	5.78682	ENSG00000197358	BNIP3P1
ENSG00000197360	0.39165	1.97875	0.830798	1.85293	ENSG00000197360	ZNF98
ENSG00000197361	0.926485	2.55959	1.59944	2.36605	ENSG00000197361	FBXL22
ENSG00000197362	3.5586	4.99356	8.30569	7.37643	ENSG00000197362	ZNF786
ENSG00000197363	5.87529	5.64788	9.69976	8.17536	ENSG00000197363	ZNF517
ENSG00000197364	0	0	0	0	ENSG00000197364	S100A7L2
ENSG00000197372	20.9492	31.3538	24.8834	38.4722	ENSG00000197372	ZNF675
ENSG00000197375	16.6774	10.9888	10.583	6.75327	ENSG00000197375	SLC22A5
ENSG00000197376	0.29747	0.605339	0.51465	1.26872	ENSG00000197376	AC089987.1
ENSG00000197380	4.12885	7.87091	7.08126	13.2578	ENSG00000197380	DACT3
ENSG00000197381	7.5972	25.1865	35.661	28.6523	ENSG00000197381	ADARB1
ENSG00000197385	6.33429	7.99463	4.64453	5.07652	ENSG00000197385	ZNF860
ENSG00000197386	30.8831	40.2151	36.9657	55.0349	ENSG00000197386	HTT
ENSG00000197403	0	0	0	0.0651724	ENSG00000197403	OR6N1
ENSG00000197405	5.34668	15.74	14.5517	38.7065	ENSG00000197405	C5AR1
ENSG00000197406	0.37382	0.0257358	0.0232662	0.0586174	ENSG00000197406	DIO3
ENSG00000197408	1.19759	1.81795	1.67479	3.95825	ENSG00000197408	CYP2B6
ENSG00000197409	29.7855	54.5816	19.093	22.9873	ENSG00000197409	HIST1H3D
ENSG00000197410	3.29875	8.77919	8.48235	11.0425	ENSG00000197410	DCHS2
ENSG00000197414	0.651092	1.37913	1.19132	1.52983	ENSG00000197414	GOLGA6L1
ENSG00000197415	1.6468	1.92993	2.31202	8.24347	ENSG00000197415	VEPH1
ENSG00000197416	0	0	0	0	ENSG00000197416	FABP12
ENSG00000197417	5.65428	7.29652	5.13666	5.84101	ENSG00000197417	SHPK
ENSG00000197421	0.111211	0.467388	0.471124	0.861942	ENSG00000197421	GGT3P
ENSG00000197428	0	0.05178	0.0935973	0.176076	ENSG00000197428	OR51D1
ENSG00000197429	12.2215	12.5931	16.673	15.9354	ENSG00000197429	IPP
ENSG00000197430	0.124357	1.23789	0.715912	0.725598	ENSG00000197430	OPALIN
ENSG00000197437	0	0	0	0	ENSG00000197437	OR13G1
ENSG00000197442	6.08811	17.862	14.6213	29.1735	ENSG00000197442	MAP3K5
ENSG00000197444	0.22288	0.606215	0.556657	0.556098	ENSG00000197444	OGDHL
ENSG00000197445	0.045172	0.173993	0.0786339	0.0987567	ENSG00000197445	C16orf47

ENSG00000197446	0.489716	0.581543	0.336088	1.62913	ENSG00000197446	CYP2F1
ENSG00000197448	56.2532	56.3612	44.9116	37.6476	ENSG00000197448	GSTK1
ENSG00000197451	39.5437	42.1653	54.1703	43.521	ENSG00000197451	HNRNPAB
ENSG00000197454	0	0	0	0	ENSG00000197454	OR2L5
ENSG00000197457	1.44268	4.7887	1.91224	4.40536	ENSG00000197457	STMN3
ENSG00000197459	29.7736	74.0711	16.6056	19.5494	ENSG00000197459	HIST1H2BH
ENSG00000197461	13.0574	48.8832	38.4911	20.9926	ENSG00000197461	PDGFA
ENSG00000197465	1.75511	3.77647	4.07583	5.37127	ENSG00000197465	GYPE
ENSG00000197467	1.19284	8.59187	1.16565	8.65501	ENSG00000197467	COL13A1
ENSG00000197468	0	0	0	0	ENSG00000197468	AC073648.1
ENSG00000197471	5.48506	13.0683	11.9233	23.3103	ENSG00000197471	SPN
ENSG00000197472	1.15718	8.28016	2.97908	5.44291	ENSG00000197472	ZNF695
ENSG00000197475	0.971695	1.98174	2.24608	2.83147	ENSG00000197475	ADAM3A
ENSG00000197476	2.18997	3.27786	2.29637	2.88876	ENSG00000197476	AC034105.1
ENSG00000197479	0.188731	0.370128	0.290832	0.623178	ENSG00000197479	PCDHB11
ENSG00000197483	2.12023	1.83788	2.61142	1.99621	ENSG00000197483	ZNF628
ENSG00000197487	1.50045	0	0	0	ENSG00000197487	GALP
ENSG00000197496	1.54618	1.15847	1.31223	8.39748	ENSG00000197496	SLC2A10
ENSG00000197497	9.16065	18.9949	17.0274	17.8485	ENSG00000197497	ZNF665
ENSG00000197498	12.9901	13.3783	13.272	10.2983	ENSG00000197498	RPF2
ENSG00000197502	0	0	5.74341	42.074	ENSG00000197502	AL627171.1
ENSG00000197506	3.93352	2.68547	5.06513	2.97566	ENSG00000197506	SLC28A3
ENSG00000197520	0.959592	1.22195	2.29485	4.4524	ENSG00000197520	FAM177B
ENSG00000197530	32.623	51.7185	45.6777	31.9294	ENSG00000197530	MIB2
ENSG00000197532	0	0	0	0.13803	ENSG00000197532	OR6Y1
ENSG00000197535	25.7559	38.8855	39.0682	46.3473	ENSG00000197535	MYO5A
ENSG00000197536	11.5327	24.5705	22.4406	33.872	ENSG00000197536	C5orf56
ENSG00000197540	0.266378	0.0847121	0.173338	0.0723281	ENSG00000197540	GZMM
ENSG00000197548	27.2429	51.4488	42.4119	62.1985	ENSG00000197548	ATG7
ENSG00000197549	0.191543	0.39114	0.331258	0.447651	ENSG00000197549	PRAMENP
ENSG00000197550	1.85117	8.55442	0.310813	1.34095	ENSG00000197550	AL359955.1
ENSG00000197555	27.3675	42.9703	46.0823	37.9587	ENSG00000197555	SIPA1L1
ENSG00000197557	2.18882	1.07439	1.51029	0.845224	ENSG00000197557	TTC30A
ENSG00000197561	0	0	0	0.148391	ENSG00000197561	ELANE
ENSG00000197562	8.71257	10.0123	13.8281	8.15843	ENSG00000197562	RAB40C
ENSG00000197563	43.3624	51.7307	28.3753	33.3749	ENSG00000197563	PIGN
ENSG00000197565	24.0713	59.432	73.9411	40.336	ENSG00000197565	COL4A6
ENSG00000197566	4.88679	10.8773	9.30566	12.5611	ENSG00000197566	ZNF624
ENSG00000197568	4.18801	9.63005	7.97183	12.3783	ENSG00000197568	HHLA3
ENSG00000197575	0	0.210725	0	0	ENSG00000197575	RPS17P2
ENSG00000197576	1.13563	0.461263	0.751259	0.581662	ENSG00000197576	HOXA4
ENSG00000197579	11.1423	9.6944	9.35281	7.90129	ENSG00000197579	TOPORS
ENSG00000197580	2.74827	7.69556	8.62743	12.0709	ENSG00000197580	BCO2
ENSG00000197582	0.291534	0.129774	0.246787	0.303941	ENSG00000197582	GPX1P1
ENSG00000197584	0.145181	1.27768	1.4203	1.95167	ENSG00000197584	KCNMB2
ENSG00000197586	98.8276	85.5637	47.1928	42.5926	ENSG00000197586	ENTPD6
ENSG00000197587	0.535314	0.738868	0.526649	1.13494	ENSG00000197587	DMBX1
ENSG00000197588	0.456799	0.943584	1.16783	1.6169	ENSG00000197588	KLKP1
ENSG00000197591	0	0	0	0	ENSG00000197591	OR11L1
ENSG00000197594	1.61699	1.29884	0.9145	8.5936	ENSG00000197594	ENPP1
ENSG00000197595	0.0996711	0.144113	0.217639	0.30098	ENSG00000197595	ATP11AUN
ENSG00000197599	1.6143	1.74429	1.6553	1.34779	ENSG00000197599	CCDC154
ENSG00000197601	41.47	74.5944	75.0994	58.2035	ENSG00000197601	FAR1
ENSG00000197603	12.3058	14.7103	16.5247	19.4427	ENSG00000197603	C5orf42

ENSG00000197604	0.310238	0.499633	0.427694	0.669167	ENSG00000197604	AC022532.1
ENSG00000197608	29.9216	20.1405	22.9619	27.5343	ENSG00000197608	ZNF841
ENSG00000197614	277.143	64.2383	56.5747	120.844	ENSG00000197614	MFAP5
ENSG00000197616	0.00907917	0.0357498	0.213417	0.198699	ENSG00000197616	MYH6
ENSG00000197617	0.293575	1.01149	0.873447	1.12529	ENSG00000197617	VN1R5
ENSG00000197619	9.02795	11.5482	10.1661	17.3929	ENSG00000197619	ZNF615
ENSG00000197620	0.903578	0.175417	4.5555	2.2757	ENSG00000197620	CXorf40A
ENSG00000197622	84.3839	79.3414	92.9309	46.1216	ENSG00000197622	CDC42SE1
ENSG00000197627	0	2.87508	0.94757	2.36009	ENSG00000197627	UBE2Q2P12
ENSG00000197629	0.423902	0.668643	0.739558	0.929939	ENSG00000197629	MPEG1
ENSG00000197632	796.195	135.684	95.5464	122.076	ENSG00000197632	SERPINB2
ENSG00000197635	1.34914	1.64791	3.28507	21.0453	ENSG00000197635	DPP4
ENSG00000197641	74.6516	17.8986	39.8622	16.4816	ENSG00000197641	SERPINB13
ENSG00000197646	10.7847	14.4355	4.75092	7.62529	ENSG00000197646	PDCD1LG2
ENSG00000197647	8.50975	13.3314	10.3262	11.6406	ENSG00000197647	ZNF433
ENSG00000197651	0.624848	0.666457	1.39631	1.05941	ENSG00000197651	CCER1
ENSG00000197653	1.64704	2.1354	1.39693	1.23113	ENSG00000197653	DNAH10
ENSG00000197658	0.0345014	0.128944	0.0699424	0.0591738	ENSG00000197658	SLC22A24
ENSG00000197665	0.286059	0.49434	0.231477	0	ENSG00000197665	AC007952.1
ENSG00000197674	0	0.0640256	0	0	ENSG00000197674	OR51C1P
ENSG00000197681	0.272991	1.52686	1.89E-10	0.571404	ENSG00000197681	TBC1D3
ENSG00000197683	0	0.150361	0.135899	0.170484	ENSG00000197683	KRTAP26-1
ENSG00000197692	0.302158	0.296425	0.5231	0	ENSG00000197692	CBX3P7
ENSG00000197694	100.627	102.71	133.287	105.175	ENSG00000197694	SPTAN1
ENSG00000197696	3.65476	2.62021	1.328	1.42531	ENSG00000197696	NMB
ENSG00000197697	11.9988	30.3512	11.8399	7.82133	ENSG00000197697	HIST1H2BE
ENSG00000197701	4.55816	9.62783	6.4961	7.51768	ENSG00000197701	ZNF595
ENSG00000197702	11.0827	18.4006	19.8589	39.9595	ENSG00000197702	PARVA
ENSG00000197704	0	0	0	0	ENSG00000197704	FRMPD2P1
ENSG00000197705	0.0551741	0.02415	0.176895	0.386587	ENSG00000197705	KLHL14
ENSG00000197706	0.120773	0.107069	0.145655	0.182511	ENSG00000197706	OR6C74
ENSG00000197712	37.9719	23.0016	15.3986	41.3255	ENSG00000197712	FAM114A1
ENSG00000197713	25.5289	31.1583	42.5955	28.1785	ENSG00000197713	RPE
ENSG00000197714	49.8433	50.8706	53.0551	37.8915	ENSG00000197714	ZNF460
ENSG00000197721	0	0	0	0	ENSG00000197721	CR1L
ENSG00000197723	0	0	0.239037	0.178123	ENSG00000197723	HSPB9
ENSG00000197724	7.0775	7.93946	8.51506	7.73031	ENSG00000197724	PHF2
ENSG00000197727	0	0	0.184069	0	ENSG00000197727	AL022341.1
ENSG00000197728	6.69321	11.6685	12.593	5.35274	ENSG00000197728	RPS26
ENSG00000197734	4.23176	7.26477	7.74611	12.607	ENSG00000197734	C14orf178
ENSG00000197744	0.34732	0	1.7449	0.697686	ENSG00000197744	PTMAP2
ENSG00000197745	0	0	0	0	ENSG00000197745	SCGB1D4
ENSG00000197746	416.128	384.986	422.135	300.516	ENSG00000197746	PSAP
ENSG00000197747	515.086	283.937	124.147	233.586	ENSG00000197747	S100A10
ENSG00000197748	1.41973	1.50183	1.14228	2.40468	ENSG00000197748	CFAP43
ENSG00000197753	5.09811	9.68788	8.14631	16.5426	ENSG00000197753	LHFPL5
ENSG00000197756	1425.33	1059.16	864.066	545.5	ENSG00000197756	RPL37A
ENSG00000197757	2.59641	4.83106	5.85895	13.4827	ENSG00000197757	HOXC6
ENSG00000197763	5.17003	6.37312	5.95354	4.33889	ENSG00000197763	TXNRD3
ENSG00000197766	1.31288	0.809236	0.651163	0.597389	ENSG00000197766	CFD
ENSG00000197768	0.396621	0.624673	0.734373	0.447079	ENSG00000197768	STPG3
ENSG00000197769	2.09871	4.31494	5.06412	8.97856	ENSG00000197769	MAP1LC3C
ENSG00000197771	21.3432	28.8106	23.0976	20.3024	ENSG00000197771	MCMBP
ENSG00000197774	22.6012	15.0768	28.4127	12.174	ENSG00000197774	EME2

ENSG00000197775	3.59086	5.69551	6.79634	3.98022	ENSG00000197775	DHRS4-AS1
ENSG00000197776	0.454359	1.44903	1.94809	2.89753	ENSG00000197776	KLHDC1
ENSG00000197779	4.06852	9.6573	6.95805	10.9026	ENSG00000197779	ZNF81
ENSG00000197780	24.8788	12.9567	23.1375	18.8157	ENSG00000197780	TAF13
ENSG00000197782	12.603	14.3518	12.7955	13.9242	ENSG00000197782	ZNF780A
ENSG00000197785	31.0233	29.9194	31.9647	24.5609	ENSG00000197785	ATAD3A
ENSG00000197786	0	0	0	0	ENSG00000197786	OR5B17
ENSG00000197790	0	0	0	0	ENSG00000197790	OR52M1
ENSG00000197794	0	0	0	0.368346	ENSG00000197794	IGKV7-3
ENSG00000197798	7.66297	7.90877	9.3558	7.47333	ENSG00000197798	FAM118B
ENSG00000197805	0	0	0	0	ENSG00000197805	BX649597.1
ENSG00000197808	11.3227	9.14602	14.6637	21.0004	ENSG00000197808	ZNF461
ENSG00000197815	13.1327	20.7855	24.2471	42.4202	ENSG00000197815	AC122129.1
ENSG00000197816	3.90169	3.91036	3.79378	8.88636	ENSG00000197816	CCDC180
ENSG00000197818	4.45033	8.34596	7.34838	4.61057	ENSG00000197818	SLC9A8
ENSG00000197822	27.0326	4.57401	8.58081	2.61586	ENSG00000197822	OCLN
ENSG00000197825	164.174	340.392	286.564	500.604	ENSG00000197825	AC061975.1
ENSG00000197826	1.26565	2.84011	3.18091	5.58325	ENSG00000197826	C4orf22
ENSG00000197830	1.58248	4.29791	4.55247	6.43351	ENSG00000197830	AC011385.1
ENSG00000197837	27.205	42.8775	26.2152	25.9513	ENSG00000197837	HIST4H4
ENSG00000197838	0	0.0336698	0	0.0792059	ENSG00000197838	CYP2A13
ENSG00000197841	3.79118	4.12755	4.3077	3.58013	ENSG00000197841	ZNF181
ENSG00000197844	17.0837	41.5912	41.1539	80.8294	ENSG00000197844	AL358813.1
ENSG00000197846	6.692	5.47969	3.12064	3.3013	ENSG00000197846	HIST1H2BF
ENSG00000197847	4.45307	5.83297	6.62658	9.8276	ENSG00000197847	SLC22A20
ENSG00000197849	0	0	0	0	ENSG00000197849	OR8G1
ENSG00000197851	0.0203585	0.0591693	0.0451312	0.0671919	ENSG00000197851	C7orf76
ENSG00000197852	4.61508	9.15204	10.9537	12.8274	ENSG00000197852	FAM212B
ENSG00000197857	16.5684	24.6167	22.4788	23.0249	ENSG00000197857	ZNF44
ENSG00000197858	29.7358	35.2927	21.4458	14.9443	ENSG00000197858	GPAA1
ENSG00000197859	0.360635	0.573965	0.419964	1.28709	ENSG00000197859	ADAMTSL2
ENSG00000197860	4.8124	6.64005	7.32999	9.11676	ENSG00000197860	SGTB
ENSG00000197863	7.07518	8.70883	7.78523	7.7574	ENSG00000197863	ZNF790
ENSG00000197866	0	0	0.119369	0	ENSG00000197866	OR5M12P
ENSG00000197870	0.226091	0.373584	0.58762	0.480665	ENSG00000197870	PRB3
ENSG00000197872	0.31307	0.357573	0.574682	0.38896	ENSG00000197872	FAM49A
ENSG00000197879	75.5625	89.4624	75.8653	84.3657	ENSG00000197879	MYO1C
ENSG00000197880	1.46391	2.61379	2.93706	5.1353	ENSG00000197880	MDS2
ENSG00000197882	0.276568	0.820972	1.3203	2.40934	ENSG00000197882	OR7E13P
ENSG00000197885	6.22846	3.9763	5.11742	6.33585	ENSG00000197885	NKIRAS1
ENSG00000197887	0	0.0608403	0	0	ENSG00000197887	OR1S2
ENSG00000197888	0.108199	0.260793	0.364598	0.296886	ENSG00000197888	UGT2B17
ENSG00000197889	1.63446	3.63144	3.88251	3.00871	ENSG00000197889	MEIG1
ENSG00000197891	0.0219532	0.0294981	0	0.120612	ENSG00000197891	SLC22A12
ENSG00000197892	23.0724	8.53767	6.86902	13.0508	ENSG00000197892	KIF13B
ENSG00000197893	0.0296745	0.0817281	0.0437644	0.0775989	ENSG00000197893	NRAP
ENSG00000197894	38.1606	71.9626	49.3553	43.831	ENSG00000197894	ADH5
ENSG00000197901	0.156266	0.201635	0.18487	0.200944	ENSG00000197901	SLC22A6
ENSG00000197903	66.629	84.912	36.6216	36.4928	ENSG00000197903	HIST1H2BK
ENSG00000197905	2.07448	4.40637	3.30883	5.11951	ENSG00000197905	TEAD4
ENSG00000197910	0.948937	0	2.16135	2.47667	ENSG00000197910	FAM25G
ENSG00000197912	88.9496	91.3232	100.895	120.025	ENSG00000197912	SPG7
ENSG00000197914	3.93493	8.56137	5.46116	1.86483	ENSG00000197914	HIST1H4K
ENSG00000197915	1.62024	0.893472	4.24654	5.98875	ENSG00000197915	HRNR

ENSG00000197919	0.912309	0.456125	2.2628	1.94333	ENSG00000197919	IFNA1
ENSG00000197921	4.43459	0.523035	0.275698	0.791418	ENSG00000197921	HES5
ENSG00000197927	3.44797	8.20889	8.78845	18.766	ENSG00000197927	C2orf27A
ENSG00000197928	14.4823	20.3108	28.3736	28.0939	ENSG00000197928	ZNF677
ENSG00000197930	165.035	145.581	86.1758	93.373	ENSG00000197930	ERO1A
ENSG00000197932	1.53474	0.972714	0.48334	1.6718	ENSG00000197932	F8A1
ENSG00000197933	4.47422	4.36741	2.69787	3.11685	ENSG00000197933	ZNF823
ENSG00000197935	0.281502	0.296324	0.329162	0.107474	ENSG00000197935	ZNF311
ENSG00000197937	14.693	32.4786	30.2208	47.5544	ENSG00000197937	ZNF347
ENSG00000197938	0	0.190613	0.0574127	0	ENSG00000197938	OR5H2
ENSG00000197943	1.47317	1.87618	2.28494	1.80971	ENSG00000197943	PLCG2
ENSG00000197948	41.8332	46.141	39.9387	47.7175	ENSG00000197948	FCHSD1
ENSG00000197951	7.29473	6.20643	6.14126	7.7357	ENSG00000197951	ZNF71
ENSG00000197953	0.239008	0.343284	0.287434	0.603154	ENSG00000197953	AADACL2
ENSG00000197956	2085.32	1963.36	529.039	595.736	ENSG00000197956	S100A6
ENSG00000197958	486.462	472.888	457.068	234.005	ENSG00000197958	RPL12
ENSG00000197959	0.905985	1.51405	1.54543	2.35405	ENSG00000197959	DNM3
ENSG00000197961	64.3095	57.4789	65.7607	43.8128	ENSG00000197961	ZNF121
ENSG00000197965	136.749	118.3	119.041	59.0842	ENSG00000197965	MPZL1
ENSG00000197969	29.5759	50.4035	48.1462	40.9951	ENSG00000197969	VPS13A
ENSG00000197971	23.6117	27.3529	24.4918	29.4405	ENSG00000197971	MBP
ENSG00000197976	24.7585	23.5659	31.2669	18.523	ENSG00000197976	AKAP17A
ENSG00000197977	0.13517	0.273751	0.377099	0.639718	ENSG00000197977	ELOVL2
ENSG00000197978	0	0.223713	0.298816	0.741248	ENSG00000197978	GOLGA6L9
ENSG00000197980	4.06629	4.7398	6.14574	7.1496	ENSG00000197980	LEKR1
ENSG00000197982	33.7459	22.525	26.7993	14.3705	ENSG00000197982	C1orf122
ENSG00000197984	0	0	0	0	ENSG00000197984	OR51A8P
ENSG00000197990	0	0	0	0	ENSG00000197990	ZNF734P
ENSG00000197991	0.0786089	0.160776	0.11712	0.150929	ENSG00000197991	AL592490.1
ENSG00000197992	0.22165	1.07904	0.681485	0.69544	ENSG00000197992	CLEC9A
ENSG00000197993	0.204096	0.449454	0.147002	0.38295	ENSG00000197993	KEL
ENSG00000198000	18.1577	23.8358	30.673	23.9572	ENSG00000198000	NOL8
ENSG00000198001	9.06173	15.3028	13.0396	15.0965	ENSG00000198001	IRAK4
ENSG00000198003	0.0977025	0.252428	0.150111	0.273639	ENSG00000198003	CCDC151
ENSG00000198010	0.112311	1.38214	0.779948	1.03592	ENSG00000198010	DLGAP2
ENSG00000198015	29.1411	34.5356	31.21	28.2648	ENSG00000198015	MRPL42
ENSG00000198018	14.3494	13.2986	11.0764	10.9414	ENSG00000198018	ENTPD7
ENSG00000198019	0.64138	0.23046	0.167124	0.0376837	ENSG00000198019	FCGR1B
ENSG00000198021	0	0	0	0.0449071	ENSG00000198021	SPANXA1
ENSG00000198022	0.0131877	0.0762661	0.0344739	0.0434295	ENSG00000198022	SAGE2P
ENSG00000198026	13.3198	15.4606	14.3079	14.9286	ENSG00000198026	ZNF335
ENSG00000198028	2.10247	3.27773	1.87992	1.01766	ENSG00000198028	ZNF560
ENSG00000198033	0.0384746	0	0	0.0452133	ENSG00000198033	TUBA3C
ENSG00000198034	212.825	185.176	178.894	144.524	ENSG00000198034	RPS4X
ENSG00000198035	0.657966	1.39318	0.993169	1.29319	ENSG00000198035	AGAP9
ENSG00000198039	5.27339	13.5039	11.3721	13.0239	ENSG00000198039	ZNF273
ENSG00000198040	13.0448	15.2321	24.609	18.2827	ENSG00000198040	ZNF84
ENSG00000198042	12.3072	14.7671	17.9976	10.0736	ENSG00000198042	MAK16
ENSG00000198046	5.74459	12.2311	15.8273	19.3061	ENSG00000198046	ZNF667
ENSG00000198049	0	0.0972037	0.0439068	0.120848	ENSG00000198049	AVPR1B
ENSG00000198053	15.4893	17.6493	20.9118	11.5153	ENSG00000198053	SIRPA
ENSG00000198054	1.17036	3.52098	2.66424	4.8116	ENSG00000198054	DSCR8
ENSG00000198055	12.2662	25.6593	14.4819	10.7212	ENSG00000198055	GRK6
ENSG00000198056	3.56753	12.0599	4.08056	5.71574	ENSG00000198056	PRIM1

ENSG00000198060	24.5995	27.2728	23.7145	22.6921	ENSG00000198060	MARCH5
ENSG00000198062	0	0	0	0	ENSG00000198062	POTEH
ENSG00000198064	5.93836	17.5084	26.8462	21.7761	ENSG00000198064	NPIPB13
ENSG00000198074	0.82388	3.53484	3.67009	1.87695	ENSG00000198074	AKR1B10
ENSG00000198075	0.728992	1.499	1.11903	2.03059	ENSG00000198075	SULT1C4
ENSG00000198077	0.0569674	0	0.121487	0.174809	ENSG00000198077	CYP2A7
ENSG00000198081	4.76381	8.41817	8.74165	4.5791	ENSG00000198081	ZBTB14
ENSG00000198082	0.0724045	0.0462886	0.0208964	0.103325	ENSG00000198082	H2AFB1
ENSG00000198083	0	0.0303879	0.0274648	0	ENSG00000198083	KRTAP9-9
ENSG00000198087	33.3329	30.5211	29.6025	31.9589	ENSG00000198087	CD2AP
ENSG00000198088	1.72464	5.72754	2.4891	1.23301	ENSG00000198088	NUP62CL
ENSG00000198089	45.8254	93.8997	87.3037	164.293	ENSG00000198089	SFI1
ENSG00000198090	0.115888	0.111523	0.0503948	0.0631593	ENSG00000198090	KRTAP4-6
ENSG00000198092	23.813	1.99603	1.92749	1.91882	ENSG00000198092	TMPRSS11F
ENSG00000198093	14.2661	17.6001	19.7476	14.1169	ENSG00000198093	ZNF649
ENSG00000198099	4.97974	7.72806	7.6625	10.3729	ENSG00000198099	ADH4
ENSG00000198100	16.8502	32.0916	35.856	69.9807	ENSG00000198100	AL138751.1
ENSG00000198104	0	0	0	0	ENSG00000198104	OR2T6
ENSG00000198105	5.16321	8.78141	9.30713	10.1005	ENSG00000198105	ZNF248
ENSG00000198108	1.08776	2.21216	1.56418	3.55423	ENSG00000198108	CHSY3
ENSG00000198113	16.4116	20.7088	12.0767	7.98499	ENSG00000198113	TOR4A
ENSG00000198121	14.18	20.7506	10.4964	26.0376	ENSG00000198121	LPAR1
ENSG00000198125	1.5775	3.55797	0.497051	1.27237	ENSG00000198125	MB
ENSG00000198128	0	0	0	0	ENSG00000198128	OR2L3
ENSG00000198129	0	0	0	0	ENSG00000198129	DEFB107B
ENSG00000198130	25.5361	59.0925	49.988	74.7142	ENSG00000198130	HIBCH
ENSG00000198131	40.5831	48.0783	55.7227	56.7671	ENSG00000198131	ZNF544
ENSG00000198133	2.65799	5.92022	7.13238	9.11197	ENSG00000198133	TMEM229B
ENSG00000198134	0.918162	0.776864	0	0.32099	ENSG00000198134	AC007537.1
ENSG00000198142	12.0735	11.598	16.3461	9.34228	ENSG00000198142	SOWAHC
ENSG00000198143	16.05	34.2184	31.7104	53.0193	ENSG00000198143	BX247900.1
ENSG00000198146	20.6829	16.0178	33.4012	14.4509	ENSG00000198146	ZNF770
ENSG00000198150	3.34018	4.79098	5.14199	7.61151	ENSG00000198150	AC135178.1
ENSG00000198153	0.168626	0.360818	0.0357288	0.563161	ENSG00000198153	ZNF849P
ENSG00000198155	0.697168	1.94566	1.60176	2.1243	ENSG00000198155	ZNF876P
ENSG00000198156	1.44354	1.83472	1.94146	8.40E-05	ENSG00000198156	NPIPB6
ENSG00000198157	2.61314	5.4334	6.75198	8.30573	ENSG00000198157	HMGN5
ENSG00000198160	17.3028	23.8556	22.1983	22.0896	ENSG00000198160	MIER1
ENSG00000198161	0	0	0	0	ENSG00000198161	PPIAL4C
ENSG00000198162	23.7814	32.4594	25.1727	20.9583	ENSG00000198162	MAN1A2
ENSG00000198168	10.1762	7.13689	6.26645	6.66011	ENSG00000198168	SVIP
ENSG00000198169	13.6049	12.4293	16.1463	14.51	ENSG00000198169	ZNF251
ENSG00000198171	43.5982	33.4993	32.7883	19.6256	ENSG00000198171	DDRGK1
ENSG00000198173	0.00828579	0.031839	0.0217737	0.0226356	ENSG00000198173	FAM47C
ENSG00000198176	46.3539	36.9787	35.9517	39.5029	ENSG00000198176	TFDP1
ENSG00000198178	0.213996	1.01845	1.16791	1.97647	ENSG00000198178	CLEC4C
ENSG00000198182	6.15917	6.6023	5.9627	5.78838	ENSG00000198182	ZNF607
ENSG00000198183	0	0	0.0521969	0	ENSG00000198183	BPIFA1
ENSG00000198185	2.08904	9.23313	5.45902	2.64837	ENSG00000198185	ZNF334
ENSG00000198189	4.81693	15.4429	5.86595	12.6702	ENSG00000198189	HSD17B11
ENSG00000198198	42.9235	87.4609	90.7287	162.04	ENSG00000198198	SZT2
ENSG00000198203	5.60472	6.74064	3.368	7.05602	ENSG00000198203	SULT1C2
ENSG00000198205	1.1193	2.78269	2.41155	1.61137	ENSG00000198205	ZXDA
ENSG00000198208	4.93528	10.1281	8.22876	15.6101	ENSG00000198208	RPS6KL1

ENSG00000198211	0	0	0	0	ENSG00000198211	AC092143.1
ENSG00000198216	0.281319	0.259512	0.200824	0.327868	ENSG00000198216	CACNA1E
ENSG00000198217	0	0	0	0	ENSG00000198217	OR51H2P
ENSG00000198218	29.9349	28.3229	29.051	26.9548	ENSG00000198218	QRICH1
ENSG00000198223	9.96883	24.0886	26.0248	49.2982	ENSG00000198223	CSF2RA
ENSG00000198225	1.26079	1.54043	1.9335	2.20224	ENSG00000198225	FKBP1C
ENSG00000198231	38.6529	50.9193	57.8544	67.1304	ENSG00000198231	DDX42
ENSG00000198237	0.925202	1.25615	3.8699	7.61025	ENSG00000198237	AC131392.1
ENSG00000198242	279.264	270.175	156.412	136.999	ENSG00000198242	RPL23A
ENSG00000198246	1.4502	0.892219	1.09546	1.3181	ENSG00000198246	SLC29A3
ENSG00000198250	0.116349	0.307444	0.989386	0.549671	ENSG00000198250	ANTXRL
ENSG00000198251	0.107857	0.207133	0.186971	0.316228	ENSG00000198251	CYP2A7P2
ENSG00000198252	7.72905	7.82683	9.05733	8.91553	ENSG00000198252	STYX
ENSG00000198258	178.094	96.5707	79.8663	68.9475	ENSG00000198258	UBL5
ENSG00000198261	0.133148	0.320128	0.0578531	0.434518	ENSG00000198261	OR5BB1P
ENSG00000198265	28.6004	32.1869	43.4062	40.0325	ENSG00000198265	HELZ
ENSG00000198270	5.74353	14.2635	8.39234	13.5982	ENSG00000198270	TMEM116
ENSG00000198271	0.07231	0.139084	0.0628337	0.314231	ENSG00000198271	KRTAP4-5
ENSG00000198276	15.3922	25.7411	18.4513	22.6299	ENSG00000198276	UCKL1
ENSG00000198277	0	0	0	0	ENSG00000198277	AC021146.1
ENSG00000198283	0	0.194063	0.116902	0.731599	ENSG00000198283	OR5B21
ENSG00000198284	0.163876	0.208916	0.14174	0.157331	ENSG00000198284	NUP210P1
ENSG00000198286	4.12818	6.24411	1.99625	6.6592	ENSG00000198286	CARD11
ENSG00000198298	7.27351	4.86766	7.17223	5.6681	ENSG00000198298	ZNF485
ENSG00000198300	0.576214	1.1638	0.541691	1.82483	ENSG00000198300	PEG3
ENSG00000198301	20.667	18.5883	21.4968	16.5417	ENSG00000198301	SDAD1
ENSG00000198305	1.31166	3.63058	3.61302	5.48428	ENSG00000198305	SPDYE8P
ENSG00000198307	0	0.0462886	0.0208964	0.103325	ENSG00000198307	H2AFB2
ENSG00000198312	0	0	0	0	ENSG00000198312	BMS1P9
ENSG00000198315	6.55607	10.0071	12.4732	11.4407	ENSG00000198315	ZKSCAN8
ENSG00000198324	5.10116	2.83998	4.06497	3.16766	ENSG00000198324	FAM109A
ENSG00000198326	0.27734	0.716872	0.459331	0.863491	ENSG00000198326	TMEM239
ENSG00000198327	16.6632	49.9452	25.1479	12.5595	ENSG00000198327	HIST1H4F
ENSG00000198331	2.08225	5.21181	2.23387	3.28485	ENSG00000198331	HYLS1
ENSG00000198336	0.673536	0.732107	0.466697	1.05795	ENSG00000198336	MYL4
ENSG00000198339	1.49055	4.4846	1.03023	1.3443	ENSG00000198339	HIST1H4I
ENSG00000198342	3.01215	2.50841	1.41354	1.00154	ENSG00000198342	ZNF442
ENSG00000198346	6.79718	5.06049	5.173	6.42863	ENSG00000198346	ZNF813
ENSG00000198353	1.73416	3.22799	4.57934	5.50958	ENSG00000198353	HOXC4
ENSG00000198354	0	0	0.0358019	0.269961	ENSG00000198354	DCAF12L2
ENSG00000198355	32.2575	14.9552	15.5522	12.3892	ENSG00000198355	PIM3
ENSG00000198356	28.9583	14.8423	16.3006	9.8315	ENSG00000198356	ASNA1
ENSG00000198363	146.386	216.731	68.4852	216.715	ENSG00000198363	ASPH
ENSG00000198366	11.228	39.3877	5.6326	14.4197	ENSG00000198366	HIST1H3A
ENSG00000198367	0.177806	0	0	0	ENSG00000198367	OR7A11P
ENSG00000198369	15.5052	18.0607	14.5627	21.2472	ENSG00000198369	SPRED2
ENSG00000198373	22.2909	25.9373	27.5424	41.9747	ENSG00000198373	WWP2
ENSG00000198374	9.34271	41.4092	10.234	13.5564	ENSG00000198374	HIST1H2AL
ENSG00000198380	22.3458	30.9951	36.9193	26.0838	ENSG00000198380	GFPT1
ENSG00000198382	16.0118	25.7257	27.3829	35.9544	ENSG00000198382	UVRAG
ENSG00000198384	0	0.0227236	0.123125	0.0854242	ENSG00000198384	TPTE2P3
ENSG00000198388	92.7736	205.372	171.581	222.538	ENSG00000198388	AC092291.1
ENSG00000198390	0	0	0	0.0959115	ENSG00000198390	KRTAP13-1
ENSG00000198393	6.03099	9.72134	18.665	13.4229	ENSG00000198393	ZNF26

ENSG00000198398	0	0.0775581	0.105159	0.397588	ENSG00000198398	TMEM207
ENSG00000198399	25.961	24.0976	21.3707	19.349	ENSG00000198399	ITSN2
ENSG00000198400	0.282424	0.297824	0.227496	0.701347	ENSG00000198400	NTRK1
ENSG00000198406	73.4732	38.4393	23.0517	8.67563	ENSG00000198406	BZW1P2
ENSG00000198408	80.2203	108.394	114.174	114.402	ENSG00000198408	MGEA5
ENSG00000198414	0.072023	0.133787	0.0559057	0.289451	ENSG00000198414	TATDN2P1
ENSG00000198416	0.853516	0.973987	1.43837	0.467314	ENSG00000198416	ZNF658B
ENSG00000198417	2.55623	1.86242	0.944183	1.58723	ENSG00000198417	MT1F
ENSG00000198420	20.9827	25.3737	19.1572	38.9724	ENSG00000198420	TCAF1
ENSG00000198429	2.73277	3.56797	2.28389	4.77035	ENSG00000198429	ZNF69
ENSG00000198431	73.8749	95.505	34.3937	82.6573	ENSG00000198431	TXNRD1
ENSG00000198434	13.5053	20.9034	21.0881	24.1452	ENSG00000198434	AF241725.1
ENSG00000198435	3.30799	0.690756	0.951273	1.30018	ENSG00000198435	NRARP
ENSG00000198440	16.6953	18.4278	27.2873	33.0396	ENSG00000198440	ZNF583
ENSG00000198443	0.0479722	0.0466247	0.0417472	0.104813	ENSG00000198443	KRTAP4-1
ENSG00000198444	0	0	0.580008	0.104487	ENSG00000198444	F8A2
ENSG00000198445	0	0.0266685	0	0	ENSG00000198445	CCT8L2
ENSG00000198452	0	0	0	0	ENSG00000198452	OR14L1P
ENSG00000198453	9.23787	12.851	12.61	18.5005	ENSG00000198453	ZNF568
ENSG00000198454	0.316997	0.182966	0.220487	0	ENSG00000198454	PRR31
ENSG00000198455	3.4834	4.46053	3.95401	2.64972	ENSG00000198455	ZXDB
ENSG00000198457	0	0	0.140536	0	ENSG00000198457	CYP21A2
ENSG00000198464	9.82299	15.579	15.7742	28.74	ENSG00000198464	ZNF480
ENSG00000198466	20.555	23.7963	30.4181	47.5376	ENSG00000198466	ZNF587
ENSG00000198467	16.909	77.3539	61.8878	146.321	ENSG00000198467	TPM2
ENSG00000198471	0.0437245	0.547396	0.435695	0.191246	ENSG00000198471	RTP2
ENSG00000198477	0.450939	0.866765	0.767587	1.53933	ENSG00000198477	ZNF280B
ENSG00000198478	8.35255	1.95717	2.69923	1.83644	ENSG00000198478	SH3BGRL2
ENSG00000198482	8.8996	13.9951	9.41869	9.83965	ENSG00000198482	ZNF808
ENSG00000198483	0.97507	0.140633	0.468997	0.21142	ENSG00000198483	ANKRD35
ENSG00000198488	0.231574	0.474435	0.524005	0.815757	ENSG00000198488	B3GNT6
ENSG00000198492	34.4657	27.9554	40.06	27.4606	ENSG00000198492	YTHDF2
ENSG00000198496	6.94627	14.552	28.7315	17.5678	ENSG00000198496	NBR2
ENSG00000198498	15.1981	22.998	18.4164	20.5247	ENSG00000198498	TMA16
ENSG00000198502	0.0787669	0.226961	0.412561	0.516162	ENSG00000198502	HLA-DRB5
ENSG00000198513	9.26695	7.10272	4.10203	5.39547	ENSG00000198513	ATL1
ENSG00000198515	7.45661	4.39666	5.04549	6.25208	ENSG00000198515	CNGA1
ENSG00000198517	16.2317	13.3037	12.1588	8.62975	ENSG00000198517	MAFK
ENSG00000198518	12.3712	18.8647	11.29	7.58545	ENSG00000198518	HIST1H4E
ENSG00000198520	2.99545	4.45088	4.53399	3.64029	ENSG00000198520	C1orf228
ENSG00000198521	7.60967	13.6939	9.04973	15.6242	ENSG00000198521	ZNF43
ENSG00000198522	24.3916	15.4658	9.81603	10.6114	ENSG00000198522	GPN1
ENSG00000198523	1.01903	3.28109	2.15965	4.33949	ENSG00000198523	PLN
ENSG00000198526	0.0710339	0.0342348	0.0927774	0.15553	ENSG00000198526	PABPC1P2
ENSG00000198535	0.529915	0.829857	0.96543	1.83173	ENSG00000198535	C2CD4A
ENSG00000198538	11.3743	17.3497	15.0651	16.62	ENSG00000198538	ZNF28
ENSG00000198542	0.695011	2.15482	0.445958	6.07752	ENSG00000198542	ITGBL1
ENSG00000198546	6.16652	9.76066	3.49159	4.63666	ENSG00000198546	ZNF511
ENSG00000198551	11.2244	12.5405	13.5493	14.6464	ENSG00000198551	ZNF627
ENSG00000198553	1.16526	2.65674	2.85614	3.81626	ENSG00000198553	KCNRG
ENSG00000198554	4.13708	12.7305	4.70643	8.41931	ENSG00000198554	WDHD1
ENSG00000198555	0.195045	0.274803	0.145896	0.324075	ENSG00000198555	AC133561.1
ENSG00000198556	13.2606	17.3993	19.555	23.9942	ENSG00000198556	ZNF789
ENSG00000198558	15.2229	38.1146	10.1086	10.7695	ENSG00000198558	HIST1H4L

ENSG00000198561	150.268	125.137	125.494	148.749	ENSG00000198561	CTNND1
ENSG00000198563	8.31802	12.8355	9.05207	9.78071	ENSG00000198563	DDX39B
ENSG00000198566	2.65E-07	0.168866	0.940751	0.197285	ENSG00000198566	ZNF658B
ENSG00000198569	0.802935	0.54924	1.27486	0.463717	ENSG00000198569	SLC34A3
ENSG00000198570	0.578606	1.18331	0.660361	1.59584	ENSG00000198570	RD3
ENSG00000198573	0.112742	0.861293	0.811569	0.402848	ENSG00000198573	SPANXC
ENSG00000198574	0.309441	2.10363	0.249878	1.68774	ENSG00000198574	SH2D1B
ENSG00000198576	0.371894	0.0662899	0.358896	0.660525	ENSG00000198576	ARC
ENSG00000198580	0.73908	0.663201	0.599478	1.04792	ENSG00000198580	AC073343.1
ENSG00000198585	3.27159	4.27536	2.99091	3.67498	ENSG00000198585	NUDT16
ENSG00000198586	15.5678	23.0342	24.645	28.0158	ENSG00000198586	TLK1
ENSG00000198589	29.5047	51.7208	40.9729	44.0253	ENSG00000198589	LRBA
ENSG00000198590	4.61286	9.29814	9.83093	14.8645	ENSG00000198590	C3orf35
ENSG00000198597	0.445551	0.487195	0.911658	1.1797	ENSG00000198597	ZNF536
ENSG00000198598	20.3807	17.2479	16.1473	17.7339	ENSG00000198598	MMP17
ENSG00000198601	0	0	0	0	ENSG00000198601	OR2M2
ENSG00000198604	33.3807	40.9933	37.6735	45.937	ENSG00000198604	BAZ1A
ENSG00000198610	0.289206	1.27946	0.864358	1.33329	ENSG00000198610	AKR1C4
ENSG00000198612	27.7203	37.5164	23.6085	26.1293	ENSG00000198612	COPS8
ENSG00000198618	1.0553	1.59556	0	0	ENSG00000198618	PPIAP22
ENSG00000198624	10.1942	18.2696	12.759	27.1327	ENSG00000198624	CCDC69
ENSG00000198625	15.8993	32.7151	45.8002	49.6281	ENSG00000198625	MDM4
ENSG00000198626	0.970615	0.814882	0.560045	1.58068	ENSG00000198626	RYR2
ENSG00000198632	0.264716	2.15819	0.411607	1.57097	ENSG00000198632	AC004878.3
ENSG00000198633	0.349921	0.381424	0.434147	0.923288	ENSG00000198633	ZNF534
ENSG00000198642	12.5117	12.047	15.0316	11.4965	ENSG00000198642	KLHL9
ENSG00000198643	1.11498	0.302018	0.0778895	0.0978286	ENSG00000198643	FAM3D
ENSG00000198646	6.32586	8.36262	8.3689	11.8599	ENSG00000198646	NCOA6
ENSG00000198648	16.3948	15.8193	10.5752	14.2636	ENSG00000198648	STK39
ENSG00000198650	0.46869	0.97631	1.25694	1.89316	ENSG00000198650	TAT
ENSG00000198657	0.0630141	0	0	0	ENSG00000198657	OR8B4
ENSG00000198658	0.0941782	0.398388	0.718663	0.289004	ENSG00000198658	ABHD17AP1
ENSG00000198663	41.1439	36.4995	29.734	17.9558	ENSG00000198663	C6orf89
ENSG00000198668	318.234	171.795	93.6864	107.895	ENSG00000198668	CALM1
ENSG00000198670	0.00829085	0.0160271	0.0144643	0	ENSG00000198670	LPA
ENSG00000198673	9.04555	20.5556	21.5335	33.2713	ENSG00000198673	FAM19A2
ENSG00000198674	0	0.0594724	0.16124	0.0673179	ENSG00000198674	OR10G6
ENSG00000198677	55.08	60.4512	46.8164	68.8485	ENSG00000198677	TTC37
ENSG00000198678	0.0668316	0.192817	0.0580758	0.145391	ENSG00000198678	AC089987.2
ENSG00000198680	4.37102	5.68443	5.54578	3.54841	ENSG00000198680	TUSC1
ENSG00000198681	0	0.0615823	0.0491844	0.157109	ENSG00000198681	MAGEA1
ENSG00000198682	0.642372	1.66681	0.915914	7.09445	ENSG00000198682	PAPSS2
ENSG00000198683	6.06385	10.8363	7.16758	11.0003	ENSG00000198683	AC012615.1
ENSG00000198685	0.447993	0.419965	0.674924	0.848555	ENSG00000198685	LINC01565
ENSG00000198689	6.89976	7.33748	4.42591	3.33141	ENSG00000198689	SLC9A6
ENSG00000198690	13.8339	22.3773	28.2007	21.5041	ENSG00000198690	FAN1
ENSG00000198691	0.00725287	0.0980024	0.710622	0.912386	ENSG00000198691	ABCA4
ENSG00000198692	14.9748	12.6683	9.24137	1.52919	ENSG00000198692	EIF1AY
ENSG00000198695	156.365	290.691	218.631	334.338	ENSG00000198695	MT-ND6
ENSG00000198700	17.064	25.1082	21.0352	19.5198	ENSG00000198700	IPO9
ENSG00000198703	0	0.0637807	0	0.0721459	ENSG00000198703	OR10R3P
ENSG00000198704	0.093196	0.677374	0.498851	1.02066	ENSG00000198704	GPX6
ENSG00000198707	4.18102	14.4363	10.9268	16.7944	ENSG00000198707	CEP290
ENSG00000198711	0.299078	0.954953	0.704214	0.811676	ENSG00000198711	SSBP3-AS1

ENSG00000198712	3164.04	2696.1	4304.41	4579.73	ENSG00000198712	MT-CO2
ENSG00000198715	46.3676	36.7635	26.0277	38.3726	ENSG00000198715	GLMP
ENSG00000198718	11.424	18.25	17.3415	18.9589	ENSG00000198718	TOGARAM1
ENSG00000198719	1.97433	13.2524	12.934	8.20266	ENSG00000198719	DLL1
ENSG00000198720	5.63479	5.98843	8.7485	8.59586	ENSG00000198720	ANKRD13B
ENSG00000198721	10.3325	22.6584	9.08829	9.89045	ENSG00000198721	ECI2
ENSG00000198722	7.45844	12.0491	8.42184	5.42121	ENSG00000198722	UNC13B
ENSG00000198723	1.90392	4.16516	3.69516	4.91858	ENSG00000198723	TEX45
ENSG00000198727	413.837	436.956	746.026	974.568	ENSG00000198727	MT-CYB
ENSG00000198728	46.0746	53.9288	83.4468	34.3705	ENSG00000198728	LDB1
ENSG00000198729	27.5448	20.3451	33.4949	9.5064	ENSG00000198729	PPP1R14C
ENSG00000198730	14.5126	12.94	15.9615	13.3017	ENSG00000198730	CTR9
ENSG00000198732	47.9843	19.5293	8.3063	18.0541	ENSG00000198732	SMOC1
ENSG00000198734	0.135972	0.0657408	0.102909	0.437194	ENSG00000198734	F5
ENSG00000198736	2.83185	3.04251	3.37392	1.70022	ENSG00000198736	MSRB1
ENSG00000198738	0	0	0	0	ENSG00000198738	SMIM11P1
ENSG00000198739	0.535253	3.64491	1.37673	2.26516	ENSG00000198739	LRRTM3
ENSG00000198740	6.36945	8.04047	6.61362	10.7798	ENSG00000198740	ZNF652
ENSG00000198742	46.4022	33.2391	27.2278	36.4678	ENSG00000198742	SMURF1
ENSG00000198743	0.105551	0.188094	0.0692291	1.14589	ENSG00000198743	SLC5A3
ENSG00000198744	1.392	0.740857	2.152	1.32307	ENSG00000198744	MTCO3P12
ENSG00000198746	3.63299	3.2069	5.71291	3.9955	ENSG00000198746	GPATCH3
ENSG00000198750	3.69689	1.20781	1.99388	5.04746	ENSG00000198750	GATSL2
ENSG00000198752	45.5481	49.9146	48.527	60.1476	ENSG00000198752	CDC42BPB
ENSG00000198753	5.89402	5.61367	7.91293	5.73892	ENSG00000198753	PLXNB3
ENSG00000198754	0.217893	0.26831	0.275596	0.237073	ENSG00000198754	OXCT2
ENSG00000198755	458.609	452.709	378.383	192.506	ENSG00000198755	RPL10A
ENSG00000198756	0.167657	0.613116	0.526653	0.723332	ENSG00000198756	COLGALT2
ENSG00000198758	0.265599	0	0.0249464	0.0263058	ENSG00000198758	EPS8L3
ENSG00000198759	0.023305	0.11233	0.323088	0.0512859	ENSG00000198759	EGFL6
ENSG00000198763	188.767	196.854	399.724	631.149	ENSG00000198763	MT-ND2
ENSG00000198765	3.08267	19.1163	21.6276	38.6016	ENSG00000198765	SYCP1
ENSG00000198768	1.13558	1.98447	1.00802	4.99833	ENSG00000198768	APCDD1L
ENSG00000198771	5.84111	12.5778	8.9794	16.734	ENSG00000198771	RCSD1
ENSG00000198774	2.80584	3.85149	5.24083	1.85095	ENSG00000198774	RASSF9
ENSG00000198780	11.6356	18.0042	25.0241	9.53574	ENSG00000198780	FAM169A
ENSG00000198783	6.74663	5.27912	6.25069	5.10123	ENSG00000198783	ZNF830
ENSG00000198785	0.403917	1.03645	0.371458	0.569014	ENSG00000198785	GRIN3A
ENSG00000198786	221.236	295.127	324.817	616.863	ENSG00000198786	MT-ND5
ENSG00000198787	0.149386	0	0	0	ENSG00000198787	OR4D12P
ENSG00000198788	0.0606328	0.145558	0.0663606	0.101999	ENSG00000198788	MUC2
ENSG00000198791	31.1441	35.212	34.5102	30.2102	ENSG00000198791	CNOT7
ENSG00000198792	40.0205	35.0746	32.2009	35.2462	ENSG00000198792	TMEM184B
ENSG00000198793	20.2224	24.8957	24.3322	21.1971	ENSG00000198793	MTOR
ENSG00000198794	1.76133	1.25917	1.33321	2.59704	ENSG00000198794	SCAMP5
ENSG00000198795	0.90249	0.619835	1.20081	11.7544	ENSG00000198795	ZNF521
ENSG00000198796	0.495346	2.61933	2.74273	12.0205	ENSG00000198796	ALPK2
ENSG00000198797	0.507353	0.46117	0.8881	0.579969	ENSG00000198797	BRINP2
ENSG00000198798	0.0242256	0.0935922	0.0851352	0.1873	ENSG00000198798	MAGEB3
ENSG00000198799	13.0383	17.3359	19.8475	20.746	ENSG00000198799	LRIG2
ENSG00000198804	4870.96	4773.58	7639.9	7911.8	ENSG00000198804	MT-CO1
ENSG00000198805	90.109	53.4207	23.3633	31.1904	ENSG00000198805	PNP
ENSG00000198807	0.837163	1.01678	0.595143	0.435321	ENSG00000198807	PAX9
ENSG00000198812	0.482253	0.698678	0.906307	0.923361	ENSG00000198812	LRRC10

ENSG00000198814	1.94084	3.90859	2.7613	7.27789	ENSG00000198814	GK
ENSG00000198815	16.6422	19.3254	19.5881	19.0098	ENSG00000198815	FOXJ3
ENSG00000198816	3.84133	4.46501	5.75503	7.60448	ENSG00000198816	ZNF358
ENSG00000198818	31.1123	31.2448	24.5077	24.8428	ENSG00000198818	SFT2D1
ENSG00000198821	1.24517	1.44905	0.771971	1.27073	ENSG00000198821	CD247
ENSG00000198822	0.0663034	0.0898596	0.299686	0.148553	ENSG00000198822	GRM3
ENSG00000198824	4.55746	7.08079	6.25073	11.3664	ENSG00000198824	CHAMP1
ENSG00000198825	10.6997	14.5964	8.24597	11.0738	ENSG00000198825	INPP5F
ENSG00000198826	3.68129	21.2672	4.47088	13.1243	ENSG00000198826	ARHGAP11A
ENSG00000198829	0.0524621	0.199666	0.10188	0.441042	ENSG00000198829	SUCNR1
ENSG00000198830	48.6473	116.056	64.8506	64.0131	ENSG00000198830	HMGN2
ENSG00000198832	6.88916	6.53584	12.2628	19.9842	ENSG00000198832	SELENOM
ENSG00000198833	9.6979	6.38245	5.8541	6.14563	ENSG00000198833	UBE2J1
ENSG00000198835	1.4849	1.82449	0.753843	0.689746	ENSG00000198835	GJC2
ENSG00000198836	79.9354	85.0024	72.3229	75.5314	ENSG00000198836	OPA1
ENSG00000198837	14.0813	18.0712	26.6052	24.1352	ENSG00000198837	DENND4B
ENSG00000198838	4.19493	3.23059	7.88364	7.71846	ENSG00000198838	RYR3
ENSG00000198839	3586.69	3688.51	3661.66	1448.92	ENSG00000198839	ZNF277
ENSG00000198840	918.942	716.571	1510.44	1618.54	ENSG00000198840	MT-ND3
ENSG00000198841	4.68392	4.09207	4.95102	3.23467	ENSG00000198841	KTI12
ENSG00000198842	0.203941	0.545365	0.719779	0.527946	ENSG00000198842	DUSP27
ENSG00000198843	110.973	50.5095	37.1005	24.4455	ENSG00000198843	SELENOT
ENSG00000198844	2.50931	2.92268	3.32364	5.51897	ENSG00000198844	ARHGEF15
ENSG00000198846	0.249672	0.433095	0.413325	0.975378	ENSG00000198846	TOX
ENSG00000198848	0.385996	0.0500528	0.135057	0.617126	ENSG00000198848	CES1
ENSG00000198851	0.201273	0.202082	0.408102	0.43784	ENSG00000198851	CD3E
ENSG00000198853	7.99803	7.74895	6.2782	12.2047	ENSG00000198853	RUSC2
ENSG00000198854	0	0.0666699	0.0602406	0.678307	ENSG00000198854	C1orf68
ENSG00000198855	6.07677	7.20174	7.1525	8.48766	ENSG00000198855	FICD
ENSG00000198856	78.7194	60.8444	41.6157	45.3518	ENSG00000198856	OSTC
ENSG00000198857	0.266764	0.622681	0.182435	2.14858	ENSG00000198857	HSD3BP5
ENSG00000198858	35.5968	38.2248	37.8826	27.1272	ENSG00000198858	R3HDM4
ENSG00000198860	22.595	53.3376	50.3116	53.8605	ENSG00000198860	TSEN15
ENSG00000198862	27.4092	30.7266	26.2417	26.6023	ENSG00000198862	LTN1
ENSG00000198863	6.83072	6.11074	9.40444	9.0012	ENSG00000198863	RUNDC1
ENSG00000198865	0.622054	1.50979	2.48911	1.91991	ENSG00000198865	CCDC152
ENSG00000198868	0	0	0	0	ENSG00000198868	MTND4LP30
ENSG00000198870	1.92306	5.80987	7.25688	8.84061	ENSG00000198870	STKLD1
ENSG00000198873	2.74752	4.38664	1.61311	4.37543	ENSG00000198873	GRK5
ENSG00000198874	12.0824	13.665	13.6277	10.3284	ENSG00000198874	TYW1
ENSG00000198876	21.2613	11.1476	12.11	7.09449	ENSG00000198876	DCAF12
ENSG00000198877	0	0	0	0	ENSG00000198877	OR5D13
ENSG00000198879	0.954235	0.827594	0.80973	1.64352	ENSG00000198879	SFMBT2
ENSG00000198881	0	0.115781	0	0	ENSG00000198881	ASB12
ENSG00000198883	0.0880032	0.119891	0.0906927	0.145303	ENSG00000198883	PNMA5
ENSG00000198885	1.71976	1.97238	0.756016	1.18174	ENSG00000198885	ITPRIPL1
ENSG00000198886	658.599	554.89	824.831	1328.63	ENSG00000198886	MT-ND4
ENSG00000198887	19.5008	24.8228	16.0114	25.7624	ENSG00000198887	SMC5
ENSG00000198888	398.179	460.092	776.95	791.853	ENSG00000198888	MT-ND1
ENSG00000198889	0.0805411	0.170873	0.0842683	0.194955	ENSG00000198889	DCAF12L1
ENSG00000198890	2.86473	2.54476	3.66419	2.95174	ENSG00000198890	PRMT6
ENSG00000198892	2.58072	1.20837	1.39316	2.35149	ENSG00000198892	SHISA4
ENSG00000198894	13.3642	6.82845	10.2583	6.78346	ENSG00000198894	CIPC
ENSG00000198898	75.5193	47.8438	42.0337	40.7067	ENSG00000198898	CAPZA2

ENSG00000198899	967.58	698.956	1539.52	1932.57	ENSG00000198899	MT-ATP6
ENSG00000198900	14.8254	18.0142	14.5821	23.2574	ENSG00000198900	TOP1
ENSG00000198901	17.7549	79.2597	18.2452	44.0441	ENSG00000198901	PRC1
ENSG00000198908	2.71971	5.09063	4.35953	7.05143	ENSG00000198908	BHLHB9
ENSG00000198909	7.48179	10.3902	6.05398	13.6964	ENSG00000198909	MAP3K3
ENSG00000198910	13.6504	22.3638	20.7924	19.0336	ENSG00000198910	L1CAM
ENSG00000198911	70.9889	95.5742	64.0438	67.8419	ENSG00000198911	SREBF2
ENSG00000198912	8.44683	10.9307	11.7646	9.38544	ENSG00000198912	C1orf174
ENSG00000198914	0.161705	0.227063	0.252557	0.47116	ENSG00000198914	POU3F3
ENSG00000198915	6.49378	4.57626	7.65818	5.12869	ENSG00000198915	RASGEF1A
ENSG00000198917	18.4294	16.4735	14.181	11.5451	ENSG00000198917	SPOUT1
ENSG00000198918	784.801	619.727	388.618	283.967	ENSG00000198918	RPL39
ENSG00000198919	3.35763	6.48489	4.93721	6.95502	ENSG00000198919	DZIP3
ENSG00000198920	13.7337	19.3253	29.0654	20.2144	ENSG00000198920	KIAA0753
ENSG00000198923	0	0.755747	0.665269	0	ENSG00000198923	AC011611.1
ENSG00000198924	2.84544	5.04314	4.18868	2.88803	ENSG00000198924	DCLRE1A
ENSG00000198925	31.8172	42.4115	36.807	21.8378	ENSG00000198925	ATG9A
ENSG00000198929	1.31545	1.09207	1.00684	1.60567	ENSG00000198929	NOS1AP
ENSG00000198930	0.0301358	0.0576578	0.0315043	0.0669767	ENSG00000198930	CSAG1
ENSG00000198931	77.2774	54.7733	67.1708	35.7261	ENSG00000198931	APRT
ENSG00000198932	0.518678	0.953886	0.828116	2.03246	ENSG00000198932	GPRASP1
ENSG00000198933	7.32319	4.55406	6.44538	6.34571	ENSG00000198933	TBKBP1
ENSG00000198934	0.997661	0.982963	0.640176	1.00701	ENSG00000198934	MAGEE1
ENSG00000198937	13.0568	7.90548	4.43247	7.02067	ENSG00000198937	CCDC167
ENSG00000198938	9426.33	8208.77	11783.2	9224.1	ENSG00000198938	MT-CO3
ENSG00000198939	1.12874	2.11353	1.36923	1.90511	ENSG00000198939	ZFP2
ENSG00000198944	0.0629499	0.121383	0.0274406	0.225038	ENSG00000198944	SOWAHA
ENSG00000198945	12.0514	11.7047	9.77947	25.6035	ENSG00000198945	L3MBTL3
ENSG00000198946	0.432239	0.15145	0.222436	0.3788	ENSG00000198946	SSX4B
ENSG00000198947	26.1527	48.1297	52.4714	100.51	ENSG00000198947	DMD
ENSG00000198948	7.26053	3.75765	5.3889	3.45795	ENSG00000198948	MFAP3L
ENSG00000198951	19.3604	26.999	7.9418	10.836	ENSG00000198951	NAGA
ENSG00000198952	46.5448	37.4294	48.2992	25.9935	ENSG00000198952	SMG5
ENSG00000198954	19.988	15.6567	14.151	19.9507	ENSG00000198954	KIF1BP
ENSG00000198959	11.0954	19.4495	5.83694	49.0538	ENSG00000198959	TGM2
ENSG00000198960	10.1879	6.91126	7.93171	5.2887	ENSG00000198960	ARMCX6
ENSG00000198961	24.0758	24.1902	21.621	28.1034	ENSG00000198961	PJA2
ENSG00000198963	0.762723	1.44944	2.40727	4.69292	ENSG00000198963	RORB
ENSG00000198964	21.1408	38.5532	24.5128	12.748	ENSG00000198964	SGMS1
ENSG00000198965	0.061156	0.058843	0.212713	0.199839	ENSG00000198965	OR10R2
ENSG00000198967	0	0	0	0	ENSG00000198967	OR10Z1
ENSG00000203257	3.92322	3.3163	3.05321	7.27276	ENSG00000203257	AL691479.1
ENSG00000203260	8.07424	15.4405	14.9101	28.3366	ENSG00000203260	AL356475.1
ENSG00000203262	0.79037	2.19852	1.70507	2.50327	ENSG00000203262	AL137845.1
ENSG00000203268	0.102965	0	0	0.22232	ENSG00000203268	AL445199.1
ENSG00000203276	4.38877	10.4397	9.32044	16.8842	ENSG00000203276	AL353898.2
ENSG00000203281	16.6682	32.6639	31.7653	54.656	ENSG00000203281	AL590489.1
ENSG00000203284	11.0544	40.5743	34.8004	61.4067	ENSG00000203284	AL591516.1
ENSG00000203285	32.7696	67.8597	55.1965	89.0778	ENSG00000203285	AL591516.2
ENSG00000203286	22.8465	41.6812	32.7408	56.6321	ENSG00000203286	Metazoa_SRP
ENSG00000203301	0.590511	1.19641	1.19652	2.17001	ENSG00000203301	AL590822.1
ENSG00000203305	1.21216	2.03362	2.09846	3.23975	ENSG00000203305	AC010525.1
ENSG00000203306	22.4812	31.7826	24.5123	24.5645	ENSG00000203306	AP001007.1
ENSG00000203314	20.0814	33.2256	19.0319	40.9492	ENSG00000203314	AC015815.1

ENSG00000203315	15.987	41.2229	30.2163	69.8281	ENSG00000203315	AC015815.2
ENSG00000203316	28.1282	66.3357	82.9217	81.1369	ENSG00000203316	AC015815.3
ENSG00000203317	9.82988	12.7292	0	0	ENSG00000203317	AC015815.4
ENSG00000203318	31.5987	53.7341	49.0005	98.7647	ENSG00000203318	AC015815.5
ENSG00000203326	34.3692	48.742	41.554	59.0941	ENSG00000203326	ZNF525
ENSG00000203334	0.379188	1.23721	1.0962	1.62515	ENSG00000203334	AP003027.1
ENSG00000203343	5.2938	4.85605	6.71666	11.5898	ENSG00000203343	AC009107.1
ENSG00000203344	0.927904	2.2442	1.95346	3.99772	ENSG00000203344	AC018696.2
ENSG00000203346	44.875	120.403	118.307	230.641	ENSG00000203346	AL162458.1
ENSG00000203363	0.45686	1.44642	1.96876	5.18705	ENSG00000203363	AC012454.1
ENSG00000203377	18.0433	25.7543	34.6619	57.472	ENSG00000203377	AC131568.1
ENSG00000203384	24.0271	56.1316	42.262	72.5115	ENSG00000203384	AL591516.3
ENSG00000203387	2.28629	4.18744	3.08374	8.08686	ENSG00000203387	AC074019.1
ENSG00000203392	2.10471	4.04175	4.65495	6.14875	ENSG00000203392	AC105020.1
ENSG00000203396	0.931426	0.913904	0.619523	1.14912	ENSG00000203396	AL512646.1
ENSG00000203397	0.148688	0.284645	1.15049	1.91762	ENSG00000203397	AL139400.1
ENSG00000203400	6.95361	11.828	15.829	32.0098	ENSG00000203400	AP001187.1
ENSG00000203401	1.76591	2.58565	4.1576	5.83847	ENSG00000203401	AC009061.1
ENSG00000203403	1.40566	2.7918	3.34291	4.66463	ENSG00000203403	AC020907.2
ENSG00000203408	0.134182	0.542945	0.236361	0.291894	ENSG00000203408	OR6C71P
ENSG00000203411	99.3005	234.557	192.037	409.612	ENSG00000203411	Metazoa_SRP
ENSG00000203413	0	0	0.291539	0.0608115	ENSG00000203413	ACTBP6
ENSG00000203414	0.441677	1.22152	0.64812	1.39186	ENSG00000203414	BTBD7P1
ENSG00000203415	0.92746	2.66347	2.44566	3.90931	ENSG00000203415	AC016734.1
ENSG00000203416	3.22403	13.8078	12.0799	29.0303	ENSG00000203416	FAM32BP
ENSG00000203418	23.9639	36.9952	42.2252	68.4736	ENSG00000203418	AC131571.1
ENSG00000203421	18.3358	7.90465	13.7589	52.9721	ENSG00000203421	AC140061.2
ENSG00000203422	68.7257	256.234	131.331	257.938	ENSG00000203422	AC140061.3
ENSG00000203423	61.3953	180.134	79.7279	225.68	ENSG00000203423	AC140061.4
ENSG00000203424	23.8221	54.156	72.1006	51.982	ENSG00000203424	AC140061.5
ENSG00000203425	47.1643	217.575	178.741	279.804	ENSG00000203425	AC140061.6
ENSG00000203426	197.204	440.738	328.658	488.096	ENSG00000203426	AC140061.7
ENSG00000203427	27.3656	85.036	92.1612	72.5822	ENSG00000203427	AC140061.8
ENSG00000203428	87.4117	197.548	204.948	305.339	ENSG00000203428	AC140061.9
ENSG00000203430	69.7345	93.9269	80.5946	106.435	ENSG00000203430	AC140061.10
ENSG00000203431	2.8393	65.1676	73.1008	120.004	ENSG00000203431	AC140061.11
ENSG00000203432	43.6798	120.755	154.608	260.608	ENSG00000203432	AC008147.1
ENSG00000203433	0	44.7463	42.7501	94.8344	ENSG00000203433	AC008147.2
ENSG00000203435	0.946672	1.83268	0.761761	4.36212	ENSG00000203435	E2F3P2
ENSG00000203436	15.7393	25.0415	25.8459	52.3745	ENSG00000203436	Metazoa_SRP
ENSG00000203437	1.67866	3.17181	2.21374	6.37841	ENSG00000203437	AC022080.1
ENSG00000203438	10.8399	26.9424	28.7649	42.875	ENSG00000203438	AL512625.1
ENSG00000203442	41.927	58.085	49.6905	100.379	ENSG00000203442	AC008555.1
ENSG00000203443	35.4987	64.8078	50.597	119.57	ENSG00000203443	AC092964.1
ENSG00000203457	13.5619	16.8348	19.7029	21.4951	ENSG00000203457	AC068896.1
ENSG00000203462	1.10664	3.37447	2.78768	7.26907	ENSG00000203462	AC093392.1
ENSG00000203465	13.3479	18.1783	15.8166	30.5261	ENSG00000203465	AC061975.2
ENSG00000203471	25.4152	22.0459	28.8543	72.9042	ENSG00000203471	AL359697.1
ENSG00000203473	31.0755	51.1769	54.4959	103.889	ENSG00000203473	AC105036.1
ENSG00000203477	5.94664	32.849	18.2656	40.8891	ENSG00000203477	AC061975.3
ENSG00000203478	19.6295	37.5173	27.3088	48.5556	ENSG00000203478	AC061975.4
ENSG00000203479	27.7844	53.8147	48.2534	81.4988	ENSG00000203479	AC061975.5
ENSG00000203480	29.2723	45.0012	37.55	98.3459	ENSG00000203480	AC061975.6
ENSG00000203482	46.5955	100.378	92.6336	189.338	ENSG00000203482	AC061975.7

ENSG00000203483	31.3195	44.7684	58.2872	104.219	ENSG00000203483	AC100852.1
ENSG00000203484	24.3826	38.5561	32.9079	103.141	ENSG00000203484	AC100852.2
ENSG00000203485	39.1077	75.1252	46.9956	59.8568	ENSG00000203485	INF2
ENSG00000203489	2.49612	4.75006	4.78968	8.29711	ENSG00000203489	HMGB1P39
ENSG00000203492	0	0	0.00828591	0	ENSG00000203492	AL645937.1
ENSG00000203504	2.70182	4.79063	5.36284	9.12638	ENSG00000203504	AC131571.2
ENSG00000203505	21.948	38.2611	27.6883	48.5854	ENSG00000203505	AC003079.1
ENSG00000203507	8.15377	20.72	19.0325	42.3091	ENSG00000203507	AC103801.1
ENSG00000203511	12.1466	23.6359	21.2244	41.0327	ENSG00000203511	AL353662.1
ENSG00000203512	68.2292	144.13	121.432	211.233	ENSG00000203512	AL353662.2
ENSG00000203513	27.3877	34.8757	35.5367	52.4267	ENSG00000203513	AL353662.3
ENSG00000203518	30.4247	66.9384	57.1488	117.058	ENSG00000203518	AL023807.1
ENSG00000203523	0	0.0664927	0	0.0751695	ENSG00000203523	TAS2R2P
ENSG00000203531	3.11612	4.35938	4.56169	6.95426	ENSG00000203531	AC104772.1
ENSG00000203542	7.51223	34.8605	31.9197	67.7888	ENSG00000203542	AL353671.1
ENSG00000203543	35.0577	56.8627	54.7779	135.89	ENSG00000203543	AL353671.2
ENSG00000203544	20.8565	45.9166	36.0739	62.7097	ENSG00000203544	BX248133.1
ENSG00000203546	8.26453	12.8503	11.3843	17.52	ENSG00000203546	AL139353.1
ENSG00000203547	9.20249	22.9015	16.1381	55.711	ENSG00000203547	AL135901.1
ENSG00000203560	0	0.258417	0.0583755	0.292266	ENSG00000203560	OR52J1P
ENSG00000203562	1.50253	2.85956	3.58915	1.61177	ENSG00000203562	AC003079.1
ENSG00000203563	7.9216	25.8985	18.4688	35.2045	ENSG00000203562	AC004771.1
ENSG00000203572	5.50439	19.5687	20.4648	19.8142	ENSG00000203572	AC090519.3
ENSG00000203573	93.0864	184.719	196.338	334.436	ENSG00000203573	Metazoa_SRP
ENSG00000203574	39.823	66.9565	78.4524	152.899	ENSG00000203574	AC090519.5
ENSG00000203575	29.4595	70.874	58.9335	133.025	ENSG00000203575	AC090519.6
ENSG00000203576	93.826	176.647	175.116	264.575	ENSG00000203576	AC090519.7
ENSG00000203578	26.2514	52.982	32.0518	73.6993	ENSG00000203578	AC073940.1
ENSG00000203581	0.134182	0.181858	0.233201	1.09563	ENSG00000203581	OR1F2P
ENSG00000203583	1.74086	1.05578	3.61765	2.92874	ENSG00000203583	AL021707.1
ENSG00000203589	10.5954	20.8133	22.6031	40.0334	ENSG00000203589	RP5-886K2.1
ENSG00000203594	18.1541	34.0268	18.1568	59.4634	ENSG00000203594	AC116351.1
ENSG00000203602	0.73376	2.42088	2.09438	0.931814	ENSG00000203602	AL137059.1
ENSG00000203606	0.483844	0.646551	1.00981	1.2469	ENSG00000203606	AC004832.1
ENSG00000203614	0.491043	2.0313	1.38681	2.65147	ENSG00000203614	AL512652.1
ENSG00000203615	102.49	173.27	146.431	241.995	ENSG00000203615	AC069200.1
ENSG00000203616	0	0	0	0	ENSG00000203616	RHOT1P2
ENSG00000203618	0.744525	0.440859	0.459166	2.73757	ENSG00000203618	GP1BB
ENSG00000203623	2.36123	2.70737	3.73633	0	ENSG00000203623	C6orf47
ENSG00000203624	3.6819	4.08555	4.50723	3.12515	ENSG00000203624	MRPS18B
ENSG00000203630	4.50988	8.54162	8.40737	14.6294	ENSG00000203630	AL136531.1
ENSG00000203632	1.32119	3.85347	3.22181	3.77765	ENSG00000203632	AC007690.1
ENSG00000203644	7.14023	11.6797	8.57935	15.2812	ENSG00000203644	AC083799.1
ENSG00000203647	1.53093	1.83088	1.48784	4.3202	ENSG00000203647	AC106827.1
ENSG00000203648	0	0	0	0.392281	ENSG00000203648	AC007618.1
ENSG00000203652	0.108334	0.20876	0.597507	0.890271	ENSG00000203652	AC099048.1
ENSG00000203659	1.60584	2.35647	3.31603	6.54763	ENSG00000203659	AL353671.3
ENSG00000203661	0.0303631	0.10551	0.052806	0	ENSG00000203661	OR2T5
ENSG00000203663	0	0.102499	0.0926392	0.174289	ENSG00000203663	OR2L2
ENSG00000203664	0	0	0	0	ENSG00000203664	OR2W5
ENSG00000203666	3.93429	6.57413	7.30607	10.9483	ENSG00000203666	EFCAB2
ENSG00000203667	16.8885	19.263	23.1478	24.5401	ENSG00000203667	COX20
ENSG00000203668	7.8518	6.6526	5.77734	9.34252	ENSG00000203668	CHML
ENSG00000203684	1.77617	2.30284	2.64757	1.02286	ENSG00000203684	IBA57-AS1

ENSG00000203685	8.2494	2.33851	2.46875	37.8002	ENSG00000203685	STUM
ENSG00000203690	0.447572	0.64362	0.443942	0.353492	ENSG00000203690	TCP10
ENSG00000203691	0.983047	2.48925	1.3459	1.5777	ENSG00000203691	AC092811.1
ENSG00000203697	61.6461	16.1369	11.8932	23.1335	ENSG00000203697	CAPN8
ENSG00000203705	13.0515	20.1358	19.4854	22.1647	ENSG00000203705	TATDN3
ENSG00000203710	1.59973	3.08802	3.261	3.97989	ENSG00000203710	CR1
ENSG00000203711	0.808825	1.25577	0.846799	1.73588	ENSG00000203711	C6orf99
ENSG00000203722	28.9931	10.6858	23.3729	4.91568	ENSG00000203722	RAET1G
ENSG00000203724	2.51235	0.580348	0.419263	0.390184	ENSG00000203724	C1orf53
ENSG00000203727	1.43497	2.25231	1.42921	2.47515	ENSG00000203727	SAMD5
ENSG00000203730	0.278874	0.349737	0.50047	0.8547	ENSG00000203730	TEDDM1
ENSG00000203733	0	0.0659668	0.0596058	0.074582	ENSG00000203733	GJE1
ENSG00000203734	0.61259	1.59147	1.62362	1.59627	ENSG00000203734	ECT2L
ENSG00000203737	0.75097	1.90355	1.43917	2.50907	ENSG00000203737	GPR52
ENSG00000203740	0	0.0895544	0	0.201597	ENSG00000203740	METTL11B
ENSG00000203747	0	0.0468457	0.0633198	0.0534015	ENSG00000203747	FCGR3A
ENSG00000203756	0	0	0.232772	0.288164	ENSG00000203756	TMEM244
ENSG00000203757	0	0	0	0	ENSG00000203757	OR6K3
ENSG00000203758	0	0.126754	0.114535	0.215083	ENSG00000203758	OR10T1P
ENSG00000203760	5.57325	12.0594	2.19027	5.38683	ENSG00000203760	CENPW
ENSG00000203761	5.28529	7.01776	7.26142	5.4	ENSG00000203761	MSTO2P
ENSG00000203772	1.07348	1.89053	3.58715	2.86524	ENSG00000203772	SPRN
ENSG00000203778	1.182	2.45831	1.65693	2.22552	ENSG00000203778	FAM229B
ENSG00000203780	7.56869	9.3858	12.8307	12.8619	ENSG00000203780	FANK1
ENSG00000203781	0	0	0	0	ENSG00000203781	AL591704.1
ENSG00000203782	0.0978322	0.047739	0.0441875	0	ENSG00000203782	LOR
ENSG00000203783	0.291154	0.235447	0.170071	1.58966	ENSG00000203783	PRR9
ENSG00000203784	0.142437	0	0	0	ENSG00000203784	LELP1
ENSG00000203785	2.25829	1.91067	3.34956	3.80316	ENSG00000203785	SPRR2E
ENSG00000203786	0.811923	0.085745	0.0775203	0.84393	ENSG00000203786	KPRP
ENSG00000203791	11.1183	16.1501	15.0964	17.7314	ENSG00000203791	EEF1AKMT2
ENSG00000203795	0.118741	0.113955	0.102909	0.12774	ENSG00000203795	FAM24A
ENSG00000203797	0	0.0610577	0.133526	0.134179	ENSG00000203797	DDO
ENSG00000203799	1.69802	4.07595	3.42353	4.21724	ENSG00000203799	CCDC162P
ENSG00000203804	1.91663	3.11051	2.50042	2.73838	ENSG00000203804	ADAMTSL4-AS1
ENSG00000203805	0.217263	0.43609	0.227546	0.331161	ENSG00000203805	PLPP4
ENSG00000203811	1.83986	7.54592	2.14069	2.30046	ENSG00000203811	HIST2H3C
ENSG00000203812	57.6173	74.4969	39.4664	29.6576	ENSG00000203812	HIST2H2AA3
ENSG00000203813	22.9001	84.8533	25.9921	20.0471	ENSG00000203813	HIST2H3H
ENSG00000203814	18.579	35.4706	15.0314	11.594	ENSG00000203814	HIST2H2BF
ENSG00000203815	0.277636	0.744755	1.62837	1.34367	ENSG00000203815	FAM231D
ENSG00000203817	0.420672	3.55804	1.06993	1.5823	ENSG00000203817	FAM72C
ENSG00000203818	0.136214	1.0188	2.63203	0.820883	ENSG00000203818	HIST2H3PS2
ENSG00000203819	1.58232	0.925699	1.03643	0.532753	ENSG00000203819	HIST2H2BC
ENSG00000203825	0.0218555	0.0349822	0.0376105	0.107764	ENSG00000203825	AC239859.1
ENSG00000203827	0	0	4.60806	0.0508975	ENSG00000203827	NBPF16
ENSG00000203832	6.60863	8.23889	9.77265	15.7187	ENSG00000203832	NBPF20
ENSG00000203835	0.00320998	0.0154325	0.0250474	0.00837705	ENSG00000203835	ABHD17AP1
ENSG00000203836	26.2615	47.27	44.696	55.399	ENSG00000203836	NBPF24
ENSG00000203837	65.7901	35.9206	48.9952	18.077	ENSG00000203837	PNLIPRP3
ENSG00000203843	4.45973	8.21794	6.55613	11.246	ENSG00000203843	PFN1P2
ENSG00000203852	1.83986	7.54592	2.14069	2.30046	ENSG00000203852	HIST2H3A
ENSG00000203855	0	0.200189	0.117614	1.02363	ENSG00000203855	HSD3BP4

ENSG00000203857	0.449932	0.574782	0.761371	1.67615	ENSG00000203857	HSD3B1
ENSG00000203858	0	0.43872	0.325867	0.8993	ENSG00000203858	HSD3BP2
ENSG00000203859	0.292836	0.706701	0.598062	1.03835	ENSG00000203859	HSD3B2
ENSG00000203863	1.27822	2.27607	1.91144	3.13278	ENSG00000203863	AL079342.1
ENSG00000203864	0	0.220704	0	0	ENSG00000203864	C1orf137
ENSG00000203867	2.13984	2.85607	3.33387	5.94612	ENSG00000203867	RBM20
ENSG00000203870	0.179343	0.559581	0.807398	0.873788	ENSG00000203870	SMIM9
ENSG00000203871	1.25737	1.80934	2.08996	2.16905	ENSG00000203871	C6orf164
ENSG00000203872	2.08212	5.16467	5.66356	7.41778	ENSG00000203872	C6orf163
ENSG00000203876	0.477289	0.644027	0.37532	1.08346	ENSG00000203876	ADD3-AS1
ENSG00000203877	0.286447	0.137355	0	0.787017	ENSG00000203877	RIPPLY2
ENSG00000203878	0.347796	0.514315	0.329066	0.512565	ENSG00000203878	CHIAP2
ENSG00000203879	15.6236	18.2667	17.7231	18.1408	ENSG00000203879	GDI1
ENSG00000203880	23.0922	28.1236	32.8655	33.2014	ENSG00000203880	PCMTD2
ENSG00000203883	0	0	0.0866929	0.109091	ENSG00000203883	SOX18
ENSG00000203896	6.02317	5.37954	7.00182	4.42003	ENSG00000203896	LIME1
ENSG00000203902	0	0.120955	0	0	ENSG00000203902	PNMA6B
ENSG00000203907	0.787369	0.877338	1.56115	1.58902	ENSG00000203907	OOEP
ENSG00000203908	0.241775	0.581886	0.369369	0.724316	ENSG00000203908	KHDC3L
ENSG00000203909	0	0.287626	0.173201	0.862574	ENSG00000203909	DPPA5
ENSG00000203910	0.462218	2.1927	1.83633	2.97945	ENSG00000203910	C1orf146
ENSG00000203914	0.334992	0.461879	0.0968379	0.608492	ENSG00000203914	HSP90B3P
ENSG00000203923	0	0	0	0.0253899	ENSG00000203923	SPANXN1
ENSG00000203924	0	0	0	0.0422059	ENSG00000203924	SPANXN2
ENSG00000203926	0	0	0	0.0449071	ENSG00000203926	SPANXA2
ENSG00000203930	0.88814	2.00631	2.09369	5.64339	ENSG00000203930	LINC00632
ENSG00000203933	0	0.0890873	0.0410391	0	ENSG00000203933	CXorf66
ENSG00000203942	0.143917	0.0461882	0.125242	0	ENSG00000203942	C10orf62
ENSG00000203943	5.40781	4.14364	7.37142	3.51221	ENSG00000203943	SAMD13
ENSG00000203950	6.28753	6.43328	4.86408	6.46609	ENSG00000203950	RTL8A
ENSG00000203952	0.407894	0.687799	0.730931	1.76158	ENSG00000203952	CCDC160
ENSG00000203963	1.16895	1.88386	2.4431	3.92142	ENSG00000203963	C1orf141
ENSG00000203965	3.2945	8.02258	6.29993	5.22192	ENSG00000203965	EFCAB7
ENSG00000203970	0	0	0	0	ENSG00000203970	DEFB110
ENSG00000203972	0	0	0	0.135272	ENSG00000203972	GLYATL3
ENSG00000203985	0.38054	0.320256	0.0720204	0	ENSG00000203985	LDLRAD1
ENSG00000203989	0	0.0489826	0.0737983	0.148568	ENSG00000203989	RHOXF2B
ENSG00000203993	8.82473	11.1051	11.2691	8.3658	ENSG00000203993	ARRDC1-AS1
ENSG00000203995	1.46908	3.11237	2.31603	3.69408	ENSG00000203995	ZYG11A
ENSG00000204001	0.0210358	0.24666	0.167181	0.279088	ENSG00000204001	LCN8
ENSG00000204003	0	0	0	0	ENSG00000204003	AL355987.1
ENSG00000204006	0.0883029	1.3784	1.03918	0.333354	ENSG00000204006	C1orf185
ENSG00000204007	0	0	0	0	ENSG00000204007	GLT6D1
ENSG00000204010	0.372025	0.331384	0.356276	0.441311	ENSG00000204010	IFIT1B
ENSG00000204019	0.333371	0.0643923	0	0	ENSG00000204019	CT83
ENSG00000204020	0.800129	0.337004	0.348109	0.0546057	ENSG00000204020	LIPN
ENSG00000204021	5.65582	0.793254	1.04811	0.319237	ENSG00000204021	LIPK
ENSG00000204022	0.100276	0.0890531	0.36248	0.703163	ENSG00000204022	LIPJ
ENSG00000204031	0	0.290453	0	0	ENSG00000204031	LCN1P2
ENSG00000204033	0.309787	0.206848	0.469373	0.451041	ENSG00000204033	LRIT2
ENSG00000204038	0.49421	1.92882	2.23457	1.34674	ENSG00000204038	AL359195.1
ENSG00000204049	1.32878	4.53446	2.5737	3.67447	ENSG00000204049	AL391421.1
ENSG00000204052	0.29087	0.433358	0.415223	0.377343	ENSG00000204052	LRRC73
ENSG00000204053	0	0	0	0	ENSG00000204053	MYCLP1

ENSG00000204060	0.393883	0.180309	0.467365	0.229364	ENSG00000204060	FOXO6
ENSG00000204065	0	0	0	0	ENSG00000204065	TCEAL5
ENSG00000204070	19.187	12.2973	12.2781	9.50523	ENSG00000204070	SYS1
ENSG00000204071	0	0.026875	0.0758672	0.154267	ENSG00000204071	TCEAL6
ENSG00000204072	2.05572	0.895161	0.356389	1.31157	ENSG00000204072	ARMCX7P
ENSG00000204084	12.3514	14.5573	16.983	29.0687	ENSG00000204084	INPP5B
ENSG00000204086	0.413346	0.723966	0.490817	0.946352	ENSG00000204086	RPA4
ENSG00000204099	0	0.458206	0.0223601	0	ENSG00000204099	NEU4
ENSG00000204103	1.4871	0.612136	4.09931	2.59098	ENSG00000204103	MAFB
ENSG00000204104	5.31106	4.45809	8.09006	7.2488	ENSG00000204104	TRAF3IP1
ENSG00000204113	0.664492	3.90447	5.95725	4.58881	ENSG00000204113	BMP2KL
ENSG00000204116	1.60769	2.6757	2.31614	2.80758	ENSG00000204116	CHIC1
ENSG00000204118	0.365066	0.469878	0.554332	1.04492	ENSG00000204118	NAP1L6
ENSG00000204120	43.2674	74.0873	65.5261	93.9307	ENSG00000204120	GIGYF2
ENSG00000204121	0.0983349	0.0631666	0.0571017	0.25151	ENSG00000204121	ECEL1P1
ENSG00000204128	0.015087	0.0574818	0.0409388	0.0979545	ENSG00000204128	C2orf72
ENSG00000204130	21.3817	25.4149	22.5833	31.9118	ENSG00000204130	RUFY2
ENSG00000204131	0.0655167	0.0471888	0.154785	2.44569	ENSG00000204131	NHSL2
ENSG00000204136	0.280723	0.495192	1.04395	0.776959	ENSG00000204136	GGTA1P
ENSG00000204138	10.225	11.2722	12.4957	17.0933	ENSG00000204138	PHACTR4
ENSG00000204140	0	0.119678	0.10807	0	ENSG00000204140	CLPSL1
ENSG00000204147	3.20749	5.52317	4.61425	4.22911	ENSG00000204147	ASAH2B
ENSG00000204149	3.22219	3.73673	5.77481	4.16157	ENSG00000204149	AGAP6
ENSG00000204150	0.0505101	0.522991	0.378531	0.331979	ENSG00000204150	CTGLF11P
ENSG00000204152	5.89493	4.76004	10.7975	9.54215	ENSG00000204152	TIMM23B
ENSG00000204160	17.322	13.6851	13.3243	9.38099	ENSG00000204160	ZDHHC18
ENSG00000204161	1.22239	1.55564	1.1579	2.8064	ENSG00000204161	C10orf128
ENSG00000204164	0.862567	1.6178	4.0092	3.70367	ENSG00000204164	BMS1P5
ENSG00000204165	0.0737425	0	0	0	ENSG00000204165	CXorf65
ENSG00000204169	0.0316254	1.2165	0.473063	0.0876141	ENSG00000204169	AGAP7
ENSG00000204172	4.04156	8.56197	13.5675	12.9847	ENSG00000204172	AGAP9
ENSG00000204173	2.16144	3.68923	4.36106	7.44443	ENSG00000204173	LRRC37A5P
ENSG00000204174	0.354691	0.139271	0.421482	0.22047	ENSG00000204174	NPY4R
ENSG00000204175	2.41686	1.09672	0.945521	0.595574	ENSG00000204175	GPRIN2
ENSG00000204176	2.55573	4.60078	7.39189	9.74629	ENSG00000204176	SYT15
ENSG00000204177	2.07148	6.03178	8.9639	7.67958	ENSG00000204177	BMS1P1
ENSG00000204178	15.6207	14.3429	10.3475	8.94587	ENSG00000204178	TMEM57
ENSG00000204179	1.64981	4.95595	3.65297	3.044	ENSG00000204179	PTPN20
ENSG00000204183	0.63772	0.643779	1.73185	2.10237	ENSG00000204183	GDF5OS
ENSG00000204186	2.46899	5.01293	4.46956	3.81067	ENSG00000204186	ZDBF2
ENSG00000204188	0	0.249401	0	0.423275	ENSG00000204188	GGNBP1
ENSG00000204193	0	0.0307111	0	0.279546	ENSG00000204193	TXNDC8
ENSG00000204194	0	0.313397	0	0	ENSG00000204194	RPL12P1
ENSG00000204195	0.17632	0.907694	0.339541	0.869185	ENSG00000204195	AWAT1
ENSG00000204196	0	0.882769	0	0	ENSG00000204196	RPL12P16
ENSG00000204197	0.157775	6.00E-10	0	0.570845	ENSG00000204197	KIFC1
ENSG00000204209	7.07035	6.18748	5.54839	2.69061	ENSG00000204209	DAXX
ENSG00000204217	23.506	21.0591	22.5743	26.0774	ENSG00000204217	BMPR2
ENSG00000204219	1.83686	3.43453	2.60352	4.36193	ENSG00000204219	TCEA3
ENSG00000204220	5.71416	3.94017	5.17631	2.52165	ENSG00000204220	PFDN6
ENSG00000204221	3.55765	5.32633	4.7322	6.88796	ENSG00000204221	WDR46
ENSG00000204227	0	2.37574	2.34196	0.817843	ENSG00000204227	RING1
ENSG00000204228	1.5288	1.62628	2.07747	0.55839	ENSG00000204228	HSD17B8
ENSG00000204231	0.770594	0.900677	1.42709	0.954922	ENSG00000204231	RXRB

ENSG00000204237	13.8818	16.451	20.6072	7.36263	ENSG00000204237	OXLD1
ENSG00000204246	0	0.157955	0.0951722	0.179012	ENSG00000204246	OR13C3
ENSG00000204248	0	0.0189021	0.03417	0.0424258	ENSG00000204248	COL11A2
ENSG00000204252	5.72E-05	0.324416	0.10432	1.04653	ENSG00000204252	HLA-DOA
ENSG00000204253	0	0.0932286	0.353874	0	ENSG00000204253	HNRNPCP2
ENSG00000204256	41.5543	33.4442	40.2468	25.7446	ENSG00000204256	BRD2
ENSG00000204257	0.216875	0.322965	1.09932	1.11209	ENSG00000204257	HLA-DMA
ENSG00000204262	10.7842	24.8188	81.3011	225.056	ENSG00000204262	COL5A2
ENSG00000204264	1.10486	0.54819	1.3866	1.30105	ENSG00000204264	PSMB8
ENSG00000204267	7.90038	12.9907	12.502	0.591091	ENSG00000204267	TAP2
ENSG00000204271	2.37866	2.65581	5.78944	1.48772	ENSG00000204271	SPIN3
ENSG00000204276	0	0	0	0	ENSG00000204276	HLA-DQA2
ENSG00000204278	0.122814	0.243727	0.302707	0.716808	ENSG00000204278	TMEM235
ENSG00000204279	0	0	0	0.0963959	ENSG00000204279	PAGE3
ENSG00000204283	0.224073	0.349654	0.38082	0.483723	ENSG00000204283	LINC01973
ENSG00000204287	0	0	0	0	ENSG00000204287	HLA-DRA
ENSG00000204290	0	0.0646215	0.0389217	0	ENSG00000204290	BTNL2
ENSG00000204291	2.30673	3.51565	3.6507	6.92268	ENSG00000204291	COL15A1
ENSG00000204293	0	0	0	0	ENSG00000204293	OR8B2
ENSG00000204296	0.0337601	0	0	0	ENSG00000204296	C6orf10
ENSG00000204300	0.0547615	0	0.0476362	0	ENSG00000204300	TMEM225
ENSG00000204301	0.0774347	0.271779	0.0796164	0.236413	ENSG00000204301	NOTCH4
ENSG00000204304	2.51235	3.12678	5.14231	3.36238	ENSG00000204304	PBX2
ENSG00000204305	0.427474	0.559219	0.554064	0.370417	ENSG00000204305	AGER
ENSG00000204306	0	0	0	0	ENSG00000204306	AP002348.1
ENSG00000204308	1.85056	2.23275	2.98611	1.51903	ENSG00000204308	RNF5
ENSG00000204310	0	0	1.41835	3.93588	ENSG00000204310	AGPAT1
ENSG00000204311	0.685234	1.30306	2.07238	2.48254	ENSG00000204311	DFNB59
ENSG00000204314	0.0315493	0.0750009	0.16353	0.116243	ENSG00000204314	PRRT1
ENSG00000204315	1.03011	1.49737	0.476154	0.430663	ENSG00000204315	FKBPL
ENSG00000204316	34.6395	48.952	35.9161	23.7066	ENSG00000204316	MRPL38
ENSG00000204323	3.91201	1.88954	3.24891	2.0814	ENSG00000204323	SMIM5
ENSG00000204334	0.234793	1.41314	2.64554	0.434061	ENSG00000204334	ERICH2
ENSG00000204335	0.0276852	0.885342	0.144732	0	ENSG00000204335	SP5
ENSG00000204338	0.163861	0.087706	0	0.0843649	ENSG00000204338	CYP21A1P
ENSG00000204344	3.09598	1.79219	2.1609	1.39658	ENSG00000204344	STK19
ENSG00000204345	1.35674	2.4942	1.62459	4.00746	ENSG00000204345	CD300LD
ENSG00000204347	0	0	0	0	ENSG00000204347	BTBD17
ENSG00000204348	1.99949	2.4991	2.10477	1.17143	ENSG00000204348	DXO
ENSG00000204351	3.32399	6.78675	2.85225	2.20424	ENSG00000204351	SKIV2L
ENSG00000204352	0	0	0	0.0667429	ENSG00000204352	C9orf129
ENSG00000204356	11.1048	12.3645	12.0847	2.68622	ENSG00000204356	NELFE
ENSG00000204359	0.029918	0.884498	0.473058	0.516727	ENSG00000204359	CFB
ENSG00000204361	2.18007	2.98298	2.65077	5.48802	ENSG00000204361	NXPE2
ENSG00000204363	0	0	0	0	ENSG00000204363	SPANXN5
ENSG00000204364	1.48007	2.88554	2.45771	4.47454	ENSG00000204364	C2
ENSG00000204365	0.766335	2.39789	1.82327	3.5817	ENSG00000204365	C10orf126
ENSG00000204366	0.256112	0.212818	0	0.639599	ENSG00000204366	ZBTB12
ENSG00000204368	0	0	0.096946	0	ENSG00000204368	AC245047.1
ENSG00000204370	27.5532	29.8351	24.2967	22.6363	ENSG00000204370	SDHD
ENSG00000204371	0.78392	1.11679	1.2282	2.39349	ENSG00000204371	EHMT2
ENSG00000204375	0	0	0	0	ENSG00000204375	XAGE1E
ENSG00000204376	0	0	0	0	ENSG00000204376	XAGE1D
ENSG00000204377	10.381	19.9541	17.9958	25.5711	ENSG00000204377	C1orf134

ENSG00000204379	0	0	0	0	ENSG00000204379	XAGE1A
ENSG00000204381	15.501	7.28407	12.198	18.5019	ENSG00000204381	LAYN
ENSG00000204382	0	0.0443425	0	0	ENSG00000204382	XAGE1B
ENSG00000204385	0.0393897	0.290961	0.258819	0.412492	ENSG00000204385	SLC44A4
ENSG00000204386	4.65105	3.54583	2.17492	1.03442	ENSG00000204386	NEU1
ENSG00000204387	7.88264	13.6079	25.4556	7.1227	ENSG00000204387	C6orf48
ENSG00000204388	0.636273	0	0	6.80E-06	ENSG00000204388	HSPA1B
ENSG00000204389	5.17E-06	0	0	0	ENSG00000204389	HSPA1A
ENSG00000204390	0	0	0.0897543	0	ENSG00000204390	HSPA1L
ENSG00000204392	1.80946	3.03656	2.08593	1.50939	ENSG00000204392	LSM2
ENSG00000204393	0	0.29362	0.066118	0.247105	ENSG00000204393	AL133343.1
ENSG00000204394	2.80712	7.18785	5.91591	8.61059	ENSG00000204394	VARS
ENSG00000204396	1.02425	1.71745	2.89525	2.54589	ENSG00000204396	VWA7
ENSG00000204397	1.63696	4.27681	2.76303	1.41266	ENSG00000204397	CARD16
ENSG00000204398	0.0327991	0	0.157364	0.0719051	ENSG00000204398	AL359649.1
ENSG00000204399	0	0	0	0	ENSG00000204399	AC012306.1
ENSG00000204403	0	0.272158	0	0.0791213	ENSG00000204403	CASP12
ENSG00000204406	16.7431	34.9643	41.8858	47.7023	ENSG00000204406	MBD5
ENSG00000204410	11.9541	28.2104	14.7191	31.7088	ENSG00000204410	MSH5
ENSG00000204414	0.144017	0.0692533	0.16982	0.0864036	ENSG00000204414	CSHL1
ENSG00000204420	0.109742	0	0.33214	0.143017	ENSG00000204420	MPIG6B
ENSG00000204421	0.329801	0	0.241696	0	ENSG00000204421	LY6G6C
ENSG00000204422	0	0	0	0.118175	ENSG00000204422	AL662899.1
ENSG00000204424	0.0272928	0.112493	0.0254114	0.0148391	ENSG00000204424	LY6G6F
ENSG00000204427	2.13871	2.80265	2.88325	1.64317	ENSG00000204427	ABHD16A
ENSG00000204428	1.33202	2.04853	1.46105	3.34325	ENSG00000204428	LY6G5C
ENSG00000204429	0	0	0	0	ENSG00000204429	AL451142.1
ENSG00000204434	0.0361091	0.122434	0.064357	0.138923	ENSG00000204434	POTEKP
ENSG00000204435	1.18829	1.24558	2.63879	4.96513	ENSG00000204435	CSNK2B
ENSG00000204437	0	0	0	0.0349224	ENSG00000204437	CTSLP6
ENSG00000204438	2.24011	0.903242	1.2865	0.267307	ENSG00000204438	GPANK1
ENSG00000204439	0	0	0	0	ENSG00000204439	C6orf47
ENSG00000204442	0.320462	0.744033	0.827235	1.48847	ENSG00000204442	FAM155A
ENSG00000204444	0.624559	1.157	1.1778	0.987048	ENSG00000204444	APOM
ENSG00000204446	0.135533	0.307009	0.266035	0.666367	ENSG00000204446	C9orf170
ENSG00000204449	0	0	0	0	ENSG00000204449	TRIM49C
ENSG00000204450	0.0244478	0.109148	0	0.0805752	ENSG00000204450	TRIM64
ENSG00000204455	0	0	0	0	ENSG00000204455	TRIM51BP
ENSG00000204456	0	0	0	0	ENSG00000204456	AP003122.1
ENSG00000204463	7.14606	26.8938	9.72521	12.2119	ENSG00000204463	BAG6
ENSG00000204464	7.91956	7.34896	6.02815	10.7454	ENSG00000204464	C1orf195
ENSG00000204469	1.88462	6.26914	7.4302	4.42253	ENSG00000204469	PRRC2A
ENSG00000204471	0	0	0	0	ENSG00000204471	TBC1D3P4
ENSG00000204472	0.128048	0.179373	0.160375	0.21663	ENSG00000204472	AIF1
ENSG00000204475	0	0	0	0	ENSG00000204475	NCR3
ENSG00000204478	0	0	0	0	ENSG00000204478	PRAMEF20
ENSG00000204479	0.0829853	0.199376	0.199984	0.31729	ENSG00000204479	PRAMEF17
ENSG00000204480	0	0	0	0.345473	ENSG00000204480	PRAMEF19
ENSG00000204481	0.0777996	0	0.137767	0.192762	ENSG00000204481	PRAMEF14
ENSG00000204482	0	0	0.112516	0	ENSG00000204482	LST1
ENSG00000204485	0.0269268	0.0299899	0.0268323	0.0675634	ENSG00000204485	XX-FW84067D5.1
ENSG00000204486	0	0	0	0	ENSG00000204486	PRAMEF21
ENSG00000204487	0.013508	0	0.0359938	0.0362078	ENSG00000204487	LTB

ENSG00000204488	0.323555	0.458872	0.455289	0.435102	ENSG00000204488	PRAMEF16
ENSG00000204490	0.222879	0.099013	0.196978	0.0453146	ENSG00000204490	TNF
ENSG00000204491	0	0	0	0	ENSG00000204491	PRAMEF18
ENSG00000204495	0	0	0	0	ENSG00000204495	PRAMEF13
ENSG00000204498	0.096051	0.158659	0.385354	0.191227	ENSG00000204498	NFKBIL1
ENSG00000204501	0	0	0	0	ENSG00000204501	PRAMEF15
ENSG00000204502	0	0	0	0	ENSG00000204502	PRAMEF5
ENSG00000204503	0.13646	0.302762	0.22006	0	ENSG00000204503	PRAMEF3
ENSG00000204505	0	0	0	0	ENSG00000204505	PRAMEF9
ENSG00000204508	0	0	0	0	ENSG00000204508	PRAMEF22
ENSG00000204510	0.0281335	0.0299899	0.0268323	0.0675634	ENSG00000204510	PRAMEF7
ENSG00000204511	0.0916753	0	0	0	ENSG00000204511	MCCD1
ENSG00000204513	0	0	0	0	ENSG00000204513	PRAMEF11
ENSG00000204514	32.2786	48.6182	55.7117	69.9851	ENSG00000204514	ZNF814
ENSG00000204516	0.730322	2.77674	1.88992	2.63457	ENSG00000204516	MICB
ENSG00000204518	0	0.0353044	0.0319135	0.0401362	ENSG00000204518	AADACL4
ENSG00000204519	5.96617	6.40468	7.32595	6.02315	ENSG00000204519	ZNF551
ENSG00000204520	0	0	0	0	ENSG00000204520	MICA
ENSG00000204524	8.06964	7.14068	9.66626	8.26843	ENSG00000204524	ZNF805
ENSG00000204525	0.428203	0.0632179	1.01496	0.108944	ENSG00000204525	HLA-C
ENSG00000204529	0	0	0	0	ENSG00000204529	GUCY2EP
ENSG00000204531	2.05477	4.48023	6.05149	8.98866	ENSG00000204531	POU5F1
ENSG00000204532	0	0.11849	0.0279413	0.0702625	ENSG00000204532	ZSCAN5C
ENSG00000204533	0.558173	0.536366	1.6958	1.4087	ENSG00000204533	AC024580.1
ENSG00000204536	6.41172	14.4506	9.64932	7.21488	ENSG00000204536	CCHCR1
ENSG00000204538	0	0	0	0	ENSG00000204538	PSORS1C2
ENSG00000204539	1.79343	0	1.91044	0.0369284	ENSG00000204539	CDSN
ENSG00000204540	1.38157	3.77178	4.68466	7.02734	ENSG00000204540	PSORS1C1
ENSG00000204542	0.357191	0.0509367	0.0789204	0.332033	ENSG00000204542	C6orf15
ENSG00000204544	0	0	0	0	ENSG00000204544	MUC21
ENSG00000204547	7.26263	13.2781	9.64574	15.9358	ENSG00000204547	DEFB122
ENSG00000204548	0.346219	0.165745	0	0	ENSG00000204548	DEFB121
ENSG00000204555	0	0.922574	0.842769	2.10059	ENSG00000204555	CFTRP3
ENSG00000204556	0	3.79573	2.59943	2.14534	ENSG00000204556	AL450124.1
ENSG00000204560	4.19729	2.47104	2.17439	1.77552	ENSG00000204560	DHX16
ENSG00000204564	4.94301	4.5653	3.16746	2.03156	ENSG00000204564	C6orf136
ENSG00000204566	0	0	0.178302	0.443779	ENSG00000204566	C10orf115
ENSG00000204568	5.27832	9.02316	7.79076	3.86115	ENSG00000204568	MRPS18B
ENSG00000204569	5.47728	9.3916	7.5678	5.75724	ENSG00000204569	PPP1R10
ENSG00000204571	0	0.116665	0.494865	0	ENSG00000204571	KRTAP5-11
ENSG00000204572	0	0.14041	0.150681	0.156684	ENSG00000204572	KRTAP5-10
ENSG00000204574	5.60087	1.38006	5.82304	10.8539	ENSG00000204574	ABCF1
ENSG00000204576	0.973382	1.07624	1.46096	0.835447	ENSG00000204576	PRR3
ENSG00000204577	0.458517	0.435275	0.526231	0.117199	ENSG00000204577	LILRB3
ENSG00000204580	272.345	84.9186	185.681	64.3954	ENSG00000204580	DDR1
ENSG00000204590	4.7918	2.11576	2.67785	2.50199	ENSG00000204590	GNL1
ENSG00000204592	19.219	6.72749	2.56494	0.358481	ENSG00000204592	HLA-E
ENSG00000204595	0	0	0.293353	0	ENSG00000204595	DPRX
ENSG00000204599	1.40869	1.16201	0.860284	0.269129	ENSG00000204599	TRIM39
ENSG00000204604	11.6458	13.54	13.1398	8.78688	ENSG00000204604	ZNF468
ENSG00000204610	0.236957	0.738629	0.141309	0.215334	ENSG00000204610	TRIM15
ENSG00000204611	12.4543	22.3813	18.5718	23.3792	ENSG00000204611	ZNF616
ENSG00000204612	0	0.0908103	0.0822692	0.425984	ENSG00000204612	FOXB2

ENSG00000204613	0	0	0	0	ENSG00000204613	TRIM10
ENSG00000204614	0.00462984	0.00875722	0.0165025	0	ENSG00000204614	TRIM40
ENSG00000204616	0.347473	0.221934	0.144599	0.557281	ENSG00000204616	TRIM31
ENSG00000204618	1.66172	0.922352	0.663665	1.08063	ENSG00000204618	RNF39
ENSG00000204619	0	0	0	0	ENSG00000204619	PPP1R11
ENSG00000204620	1.83827	2.54679	2.01658	4.33132	ENSG00000204620	AC115618.1
ENSG00000204622	0.111634	0.322334	0.0133325	0.102342	ENSG00000204622	HLA-J
ENSG00000204624	0.0388437	0.262427	0.161859	0.103759	ENSG00000204624	DISP3
ENSG00000204628	716.608	777.684	590.056	367.562	ENSG00000204628	RACK1
ENSG00000204632	15.7666	1.56069	0.229717	0	ENSG00000204632	HLA-G
ENSG00000204634	27.522	60.7789	51.7413	70.7759	ENSG00000204634	TBC1D8
ENSG00000204637	0	0	0	0	ENSG00000204637	AC068538.1
ENSG00000204640	0	0	0	0	ENSG00000204640	NMS
ENSG00000204642	17.8314	7.17143	1.70574	4.56501	ENSG00000204642	HLA-F
ENSG00000204644	0.597048	0.883221	0.053838	0.24367	ENSG00000204644	ZFP57
ENSG00000204645	0	0	0	0	ENSG00000204645	SSX4
ENSG00000204648	0	0	0	0	ENSG00000204648	SSX9
ENSG00000204650	22.0762	36.7761	35.3681	33.3562	ENSG00000204650	LINC02210
ENSG00000204652	0	0	0	0	ENSG00000204652	RPS26P8
ENSG00000204653	2.40416	1.43467	5.46374	1.68269	ENSG00000204653	ASPDH
ENSG00000204655	1.18349	1.69103	0.843862	0.857854	ENSG00000204655	MOG
ENSG00000204657	0.0330719	0.060823	0.0385538	0.0189047	ENSG00000204657	OR2H2
ENSG00000204658	0	0	0	0	ENSG00000204658	CST9LP2
ENSG00000204659	0.112225	0.389648	0.479881	0.359588	ENSG00000204659	CBY3
ENSG00000204661	0.469867	1.20235	1.51067	2.47839	ENSG00000204661	C5orf60
ENSG00000204662	0	0	0	0.192964	ENSG00000204662	CST9LP1
ENSG00000204663	0	0.100644	0.0454816	0.171163	ENSG00000204663	CST13P
ENSG00000204669	0.921365	3.06355	3.47448	4.76288	ENSG00000204669	C9orf57
ENSG00000204670	0	0	0	0	ENSG00000204670	IGKV1OR2-3
ENSG00000204671	0.140812	0	0.0608936	0	ENSG00000204671	IL31
ENSG00000204673	7.08438	6.3099	8.80841	7.15483	ENSG00000204673	AKT1S1
ENSG00000204677	5.76735	10.2304	7.5277	16.3647	ENSG00000204677	FAM153C
ENSG00000204681	10.1629	17.5055	11.66	31.35	ENSG00000204681	GABBR1
ENSG00000204682	1.60591	1.1011	1.08567	1.63572	ENSG00000204682	CASC10
ENSG00000204683	0.24764	0.71295	0.214601	0.266168	ENSG00000204683	C10orf113
ENSG00000204687	0	0	0	0	ENSG00000204687	MAS1L
ENSG00000204688	0.0440785	0.10084	0.119165	0.128925	ENSG00000204688	OR2H1
ENSG00000204689	0	0.00838819	0.0181864	0	ENSG00000204689	OR10C1
ENSG00000204690	0	0.0114325	0.0103321	0.0258921	ENSG00000204690	OR12D2
ENSG00000204692	0.0151711	0.0536059	0.0442655	0.0942871	ENSG00000204692	OR12D3
ENSG00000204694	0.21123	0.457168	0.423707	0.844127	ENSG00000204694	OR11A1
ENSG00000204695	0	0	0	0	ENSG00000204695	OR14J1
ENSG00000204697	0.0144218	0	0.05347	0	ENSG00000204697	AL672167.2
ENSG00000204699	0.159906	0.310465	0.275429	0.511637	ENSG00000204699	UBTFL3
ENSG00000204700	0	0	0	0	ENSG00000204700	OR2J2
ENSG00000204701	0	0	0.00605942	0	ENSG00000204701	OR2J3
ENSG00000204702	0	0.0224316	0.118574	0.193776	ENSG00000204702	OR2J1
ENSG00000204703	0	0.0131907	0.0059608	0	ENSG00000204703	OR2B3
ENSG00000204704	0	0	0	0	ENSG00000204704	OR2W1
ENSG00000204705	0.159906	0.310465	0.275429	0.511637	ENSG00000204705	UBTFL5
ENSG00000204709	0	0.0269191	0	0	ENSG00000204709	LINC01556
ENSG00000204710	0.124815	0.36026	0.218175	0	ENSG00000204710	SPDYC
ENSG00000204711	0	0	0	0.14232	ENSG00000204711	C9orf135
ENSG00000204713	3.55254	8.17359	6.33091	6.80266	ENSG00000204713	TRIM27

ENSG00000204717	0	0	0	0	ENSG00000204717	AC073464.1
ENSG00000204718	0.0943836	0	0.0819222	0	ENSG00000204718	CNN2P12
ENSG00000204740	0.285652	0.488921	0.28072	1.17015	ENSG00000204740	MALRD1
ENSG00000204745	0.698876	1.12858	0.670405	1.19373	ENSG00000204745	AC083899.1
ENSG00000204752	0.622038	1.14071	1.42834	2.65213	ENSG00000204752	AC025278.1
ENSG00000204764	13.6076	26.5325	21.7781	29.4167	ENSG00000204764	RANBP17
ENSG00000204767	0.27584	1.14809	0.648598	2.2552	ENSG00000204767	FAM196B
ENSG00000204771	5.79326	6.50343	8.98801	10.0931	ENSG00000204771	CTD-3232M19.2
ENSG00000204775	0.113454	3.64278	7.87721	3.12797	ENSG00000204775	KM-PA-2
ENSG00000204776	12.943	9.18268	0.483852	0.750082	ENSG00000204776	IGKV1OR-3
ENSG00000204778	1.92401	0.956532	1.10395	0.439191	ENSG00000204778	CBWD4P
ENSG00000204779	0	0.125797	0.14723	0.0934774	ENSG00000204779	FOXD4L5
ENSG00000204780	0	0	0	0	ENSG00000204780	IGKV1OR9-1
ENSG00000204787	0	0	0	0	ENSG00000204787	REG1CP
ENSG00000204788	1.19625	3.69327	2.76434	3.12748	ENSG00000204788	CR769776.1
ENSG00000204789	2.27786	4.9304	4.10148	4.0462	ENSG00000204789	ZNF204P
ENSG00000204790	20.8522	44.7175	56.3541	48.4825	ENSG00000204790	AL163540.1
ENSG00000204793	0	0	0	0	ENSG00000204793	FOXD4L6
ENSG00000204794	6.56356	14.7969	14.933	39.0923	ENSG00000204794	PGM5P1
ENSG00000204801	0	0	0	0	ENSG00000204801	FGF7P7
ENSG00000204805	0.764386	1.5432	0.977597	9.71591	ENSG00000204805	FAM27E4
ENSG00000204807	0.0820539	0.748358	0.602446	0.971319	ENSG00000204807	FAM27E2
ENSG00000204813	0	0	0	0	ENSG00000204813	RP11-34H11.3
ENSG00000204814	0.216056	2.7022	3.00743	1.27347	ENSG00000204814	AL935212.1
ENSG00000204816	0.102809	0	0.286228	0.120628	ENSG00000204816	FGF7P5
ENSG00000204818	0	0.173571	0	0.18125	ENSG00000204818	ADGRF5P2
ENSG00000204822	17.3011	14.7144	13.2833	11.6464	ENSG00000204822	MRPL53
ENSG00000204828	0.0371732	0.18091	0.351634	0.280432	ENSG00000204828	FOXD4L2
ENSG00000204839	18.4233	26.1552	6.74312	9.35031	ENSG00000204839	MROH6
ENSG00000204842	27.3769	39.2131	42.076	69.5287	ENSG00000204842	ATXN2
ENSG00000204843	46.732	60.4897	58.5958	58.5758	ENSG00000204843	DCTN1
ENSG00000204848	0	0	0	0.00164584	ENSG00000204848	SPATA31A2
ENSG00000204849	0	0	0	0.0127352	ENSG00000204849	SPATA31A1
ENSG00000204850	0	0.103418	0	0	ENSG00000204850	AC011484.1
ENSG00000204851	0.0993397	0.299319	0.0868517	0.597181	ENSG00000204851	PNMA8B
ENSG00000204852	21.3093	41.9619	41.5282	55.1875	ENSG00000204852	TCTN1
ENSG00000204856	4.54595	9.27772	9.18608	12.5073	ENSG00000204856	FAM216A
ENSG00000204859	10.5702	25.4932	17.8948	11.4472	ENSG00000204859	ZBTB48
ENSG00000204866	29.4962	5.13255	10.1009	11.052	ENSG00000204866	IGFL2
ENSG00000204869	9.63358	23.9729	20.7559	27.3911	ENSG00000204869	IGFL4
ENSG00000204872	0	0.0958755	0.519604	0.431287	ENSG00000204872	NAT8B
ENSG00000204873	0	0.114522	0.0519826	0.433719	ENSG00000204873	KRTAP9-3
ENSG00000204876	0.545175	1.2861	1.15757	2.6936	ENSG00000204876	AC021218.1
ENSG00000204880	0	0.0502899	0.0454162	0.342138	ENSG00000204880	KRTAP4-8
ENSG00000204882	0.153728	0.111192	0.100467	0.0861881	ENSG00000204882	GPR20
ENSG00000204887	0	0	0	0	ENSG00000204887	KRTAP1-4
ENSG00000204889	0.157619	0.306264	0.270826	0.323529	ENSG00000204889	KRT40
ENSG00000204894	22.6588	46.8502	32.1999	16.5187	ENSG00000204894	AC104692.1
ENSG00000204897	0	0.0330896	0.0299097	0.112892	ENSG00000204897	KRT25
ENSG00000204899	5.47209	8.46923	4.82337	6.49321	ENSG00000204899	MZT1
ENSG00000204904	0.466149	0.613771	0.636461	0.692479	ENSG00000204904	LINC01545
ENSG00000204909	29.5325	68.85	68.6416	181.153	ENSG00000204909	SPINK9
ENSG00000204913	0	0	0	0	ENSG00000204913	LRRC3C
ENSG00000204915	0	0	0.0290007	0.0726033	ENSG00000204915	AC234772.1

ENSG00000204918	0	0	0	0	ENSG00000204918	PRR20B
ENSG00000204919	0	0	0	0	ENSG00000204919	PRR20A
ENSG00000204920	7.25595	11.4043	11.5992	8.27971	ENSG00000204920	ZNF155
ENSG00000204922	7.69624	7.00259	6.6734	5.90628	ENSG00000204922	UQCC3
ENSG00000204923	1.00523	2.31582	2.01604	2.8051	ENSG00000204923	FBXO48
ENSG00000204928	0.0883029	0	0	0	ENSG00000204928	GRXCR2
ENSG00000204930	1.28853	2.30155	2.34833	4.38635	ENSG00000204930	FAM221B
ENSG00000204933	0	0	0	0	ENSG00000204933	CD177P1
ENSG00000204936	0.765896	1.30749	1.1365	1.6847	ENSG00000204936	CD177
ENSG00000204941	4.55694	3.9906	3.86172	8.3569	ENSG00000204941	PSG5
ENSG00000204946	5.80004	10.0877	13.0886	10.9313	ENSG00000204946	ZNF783
ENSG00000204947	2.89619	3.01527	4.98312	3.2334	ENSG00000204947	ZNF425
ENSG00000204950	0.101323	0.171729	0.176599	0.34519	ENSG00000204950	LRRC10B
ENSG00000204952	0.122622	0.0749941	0.154604	0.162716	ENSG00000204952	FBXO47
ENSG00000204954	5.98976	9.28878	7.34789	6.24578	ENSG00000204954	C12orf73
ENSG00000204956	0.228891	0.112414	0.179222	0.15516	ENSG00000204956	PCDHGA1
ENSG00000204957	1.29752	1.78751	2.16567	2.76194	ENSG00000204957	AC006486.1
ENSG00000204959	22.0961	10.4083	9.2051	5.26246	ENSG00000204959	ARHGEF34P
ENSG00000204960	0.175174	0.212812	0.171189	0.578315	ENSG00000204960	BLACE
ENSG00000204961	0.168364	0.363334	0.267812	0.433784	ENSG00000204961	PCDHA9
ENSG00000204962	0	0	0	0.0138936	ENSG00000204962	PCDHA8
ENSG00000204963	0.0134697	0.0232998	0.0306727	0.0813906	ENSG00000204963	PCDHA7
ENSG00000204965	0.0238848	0.0331103	0.0197264	0.0792427	ENSG00000204965	PCDHA5
ENSG00000204967	0.116349	0.0439262	0.0964955	0.0663163	ENSG00000204967	PCDHA4
ENSG00000204969	0.0279167	0.109821	0.0708882	0.151641	ENSG00000204969	PCDHA2
ENSG00000204970	0.0537674	0.0103695	0	0.0456136	ENSG00000204970	PCDHA1
ENSG00000204977	17.7024	18.0233	15.7678	16.2724	ENSG00000204977	TRIM13
ENSG00000204978	0.265745	0.774309	0.999446	1.23192	ENSG00000204978	ERICH4
ENSG00000204979	0	0.0790889	0.304562	0.457504	ENSG00000204979	MS4A13
ENSG00000204982	1.26655	0	0	0	ENSG00000204982	PRSS3P4
ENSG00000204983	0.756819	0.237366	0.444456	0.759485	ENSG00000204983	PRSS1
ENSG00000204989	0	0	0	0	ENSG00000204989	OR4D8P
ENSG00000204991	8.13865	14.2947	12.6286	22.3024	ENSG00000204991	SPIRE2
ENSG00000204993	0	0.0298243	0	0.0335005	ENSG00000204993	AC139712.1
ENSG00000205002	1.3817	2.32325	2.11865	5.68837	ENSG00000205002	AARD
ENSG00000205018	0.0313893	0.060494	0.0820296	0.137672	ENSG00000205018	AC092384.1
ENSG00000205020	0	0.065814	0.224396	0.743588	ENSG00000205020	CCL4L1
ENSG00000205021	0	0	0	0.0928069	ENSG00000205021	CCL3L1
ENSG00000205022	0.0747057	0.179614	0.121765	0.169483	ENSG00000205022	PABPN1L
ENSG00000205025	0.0470206	0.0963031	0.0997123	0.0508468	ENSG00000205025	OR5G5P
ENSG00000205029	0	0	0	0	ENSG00000205029	OR5D16
ENSG00000205030	0.133663	0.0147948	0.174713	0.14623	ENSG00000205030	OR5L2
ENSG00000205035	0	0	0.0791077	0.0568424	ENSG00000205035	AC136759.1
ENSG00000205038	0.168606	0.477069	0.115224	0.269427	ENSG00000205038	PKHD1L1
ENSG00000205044	0	0.0756228	0	0	ENSG00000205044	AC027369.1
ENSG00000205045	18.9725	40.9806	39.5599	63.219	ENSG00000205045	SLFN12L
ENSG00000205047	0.804986	0.792898	1.8882	1.34402	ENSG00000205047	FLJ00104
ENSG00000205057	0.0984676	0	0.170946	0	ENSG00000205057	CLLU1OS
ENSG00000205060	10.1009	13.7548	7.81085	11.1888	ENSG00000205060	SLC35B4
ENSG00000205076	88.4419	7.21902	34.2934	2.48098	ENSG00000205076	LGALS7
ENSG00000205078	7.74136	18.6196	7.15946	2.0547	ENSG00000205078	SYCE1L
ENSG00000205081	0.00976883	0.0394198	0.051094	0.133379	ENSG00000205081	CXorf30
ENSG00000205084	8.2196	10.1442	10.1714	5.59558	ENSG00000205084	TMEM231
ENSG00000205085	7.16272	16.6724	19.8439	27.8162	ENSG00000205085	FAM71F2

ENSG00000205086	2.20046	4.24922	3.77971	6.93114	ENSG00000205086	C2orf91
ENSG00000205089	0.701117	1.54842	0.994515	0.785773	ENSG00000205089	CCNI2
ENSG00000205090	0.561295	0.446963	1.85691	1.71505	ENSG00000205090	TMEM240
ENSG00000205097	0.0493108	0.215285	0.169466	0.477668	ENSG00000205097	FRG2
ENSG00000205100	0.857964	0.687737	0.753333	1.7778	ENSG00000205100	HSP90AA4P
ENSG00000205105	0	0	0	0	ENSG00000205105	COX17P1
ENSG00000205106	0	0.101712	0.0918567	0	ENSG00000205106	DKFZp779M0652
ENSG00000205108	0.0638153	0.461294	0.424103	1.00487	ENSG00000205108	FAM205A
ENSG00000205111	0.541036	0.643267	0.42513	0.540371	ENSG00000205111	CDKL4
ENSG00000205116	0.312399	0	0	0.67446	ENSG00000205116	TMEM88B
ENSG00000205126	0	0	0	0	ENSG00000205126	ACCSL
ENSG00000205129	0.676083	0.96734	1.97323	2.66346	ENSG00000205129	C4orf47
ENSG00000205133	10.3506	23.1678	18.8714	24.6446	ENSG00000205133	TRIQK
ENSG00000205138	6.73359	5.60344	7.01581	2.27268	ENSG00000205138	SDHAF1
ENSG00000205143	0.165809	0.0798475	0.180437	0.0455577	ENSG00000205143	ARID3C
ENSG00000205147	3.24802	6.77213	8.52247	11.0428	ENSG00000205147	AC016586.1
ENSG00000205148	0.231241	1.32496	0.398923	0.976457	ENSG00000205148	AC016251.1
ENSG00000205155	74.3619	42.7641	23.6621	15.6295	ENSG00000205155	PSENEN
ENSG00000205174	0	0	0	0	ENSG00000205174	C7orf66
ENSG00000205176	1.86172	4.05249	3.64827	8.37928	ENSG00000205176	REXO1L1P
ENSG00000205177	13.6873	15.4885	1.86979	10.7679	ENSG00000205177	C11orf91
ENSG00000205184	0	0.21787	0.157542	0.0494637	ENSG00000205184	SLC10A5P1
ENSG00000205186	0	0.14692	0	0	ENSG00000205186	FABP9
ENSG00000205189	2.0375	3.23271	2.97182	4.86331	ENSG00000205189	ZBTB10
ENSG00000205208	3.0621	3.72634	3.82722	3.60984	ENSG00000205208	C4orf46
ENSG00000205209	0.919408	2.83009	3.39155	4.1835	ENSG00000205209	SCGB2B2
ENSG00000205212	0.990807	1.42141	1.41336	1.81801	ENSG00000205212	CCDC144NL
ENSG00000205213	20.071	41.5614	17.7388	22.6883	ENSG00000205213	LGR4
ENSG00000205215	4.41076	12.5513	6.53224	14.2147	ENSG00000205215	KRT17P7
ENSG00000205217	0.227485	0.884457	0.808994	0.773549	ENSG00000205217	FAM106B
ENSG00000205220	13.1333	11.6102	7.84647	8.42702	ENSG00000205220	PSMB10
ENSG00000205221	0.15127	0.1789	0.259545	0.455835	ENSG00000205221	VIT
ENSG00000205236	1.51074	2.64344	2.03563	2.32804	ENSG00000205236	AC105052.1
ENSG00000205238	1.93252	5.5771	6.599	13.0005	ENSG00000205238	SPDYE2
ENSG00000205240	0.308432	0.953547	0.357102	0.889224	ENSG00000205240	OR7E36P
ENSG00000205246	50.465	3.54835	9.99203	15.7893	ENSG00000205246	RPSAP58
ENSG00000205250	45.2703	40.333	48.176	29.8035	ENSG00000205250	E2F4
ENSG00000205267	0	0	0	0	ENSG00000205267	DGAT2L7P
ENSG00000205268	20.0484	59.3727	34.2418	41.585	ENSG00000205268	PDE7A
ENSG00000205269	0.458298	0.7116	0.418552	1.04154	ENSG00000205269	TMEM170B
ENSG00000205271	1.16974	3.38918	3.26757	4.16473	ENSG00000205271	CSPG4P10
ENSG00000205274	0	0	0	0	ENSG00000205274	TRBV20OR9-2
ENSG00000205275	1.5941	2.07044	3.85986	1.71608	ENSG00000205275	CSPG4P9
ENSG00000205277	0.609828	0.291941	0.263713	1.26124	ENSG00000205277	MUC12
ENSG00000205279	0	0	0.183894	0.46857	ENSG00000205279	CTXN3
ENSG00000205281	0	0.29192	0.298816	0.8194	ENSG00000205281	GOLGA6L10
ENSG00000205300	0.0984676	0	0.0854729	0.319257	ENSG00000205300	AL356414.1
ENSG00000205301	0.105943	0.904411	0.93486	1.02648	ENSG00000205301	MGAT4D
ENSG00000205302	31.9882	21.1799	22.9079	16.6975	ENSG00000205302	SNX2
ENSG00000205307	0.282252	0.695271	0.531394	0.0475663	ENSG00000205307	SAP25
ENSG00000205309	1.4341	5.00944	3.67319	3.94433	ENSG00000205309	NT5M
ENSG00000205312	0.148142	0.386436	0.388645	0.99242	ENSG00000205312	KRT17P4
ENSG00000205318	0.102084	0.0823424	0	0.0557217	ENSG00000205318	GCNT6
ENSG00000205323	34.7434	32.7458	28.7248	28.7749	ENSG00000205323	SARNP

ENSG00000205327	0	0.0640255	0	0	ENSG00000205327	OR6C68
ENSG00000205328	0.0566152	0	0	0.123459	ENSG00000205328	OR6C65
ENSG00000205329	0	0.0642722	0	0	ENSG00000205329	OR6C3
ENSG00000205330	0	0.0552686	0	0	ENSG00000205330	OR6C1
ENSG00000205331	0.141685	0.136244	0.123103	0.307925	ENSG00000205331	OR6C72P
ENSG00000205333	0.0755322	0.167539	0.215955	0.208707	ENSG00000205333	GOLGA2P1
ENSG00000205334	0.552427	1.3043	0.991311	1.9504	ENSG00000205334	LINC01460
ENSG00000205336	96.6859	122.782	154.078	54.8717	ENSG00000205336	ADGRG1
ENSG00000205339	63.7049	90.312	56.6072	75.2688	ENSG00000205339	IPO7
ENSG00000205352	49.1197	31.9272	44.299	35.5901	ENSG00000205352	PRR13
ENSG00000205356	15.653	15.2303	13.1777	18.7506	ENSG00000205356	TECPR1
ENSG00000205358	0.0964968	0.206844	0.260388	0.228841	ENSG00000205358	MT1H
ENSG00000205359	0	0.10329	0.0207295	0.156593	ENSG00000205359	SLCO6A1
ENSG00000205360	0	0	0	0	ENSG00000205360	MT1CP
ENSG00000205361	0	0	0	0	ENSG00000205361	MT1DP
ENSG00000205362	0	0	0	0.230743	ENSG00000205362	MT1A
ENSG00000205363	3.54598	0.368738	1.44465	0.890208	ENSG00000205363	C15orf59
ENSG00000205364	0	0.0807723	0	0.110658	ENSG00000205364	MT1M
ENSG00000205403	1.09933	1.82578	1.48221	3.6774	ENSG00000205403	CFI
ENSG00000205409	0	0.0628199	0	0	ENSG00000205409	OR52E6
ENSG00000205412	0.0655468	0.125908	0.114337	0.156387	ENSG00000205412	HNRNPA1P20
ENSG00000205413	57.1378	11.3899	9.29478	15.6613	ENSG00000205413	SAMD9
ENSG00000205420	6190.68	2107.88	2330.26	1812.43	ENSG00000205420	KRT6A
ENSG00000205423	21.0374	21.5598	19.7777	17.3703	ENSG00000205423	CNEP1R1
ENSG00000205426	0	0	0	0.0557622	ENSG00000205426	KRT81
ENSG00000205433	0	0	0	0	ENSG00000205433	SNRPGP6
ENSG00000205436	0.586656	1.34331	0.743424	1.74457	ENSG00000205436	EXOC3L4
ENSG00000205439	0	0	0	0	ENSG00000205439	KRTAP12-3
ENSG00000205441	0	0	0	0	ENSG00000205441	KRTAP10-7
ENSG00000205442	0	0	0.0422145	0.105977	ENSG00000205442	IZUMO3
ENSG00000205445	0	0	0.106579	0.650835	ENSG00000205445	KRTAP10-2
ENSG00000205449	0	0.113739	0	0	ENSG00000205449	NBPF22P
ENSG00000205456	0	0.435302	0.183656	0.604493	ENSG00000205456	TP53TG3D
ENSG00000205457	0.409621	0.421649	0.449766	0.553889	ENSG00000205457	TP53TG3C
ENSG00000205464	1.49874	4.32529	4.27839	5.90599	ENSG00000205464	ATP6AP1L
ENSG00000205476	27.455	25.8718	26.1531	13.3297	ENSG00000205476	CCDC85C
ENSG00000205482	0.150237	2.25929	2.69038	2.0538	ENSG00000205482	SPDYE18
ENSG00000205485	9.65388	21.6875	18.6095	16.3136	ENSG00000205485	AC004980.1
ENSG00000205494	0.162254	0.062506	0.140901	0.363646	ENSG00000205494	OR52A4P
ENSG00000205495	0	0	0	0	ENSG00000205495	OR52J3
ENSG00000205496	0.0663187	0.191342	0.057632	0.0721459	ENSG00000205496	OR51A2
ENSG00000205497	0	0	0	0	ENSG00000205497	OR51A4
ENSG00000205502	0.18272	0.352051	0.102511	1.459	ENSG00000205502	C2CD4B
ENSG00000205505	0	0	0	0	ENSG00000205505	AC006014.10
ENSG00000205506	0	0	0.270663	0	ENSG00000205506	AC004878.6
ENSG00000205508	0	0	0	0	ENSG00000205508	AC004878.5
ENSG00000205509	0.545955	0.800993	1.54925	0.598673	ENSG00000205509	AC138783.11
ENSG00000205517	1.4601	3.2093	3.57487	7.98528	ENSG00000205517	RGL3
ENSG00000205531	77.4886	101.926	87.9135	93.0768	ENSG00000205531	NAP1L4
ENSG00000205534	4.56941	8.49761	8.72466	3.30368	ENSG00000205534	SMG1P2
ENSG00000205542	746.952	337.324	269.006	488.711	ENSG00000205542	TMSB4X
ENSG00000205544	43.5696	36.3236	17.0586	19.044	ENSG00000205544	TMEM256
ENSG00000205549	0.466456	0.44554	0.402349	1.23107	ENSG00000205549	C9orf92
ENSG00000205560	6.98911	22.5622	28.625	10.5371	ENSG00000205560	CPT1B

ENSG00000205565	0.768103	1.01081	1.78033	0.663019	ENSG00000205565	RP11-497H16.6
ENSG00000205571	9.57014	3.24211	11.3561	8.68886	ENSG00000205571	SMN2
ENSG00000205572	9.61661	6.94668	10.5785	9.60199	ENSG00000205572	SERF1B
ENSG00000205578	0.124828	0.143715	0.360444	0.169192	ENSG00000205578	POM121B
ENSG00000205579	0	0	0.738922	0	ENSG00000205579	DYNLL1P1
ENSG00000205580	1.08464	2.75109	3.28549	4.25976	ENSG00000205580	AC006995.8
ENSG00000205581	130.831	120.089	99.6152	75.5257	ENSG00000205581	HMGN1
ENSG00000205583	14.2586	13.5269	25.1544	12.6815	ENSG00000205583	STAG3L1
ENSG00000205584	0.294268	0	0	0	ENSG00000205584	AC211476.1
ENSG00000205592	1.76041	4.64827	4.98617	3.11326	ENSG00000205592	MUC19
ENSG00000205593	1.4542	2.44528	5.62987	3.76896	ENSG00000205593	DENND6B
ENSG00000205595	23.6341	53.5205	27.7122	16.5685	ENSG00000205595	AREGB
ENSG00000205596	0	0	0	0	ENSG00000205596	AC068533.1
ENSG00000205609	30.0145	33.4392	16.369	16.9168	ENSG00000205609	EIF3CL
ENSG00000205625	2.7507	7.31339	7.82919	12.1952	ENSG00000205625	AL591499.1
ENSG00000205629	19.8519	16.9817	20.6734	23.8425	ENSG00000205629	LCMT1
ENSG00000205639	1.49552	2.57478	1.94314	3.09058	ENSG00000205639	MFSD2B
ENSG00000205642	0	0	0.443285	0	ENSG00000205642	VCX3B
ENSG00000205643	3.08252	5.53109	3.68465	3.00759	ENSG00000205643	CDPF1
ENSG00000205644	1.0954	3.69926	1.21621	11.7975	ENSG00000205644	AC025186.1
ENSG00000205649	10.923	31.0554	29.4281	67.6902	ENSG00000205649	HTN3
ENSG00000205659	4.05469	6.55736	8.18946	12.5325	ENSG00000205659	LIN52
ENSG00000205664	87.3071	52.5067	77.8192	108.951	ENSG00000205664	BX890604.1
ENSG00000205667	0.0302361	0.0291374	0.0526809	0.0331622	ENSG00000205667	ARSH
ENSG00000205669	0	0.0702182	0	0	ENSG00000205669	ACOT6
ENSG00000205670	6.65876	10.66	10.4795	12.594	ENSG00000205670	SMIM11A
ENSG00000205677	0	0	0	0	ENSG00000205677	LYPLA2P1
ENSG00000205678	2.10041	5.1164	4.73752	8.32805	ENSG00000205678	TECRL
ENSG00000205683	0.681474	2.73475	1.42268	12.82	ENSG00000205683	DPF3
ENSG00000205693	0.0600928	0	0.104514	0.261882	ENSG00000205693	MANSC4
ENSG00000205695	0.0363646	0.14013	0.126671	0.238975	ENSG00000205695	AL390205.1
ENSG00000205702	1.68776	3.5902	5.19266	1.12643	ENSG00000205702	CYP2D7
ENSG00000205704	0.179016	0.189555	0.174036	0.598788	ENSG00000205704	LINC00634
ENSG00000205707	7.49035	8.78244	11.9831	8.22218	ENSG00000205707	ETFRF1
ENSG00000205710	1.50948	1.43228	1.93825	1.32841	ENSG00000205710	C17orf107
ENSG00000205716	0	0	0.185138	0	ENSG00000205716	FAM183DP
ENSG00000205718	0.0421418	0	0	0	ENSG00000205718	MBD3L4
ENSG00000205726	24.8771	31.3191	21.1386	46.2976	ENSG00000205726	ITSN1
ENSG00000205730	8.5101	13.3102	10.7771	17.6203	ENSG00000205730	ITPRIPL2
ENSG00000205740	1.00648	2.01431	1.55961	3.40587	ENSG00000205740	AL359878.1
ENSG00000205744	9.73776	6.70599	9.57825	3.25251	ENSG00000205744	DENND1C
ENSG00000205745	0.117405	0.187538	0.204239	0.213352	ENSG00000205745	AC083864.1
ENSG00000205746	40.7622	117.522	139.55	57.0181	ENSG00000205746	AC126755.1
ENSG00000205754	1.98832	6.11587	4.32997	12.798	ENSG00000205754	SLCO1B7
ENSG00000205755	0.683089	0.762654	0.564894	1.24779	ENSG00000205755	CRLF2
ENSG00000205758	27.7462	41.1154	38.7198	67.3836	ENSG00000205758	CRYZL1
ENSG00000205763	6.62681	10.3769	10.9475	7.1171	ENSG00000205763	RP9P
ENSG00000205765	7.20397	6.9678	8.09305	8.92709	ENSG00000205765	C5orf51
ENSG00000205767	0	0	0	0	ENSG00000205767	AL136038.1
ENSG00000205771	3.73919	8.28765	8.40856	9.76984	ENSG00000205771	CATSPER2P1
ENSG00000205775	0	0	0	0	ENSG00000205775	GAGE2E
ENSG00000205777	0.201861	0.401905	0.282222	0.520517	ENSG00000205777	GAGE1
ENSG00000205784	0.339455	0.377195	0.559447	0.546744	ENSG00000205784	ARRDC5
ENSG00000205791	0.397447	1.59184	1.7683	2.83542	ENSG00000205791	LOH12CR2

ENSG00000205794	1.12892	2.2646	1.55228	2.18388	ENSG00000205794	AC098591.1
ENSG00000205795	0.306657	0.570633	0.992654	0.997929	ENSG00000205795	CYS1
ENSG00000205808	8.23899	7.90016	7.66143	2.12244	ENSG00000205808	PLPP6
ENSG00000205809	0.636221	0.581121	1.09192	2.2604	ENSG00000205809	KLRC2
ENSG00000205810	0	0.205394	0	1.24648	ENSG00000205810	KLRC3
ENSG00000205821	0	0	0	0	ENSG00000205821	AC006435.1
ENSG00000205822	1.09268	1.39589	2.52292	3.85822	ENSG00000205822	TPTE2P6
ENSG00000205832	0.0854174	0.0819134	0.0864058	0.110079	ENSG00000205832	C16orf96
ENSG00000205835	0.257453	0.261591	0.258894	0.345835	ENSG00000205835	GMNC
ENSG00000205838	0.312099	0.503928	1.48524	0.840325	ENSG00000205838	TTC23L
ENSG00000205846	0.170353	0.558049	0.626353	0.597372	ENSG00000205846	CLEC6A
ENSG00000205847	0	0.073843	0.173748	0.0797615	ENSG00000205847	OR7E91P
ENSG00000205850	0	0.393359	0.294749	0	ENSG00000205850	AL359736.1
ENSG00000205853	1.78017	1.659	1.81085	1.4349	ENSG00000205853	RFPL3S
ENSG00000205856	0.49943	0.895498	0.601397	0.745535	ENSG00000205856	C22orf42
ENSG00000205857	0.199338	0.581058	1.04455	1.75099	ENSG00000205857	NANOGNB
ENSG00000205858	1.11424	1.57068	2.49815	3.054	ENSG00000205858	LRRC72
ENSG00000205863	0.139425	0.447177	0.688983	0.380774	ENSG00000205863	C1QTNF9B
ENSG00000205864	0	0	0	0	ENSG00000205864	KRTAP5-6
ENSG00000205867	0.417657	0.365486	0.471891	0.832996	ENSG00000205867	KRTAP5-2
ENSG00000205869	0.147854	0.0637807	0.230528	0.216438	ENSG00000205869	KRTAP5-1
ENSG00000205871	0	0.102492	0	0	ENSG00000205871	AC068724.1
ENSG00000205879	0.0293591	0.292821	0.569321	0.462754	ENSG00000205879	FAM90A2P
ENSG00000205882	0	0.0555138	0.0501713	0.440173	ENSG00000205882	DEFB134
ENSG00000205883	0	0	0	0	ENSG00000205883	DEFB135
ENSG00000205884	0	0	0	0	ENSG00000205884	DEFB136
ENSG00000205897	0	0	0.0589195	0.13215	ENSG00000205897	OR7E136P
ENSG00000205898	0.25003	0	0.542234	0.700876	ENSG00000205898	AC019155.1
ENSG00000205899	0	0	0	0	ENSG00000205899	BHLHA9
ENSG00000205903	9.11068	7.60742	15.4372	11.7389	ENSG00000205903	ZNF316
ENSG00000205916	0	0	0	0.00407971	ENSG00000205916	DAZ4
ENSG00000205918	5.97535	7.55454	8.14674	9.58107	ENSG00000205918	PDPK2P
ENSG00000205922	1.36246	1.61811	2.01298	6.50319	ENSG00000205922	ONECUT3
ENSG00000205923	0.0880538	2.91245	2.12988	3.57545	ENSG00000205923	CEMP1
ENSG00000205927	0.177294	0.304114	0.184273	0.373252	ENSG00000205927	OLIG2
ENSG00000205929	0.950377	2.0556	2.17171	3.35949	ENSG00000205929	C21orf62
ENSG00000205930	1.19986	1.99328	2.09467	2.74547	ENSG00000205930	C21orf62-AS1
ENSG00000205936	0	0	0	0	ENSG00000205936	PPP1R12BP2
ENSG00000205937	54.5597	58.4852	62.3079	52.4492	ENSG00000205937	RNPS1
ENSG00000205940	1.1234	1.23185	1.06676	1.12387	ENSG00000205940	HSP90AB2P
ENSG00000205944	0	0	0	0	ENSG00000205944	DAZ2
ENSG00000205946	0	0	0	0	ENSG00000205946	USP17L6P
ENSG00000205955	0.0510997	0.222696	0.168409	0.35143	ENSG00000205955	HSP90AA5P
ENSG00000205971	0	0.0790903	0.107236	0.628921	ENSG00000205971	AC074389.1
ENSG00000205976	0.0377	0.319791	0.176461	0.171391	ENSG00000205976	AC091951.1
ENSG00000205978	6.32982	9.47817	9.19671	4.73273	ENSG00000205978	NYNRIN
ENSG00000205981	15.9736	13.9616	15.8677	9.95002	ENSG00000205981	DNAJC19
ENSG00000205989	0.222971	0	0.815236	0.228364	ENSG00000205989	DEFB109C
ENSG00000206013	0.359919	0	0.0781121	0.0973796	ENSG00000206013	IFITM5
ENSG00000206014	0	0	0	0	ENSG00000206014	OR7E161P
ENSG00000206026	0.324313	0.754504	0.732156	1.23584	ENSG00000206026	SMIM21
ENSG00000206034	0.222971	0	0.815236	0.228364	ENSG00000206034	DEFB109B
ENSG00000206042	0	0	0	0	ENSG00000206042	DEFA7P
ENSG00000206043	0.0939525	0.191327	0.154785	0.115381	ENSG00000206043	C18orf63

ENSG00000206044	0.332871	0.896358	1.0185	0.506937	ENSG00000206044	AC005841.1
ENSG00000206047	0	0.398986	0.360325	0.663008	ENSG00000206047	DEFA1
ENSG00000206052	0.766264	1.9003	2.14285	2.60243	ENSG00000206052	DOK6
ENSG00000206053	44.8764	31.4432	33.5215	27.1578	ENSG00000206053	JPT2
ENSG00000206066	0	0.194185	0	0	ENSG00000206066	IGLL3P
ENSG00000206069	0.367146	0.969792	1.1294	0.829829	ENSG00000206069	TMEM211
ENSG00000206072	0.40656	0.885783	0.681499	1.77501	ENSG00000206072	SERPINB11
ENSG00000206073	7.5433	1.88806	2.69042	2.76993	ENSG00000206073	SERPINB4
ENSG00000206075	633.097	266.477	254.103	175.982	ENSG00000206075	SERPINB5
ENSG00000206077	3.45145	0.202582	0.13673	0.249169	ENSG00000206077	ZDHHC11B
ENSG00000206082	3.19138	8.67681	9.24063	10.3672	ENSG00000206082	LINC01002
ENSG00000206090	0.139	0	0	0	ENSG00000206090	AP000350.1
ENSG00000206102	0	0	0	0	ENSG00000206102	KRTAP19-8
ENSG00000206104	0	0	0	0	ENSG00000206104	KRTAP20-3
ENSG00000206105	0.615517	1.72768	0.515716	1.86079	ENSG00000206105	KRTAP20-4
ENSG00000206106	0	0	0	0	ENSG00000206106	KRTAP22-2
ENSG00000206107	0	0	0	0.107216	ENSG00000206107	KRTAP27-1
ENSG00000206120	0.29607	0.528456	0.736654	0.855165	ENSG00000206120	EGFEM1P
ENSG00000206127	0.0746416	1.49319	1.2202	0.364538	ENSG00000206127	GOLGA8O
ENSG00000206144	0	0.0251563	0.0453389	0.114507	ENSG00000206144	AC022034.1
ENSG00000206145	0.692782	3.02098	1.19655	2.97886	ENSG00000206145	P2RX6P
ENSG00000206147	0	0.498742	0.754325	0.180324	ENSG00000206147	RPL23AP57
ENSG00000206149	9.75075	14.2443	19.6027	13.9869	ENSG00000206149	HERC2P9
ENSG00000206150	0.0576088	0	0.0428766	0.0513946	ENSG00000206150	RNASE13
ENSG00000206159	19.0273	27.4104	24.7357	36.6743	ENSG00000206159	GYG2P1
ENSG00000206168	0	0	0.268706	0	ENSG00000206168	Z69890.1
ENSG00000206172	0	0	0	0	ENSG00000206172	HBA1
ENSG00000206177	0	0	0	0	ENSG00000206177	HBM
ENSG00000206178	0	0	0	0	ENSG00000206178	HBZP1
ENSG00000206181	0.0539631	0.233132	0.595986	0.67512	ENSG00000206181	ELOA2
ENSG00000206190	0.248738	0.677832	0.849999	2.91374	ENSG00000206190	ATP10A
ENSG00000206192	0.0185755	0.224497	0.0370986	0	ENSG00000206192	ANKRD20A9P
ENSG00000206199	2.91599	5.28334	2.98465	3.92621	ENSG00000206199	ANKUB1
ENSG00000206203	0	0	0	0	ENSG00000206203	TSSK2
ENSG00000206206	0.794617	0.498114	1.84831	3.32793	ENSG00000206206	DAXX
ENSG00000206208	23.3603	60.5021	37.3845	20.9258	ENSG00000206208	TAPBP
ENSG00000206228	0	0	0	0	ENSG00000206228	HNRNPA1P4
ENSG00000206235	0.733398	4.55847	0.66121	0.591079	ENSG00000206235	TAP2
ENSG00000206237	0	0	0	0	ENSG00000206237	HLA-DQB1
ENSG00000206240	0.0366969	0	0	0.0909167	ENSG00000206240	HLA-DRB1
ENSG00000206245	0.0821168	0.0575378	0.161802	0.494349	ENSG00000206245	C6orf10
ENSG00000206256	0.0409104	0.251919	0.417516	1.7286	ENSG00000206256	PPT2
ENSG00000206258	1.61453	0.186454	0.545793	0.640769	ENSG00000206258	TNXB
ENSG00000206260	0.489313	1.52482	1.13218	2.2383	ENSG00000206260	PRR23A
ENSG00000206262	0.990292	2.29131	2.50745	4.12058	ENSG00000206262	FOXL2NB
ENSG00000206268	4.30996	3.46615	2.38813	2.98449	ENSG00000206268	NELFE
ENSG00000206279	3.56876	3.894	3.94832	1.25481	ENSG00000206279	DAXX
ENSG00000206280	3.37329	0.00954843	0	0	ENSG00000206280	ZBTB22
ENSG00000206281	25.6708	1.95436	4.2942	12.0705	ENSG00000206281	TAPBP
ENSG00000206282	8.91918	7.76267	4.14572	3.66756	ENSG00000206282	RGL2
ENSG00000206283	5.34729	2.40943	3.02846	5.57404	ENSG00000206283	PFDN6
ENSG00000206284	14.6143	1.20558	1.13863	1.37608	ENSG00000206284	WDR46
ENSG00000206285	2.90332	0	0.715115	1.53111	ENSG00000206285	B3GALT4
ENSG00000206286	6.0477	0.562313	1.03124	1.56312	ENSG00000206286	VPS52

ENSG00000206287	6.73865	3.75922	5.56762	0	ENSG00000206287	RING1
ENSG00000206288	8.10034	7.04224	6.12923	6.51393	ENSG00000206288	SLC39A7
ENSG00000206289	9.04598	1.60346	1.53736	0.954922	ENSG00000206289	RXRB
ENSG00000206290	0	0.0476721	0.0752155	0.0424258	ENSG00000206290	COL11A2
ENSG00000206291	0.015404	0	0.0767526	0	ENSG00000206291	HLA-DPA1
ENSG00000206292	0	0.0184165	7.60E-05	0.0387109	ENSG00000206292	HLA-DOA
ENSG00000206297	3.97772	4.76897	4.68948	3.88382	ENSG00000206297	TAP1
ENSG00000206298	1.10486	0.54819	1.3866	1.30105	ENSG00000206298	PSMB8
ENSG00000206299	0.733398	14.08	1.7986	6.2756	ENSG00000206299	TAP2
ENSG00000206301	0	0	0.0899246	1.65918	ENSG00000206301	HLA-DQA2
ENSG00000206302	0	0	0	0	ENSG00000206302	HLA-DQB1
ENSG00000206305	0.0443433	0	0	0.0600458	ENSG00000206305	HLA-DQA1
ENSG00000206306	0.0366969	0	0	0.0909167	ENSG00000206306	HLA-DRB1
ENSG00000206308	0.132708	0.0207335	0.166196	0.116951	ENSG00000206308	HLA-DRA
ENSG00000206310	0	0	0	0	ENSG00000206310	C6orf10
ENSG00000206312	0.0774347	0.271779	0.424242	0.236413	ENSG00000206312	NOTCH4
ENSG00000206314	0.26308	0.0707527	0.25712	0.0988522	ENSG00000206314	GPSM3
ENSG00000206315	1.66598	1.23411	0.68902	0.826113	ENSG00000206315	PBX2
ENSG00000206320	0.588993	1.16103	1.17473	1.07712	ENSG00000206320	AGER
ENSG00000206324	4.49328	0	0.758657	3.4111	ENSG00000206324	AGPAT1
ENSG00000206329	2.20719	2.71248	2.21686	1.12312	ENSG00000206329	PPT2
ENSG00000206331	0.0315493	1.44929	0.784148	1.3553	ENSG00000206331	PRRT1
ENSG00000206338	0	0.938591	1.12825	3.82517	ENSG00000206338	CYP21A2
ENSG00000206340	0.437181	0.183949	0.890531	0.512031	ENSG00000206340	C4A
ENSG00000206341	4.96637	4.64275	3.8801	2.48884	ENSG00000206341	HLA-H
ENSG00000206342	0.639573	0.464258	4.29893	0.727323	ENSG00000206342	STK19
ENSG00000206344	0.843751	6.15606	2.67661	5.65017	ENSG00000206344	HCG27
ENSG00000206346	0.757898	1.00096	2.24137	1.07671	ENSG00000206346	DXO
ENSG00000206353	8.10942	7.81457	9.08597	7.06332	ENSG00000206353	SKIV2L
ENSG00000206355	2.93235	0	6.10041	2.04872	ENSG00000206355	CCHCR1
ENSG00000206356	7.88552	4.4065	3.4565	6.26053	ENSG00000206356	AC114324.1
ENSG00000206357	4.30996	3.46615	2.38813	2.98449	ENSG00000206357	NELFE
ENSG00000206366	0	0.36058	0.765972	0.471794	ENSG00000206366	ZBTB12
ENSG00000206372	0.291039	0.225961	0.301166	0.307951	ENSG00000206372	C2
ENSG00000206376	1.62967	3.87586	6.08949	7.63053	ENSG00000206376	EHMT2
ENSG00000206378	0	0.388896	0.11263	0.175459	ENSG00000206378	SLC44A4
ENSG00000206379	1.28296	2.5267	0.96359	2.48666	ENSG00000206379	FLOT1
ENSG00000206380	15.4939	23.7762	42.7954	13.313	ENSG00000206380	C6orf48
ENSG00000206383	0.232265	0.119065	0.0689541	0.135567	ENSG00000206383	HSPA1L
ENSG00000206384	0.448977	0.449361	0.673473	0.729788	ENSG00000206384	COL6A6
ENSG00000206394	48.3287	53.2822	22.9215	21.5914	ENSG00000206394	CLIC1
ENSG00000206395	0.365304	2.25855	0.892104	1.57402	ENSG00000206395	DDAH2
ENSG00000206396	0.181329	0.151186	0	0.303335	ENSG00000206396	MPIG6B
ENSG00000206398	0	1.66934	1.3334	2.0363	ENSG00000206398	LY6G6C
ENSG00000206401	0.0327523	0	0	0	ENSG00000206401	LY6G6E
ENSG00000206402	0.0302896	0.0578806	0	0.032054	ENSG00000206402	LY6G6D
ENSG00000206403	0.550835	1.2519	1.34503	2.89883	ENSG00000206403	ABHD16A
ENSG00000206404	0.0973281	0.0758412	0	0.0644326	ENSG00000206404	LY6G5C
ENSG00000206406	1.18829	12.2013	4.38774	8.72403	ENSG00000206406	CSNK2B
ENSG00000206408	0	0.74578	0.291819	1.01343	ENSG00000206408	GPANK1
ENSG00000206409	0.164783	0.252772	0.0998859	0.157885	ENSG00000206409	APOM
ENSG00000206412	13.7553	4.56267	3.3693	13.1864	ENSG00000206412	GNL1
ENSG00000206418	23.7434	26.33	24.8391	23.9695	ENSG00000206418	RAB12
ENSG00000206422	0	0.130727	0.178992	0.0739081	ENSG00000206422	LRRC30

ENSG00000206427	1.1185	8.16453	7.68887	15.2385	ENSG00000206427	PRRC2A
ENSG00000206428	0.128048	0.290488	0.160375	0.21663	ENSG00000206428	AIF1
ENSG00000206430	0	0	0	0	ENSG00000206430	NCR3
ENSG00000206432	0.117852	0.22849	0.128437	0.979461	ENSG00000206432	TMEM200C
ENSG00000206433	0.479817	1.16548	1.78612	2.03075	ENSG00000206433	LST1
ENSG00000206435	3.87866	11.3498	6.10389	0.00168656	ENSG00000206435	HLA-C
ENSG00000206437	0.013508	0	0.0359938	0.0362078	ENSG00000206437	LTB
ENSG00000206439	0.222879	0.099013	0.196978	0.0453146	ENSG00000206439	TNF
ENSG00000206440	1.27859	1.68772	2.62759	1.01061	ENSG00000206440	NFKBIL1
ENSG00000206444	0.0711381	0.145386	3.04139	1.11379	ENSG00000206444	HLA-V
ENSG00000206445	0.00314444	0.0186652	0.023055	0.174972	ENSG00000206445	ATP6V1G2
ENSG00000206447	0.0916753	0.264657	0.272079	0.660025	ENSG00000206447	MCCD1
ENSG00000206448	0	0.574988	0.894536	0.360965	ENSG00000206448	PPIAP30
ENSG00000206449	0.395785	2.73539	1.81284	3.0827	ENSG00000206449	MICB
ENSG00000206450	6.0586	44.095	33.3001	22.9286	ENSG00000206450	HLA-B
ENSG00000206452	53.8238	29.8638	7.37365	0.268983	ENSG00000206452	HLA-C
ENSG00000206454	0.0792565	0.253763	0	0.291808	ENSG00000206454	POU5F1
ENSG00000206455	0.402607	0	0.0670335	0	ENSG00000206455	TCF19
ENSG00000206457	3.135	5.29394	1.96181	9.19829	ENSG00000206457	CCHCR1
ENSG00000206458	0.0416757	0	0.367557	0	ENSG00000206458	PSORS1C1
ENSG00000206459	0	0	0.319568	0	ENSG00000206459	PSORS1C2
ENSG00000206460	0	0	0	0	ENSG00000206460	CDSN
ENSG00000206461	1.42876	0	1.1575	0	ENSG00000206461	C6orf15
ENSG00000206463	0.0197449	0	0.0588856	0.304789	ENSG00000206463	MUC21
ENSG00000206465	0	0	0	0	ENSG00000206465	SFTA2
ENSG00000206466	2.04236	3.60359	1.27243	6.09971	ENSG00000206466	GABBR1
ENSG00000206467	0.0330719	0	0.0385538	0.0189047	ENSG00000206467	OR2H2
ENSG00000206468	0	0	0	0	ENSG00000206468	UBD
ENSG00000206470	0	0	0	0	ENSG00000206470	MAS1L
ENSG00000206471	0.0440785	0.10084	0.119165	0.128925	ENSG00000206471	OR2H1
ENSG00000206472	0.21123	0.457168	0.423707	0.844127	ENSG00000206472	OR11A1
ENSG00000206474	0	0.00838819	0.0075842	0	ENSG00000206474	OR10C1
ENSG00000206476	3.6052	0.979433	4.42276	1.40908	ENSG00000206476	VARS2
ENSG00000206478	85.0597	0	36.8167	50.1516	ENSG00000206478	IER3
ENSG00000206480	1.28296	2.5267	0.96359	2.48666	ENSG00000206480	FLOT1
ENSG00000206481	1.32993	0.568341	1.95986	4.47642	ENSG00000206481	MDC1
ENSG00000206483	0	0.258388	0.155687	0.291149	ENSG00000206483	TXNRD3NB
ENSG00000206484	0.463793	1.24111	0.515031	0.408103	ENSG00000206484	NRM
ENSG00000206485	0.230442	0.49399	0.566592	0.220399	ENSG00000206485	PPP1R18
ENSG00000206486	0.173831	0.0946672	0.00204424	0.237523	ENSG00000206486	DHX16
ENSG00000206487	1.54806	2.26487	0.849077	1.82576	ENSG00000206487	C6orf136
ENSG00000206488	0.449589	0.763134	1.27499	0.973813	ENSG00000206488	ATAT1
ENSG00000206489	11.5578	7.66422	13.4411	14.644	ENSG00000206489	PPP1R10
ENSG00000206490	3.61336	5.3999	6.92217	7.77632	ENSG00000206490	ABCF1
ENSG00000206491	1.24177	1.79606	3.14341	2.86624	ENSG00000206491	PRR3
ENSG00000206492	2.29229	3.70852	2.77643	4.5276	ENSG00000206492	GNL1
ENSG00000206493	16.4661	29.8937	16.2765	16.1278	ENSG00000206493	HLA-E
ENSG00000206495	0.0286555	0.2096	3.42437	6.46546	ENSG00000206495	TRIM39
ENSG00000206500	0	0	0	0	ENSG00000206500	RNF39
ENSG00000206501	0	0	0.162302	0	ENSG00000206501	PPP1R11
ENSG00000206502	0	0	0	0	ENSG00000206502	ZNRD1
ENSG00000206503	127.815	57.2907	12.8843	0.390274	ENSG00000206503	HLA-A
ENSG00000206505	9.96399	2.96592	5.4213	0	ENSG00000206505	HLA-A
ENSG00000206506	28.7608	2.77339	3.77006	8.12519	ENSG00000206506	HLA-G

ENSG00000206507	0.00510344	0.291853	0.600953	0.11726	ENSG00000206507	HLA-V
ENSG00000206509	0.73055	6.07825	3.47303	2.35358	ENSG00000206509	HLA-F
ENSG00000206510	0.597048	0.883221	0.053838	0.24367	ENSG00000206510	ZFP57
ENSG00000206511	1.95594	3.16553	1.27243	5.60608	ENSG00000206511	GABBR1
ENSG00000206512	0.0330719	0.060823	0.0385538	0.0189047	ENSG00000206512	OR2H2
ENSG00000206513	0	0	0	0	ENSG00000206513	UBD
ENSG00000206515	0	0	0	0	ENSG00000206515	MAS1L
ENSG00000206516	0.0440785	0.10084	0.119165	0.128925	ENSG00000206516	OR2H1
ENSG00000206517	0.21123	0.457168	0.423707	0.844127	ENSG00000206517	OR11A1
ENSG00000206519	0.0288811	0.0197876	0.0178653	0	ENSG00000206519	BX000688.1
ENSG00000206522	0	0	0.00605942	0	ENSG00000206522	OR2J3
ENSG00000206523	0.0332871	0	0	0.0136277	ENSG00000206523	OR2J1
ENSG00000206524	0	0.0131907	0.0059608	0	ENSG00000206524	OR2B3
ENSG00000206525	0	0	0	0	ENSG00000206525	OR2W1
ENSG00000206526	0	0.0269191	0	0	ENSG00000206526	LINC01556
ENSG00000206527	115.579	89.8841	85.8037	70.0103	ENSG00000206527	HACD2
ENSG00000206530	4.69949	8.40652	10.4981	11.018	ENSG00000206530	CFAP44
ENSG00000206531	0.678901	2.10313	2.34785	4.53825	ENSG00000206531	CD200R1L
ENSG00000206532	0.569571	0.967631	0.22923	2.10092	ENSG00000206532	AC117402.1
ENSG00000206535	0.431299	1.08997	0.809123	1.46979	ENSG00000206535	LNP1
ENSG00000206536	0.0643435	0	0	0	ENSG00000206536	OR5K3
ENSG00000206538	24.0931	3.05164	6.38318	23.4331	ENSG00000206538	VGLL3
ENSG00000206549	0.0459323	0.0884574	0.279838	0	ENSG00000206549	PRSS50
ENSG00000206557	0.164034	0.490419	0.399415	0.641313	ENSG00000206557	TRIM71
ENSG00000206559	2.68964	6.67753	6.94967	7.89827	ENSG00000206559	ZCWPW2
ENSG00000206560	15.1109	33.5969	20.7748	57.5351	ENSG00000206560	ANKRD28
ENSG00000206561	0.524668	1.63597	3.71661	2.86182	ENSG00000206561	COLQ
ENSG00000206562	13.3655	22.6537	19.8775	22.7256	ENSG00000206562	METTL6
ENSG00000206579	0.325959	0.564295	0.505656	1.00574	ENSG00000206579	XKR4
ENSG00000211445	46.2495	28.8812	18.4768	21.1869	ENSG00000211445	GPX3
ENSG00000211448	2.22367	2.51317	2.70019	5.7789	ENSG00000211448	DIO2
ENSG00000211450	48.1268	34.2757	28.6347	23.9767	ENSG00000211450	SELENOH
ENSG00000211451	15.6708	41.6035	40.6108	74.2708	ENSG00000211451	GNRHR2
ENSG00000211452	0.286519	0.502096	0.805496	1.22158	ENSG00000211452	DIO1
ENSG00000211454	9.37997	13.5784	16.0217	19.2797	ENSG00000211454	AKR7L
ENSG00000211455	24.8083	23.1607	27.4929	26.4315	ENSG00000211455	STK38L
ENSG00000211456	15.628	24.9667	20.6096	24.7994	ENSG00000211456	SACM1L
ENSG00000211460	21.263	19.1058	21.7213	16.2855	ENSG00000211460	TSN
ENSG00000211584	13.591	15.9019	11.3408	12.7514	ENSG00000211584	SLC48A1
ENSG00000211592	0	0	0.246681	0	ENSG00000211592	IGKC
ENSG00000211593	0	0	0	0	ENSG00000211593	IGKJ5
ENSG00000211594	0	0	0	0	ENSG00000211594	IGKJ4
ENSG00000211595	0	0	0	0	ENSG00000211595	IGKJ3
ENSG00000211596	0	0	0	0	ENSG00000211596	IGKJ2
ENSG00000211597	1.32947	0	0	0	ENSG00000211597	IGKJ1
ENSG00000211598	0	0	0	0	ENSG00000211598	IGKV4-1
ENSG00000211599	0.207032	0	0	0	ENSG00000211599	IGKV5-2
ENSG00000211611	0	0	0	0	ENSG00000211611	IGKV6-21
ENSG00000211619	0	0	0	0	ENSG00000211619	IGKV2-40
ENSG00000211623	0	0	0	0	ENSG00000211623	IGKV2D-26
ENSG00000211625	0	0	0	0	ENSG00000211625	IGKV3D-20
ENSG00000211626	0	0	0	0	ENSG00000211626	IGKV6D-41
ENSG00000211630	0	0	0.474795	0	ENSG00000211630	IGKV1D-13
ENSG00000211632	0	0	0	0	ENSG00000211632	IGKV3D-11

ENSG00000211633	0	0	0	0	ENSG00000211633	IGKV1D-42
ENSG00000211637	0	0.37985	0	0.210566	ENSG00000211637	IGLV4-69
ENSG00000211638	0	0	0	0	ENSG00000211638	IGLV8-61
ENSG00000211639	0	0.240072	0	0.265076	ENSG00000211639	IGLV4-60
ENSG00000211640	0.352226	0.333389	0.405745	0.125391	ENSG00000211640	IGLV6-57
ENSG00000211641	0.19345	1.11722	1.34619	0.821369	ENSG00000211641	IGLV11-55
ENSG00000211642	0	0	0	0.522993	ENSG00000211642	IGLV10-54
ENSG00000211643	11.4075	12.3436	17.1907	6.04498	ENSG00000211643	IGLV5-52
ENSG00000211644	1.71003	2.38404	4.91879	0.904422	ENSG00000211644	IGLV1-51
ENSG00000211645	0	0.801005	0	0	ENSG00000211645	IGLV1-50
ENSG00000211647	0	0	0	0.513815	ENSG00000211647	IGLV5-48
ENSG00000211648	0	0	0.179448	0	ENSG00000211648	IGLV1-47
ENSG00000211649	0	0	0	0	ENSG00000211649	IGLV7-46
ENSG00000211650	0	0	0.186647	0	ENSG00000211650	IGLV5-45
ENSG00000211651	0	0	0	0	ENSG00000211651	IGLV1-44
ENSG00000211652	0	0	0	0	ENSG00000211652	IGLV7-43
ENSG00000211653	0	0	0	0	ENSG00000211653	IGLV1-40
ENSG00000211654	0.240033	0	0	0.25142	ENSG00000211654	IGLV5-37
ENSG00000211655	0	0	0	0.233339	ENSG00000211655	IGLV1-36
ENSG00000211656	0	0	0	0	ENSG00000211656	IGLV2-33
ENSG00000211657	0	0	0	0	ENSG00000211657	IGLV3-32
ENSG00000211658	0	0	0	0	ENSG00000211658	IGLV3-27
ENSG00000211659	0	0	0	0	ENSG00000211659	IGLV3-25
ENSG00000211660	0	0	0	0	ENSG00000211660	IGLV2-23
ENSG00000211661	0	0.197155	0.178161	0	ENSG00000211661	IGLV3-22
ENSG00000211662	0	0	0	0	ENSG00000211662	IGLV3-21
ENSG00000211663	0	0	0	0.24825	ENSG00000211663	IGLV3-19
ENSG00000211664	0	0	0	0	ENSG00000211664	IGLV2-18
ENSG00000211665	0	0.706717	1.02346	2.00277	ENSG00000211665	IGLV3-16
ENSG00000211666	0	0	0	0	ENSG00000211666	IGLV2-14
ENSG00000211667	0	0	0	0	ENSG00000211667	IGLV3-12
ENSG00000211668	0	0	0	0	ENSG00000211668	IGLV2-11
ENSG00000211669	0	0	0	0	ENSG00000211669	IGLV3-10
ENSG00000211670	0	0	0	0	ENSG00000211670	IGLV3-9
ENSG00000211671	0	0	0	0	ENSG00000211671	IGLV2-8
ENSG00000211672	0	0	0	0	ENSG00000211672	IGLV4-3
ENSG00000211673	0	0	0	0	ENSG00000211673	IGLV3-1
ENSG00000211674	0	0	0	0	ENSG00000211674	IGLJ1
ENSG00000211675	0	0	0	0	ENSG00000211675	IGLC1
ENSG00000211676	0	0	0	0	ENSG00000211676	IGLJ2
ENSG00000211677	0	0	0.0738479	0	ENSG00000211677	IGLC2
ENSG00000211678	0	0	0.860772	0	ENSG00000211678	IGLJ3
ENSG00000211679	0	0	0.0738479	0	ENSG00000211679	IGLC3
ENSG00000211680	0	0	0	0	ENSG00000211680	IGLJ4
ENSG00000211681	0	0	0	0	ENSG00000211681	IGLJ5
ENSG00000211682	0	0	0	0	ENSG00000211682	IGLJ6
ENSG00000211684	0	0	0	0	ENSG00000211684	IGLJ7
ENSG00000211685	0	0	0.160116	0	ENSG00000211685	IGLC7
ENSG00000211687	0	0	0	0	ENSG00000211687	TRGJ2
ENSG00000211688	0	0	0	0	ENSG00000211688	TRGJP2
ENSG00000211689	0	0.019453	0.0790643	0.102377	ENSG00000211689	TRGC1
ENSG00000211690	0	0	0	0	ENSG00000211690	TRGJ1
ENSG00000211691	0	0	0	0	ENSG00000211691	TRGJP
ENSG00000211692	0	0	0	0	ENSG00000211692	TRGJP1

ENSG00000211693	0	0	0	0	ENSG00000211693	TRGV11
ENSG00000211694	0	0	0	0.157114	ENSG00000211694	TRGV10
ENSG00000211695	0.131696	0.381153	0.517538	0.634942	ENSG00000211695	TRGV9
ENSG00000211696	0	0	0	0	ENSG00000211696	TRGV8
ENSG00000211697	0	0	0	0	ENSG00000211697	TRGV5
ENSG00000211698	0	0	0.0851512	0	ENSG00000211698	TRGV4
ENSG00000211699	0	0	0	0	ENSG00000211699	TRGV3
ENSG00000211701	0	0	0	0	ENSG00000211701	TRGV1
ENSG00000211706	0	0	0	0.112631	ENSG00000211706	TRBV6-1
ENSG00000211707	0	0	0	0	ENSG00000211707	TRBV7-1
ENSG00000211710	0	0	0	0	ENSG00000211710	TRBV4-1
ENSG00000211713	0	0	0	0	ENSG00000211713	TRBV6-4
ENSG00000211714	0	0.206683	0.0933234	0.114374	ENSG00000211714	TRBV7-3
ENSG00000211715	0	0	0	0	ENSG00000211715	TRBV5-3
ENSG00000211716	0.111335	0.425329	0.200454	0	ENSG00000211716	TRBV9
ENSG00000211717	0	0	0	0	ENSG00000211717	TRBV10-1
ENSG00000211720	0	0	0	0	ENSG00000211720	TRBV11-1
ENSG00000211721	0	0	0	0.14502	ENSG00000211721	TRBV6-5
ENSG00000211724	0	0	0	0	ENSG00000211724	TRBV6-6
ENSG00000211725	0	0	0	0	ENSG00000211725	TRBV5-5
ENSG00000211727	0	0	0	0	ENSG00000211727	TRBV7-6
ENSG00000211728	0	0	0	0.241055	ENSG00000211728	TRBV5-6
ENSG00000211731	0	0.131396	0	0	ENSG00000211731	TRBV5-7
ENSG00000211732	0	0	0	0.14404	ENSG00000211732	TRBV6-9
ENSG00000211734	0	0	0	0	ENSG00000211734	TRBV5-1
ENSG00000211739	0	0	0	0	ENSG00000211739	TRBV12-2
ENSG00000211745	0	0	0	0	ENSG00000211745	TRBV4-2
ENSG00000211746	0.197986	0	0.228655	0.424848	ENSG00000211746	TRBV19
ENSG00000211747	0	0	0	0	ENSG00000211747	TRBV20-1
ENSG00000211749	0	0	0	0	ENSG00000211749	TRBV23-1
ENSG00000211750	0	0	0	0	ENSG00000211750	TRBV24-1
ENSG00000211751	0	0	0	0	ENSG00000211751	AC245427.1
ENSG00000211752	0	0	0	0	ENSG00000211752	TRBV27
ENSG00000211753	0	0	0	0	ENSG00000211753	TRBV28
ENSG00000211764	0	0	0	0	ENSG00000211764	TRBJ2-1
ENSG00000211765	0	0	0	0	ENSG00000211765	TRBJ2-2
ENSG00000211766	0	0	0	0	ENSG00000211766	TRBJ2-2P
ENSG00000211767	0	0	0	0	ENSG00000211767	TRBJ2-3
ENSG00000211768	0	0	0	0	ENSG00000211768	TRBJ2-4
ENSG00000211769	0	0	0	0	ENSG00000211769	TRBJ2-5
ENSG00000211770	0	0	0	0	ENSG00000211770	TRBJ2-6
ENSG00000211771	0	0	0	0	ENSG00000211771	TRBJ2-7
ENSG00000211772	0	0	0	0.0938673	ENSG00000211772	TRBC2
ENSG00000211776	0	0	0	0	ENSG00000211776	TRAV2
ENSG00000211777	0	0.138099	0.249375	0.465782	ENSG00000211777	TRAV3
ENSG00000211778	0	0	0	0	ENSG00000211778	TRAV4
ENSG00000211779	0	0	0	0	ENSG00000211779	TRAV5
ENSG00000211780	0.630986	1.20621	1.08921	2.48059	ENSG00000211780	TRAV6
ENSG00000211781	0	0	0	0	ENSG00000211781	TRAV7
ENSG00000211782	0	0	0	0.175851	ENSG00000211782	TRAV8-1
ENSG00000211783	0	0	0	0	ENSG00000211783	TRAV9-1
ENSG00000211784	0	0	0	0.246214	ENSG00000211784	TRAV10
ENSG00000211785	0.280632	0	0.723139	0.881184	ENSG00000211785	TRAV12-1
ENSG00000211786	0	0	0	0.136889	ENSG00000211786	TRAV8-2

ENSG00000211787	0	0	0	0	ENSG00000211787	TRAV8-3
ENSG00000211788	0	0	0.219156	0	ENSG00000211788	TRAV13-1
ENSG00000211789	0.180889	0	0	0	ENSG00000211789	TRAV12-2
ENSG00000211790	0	0	0	0	ENSG00000211790	TRAV8-4
ENSG00000211791	0	0	0	0	ENSG00000211791	TRAV13-2
ENSG00000211792	0	0	0	0	ENSG00000211792	TRAV14DV4
ENSG00000211793	0	0	0	0	ENSG00000211793	TRAV9-2
ENSG00000211794	0	0	0	0	ENSG00000211794	TRAV12-3
ENSG00000211795	0	0	0	0	ENSG00000211795	TRAV8-6
ENSG00000211796	0	0	0	0	ENSG00000211796	TRAV16
ENSG00000211797	0	0	0	0	ENSG00000211797	TRAV17
ENSG00000211798	0	0	0	0	ENSG00000211798	TRAV18
ENSG00000211799	0	0	0	0	ENSG00000211799	TRAV19
ENSG00000211800	0.62597	1.79544	0.72065	0.663008	ENSG00000211800	TRAV20
ENSG00000211801	0	0	0	0	ENSG00000211801	TRAV21
ENSG00000211802	0	0	0.146738	0	ENSG00000211802	TRAV22
ENSG00000211803	0	0	0	0	ENSG00000211803	TRAV23DV6
ENSG00000211804	0	0	0	0	ENSG00000211804	TRDV1
ENSG00000211805	0	0	0	0	ENSG00000211805	TRAV24
ENSG00000211806	0	0	0	0	ENSG00000211806	TRAV25
ENSG00000211807	0.137202	0.131628	0.118807	0	ENSG00000211807	TRAV26-1
ENSG00000211808	0	0.265474	0	0	ENSG00000211808	TRAV8-7
ENSG00000211809	0	0	0	0	ENSG00000211809	TRAV27
ENSG00000211810	0	0	0	0	ENSG00000211810	TRAV29DV5
ENSG00000211812	0	0	0	0	ENSG00000211812	TRAV26-2
ENSG00000211813	0	0	0	0.281347	ENSG00000211813	TRAV34
ENSG00000211814	1.77383	4.21334	0.761595	2.78246	ENSG00000211814	TRAV35
ENSG00000211815	0	0	0	0	ENSG00000211815	TRAV36DV7
ENSG00000211816	0	0	0.679496	0	ENSG00000211816	TRAV38-1
ENSG00000211817	0	0	0	0	ENSG00000211817	TRAV38-2DV8
ENSG00000211818	0	0	0.252577	0	ENSG00000211818	TRAV39
ENSG00000211819	0	0	0.272364	0	ENSG00000211819	TRAV40
ENSG00000211820	0.286547	0	0	0	ENSG00000211820	TRAV41
ENSG00000211821	0	0.137719	0	0	ENSG00000211821	TRDV2
ENSG00000211825	0	0	0	0	ENSG00000211825	TRDJ1
ENSG00000211826	4.63854	1.02125	1.01137	4.67388	ENSG00000211826	TRDJ4
ENSG00000211827	0	12.642	0	0	ENSG00000211827	TRDJ2
ENSG00000211828	0	0	0	0	ENSG00000211828	TRDJ3
ENSG00000211829	0	0	0	0	ENSG00000211829	TRDC
ENSG00000211831	0	0	0	0	ENSG00000211831	TRAJ61
ENSG00000211832	0	0	0	0	ENSG00000211832	TRAJ59
ENSG00000211833	0	0	0	0	ENSG00000211833	TRAJ58
ENSG00000211834	0	0	0	0	ENSG00000211834	TRAJ57
ENSG00000211835	0	0	0	0	ENSG00000211835	TRAJ56
ENSG00000211836	0	0	0	0	ENSG00000211836	TRAJ54
ENSG00000211837	0	0	0	0	ENSG00000211837	TRAJ53
ENSG00000211838	0	0	0	0	ENSG00000211838	TRAJ52
ENSG00000211839	0	0	0	0	ENSG00000211839	TRAJ50
ENSG00000211840	0	0	0	0	ENSG00000211840	TRAJ49
ENSG00000211841	0	0	0	0	ENSG00000211841	TRAJ48
ENSG00000211842	8.68293	0	0	0	ENSG00000211842	TRAJ47
ENSG00000211843	0	0	0	0	ENSG00000211843	TRAJ46
ENSG00000211844	0	0	0	0	ENSG00000211844	TRAJ45
ENSG00000211845	0	0	5.08104	0	ENSG00000211845	TRAJ44

ENSG00000211846	0	0	0	0	ENSG00000211846	TRAJ43
ENSG00000211847	0	0	0	0	ENSG00000211847	TRAJ42
ENSG00000211848	0	0	0	0	ENSG00000211848	TRAJ41
ENSG00000211849	0	6.8238	0	0	ENSG00000211849	TRAJ40
ENSG00000211850	0	0	0	0	ENSG00000211850	TRAJ39
ENSG00000211851	0	0	0	0	ENSG00000211851	TRAJ38
ENSG00000211852	0	0	0	0	ENSG00000211852	TRAJ37
ENSG00000211853	0	0	0	0	ENSG00000211853	TRAJ36
ENSG00000211854	0	0	0	0	ENSG00000211854	TRAJ35
ENSG00000211855	0	0	0	0	ENSG00000211855	TRAJ34
ENSG00000211856	0	0	0	0	ENSG00000211856	TRAJ33
ENSG00000211857	0	0	0	0	ENSG00000211857	TRAJ32
ENSG00000211858	0	0	0	0	ENSG00000211858	TRAJ31
ENSG00000211859	0	8.57059	0	0	ENSG00000211859	TRAJ30
ENSG00000211860	0	0	0	0	ENSG00000211860	TRAJ29
ENSG00000211861	0	0	0	0	ENSG00000211861	TRAJ28
ENSG00000211862	0	0	0	0	ENSG00000211862	TRAJ27
ENSG00000211863	0	0	0	0	ENSG00000211863	TRAJ26
ENSG00000211864	0	0	0	0	ENSG00000211864	TRAJ25
ENSG00000211865	0	0	0	0	ENSG00000211865	TRAJ24
ENSG00000211866	0	0	4.80103	0	ENSG00000211866	TRAJ23
ENSG00000211867	0	0	5.08104	0	ENSG00000211867	TRAJ22
ENSG00000211868	0	0	9.76787	0	ENSG00000211868	TRAJ21
ENSG00000211869	0	0	7.63272	0	ENSG00000211869	TRAJ20
ENSG00000211870	0	6.67216	0	0	ENSG00000211870	TRAJ19
ENSG00000211871	0	0	0	0	ENSG00000211871	TRAJ18
ENSG00000211872	0	0	0	0	ENSG00000211872	TRAJ17
ENSG00000211873	0	0	0	0	ENSG00000211873	TRAJ16
ENSG00000211874	0	0	0	0	ENSG00000211874	TRAJ15
ENSG00000211875	0	0	0	0	ENSG00000211875	TRAJ14
ENSG00000211876	0	0	0	0	ENSG00000211876	TRAJ13
ENSG00000211877	0	0	0	0	ENSG00000211877	TRAJ12
ENSG00000211878	0	0	0	0	ENSG00000211878	TRAJ11
ENSG00000211879	0	0	4.95101	0	ENSG00000211879	TRAJ10
ENSG00000211880	0	0	0	8.67027	ENSG00000211880	TRAJ9
ENSG00000211881	0	0	0	0	ENSG00000211881	TRAJ8
ENSG00000211882	0	0	0	0	ENSG00000211882	TRAJ7
ENSG00000211883	0	0	0	0	ENSG00000211883	TRAJ6
ENSG00000211884	0	0	0	8.92884	ENSG00000211884	TRAJ5
ENSG00000211885	0	6.85958	0	0	ENSG00000211885	TRAJ4
ENSG00000211886	0	0	0	0	ENSG00000211886	TRAJ3
ENSG00000211887	0	0	0	0	ENSG00000211887	TRAJ2
ENSG00000211888	0	0	0	0	ENSG00000211888	TRAJ1
ENSG00000211890	0	0	0	0	ENSG00000211890	IGHA2
ENSG00000211891	0	0.019946	0.496555	0.113285	ENSG00000211891	IGHE
ENSG00000211892	0	0.0262706	0	0	ENSG00000211892	IGHG4
ENSG00000211893	0	0	0	0	ENSG00000211893	IGHG2
ENSG00000211895	0	0	0	0	ENSG00000211895	IGHA1
ENSG00000211896	0	0.0203302	0.0523175	0.0655454	ENSG00000211896	IGHG1
ENSG00000211897	0	0	0	0	ENSG00000211897	IGHG3
ENSG00000211898	0	0.0332544	0.0446284	0.0758869	ENSG00000211898	IGHD
ENSG00000211899	0	0	0	0	ENSG00000211899	IGHM
ENSG00000211900	0	6.8238	14.0934	8.67027	ENSG00000211900	IGHJ6
ENSG00000211904	0	0	0	0	ENSG00000211904	IGHJ2

ENSG00000211905	0	0	0	0	ENSG00000211905	IGHJ1
ENSG00000211907	0	0	0	0	ENSG00000211907	IGHD1-26
ENSG00000211909	0	0	0	0	ENSG00000211909	IGHD5-24
ENSG00000211911	0	0	0	0	ENSG00000211911	IGHD3-22
ENSG00000211912	0	0	0	0	ENSG00000211912	IGHD2-21
ENSG00000211914	0	0	0	0	ENSG00000211914	IGHD6-19
ENSG00000211915	0	0	0	0	ENSG00000211915	IGHD5-18
ENSG00000211917	0	0	0	0	ENSG00000211917	IGHD3-16
ENSG00000211918	0	0	0	0	ENSG00000211918	IGHD2-15
ENSG00000211920	0	0	0	0	ENSG00000211920	IGHD6-13
ENSG00000211921	0	0	0	0	ENSG00000211921	IGHD5-12
ENSG00000211923	0	0	0	0	ENSG00000211923	IGHD3-10
ENSG00000211924	0	0	0	0	ENSG00000211924	IGHD3-9
ENSG00000211925	0	0	0	0	ENSG00000211925	IGHD2-8
ENSG00000211928	0	0	0	0	ENSG00000211928	IGHD5-5
ENSG00000211930	0	0	0	0	ENSG00000211930	IGHD3-3
ENSG00000211931	0	0	0	0	ENSG00000211931	IGHD2-2
ENSG00000211933	0	0	0	0.106823	ENSG00000211933	IGHV6-1
ENSG00000211934	0	0	0	0	ENSG00000211934	IGHV1-2
ENSG00000211935	0	0	0	0	ENSG00000211935	IGHV1-3
ENSG00000211936	0	0	0	0	ENSG00000211936	IGHV4-4
ENSG00000211937	0	0	0	0	ENSG00000211937	IGHV2-5
ENSG00000211938	0	0	0	0	ENSG00000211938	IGHV3-7
ENSG00000211939	0	0	0	0	ENSG00000211939	IGHV1-8
ENSG00000211940	0	0	0	0	ENSG00000211940	IGHV3-9
ENSG00000211941	0	0	0	0	ENSG00000211941	IGHV3-11
ENSG00000211942	0	0	0	0	ENSG00000211942	IGHV3-13
ENSG00000211943	0	0	0	0	ENSG00000211943	IGHV3-15
ENSG00000211944	0	0	0.167733	0	ENSG00000211944	IGHV3-16
ENSG00000211945	0	0	0	0	ENSG00000211945	IGHV1-18
ENSG00000211946	0	0	0	0	ENSG00000211946	IGHV3-20
ENSG00000211947	0	0	0	0	ENSG00000211947	IGHV3-21
ENSG00000211949	0	0	0	0	ENSG00000211949	IGHV3-23
ENSG00000211950	0	0	0	0	ENSG00000211950	IGHV1-24
ENSG00000211951	0	0	0	0	ENSG00000211951	IGHV2-26
ENSG00000211952	0	0	0.084493	0.103777	ENSG00000211952	IGHV4-28
ENSG00000211953	0	0	0.0410332	0	ENSG00000211953	IGHV3-30
ENSG00000211955	0	0	0.0410332	0	ENSG00000211955	IGHV3-33
ENSG00000211956	0	0	0	0	ENSG00000211956	IGHV4-34
ENSG00000211957	0	0	0	0	ENSG00000211957	IGHV3-35
ENSG00000211958	0	0	0	0	ENSG00000211958	IGHV3-38
ENSG00000211959	0	0	0	0	ENSG00000211959	IGHV4-39
ENSG00000211961	0	0	0.0890803	0	ENSG00000211961	IGHV1-45
ENSG00000211962	0	0	0	0	ENSG00000211962	IGHV1-46
ENSG00000211964	0	0	0	0	ENSG00000211964	IGHV3-48
ENSG00000211965	0	0	0	0	ENSG00000211965	IGHV3-49
ENSG00000211966	0.205433	0.0981906	0.396165	0.435371	ENSG00000211966	IGHV5-51
ENSG00000211967	0.126528	0.121421	0.219282	0.407744	ENSG00000211967	IGHV3-53
ENSG00000211968	0	0	0	0	ENSG00000211968	IGHV1-58
ENSG00000211970	0	0	0	0	ENSG00000211970	IGHV4-61
ENSG00000211972	0	0	0	0	ENSG00000211972	IGHV3-66
ENSG00000211973	0	0	0	0	ENSG00000211973	IGHV1-69
ENSG00000211974	0.0943192	0	0	0	ENSG00000211974	AC245369.1
ENSG00000211976	0.185988	0.266953	0	0.197626	ENSG00000211976	IGHV3-73

ENSG00000211978	0	0	0	0.75018	ENSG00000211978	IGHV5-78
ENSG00000211979	0	0	0	0	ENSG00000211979	IGHV7-81
ENSG00000212122	0.556963	1.24755	1.28362	1.92204	ENSG00000212122	TSSK1B
ENSG00000212123	1.70964	1.73508	6.296	1.19446	ENSG00000212123	PRR22
ENSG00000212124	0.193295	0.560465	0.363731	1.00266	ENSG00000212124	TAS2R19
ENSG00000212125	0.292621	1.27252	1.10461	1.53197	ENSG00000212125	TAS2R15P
ENSG00000212126	0.102898	0.718323	0.447358	0.403433	ENSG00000212126	TAS2R50
ENSG00000212127	0.18156	0.913382	0.610468	0.768707	ENSG00000212127	TAS2R14
ENSG00000212128	0.0819205	0.586298	0.37711	0.820575	ENSG00000212128	TAS2R13
ENSG00000212643	0.651469	0.134103	0.34614	1.74537	ENSG00000212643	ZRSR1
ENSG00000212657	0.0375269	0.197095	0.0809831	0.122208	ENSG00000212657	KRTAP16-1
ENSG00000212658	0	0.0192078	0	0.0217489	ENSG00000212658	KRTAP29-1
ENSG00000212659	0.418453	0.740686	0.882134	1.06989	ENSG00000212659	KRTAP9-6
ENSG00000212664	2.66587	5.95927	2.36956	7.59406	ENSG00000212664	AC064799.1
ENSG00000212670	3.09214	5.40788	6.72635	10.6244	ENSG00000212670	AL161915.1
ENSG00000212673	1.86596	3.87205	2.77181	5.88093	ENSG00000212673	AL136115.1
ENSG00000212695	0	0	0	0	ENSG00000212695	AL583805.1
ENSG00000212710	0.138586	0.162902	0.254078	0.43168	ENSG00000212710	CTAGE1
ENSG00000212712	0	0	0.0457625	0	ENSG00000212712	AP002414.1
ENSG00000212717	0	0	0	0	ENSG00000212717	DEFB117
ENSG00000212719	2.50039	8.24189	6.75079	6.70422	ENSG00000212719	C17orf51
ENSG00000212721	0	0.0984657	0	0.164673	ENSG00000212721	KRTAP4-11
ENSG00000212722	0	0	0	0	ENSG00000212722	KRTAP4-9
ENSG00000212724	0	0	0.0710241	0	ENSG00000212724	KRTAP2-3
ENSG00000212725	0.084147	0.325688	0.0803379	0.105987	ENSG00000212725	KRTAP2-1
ENSG00000212734	3.75916	5.20372	7.08422	3.43164	ENSG00000212734	C17orf100
ENSG00000212743	0.314529	0.818374	0.671969	1.58679	ENSG00000212743	AL137145.1
ENSG00000212747	1.10251	0.786625	1.2233	1.84432	ENSG00000212747	RTL8B
ENSG00000212768	0.0757787	0.139838	0.0805675	0	ENSG00000212768	AC114546.1
ENSG00000212769	0	0	0	0	ENSG00000212769	HMGN2P8
ENSG00000212789	0.0592156	0.261816	0	0.300324	ENSG00000212789	ST13P5
ENSG00000212802	0	0.305045	0.537827	0.346553	ENSG00000212802	RPL15P3
ENSG00000212807	0.382846	0.425753	0.355468	0.836419	ENSG00000212807	OR2A42
ENSG00000212829	0.874123	0.458984	0.581468	0.509514	ENSG00000212829	RPS26P3
ENSG00000212857	0	0	0	0.0376798	ENSG00000212857	AL356585.1
ENSG00000212864	1.02692	0.384333	0.419885	0.302663	ENSG00000212864	RNF208
ENSG00000212866	8.17734	21.0112	11.0812	18.4966	ENSG00000212866	HSPA1B
ENSG00000212884	1.48446	1.5399	0.713227	0.502619	ENSG00000212884	AC011841.1
ENSG00000212899	0	0	0.265865	0	ENSG00000212899	KRTAP3-3
ENSG00000212900	0	0.187128	0.169374	0.110631	ENSG00000212900	KRTAP3-2
ENSG00000212901	0.511816	0.29042	0	0.209109	ENSG00000212901	KRTAP3-1
ENSG00000212907	1137.05	998.009	1219.85	1979.54	ENSG00000212907	MT-ND4L
ENSG00000212916	0.549461	0.520608	0.436138	0.65368	ENSG00000212916	MAP10
ENSG00000212928	1.35892	0	0	0.341449	ENSG00000212928	AL391152.1
ENSG00000212932	0.891002	0	0	0	ENSG00000212932	RPL23AP4
ENSG00000212933	0.0898179	0	0	0	ENSG00000212933	KRTAP12-4
ENSG00000212935	0	0	0	0	ENSG00000212935	KRTAP10-3
ENSG00000212938	0	0	0	0	ENSG00000212938	KRTAP6-3
ENSG00000212951	1.69628	4.6046	5.55383	4.1739	ENSG00000212951	BX005266.1
ENSG00000212952	1.26614	0.871773	1.53547	1.04482	ENSG00000212952	BX088651.1
ENSG00000212961	1.30266	3.78895	3.13401	10.1559	ENSG00000212961	HNRNPA1P40
ENSG00000212989	0	0.338527	0	0	ENSG00000212989	AC124293.1
ENSG00000212993	0.851168	1.39117	2.05613	1.91749	ENSG00000212993	POU5F1B
ENSG00000212994	0.344735	0.351486	0.612935	0.704017	ENSG00000212994	RPS26P6

ENSG00000212997	2.17132	4.94707	4.55284	9.57393	ENSG00000212997	AC023632.1
ENSG00000212998	2.0129	4.59737	4.95926	4.45679	ENSG00000212998	RBM12B-AS1
ENSG00000212999	0	0	0.193878	0.35103	ENSG00000212999	AC117834.1
ENSG00000213002	0	0.504619	0.695418	1.7769	ENSG00000213002	AC120194.1
ENSG00000213003	0.769166	1.76229	1.01333	1.77397	ENSG00000213003	BTF3P12
ENSG00000213005	0	0.224172	0	0.251832	ENSG00000213005	PTTG3P
ENSG00000213013	1.15119	1.84265	2.38351	0.729234	ENSG00000213013	RPS15AP36
ENSG00000213014	0.617149	0.444994	0.469055	0.502364	ENSG00000213014	VN2R17P
ENSG00000213015	4.49525	4.85894	7.7984	5.47653	ENSG00000213015	ZNF580
ENSG00000213016	0	0	0	0	ENSG00000213016	AC245036.1
ENSG00000213018	0.760776	1.83645	2.77999	4.11073	ENSG00000213018	AL590762.1
ENSG00000213020	25.6037	30.0116	33.296	50.0533	ENSG00000213020	ZNF611
ENSG00000213022	19.4443	10.409	7.47315	8.80062	ENSG00000213022	KLK9
ENSG00000213023	0.0567116	0.220042	0.233275	0.393999	ENSG00000213023	SYT3
ENSG00000213024	18.4271	21.5703	19.6223	24.0611	ENSG00000213024	NUP62
ENSG00000213025	0	0	0	0	ENSG00000213025	COX20P1
ENSG00000213026	0	0	0	0	ENSG00000213026	CFL1P4
ENSG00000213028	0	0	0.0604014	0	ENSG00000213028	AL354983.1
ENSG00000213029	0	0	0	0	ENSG00000213029	SPHAR
ENSG00000213030	0.170294	0.251469	0.80793	0.19047	ENSG00000213030	CGB8
ENSG00000213032	0	0.521429	0.834589	1.51043	ENSG00000213032	NDUFA3P3
ENSG00000213033	0.820291	2.39927	1.81166	2.0917	ENSG00000213033	AURKAPS1
ENSG00000213035	0	0	0	0	ENSG00000213035	RPL23AP80
ENSG00000213036	0.50869	2.27918	3.68521	4.65188	ENSG00000213036	AL445305.1
ENSG00000213041	1.18856	1.26835	1.49916	1.15338	ENSG00000213041	AC093422.1
ENSG00000213045	0.719837	1.494	1.13177	1.31653	ENSG00000213045	AC097065.1
ENSG00000213046	0.736615	0.971837	1.56831	0.827955	ENSG00000213046	EEF1A1P32
ENSG00000213047	17.5311	17.1221	14.1323	12.4974	ENSG00000213047	DENND1B
ENSG00000213048	0.0655639	0	0.0569846	0	ENSG00000213048	OR5S1P
ENSG00000213049	0	0	0.1259	0	ENSG00000213049	HNRNPA1P34
ENSG00000213050	0.353429	1.36274	1.23229	2.07603	ENSG00000213050	TPM3P1
ENSG00000213051	0.141875	0.136531	0.123298	0.231192	ENSG00000213051	RPL5P5
ENSG00000213055	0.50244	1.54385	1.48073	2.92773	ENSG00000213055	EEF1B2P7
ENSG00000213057	0.478558	0.467837	0.453114	1.41576	ENSG00000213057	C1orf220
ENSG00000213058	1.547	2.33599	0.222901	1.65926	ENSG00000213058	AL365357.1
ENSG00000213060	0.195581	0	0.168986	0	ENSG00000213060	AL031864.1
ENSG00000213061	0	0	0.385716	0	ENSG00000213061	PFN1P11
ENSG00000213062	1.15414	0.922006	1.21277	0.304892	ENSG00000213062	AL021068.1
ENSG00000213063	0	0.167374	0.304793	0.564426	ENSG00000213063	RPL29P7
ENSG00000213064	45.6245	41.0233	34.1563	54.5442	ENSG00000213064	SFT2D2
ENSG00000213065	0	0	0	0	ENSG00000213065	AL009178.1
ENSG00000213066	9.68607	13.4025	11.6416	14.6818	ENSG00000213066	FGFR1OP
ENSG00000213067	0.0656025	0.126217	0.172643	0.144786	ENSG00000213067	AC092447.1
ENSG00000213068	0.202601	0	0.5226	0	ENSG00000213068	AL451050.1
ENSG00000213069	0.128408	0	0.222472	0	ENSG00000213069	KRT8P40
ENSG00000213070	0.120723	0.118802	0	0.131182	ENSG00000213070	HMGB3P6
ENSG00000213071	3.36545	10.9619	16.3312	34.2411	ENSG00000213071	LPAL2
ENSG00000213073	1.57882	2.91233	6.51133	4.95602	ENSG00000213073	AL353625.1
ENSG00000213075	0.0851671	0.342208	0.207445	0.26169	ENSG00000213075	RPL31P11
ENSG00000213076	0.123232	0.236528	0.106795	0.584875	ENSG00000213076	AL627422.1
ENSG00000213077	1.07684	2.24234	2.16746	3.66485	ENSG00000213077	FAM106A
ENSG00000213078	0	0	0	0	ENSG00000213078	AL390955.1
ENSG00000213079	19.8354	23.0402	24.8913	26.1531	ENSG00000213079	SCAF8
ENSG00000213080	0.133574	0.198219	0.0602114	0.287395	ENSG00000213080	AL354714.2

ENSG00000213081	0.0895226	0	0.233129	0.0968853	ENSG00000213081	AC012362.1
ENSG00000213082	0	0	0	0	ENSG00000213082	PPP1R14BP2
ENSG00000213083	0	0	0	0	ENSG00000213083	AC010731.1
ENSG00000213084	13.5138	22.6671	22.7237	56.7546	ENSG00000213084	AC008555.2
ENSG00000213085	0.825379	0.59917	0.323821	0.962292	ENSG00000213085	CFAP45
ENSG00000213087	0	0.226161	0	0	ENSG00000213087	AL356535.1
ENSG00000213088	0	0.0316232	0	0.0609409	ENSG00000213088	ACKR1
ENSG00000213089	0.335159	0.2174	0.4287	1.48917	ENSG00000213089	PDCL3P5
ENSG00000213090	0.161648	0.961571	0.633509	1.28837	ENSG00000213090	AC007256.1
ENSG00000213091	0.160398	0.153802	0	0.0867638	ENSG00000213091	PHBP1
ENSG00000213096	13.9083	13.8946	18.5202	18.0854	ENSG00000213096	ZNF254
ENSG00000213100	0.0619987	0	0.107723	0.0677669	ENSG00000213100	KRT18P68
ENSG00000213104	0	0.0827809	0.0698505	0.129133	ENSG00000213104	NPM1P46
ENSG00000213107	0	0.0463165	0	0.0525508	ENSG00000213107	AHCYP5
ENSG00000213108	0	0	0	0	ENSG00000213108	BTF3L4P3
ENSG00000213109	0.319314	0.798922	0.657954	1.64592	ENSG00000213109	AL365223.1
ENSG00000213110	0	0	0	0.197205	ENSG00000213110	AC019178.1
ENSG00000213111	0.322439	0.166132	0.234229	1.70287	ENSG00000213111	COX5BP2
ENSG00000213113	0	0	0	0	ENSG00000213113	TUBB8P8
ENSG00000213115	0	0	0	0	ENSG00000213115	AC104131.1
ENSG00000213117	0	0	0.190365	0	ENSG00000213117	AL021939.1
ENSG00000213118	0	0	0	0	ENSG00000213118	CHCHD2P4
ENSG00000213120	0	0	0.36162	0	ENSG00000213120	LIN28AP1
ENSG00000213121	82.6164	195.768	193.492	450.998	ENSG00000213121	AL590867.1
ENSG00000213122	0.62682	1.05002	0.628833	0.709725	ENSG00000213122	RPL23AP46
ENSG00000213123	12.5891	24.0419	13.6345	16.8758	ENSG00000213123	TCTEX1D2
ENSG00000213126	0	0	0	0	ENSG00000213126	AC092642.1
ENSG00000213128	0	0	0	0	ENSG00000213128	AC109327.1
ENSG00000213130	0.338949	0.733683	1.02959	0.550621	ENSG00000213130	EEF1DP5
ENSG00000213131	0.137172	0.51588	0.335829	0.611264	ENSG00000213131	YWHAZP4
ENSG00000213132	2.0758	3.97748	5.98916	5.10798	ENSG00000213132	AC022498.1
ENSG00000213133	0.187819	0.179878	1.31489	0.39922	ENSG00000213133	PPP1R14BP5
ENSG00000213135	33.8868	28.4726	35.2145	22.1169	ENSG00000213135	AC015815.6
ENSG00000213137	0.823523	1.57895	0.950159	4.27635	ENSG00000213137	ARF1P2
ENSG00000213139	2.94085	4.92401	4.33347	5.4631	ENSG00000213139	CRYGS
ENSG00000213140	0.0306141	0	0	0	ENSG00000213140	ELK2AP
ENSG00000213144	0.502261	0.488901	0.296194	0.539372	ENSG00000213144	AC084880.1
ENSG00000213145	0	0.105855	0.0665227	0.436923	ENSG00000213145	CRIP1
ENSG00000213147	0.546611	2.84441	0	0	ENSG00000213147	RPL23AP60
ENSG00000213148	0	0.325128	1.02717	0.361664	ENSG00000213148	AC073465.1
ENSG00000213149	0	0.0665812	0.0602735	0.150715	ENSG00000213149	CNN2P9
ENSG00000213150	0	0.213652	0.128705	0.453836	ENSG00000213150	AL512430.1
ENSG00000213152	0.409006	0.707882	0.63968	1.4283	ENSG00000213152	AC004217.1
ENSG00000213153	0	0.337136	0.304562	0.189914	ENSG00000213153	AP001979.1
ENSG00000213155	0	0.157537	0	0	ENSG00000213155	AC007547.1
ENSG00000213157	0	0	0	0	ENSG00000213157	AC108734.1
ENSG00000213158	1.62259	7.92571	2.49608	10.4076	ENSG00000213158	GAPDHP36
ENSG00000213159	0	0.167375	0	0	ENSG00000213159	CEND1P1
ENSG00000213160	2.50752	3.29368	4.10985	3.60899	ENSG00000213160	KLHL23
ENSG00000213165	5.08504	12.9343	12.1218	18.8677	ENSG00000213165	AC090425.1
ENSG00000213167	8.36642	29.1417	18.2316	43.643	ENSG00000213167	Metazoa_SRP
ENSG00000213169	0	0	0	0	ENSG00000213169	AC069218.1
ENSG00000213170	0	0	0	0.641563	ENSG00000213170	SAR1AP2
ENSG00000213171	0.306902	0.422245	0.515775	1.01389	ENSG00000213171	LINGO4

ENSG00000213172	0	0	0	0	ENSG00000213172	AL031985.1
ENSG00000213174	0	0	0	0	ENSG00000213174	AC026316.1
ENSG00000213176	1.48537	2.34326	1.73422	3.75226	ENSG00000213176	RPL13P6
ENSG00000213177	0	0	0	0.256115	ENSG00000213177	PRDX2P4
ENSG00000213178	56.1223	43.3465	35.7081	34.4324	ENSG00000213178	AC074033.1
ENSG00000213179	0	0	0	0	ENSG00000213179	AC006534.1
ENSG00000213180	0.646368	0.306436	1.94049	1.00972	ENSG00000213180	RPL36AP48
ENSG00000213181	0	0	0	0.0794296	ENSG00000213181	OR10N1P
ENSG00000213182	0.305844	0.147039	0.0664178	0.082999	ENSG00000213182	OR10D5P
ENSG00000213183	0	0	0	0	ENSG00000213183	RPS7P8
ENSG00000213184	0.240795	0.174122	0.368638	0.196901	ENSG00000213184	AP003040.1
ENSG00000213185	4.94322	6.10557	6.76261	4.13471	ENSG00000213185	FAM24B
ENSG00000213186	7.73404	17.9848	8.74116	12.5726	ENSG00000213186	TRIM59
ENSG00000213187	0.0832243	0	0.216061	0	ENSG00000213187	COPS5P1
ENSG00000213188	0.722418	0.538308	0.654812	0.788699	ENSG00000213188	YBX1P4
ENSG00000213189	12.6015	13.7949	16.6872	6.84821	ENSG00000213189	BTF3L4P2
ENSG00000213190	4.40382	5.84924	7.32815	4.53827	ENSG00000213190	MLLT11
ENSG00000213194	0	0	0	0	ENSG00000213194	CDK7P1
ENSG00000213197	1.29517	4.10903	2.75855	10.8432	ENSG00000213197	AC012066.1
ENSG00000213199	1.63177	1.96224	3.39833	2.34512	ENSG00000213199	ASIC3
ENSG00000213201	0	0	0	0	ENSG00000213201	FABP5P10
ENSG00000213203	1.04838	1.47734	1.54473	3.09388	ENSG00000213203	GIMAP1
ENSG00000213204	0.621467	1.09847	0.996004	0.979972	ENSG00000213204	AL049697.1
ENSG00000213205	0.0483394	0	0.0828216	0.054446	ENSG00000213205	STRADBP1
ENSG00000213209	0	0	0	0	ENSG00000213209	AC005229.1
ENSG00000213210	0	0.205103	0	0	ENSG00000213210	AC005229.2
ENSG00000213211	0	0.0471456	0	0	ENSG00000213211	KRT18P64
ENSG00000213212	0.691805	0.805102	1.5984	1.90743	ENSG00000213212	NCLP1
ENSG00000213213	5.07181	3.78738	5.00147	3.81005	ENSG00000213213	CCDC183
ENSG00000213214	13.5884	10.6419	10.5717	6.16622	ENSG00000213214	ARHGEF35
ENSG00000213215	0	0.108265	0.0489237	0	ENSG00000213215	OR2F1
ENSG00000213216	1.40122	2.89824	2.62222	1.96715	ENSG00000213216	AC007066.1
ENSG00000213218	0.0512401	0	0	0	ENSG00000213218	CSH2
ENSG00000213221	3.85089	5.9582	5.85191	4.32547	ENSG00000213221	DNLZ
ENSG00000213222	3.74354	4.94756	7.42398	16.2791	ENSG00000213222	AC093724.1
ENSG00000213225	0.250607	0.880207	1.55094	0.822827	ENSG00000213225	NOC2LP1
ENSG00000213226	0	0.0311751	0	0	ENSG00000213226	AC242426.1
ENSG00000213228	0.219944	0.824974	0.654238	1.16618	ENSG00000213228	RPL12P38
ENSG00000213231	5.67229	11.7422	8.43153	10.8718	ENSG00000213231	TCL1B
ENSG00000213232	0	0	0	0	ENSG00000213232	PPP1R2P10
ENSG00000213233	0.193796	1.93784	0.390126	2.20762	ENSG00000213233	RPL23AP62
ENSG00000213234	0.0567996	0.163383	0.499355	0.124512	ENSG00000213234	ST13P10
ENSG00000213235	0.124581	0.0803266	0.144736	0.0909702	ENSG00000213235	EEF1A1P16
ENSG00000213236	0	0.268672	0.0812954	0.162906	ENSG00000213236	YWHAZP2
ENSG00000213237	0	0	0	0	ENSG00000213237	AC008155.1
ENSG00000213238	0	0	0	0	ENSG00000213238	AC008155.2
ENSG00000213239	0	0.333284	0.108168	0.130556	ENSG00000213239	NPM1P32
ENSG00000213240	89.2508	119.705	129.51	129.594	ENSG00000213240	AC239799.1
ENSG00000213244	0.615847	4.56913	0.782917	2.33491	ENSG00000213244	HIST2H3DP1
ENSG00000213246	35.6448	17.0418	14.6778	12.92	ENSG00000213246	SUPT4H1
ENSG00000213247	0.366437	0	0.625586	2.65692	ENSG00000213247	AL355863.1
ENSG00000213250	0.0862651	0.19961	0.190113	0.278928	ENSG00000213250	RBMS2P1
ENSG00000213252	0	0	0	0.161693	ENSG00000213252	AP001282.1
ENSG00000213253	0.460664	0.295834	0	0	ENSG00000213253	RPL12P42

ENSG00000213260	0.0955376	0.273188	0	0.207777	ENSG00000213260	YWHAZP5
ENSG00000213261	0	0	0	0	ENSG00000213261	EEF1B2P6
ENSG00000213262	0	0	0	0.0842199	ENSG00000213262	VDAC2P3
ENSG00000213264	0	0	0	0.288891	ENSG00000213264	NIP7P2
ENSG00000213265	0	0.24812	0.147382	0.931234	ENSG00000213265	TSGA13
ENSG00000213269	0.251544	0.678173	0.739109	1.64537	ENSG00000213269	AC004386.1
ENSG00000213270	0	0.142514	0.257583	0.080462	ENSG00000213270	AC090680.1
ENSG00000213272	0	0	0	0.0878285	ENSG00000213272	RPL7AP9
ENSG00000213275	0	0	0	0.467988	ENSG00000213275	IFITM9P
ENSG00000213277	1.22189	3.42514	2.18138	3.05649	ENSG00000213277	MARCKSL1P1
ENSG00000213280	0.209771	1.70413	1.72167	1.94566	ENSG00000213280	AC090114.1
ENSG00000213281	17.1604	14.2868	13.1111	11.1961	ENSG00000213281	NRAS
ENSG00000213285	0	0	3.17613	0	ENSG00000213285	RPL23AP45
ENSG00000213287	1.2375	2.36586	0.712643	2.84071	ENSG00000213287	AP001102.1
ENSG00000213290	0.147969	0	0.0862068	0.0539806	ENSG00000213290	PGK1P2
ENSG00000213291	0	0	0	0	ENSG00000213291	AC010099.1
ENSG00000213293	0.515075	1.16958	0.704394	0.648193	ENSG00000213293	AC012618.1
ENSG00000213295	0	0	0	0.253243	ENSG00000213295	AC092106.1
ENSG00000213296	0	0	0	0	ENSG00000213296	AC005521.1
ENSG00000213297	2.64957	1.79718	1.68249	1.22984	ENSG00000213297	ZNF625-ZNF20
ENSG00000213300	0	0	0	0	ENSG00000213300	HNRNPA3P6
ENSG00000213301	0	0	0.20216	0.1255	ENSG00000213301	HMGB3P11
ENSG00000213302	0	0	0	0	ENSG00000213302	AC015983.1
ENSG00000213303	0.657826	1.39419	2.08961	4.08269	ENSG00000213303	AC008481.1
ENSG00000213304	0.278885	0.133865	0.121726	1.95534	ENSG00000213304	AC008481.2
ENSG00000213305	0	0.0710029	0.128163	0.322077	ENSG00000213305	HNRNPCP6
ENSG00000213307	0	0	0	0	ENSG00000213307	AC067863.1
ENSG00000213309	0	0	0	0	ENSG00000213309	AL513043.1
ENSG00000213310	0	0	0	0	ENSG00000213310	CYCSP19
ENSG00000213312	0.161984	0.155757	0.352082	0.187742	ENSG00000213312	AL135905.1
ENSG00000213315	0	0.39191	0.747277	1.91007	ENSG00000213315	AL122020.1
ENSG00000213316	0.478876	1.31159	1.05849	0.567529	ENSG00000213316	LTC4S
ENSG00000213318	0.166527	0	0	0	ENSG00000213318	AC009078.1
ENSG00000213326	0.329134	0.629125	0.872109	0.909068	ENSG00000213326	RPS7P11
ENSG00000213328	0.0700764	0.202164	0.186388	0.0761695	ENSG00000213328	AC104117.1
ENSG00000213331	0.100919	0.0970888	0	0.109099	ENSG00000213331	AC108073.1
ENSG00000213332	0.0722621	0.137493	0	0	ENSG00000213332	SLC25A5P6
ENSG00000213333	0.337843	0.705928	0.0794901	0.716976	ENSG00000213333	NPM1P50
ENSG00000213335	0	0.095774	0.0861149	0	ENSG00000213335	CLNS1AP1
ENSG00000213337	4.80879	3.71104	3.75557	3.23268	ENSG00000213337	ANKRD39
ENSG00000213338	0.014225	0	0.0247501	0.0310757	ENSG00000213338	ATF4P1
ENSG00000213339	22.4143	32.0982	42.7048	31.4339	ENSG00000213339	QTRT1
ENSG00000213341	13.5371	8.80465	11.9794	9.68106	ENSG00000213341	CHUK
ENSG00000213343	0	0	0	0	ENSG00000213343	RPL21P18
ENSG00000213344	1.00981	1.11904	0.731985	0	ENSG00000213344	PCNPP3
ENSG00000213347	6.60575	12.3355	8.06646	8.74985	ENSG00000213347	MXD3
ENSG00000213352	0	0	0	0.133502	ENSG00000213352	GAPDHP44
ENSG00000213355	0	0	0	0	ENSG00000213355	CNN2P8
ENSG00000213356	0.34271	7.25857	7.92461	8.46544	ENSG00000213356	AC018696.6
ENSG00000213358	2.5008	5.09834	3.78064	4.68128	ENSG00000213358	AC092933.1
ENSG00000213361	1.63334	1.79049	2.15497	4.07972	ENSG00000213361	AC004884.1
ENSG00000213362	0.135116	0	0.11778	0.289827	ENSG00000213362	FTH1P12
ENSG00000213363	0.232948	0	0.404157	0.626128	ENSG00000213363	RPS3P6
ENSG00000213365	0	0	0	0	ENSG00000213365	AP000593.1

ENSG00000213366	16.33	26.7537	28.4937	38.6609	ENSG00000213366	GSTM2
ENSG00000213368	0.779077	0.225917	0.654055	0.898658	ENSG00000213368	AP002383.1
ENSG00000213370	0	0	0	0	ENSG00000213370	RANP6
ENSG00000213371	0	0.0697024	0	0.0790667	ENSG00000213371	NAP1L1P3
ENSG00000213375	23.6819	38.3478	25.3469	64.3427	ENSG00000213375	AC068279.1
ENSG00000213376	0	0	0.0541593	0	ENSG00000213376	GAPDHP71
ENSG00000213380	13.6717	14.7446	15.776	15.7614	ENSG00000213380	COG8
ENSG00000213383	0	0	0	0.0809043	ENSG00000213383	AC104297.1
ENSG00000213384	0.955223	0	0.402115	2.34927	ENSG00000213384	EIF4E2P1
ENSG00000213385	0.995653	1.33215	1.16303	0.457301	ENSG00000213385	AC105052.2
ENSG00000213386	0	0	0	0	ENSG00000213386	AC022217.1
ENSG00000213390	3.11321	8.03945	2.5471	4.99141	ENSG00000213390	ARHGAP19
ENSG00000213391	0	0	0.207445	0	ENSG00000213391	AF274858.1
ENSG00000213393	0	0	0	0	ENSG00000213393	AC091980.1
ENSG00000213394	0	0	0	0.0782794	ENSG00000213394	RPSAP46
ENSG00000213397	2.9335	6.66979	6.95396	6.84704	ENSG00000213397	HAUS7
ENSG00000213398	23.2757	32.8376	33.746	30.301	ENSG00000213398	LCAT
ENSG00000213399	0	0.37482	0.0769717	0	ENSG00000213399	AC022210.1
ENSG00000213400	0	0	0.261465	0.317727	ENSG00000213400	RPL12P18
ENSG00000213401	0.000184377	0.0786797	0.0377864	0.0984552	ENSG00000213401	MAGEA12
ENSG00000213402	1.3775	4.64228	3.36284	1.59515	ENSG00000213402	PTPRCAP
ENSG00000213403	0	0	0	0	ENSG00000213403	CISD1P1
ENSG00000213406	0.863063	0.819365	0.475305	0.775784	ENSG00000213406	ANXA2P1
ENSG00000213409	0.754751	2.24788	2.25513	1.41031	ENSG00000213409	C1QBPP2
ENSG00000213410	17.7309	36.9101	33.052	58.8625	ENSG00000213410	AC009951.2
ENSG00000213411	1.76458	4.6084	6.02879	10.5283	ENSG00000213411	RBM22P2
ENSG00000213412	34.0032	8.78747	31.9564	15.0832	ENSG00000213412	HNRNPA1P33
ENSG00000213413	1.67702	1.93129	3.479	6.04084	ENSG00000213413	PVRIG
ENSG00000213414	0.111166	0	0.0322963	0.0812351	ENSG00000213414	AC008677.1
ENSG00000213416	0	0.0276239	0.0245948	0	ENSG00000213416	KRTAP4-12
ENSG00000213417	0.194096	0.540717	0.567902	0.645066	ENSG00000213417	KRTAP2-4
ENSG00000213420	2.32569	5.27299	9.53862	7.43561	ENSG00000213420	GPC2
ENSG00000213421	0	0.0800391	0	0.451615	ENSG00000213421	AC099670.1
ENSG00000213423	0	0.113743	0.252468	0.121781	ENSG00000213423	RBMX2P2
ENSG00000213424	1.17728	0.994243	0.372475	1.31624	ENSG00000213424	KRT222
ENSG00000213430	0	0	0	0.294336	ENSG00000213430	HSPD1P1
ENSG00000213431	0	0.0494854	0.044362	2.90118	ENSG00000213431	AC080014.1
ENSG00000213432	0.166546	0.258366	0.1168	0	ENSG00000213432	RPL17P34
ENSG00000213433	0.828779	0.607583	0.992965	0.505448	ENSG00000213433	AC091982.1
ENSG00000213434	0.485281	0.185739	0.0838967	0.105418	ENSG00000213434	VTI1BP2
ENSG00000213435	0	0	0	0	ENSG00000213435	ATP6V0CP3
ENSG00000213438	0.289857	0.249076	0.174051	0.452144	ENSG00000213438	YBX2P1
ENSG00000213439	0	0.0651933	0.117815	0.0737178	ENSG00000213439	OR5AC1
ENSG00000213440	0.220032	2.31506	0.677632	1.92427	ENSG00000213440	H2AFZP1
ENSG00000213442	1.53978	0	1.01387	0	ENSG00000213442	RPL18AP3
ENSG00000213443	0.605703	2.68888	2.50135	2.95386	ENSG00000213443	AC007068.1
ENSG00000213445	28.3488	22.6883	12.6374	31.0918	ENSG00000213445	SIPA1
ENSG00000213448	0	0.192829	0	0	ENSG00000213448	RPS23P2
ENSG00000213449	0	0	0	0.201008	ENSG00000213449	GAPDHP28
ENSG00000213450	0	0.0727757	0	0.0819301	ENSG00000213450	VDAC1P7
ENSG00000213451	0	0	0	0	ENSG00000213451	OR6C69P
ENSG00000213452	0	0	0	0	ENSG00000213452	AKR1B1P2
ENSG00000213453	0.251526	0.994108	0.978095	1.22144	ENSG00000213453	FTH1P3
ENSG00000213455	0.131104	0.184117	0	0	ENSG00000213455	AC093799.1

ENSG00000213461	0	0	0	0	ENSG00000213461	AL672212.1
ENSG00000213462	26.4524	22.4009	21.0828	18.346	ENSG00000213462	ERV3-1
ENSG00000213463	12.36	8.47557	9.63685	11.8005	ENSG00000213463	SYNJ2BP
ENSG00000213465	20.2704	30.3449	22.5314	28.7144	ENSG00000213465	ARL2
ENSG00000213467	0	0	0.103117	0	ENSG00000213467	HMGB1P37
ENSG00000213470	0	0	0.430155	0	ENSG00000213470	AC073594.1
ENSG00000213471	0.131402	0.0891515	0.320621	0.202028	ENSG00000213471	TTLL13P
ENSG00000213478	0.395623	0.335511	0.72312	0.534822	ENSG00000213478	CFL1P2
ENSG00000213480	0	0.0675568	0	0	ENSG00000213480	AC093816.1
ENSG00000213483	0.540232	0.550271	0	0.461217	ENSG00000213483	NDUFAF4P2
ENSG00000213484	0.155646	0.193879	0.221765	0.109945	ENSG00000213484	EIF4A1P8
ENSG00000213486	0	0	0	0	ENSG00000213486	AC108039.1
ENSG00000213487	0	0	0	0	ENSG00000213487	ASS1P4
ENSG00000213488	0	0.144056	0	0.470052	ENSG00000213488	AC008716.1
ENSG00000213489	0.0537399	0	0	0.0586319	ENSG00000213489	AL627231.1
ENSG00000213492	0.0738104	0.111083	0.033449	0.353639	ENSG00000213492	NT5C3AP1
ENSG00000213493	0	0	0.0703203	0.13281	ENSG00000213493	ACTN4P1
ENSG00000213494	0.425875	0.810841	1.09896	0.916473	ENSG00000213494	CCL14
ENSG00000213495	0	0.355938	0.482006	0.634733	ENSG00000213495	AC012498.1
ENSG00000213498	0	0.146092	0.131905	0.162893	ENSG00000213498	TPT1P13
ENSG00000213500	0	0	0	0	ENSG00000213500	LAP3P2
ENSG00000213509	0	0.304482	0.688152	0.509051	ENSG00000213509	PPIAP16
ENSG00000213512	0.02264	0.152685	0.118204	0.132119	ENSG00000213512	GBP7
ENSG00000213513	1.03331	3.61727	2.37551	2.72903	ENSG00000213513	IMPDH1P5
ENSG00000213514	0.182029	0.386008	0.482606	0.396891	ENSG00000213514	AL731556.1
ENSG00000213516	6.99673	8.10409	4.23006	5.84715	ENSG00000213516	RBMXL1
ENSG00000213519	0	0	0.326316	0.395477	ENSG00000213519	AC132008.1
ENSG00000213522	0.126631	0.24178	0.217391	0	ENSG00000213522	RAC1P5
ENSG00000213523	19.8378	14.2668	13.1974	10.9657	ENSG00000213523	SRA1
ENSG00000213525	0	0	0	0	ENSG00000213525	AL357037.1
ENSG00000213526	0	0.649831	0.121656	1.17435	ENSG00000213526	SETP8
ENSG00000213527	0	0	0	0.266309	ENSG00000213527	AC026826.1
ENSG00000213529	0	0.40377	0	0.447184	ENSG00000213529	AL359073.1
ENSG00000213530	0	0	0	0	ENSG00000213530	MTHFD2P5
ENSG00000213533	9.98961	17.7806	12.6051	10.8612	ENSG00000213533	TMEM110
ENSG00000213536	0	0	0	0	ENSG00000213536	GNG5P1
ENSG00000213538	0.131319	0.213342	0.262784	0.645065	ENSG00000213538	KRT8P41
ENSG00000213539	0.498256	0.0599709	0.380057	0.609023	ENSG00000213539	YBX1P6
ENSG00000213540	0.465348	2.04088	2.98536	2.983	ENSG00000213540	AL359504.1
ENSG00000213542	0.49772	1.7762	2.29259	1.37294	ENSG00000213542	AC007000.1
ENSG00000213543	1.27097	0.815276	0	2.22E-05	ENSG00000213543	RARRES2P2
ENSG00000213547	0	0	0	0.0729734	ENSG00000213547	VN1R64P
ENSG00000213548	0	0	0	0	ENSG00000213548	AC005522.1
ENSG00000213549	0.288226	0.588339	0.898864	1.4043	ENSG00000213549	AC005077.1
ENSG00000213551	8.1012	12.5776	11.1045	7.78538	ENSG00000213551	DNAJC9
ENSG00000213553	0.428462	0.423499	0.280246	0.124953	ENSG00000213553	RPLP0P6
ENSG00000213556	2.65622	1.25274	0	1.36091	ENSG00000213556	AL359692.1
ENSG00000213557	0	1.06229	0.239085	0.987845	ENSG00000213557	AC068050.1
ENSG00000213558	0	0	0	0	ENSG00000213558	HMGN2P32
ENSG00000213559	0	0	0	0.0741524	ENSG00000213559	HNRNPA1P64
ENSG00000213560	0	0	0	0.281082	ENSG00000213560	AC103591.1
ENSG00000213561	0.0857516	0	0	0	ENSG00000213561	AC103591.2
ENSG00000213563	6.33716	9.75774	7.69181	4.28874	ENSG00000213563	C8orf82
ENSG00000213568	0.0647892	0	0.0563592	0.070286	ENSG00000213568	HNRNPA1P13

ENSG00000213569	0	0	0	0.13463	ENSG00000213569	AL390039.1
ENSG00000213574	0.347309	0.10915	0	0	ENSG00000213574	LDHAP5
ENSG00000213578	0.281005	0.187003	0.341734	0.544478	ENSG00000213578	CPLX3
ENSG00000213579	0	0	0	0	ENSG00000213579	AL096829.1
ENSG00000213585	135.828	106.948	79.2939	91.3035	ENSG00000213585	VDAC1
ENSG00000213587	0	0.162188	0	0	ENSG00000213587	AC126120.1
ENSG00000213588	0	0	0	0	ENSG00000213588	ZBTB9
ENSG00000213590	2.88671	5.93759	7.37289	10.1092	ENSG00000213590	AL807752.1
ENSG00000213592	0.925183	1.85205	2.04917	1.76738	ENSG00000213592	AP000662.1
ENSG00000213593	68.3776	64.4869	47.621	27.6915	ENSG00000213593	TMX2
ENSG00000213594	0.0616683	0	0	0	ENSG00000213594	GAPDHP25
ENSG00000213598	0	0.235283	0	0	ENSG00000213598	AL049873.1
ENSG00000213600	2.17109	3.04378	2.97301	2.82107	ENSG00000213600	U73169.1
ENSG00000213601	0	0.183172	0.634523	0.205578	ENSG00000213601	KRT18P19
ENSG00000213604	0	0	0	0	ENSG00000213604	AC022882.1
ENSG00000213605	1.56119	4.70777	3.8396	9.94058	ENSG00000213605	AC111200.1
ENSG00000213606	0	0	0.057632	0.0753942	ENSG00000213606	AKR1B10P1
ENSG00000213607	0.139964	0.0672975	0	0	ENSG00000213607	OR4A45P
ENSG00000213608	0.279927	1.27865	0.486458	1.14102	ENSG00000213608	SLC25A14P1
ENSG00000213609	0.0836835	0.0804402	0.0731107	0	ENSG00000213609	RPL7AP50
ENSG00000213612	0.456446	0.431039	0.246761	0.772154	ENSG00000213612	FAM220CP
ENSG00000213613	1.56824	3.75011	4.06816	5.96247	ENSG00000213613	RPL11P3
ENSG00000213614	36.9845	63.6334	60.3771	53.3695	ENSG00000213614	HEXA
ENSG00000213619	34.0178	35.9531	29.3284	26.5905	ENSG00000213619	NDUFS3
ENSG00000213620	0.281031	0.806941	0.488715	0.298657	ENSG00000213620	AL121657.1
ENSG00000213621	0.0846194	0.0763771	0.0695649	0	ENSG00000213621	RPSAP54
ENSG00000213622	54.1961	151.305	147.607	251.793	ENSG00000213622	AL163952.1
ENSG00000213625	47.0757	40.9766	40.3615	45.0445	ENSG00000213625	LEPROT
ENSG00000213626	4.40071	3.81727	2.8259	7.40321	ENSG00000213626	LBH
ENSG00000213630	0	0	0	0	ENSG00000213630	BOLA3P3
ENSG00000213638	3.6106	2.92325	2.75322	2.52477	ENSG00000213638	ADAT3
ENSG00000213639	92.2274	58.878	67.0907	54.6223	ENSG00000213639	PPP1CB
ENSG00000213640	0.145491	0.277013	0.250292	0.245429	ENSG00000213640	EEF1DP4
ENSG00000213641	0	0.502414	0.448209	0.461068	ENSG00000213641	RPL7AP4
ENSG00000213642	0.122024	0	0	0	ENSG00000213642	AC016769.1
ENSG00000213643	0	0	0	0	ENSG00000213643	VN1R37P
ENSG00000213644	0	0	0	0.118244	ENSG00000213644	SAPCD2P1
ENSG00000213645	0	0	0	0.25266	ENSG00000213645	SLC25A1P3
ENSG00000213648	5.88132	6.92194	10.3439	6.40991	ENSG00000213648	SULT1A4
ENSG00000213650	0	0	0	0	ENSG00000213650	AC092447.2
ENSG00000213652	0.117663	0.340032	0.101981	0.382208	ENSG00000213652	HMGB3P30
ENSG00000213653	0	0	0	0	ENSG00000213653	RPL22P22
ENSG00000213654	0.26308	0.0707527	0.25712	0.0988522	ENSG00000213654	GPSM3
ENSG00000213655	0	0	0	0	ENSG00000213655	AC010493.1
ENSG00000213657	1.84605	0	0.202938	0	ENSG00000213657	RPL31P44
ENSG00000213658	4.35781	7.19294	7.15968	9.99703	ENSG00000213658	LAT
ENSG00000213659	0	0	0.200135	2.66757	ENSG00000213659	RSU1P3
ENSG00000213661	0	0	0	0	ENSG00000213661	AC106806.1
ENSG00000213663	0	0.156526	0.282594	0	ENSG00000213663	AC010409.1
ENSG00000213664	0	0	0	0	ENSG00000213664	AC026254.1
ENSG00000213667	0	0	0	0	ENSG00000213667	PGGT1BP1
ENSG00000213669	0.507468	0.486113	0.438791	0.540788	ENSG00000213669	AL137074.1
ENSG00000213671	0.833647	2.2079	1.7499	2.92533	ENSG00000213671	OLA1P2
ENSG00000213672	10.2606	10.8562	10.3683	7.90893	ENSG00000213672	NCKIPSD

ENSG00000213673	0	0	0.062486	0	ENSG00000213673	SLC25A5P3
ENSG00000213676	3.20544	7.03579	8.63326	18.3188	ENSG00000213676	ATF6B
ENSG00000213683	0	0	0	0.127944	ENSG00000213683	AC002056.1
ENSG00000213684	0	0.0295675	0.0267153	0.0670593	ENSG00000213684	LDHBP2
ENSG00000213686	0	0.0960097	0.00943135	0.0837891	ENSG00000213686	DUSP8P1
ENSG00000213689	4.07201	8.61077	3.8988	2.52452	ENSG00000213689	TREX1
ENSG00000213690	2.80961	0.904549	0.135555	1.66985	ENSG00000213690	AL360271.1
ENSG00000213693	1.02982	1.35445	1.94391	1.85087	ENSG00000213693	SEC14L1P1
ENSG00000213694	1.55567	3.81141	2.22277	5.74871	ENSG00000213694	S1PR3
ENSG00000213695	0.245394	0	0	0	ENSG00000213695	RPS7P14
ENSG00000213697	0	0	0	0	ENSG00000213697	CTBP2P6
ENSG00000213698	0	0	0	0	ENSG00000213698	AC240504.1
ENSG00000213699	35.7768	40.7922	46.6963	20.9071	ENSG00000213699	SLC35F6
ENSG00000213700	2.0587	2.10122	1.68729	3.26115	ENSG00000213700	RPL17P50
ENSG00000213701	0.0720021	0	0.0570035	0.07197	ENSG00000213701	SETP22
ENSG00000213702	0	0	0.132656	0	ENSG00000213702	AC008865.1
ENSG00000213703	0.627768	1.40418	1.39331	3.59301	ENSG00000213703	AL138847.1
ENSG00000213704	0.0416632	0.0800982	0.0737115	0.0929927	ENSG00000213704	EEF1A1P15
ENSG00000213706	0.143927	0.550827	0.266826	1.14504	ENSG00000213706	AL590762.2
ENSG00000213707	0.824788	0.680296	0.578802	1.33858	ENSG00000213707	HMGB1P10
ENSG00000213708	0	0	0	0	ENSG00000213708	SLC16A14P1
ENSG00000213711	0	0	0	0	ENSG00000213711	PHBP7
ENSG00000213713	8.66323	6.92077	8.94211	7.83512	ENSG00000213713	PIGCP1
ENSG00000213714	0.315006	0	0.915524	1.07515	ENSG00000213714	FAM209B
ENSG00000213716	0.62597	0.598479	1.08098	0.663008	ENSG00000213716	FABP5P5
ENSG00000213717	0	0	0	0.206805	ENSG00000213717	AC004692.1
ENSG00000213719	47.8587	52.6287	21.8263	21.5159	ENSG00000213719	CLIC1
ENSG00000213721	0.532086	3.14563	1.38218	3.40085	ENSG00000213721	HMGN2P30
ENSG00000213722	0.807257	0.391885	0.745312	0.052533	ENSG00000213722	DDAH2
ENSG00000213724	1.87727	2.6875	3.8069	5.21586	ENSG00000213724	PRDX2P2
ENSG00000213726	0	0	0	0.0961835	ENSG00000213726	RPS2P52
ENSG00000213727	0.262094	0.0704375	0	0	ENSG00000213727	AP000533.1
ENSG00000213729	0	0	0.158991	0	ENSG00000213729	AC098828.1
ENSG00000213730	0	0	0	0	ENSG00000213730	POLD2P1
ENSG00000213731	3.21293	5.51587	5.45359	9.69379	ENSG00000213731	RAB5CP1
ENSG00000213735	0.264724	1.14937	0.683722	1.41463	ENSG00000213735	ANAPC10P1
ENSG00000213736	0	0	0	0	ENSG00000213736	AC026310.1
ENSG00000213739	0	0	0	0	ENSG00000213739	AC007679.1
ENSG00000213740	0.0588153	0	0.0519879	0.251253	ENSG00000213740	SERBP1P1
ENSG00000213741	1069.74	770.182	488.479	285.69	ENSG00000213741	RPS29
ENSG00000213744	0	0	0	0	ENSG00000213744	RPS10P14
ENSG00000213747	0	0	0	0	ENSG00000213747	AL627390.1
ENSG00000213750	0	0	0	0	ENSG00000213750	AP002982.1
ENSG00000213752	0	0	0	0	ENSG00000213752	AL008718.1
ENSG00000213753	12.0669	8.59759	12.5142	7.6011	ENSG00000213753	CENPBD1P1
ENSG00000213754	0.166418	0.158095	0.216521	0.318005	ENSG00000213754	AL356317.1
ENSG00000213755	0.635182	2.28079	1.6744	1.01578	ENSG00000213755	AC093270.1
ENSG00000213757	0.437407	0.171842	0.487065	0.393612	ENSG00000213757	AC020898.1
ENSG00000213759	0.132035	0.337703	0.185829	0.53282	ENSG00000213759	UGT2B11
ENSG00000213760	0.267188	0.770878	0.54688	0.175607	ENSG00000213760	ATP6V1G2
ENSG00000213761	1.70854	4.78555	3.9685	1.04991	ENSG00000213761	MT1P1
ENSG00000213762	12.7821	12.3232	15.3558	9.55507	ENSG00000213762	ZNF134
ENSG00000213763	0.0541883	0.0522689	0	0	ENSG00000213763	ACTBP2

ENSG00000213770	0	0	0	0	ENSG00000213770	FAM210CP
ENSG00000213771	0.041371	0	0	0	ENSG00000213771	KRT8P37
ENSG00000213772	1.99521	3.07852	1.26109	5.02197	ENSG00000213772	EIF1P7
ENSG00000213774	0	0	0	0	ENSG00000213774	AC010904.1
ENSG00000213777	0.749185	1.05621	1.02316	1.21769	ENSG00000213777	AC011487.1
ENSG00000213778	0.323036	0.187022	0.225715	0.72138	ENSG00000213778	HNRNPA1P32
ENSG00000213779	0.356501	0.67168	0.887388	1.2341	ENSG00000213779	AC107956.2
ENSG00000213780	2.42888	0.280746	2.20319	2.06375	ENSG00000213780	GTF2H4
ENSG00000213781	0	0	0	0.217863	ENSG00000213781	PSMC1P2
ENSG00000213782	45.6472	32.1249	29.3376	28.116	ENSG00000213782	DDX47
ENSG00000213783	0	0	0	0	ENSG00000213783	RPL35P4
ENSG00000213785	0.120957	0.11607	0.104816	0	ENSG00000213785	AKR1B1P3
ENSG00000213786	0.171961	0.331133	0.747118	0.73251	ENSG00000213786	NHP2P2
ENSG00000213787	0	0	0.070872	0	ENSG00000213787	AC073472.1
ENSG00000213790	0.0555412	0.0541928	0.0958004	0.281774	ENSG00000213790	OLA1P1
ENSG00000213791	0	0	0	0	ENSG00000213791	AC104212.1
ENSG00000213798	0	0.313384	0.212607	0.0884234	ENSG00000213798	AC004129.1
ENSG00000213799	10.0557	9.58054	7.27714	4.78035	ENSG00000213799	ZNF845
ENSG00000213801	2.97359	5.10757	0.00116031	0.000756808	ENSG00000213801	ZNF321P
ENSG00000213809	2.2794	3.60799	5.68921	4.50526	ENSG00000213809	KLRK1
ENSG00000213816	0.351081	2.19E-07	0	2.41E-06	ENSG00000213816	CNN2P4
ENSG00000213820	0	0	0	0	ENSG00000213820	RPL13P2
ENSG00000213822	0	0.0962869	0	0.109211	ENSG00000213822	AC020914.1
ENSG00000213828	0	0.841373	3.38918	4.07631	ENSG00000213828	AC017028.1
ENSG00000213830	0.151135	0.469027	0.481014	0.242542	ENSG00000213830	CFL1P5
ENSG00000213839	8.9147	8.84441	10.3921	8.71561	ENSG00000213839	TMX2P1
ENSG00000213842	0.570316	0.550544	1.6396	1.45899	ENSG00000213842	SUGT1P2
ENSG00000213846	0.113856	1.19769	0.199854	1.03771	ENSG00000213846	AC098614.1
ENSG00000213849	0.241636	0	0.41782	0.254699	ENSG00000213849	AC104306.1
ENSG00000213851	0	0	0.122685	0	ENSG00000213851	AC098590.1
ENSG00000213853	27.972	56.7537	30.8907	35.0922	ENSG00000213853	EMP2
ENSG00000213854	0	0.067442	0.0608891	0.0763323	ENSG00000213854	CNN2P6
ENSG00000213856	0	0	0	0	ENSG00000213856	VDAC1P2
ENSG00000213857	0	0	0	0	ENSG00000213857	AL080243.1
ENSG00000213859	17.1331	5.49471	12.9821	6.74677	ENSG00000213859	KCTD11
ENSG00000213860	206.337	134.831	64.7586	43.9264	ENSG00000213860	RPL21P75
ENSG00000213862	0.0852563	0.251257	0.148606	0.493781	ENSG00000213862	AC044787.1
ENSG00000213864	0	0	0	0	ENSG00000213864	EEF1B2P2
ENSG00000213865	5.60175	8.98822	10.4266	15.6268	ENSG00000213865	C8orf44
ENSG00000213866	0	0.0705994	0.12727	0	ENSG00000213866	YBX1P10
ENSG00000213867	0	0	0	0	ENSG00000213867	AL049830.1
ENSG00000213871	0.451725	2.04072	1.93002	1.21012	ENSG00000213871	TAF9BP1
ENSG00000213872	2.06402	2.41017	3.22599	1.84291	ENSG00000213872	AC092798.1
ENSG00000213873	0	0	0.129204	0	ENSG00000213873	AC060775.1
ENSG00000213875	0	0	0	0	ENSG00000213875	AC005019.1
ENSG00000213876	0	0	0	0	ENSG00000213876	AC120057.1
ENSG00000213877	0	0	0	0	ENSG00000213877	CFL1P7
ENSG00000213880	0.0488289	0	0	0	ENSG00000213880	AL645939.1
ENSG00000213881	0.26275	0.246161	0.333707	0	ENSG00000213881	NPM1P6
ENSG00000213882	0	0	0	0	ENSG00000213882	CYB5AP4
ENSG00000213885	0.325164	0.392291	0	0	ENSG00000213885	RPL13AP7
ENSG00000213886	0	0	0.0486607	0.244023	ENSG00000213886	UBD
ENSG00000213888	2.15541	3.52871	4.14616	6.44661	ENSG00000213888	LINC01521
ENSG00000213889	2.71613	3.02533	3.14049	3.4283	ENSG00000213889	PPM1N

ENSG00000213891	0.650956	2.05821	1.98993	3.47075	ENSG00000213891	RPL3P6
ENSG00000213892	0	0.259378	0.507751	0.319299	ENSG00000213892	CEACAM16
ENSG00000213896	0	0	0.411238	0.251416	ENSG00000213896	AC109486.1
ENSG00000213900	0	0	0	0	ENSG00000213900	AL645927.1
ENSG00000213901	2.73021	3.39558	6.36286	3.67785	ENSG00000213901	SLC23A3
ENSG00000213903	7.03541	30.6651	20.5624	8.2347	ENSG00000213903	LTB4R
ENSG00000213906	6.30246	29.9333	13.9992	6.91317	ENSG00000213906	LTB4R2
ENSG00000213908	0	0.152165	0.137477	0.0858531	ENSG00000213908	CYP2A7P1
ENSG00000213911	0	0	0	0	ENSG00000213911	AL645937.2
ENSG00000213916	0	0	0	0	ENSG00000213916	AL662890.1
ENSG00000213917	0	0	0.0687729	0	ENSG00000213917	RPL5P8
ENSG00000213918	11.924	16.9754	21.6698	20.362	ENSG00000213918	DNASE1
ENSG00000213920	5.07004	5.92757	7.60823	5.3917	ENSG00000213920	MDP1
ENSG00000213921	0	0	0	0	ENSG00000213921	LEUTX
ENSG00000213922	0.167533	0.160495	0	0	ENSG00000213922	AC011500.1
ENSG00000213923	240.318	257.701	208.181	205.858	ENSG00000213923	CSNK1E
ENSG00000213924	0.0246944	0.0237861	0.0214882	0.0269685	ENSG00000213924	HNRNPH1P2
ENSG00000213925	0	0	0.433835	0	ENSG00000213925	NPM1P33
ENSG00000213926	0	0	0	0	ENSG00000213926	MSRB1P1
ENSG00000213927	1.26182	0.901541	1.23878	1.25446	ENSG00000213927	CCL27
ENSG00000213928	63.2687	125.226	85.0502	83.9768	ENSG00000213928	IRF9
ENSG00000213930	22.9707	31.8313	22.0367	25.8455	ENSG00000213930	GALT
ENSG00000213931	0.490013	0.959971	0.890146	0.964691	ENSG00000213931	HBE1
ENSG00000213934	0	0	0	0	ENSG00000213934	HBG1
ENSG00000213935	0.283959	0.725229	0.646713	0.801765	ENSG00000213935	AC092610.1
ENSG00000213937	0.274362	0.105772	0.239937	0.213802	ENSG00000213937	CLDN9
ENSG00000213938	0	0	0	0	ENSG00000213938	SEPHS1P6
ENSG00000213939	0	0.450276	1.21702	0.735369	ENSG00000213939	AC091153.1
ENSG00000213940	0	0.54501	0	0	ENSG00000213940	AC026477.1
ENSG00000213942	1.19138	1.0494	0.609101	0.745424	ENSG00000213942	AC005840.1
ENSG00000213943	0.14001	0	0	0	ENSG00000213943	KRT18P17
ENSG00000213946	0	0	0	0	ENSG00000213946	DNAJB1P1
ENSG00000213949	6.21952	17.3557	6.91769	29.0156	ENSG00000213949	ITGA1
ENSG00000213950	0.620416	0.445352	0.403755	0.332164	ENSG00000213950	RPS10P2
ENSG00000213953	17.3659	25.7118	30.5309	46.943	ENSG00000213953	AC018867.1
ENSG00000213954	0	0	0.274146	0	ENSG00000213954	ATP5HP3
ENSG00000213956	0	0	0	0	ENSG00000213956	AC112187.1
ENSG00000213958	0.0968185	0.23399	0.0824609	0.259439	ENSG00000213958	KRT18P29
ENSG00000213959	0.256181	0.983294	0.923066	0	ENSG00000213959	AL035419.1
ENSG00000213962	0.0777947	0.0747454	0.101701	0.0851459	ENSG00000213962	API5P2
ENSG00000213964	0.901703	0.300104	1.4683	2.61593	ENSG00000213964	CHCHD4P4
ENSG00000213965	15.7924	10.7757	13.4343	11.447	ENSG00000213965	NUDT19
ENSG00000213967	9.28468	19.1124	15.7549	25.3395	ENSG00000213967	ZNF726
ENSG00000213970	3.41224	3.21879	4.64762	1.76151	ENSG00000213970	AC006122.1
ENSG00000213972	0	0.195072	0.236774	0.456555	ENSG00000213972	AL024509.1
ENSG00000213973	0	0.019894	0	0	ENSG00000213973	ZNF99
ENSG00000213976	0.81798	0.671468	0.643331	0.719463	ENSG00000213976	AC010615.1
ENSG00000213977	60.9466	55.6609	54.6996	34.731	ENSG00000213977	TAX1BP3
ENSG00000213979	0.187743	0.0776168	0.0701401	0	ENSG00000213979	RPL7AP14
ENSG00000213983	80.469	105.944	95.0781	73.012	ENSG00000213983	AP1G2
ENSG00000213985	0	0	0	0	ENSG00000213985	AC078899.1
ENSG00000213987	0	0	0.278304	1.01712	ENSG00000213987	AC093151.1
ENSG00000213988	5.17927	14.0658	11.9108	17.8297	ENSG00000213988	ZNF90

ENSG00000213995	16.3855	20.5062	20.1909	13.105	ENSG00000213995	NAXD
ENSG00000213996	0	0.0598787	0.100712	0.963849	ENSG00000213996	TM6SF2
ENSG00000213997	1.5384	1.37814	0.389887	1.83891	ENSG00000213997	PGAM1P7
ENSG00000213999	0.994122	1.56378	1.77077	1.19928	ENSG00000213999	MEF2B
ENSG00000214003	0.208413	0.343151	0.451989	0.899672	ENSG00000214003	ATP5F1P3
ENSG00000214006	9.4863	21.9469	30.5499	36.3026	ENSG00000214006	AL353671.4
ENSG00000214009	0	0	0	0	ENSG00000214009	PCNAP3
ENSG00000214012	0	0	0	0	ENSG00000214012	KRT18P38
ENSG00000214013	40.4249	45.2665	41.9026	36.844	ENSG00000214013	GANC
ENSG00000214015	0	0	0	0	ENSG00000214015	RPL32P23
ENSG00000214016	0	0	0	0	ENSG00000214016	RPSAP61
ENSG00000214018	0.155111	0.51009	0.508652	0.115351	ENSG00000214018	RRM2P3
ENSG00000214019	0	0.106208	0.0637651	0.0802607	ENSG00000214019	AL034370.1
ENSG00000214020	0	0	0	0.165783	ENSG00000214020	FTLP4
ENSG00000214021	17.8088	32.8226	36.1251	36.0858	ENSG00000214021	TTLL3
ENSG00000214022	20.8799	14.2317	21.9181	15.122	ENSG00000214022	REPIN1
ENSG00000214024	0	0	0	0	ENSG00000214024	RPL23AP29
ENSG00000214025	0	0	0	0	ENSG00000214025	ATP5F1P4
ENSG00000214026	32.4114	47.5526	25.8827	25.4246	ENSG00000214026	MRPL23
ENSG00000214027	0	0.134199	0	0	ENSG00000214027	ARPC3P5
ENSG00000214029	1.2988	2.19738	2.13763	3.45767	ENSG00000214029	ZNF891
ENSG00000214031	4.18206	11.3639	9.46551	17.4112	ENSG00000214031	AC092474.1
ENSG00000214035	0	0	0.0517829	0	ENSG00000214035	AC073310.1
ENSG00000214041	0.359184	0.898255	0.624004	0.19023	ENSG00000214041	PGAM1P4
ENSG00000214042	0.179648	0.087386	0.235159	0.499586	ENSG00000214042	IFNA7
ENSG00000214045	0	0	0	0	ENSG00000214045	AC091807.1
ENSG00000214046	48.3138	60.9641	50.3402	50.3762	ENSG00000214046	SMIM7
ENSG00000214047	0	0	0	0	ENSG00000214047	RPS11P7
ENSG00000214050	7.58281	12.5283	11.4526	13.6607	ENSG00000214050	FBXO16
ENSG00000214051	0	0	0	0	ENSG00000214051	ARF4P3
ENSG00000214062	0.460297	0.445168	0.398782	0.596391	ENSG00000214062	RPL7P17
ENSG00000214063	47.8376	99.686	43.3422	44.5915	ENSG00000214063	TSPAN4
ENSG00000214064	0	0	0	0	ENSG00000214064	RPL6P5
ENSG00000214067	0.335067	0.641979	1.01401	0.894991	ENSG00000214067	AL360182.1
ENSG00000214070	0.0600233	0.231025	0.365378	0.130791	ENSG00000214070	AC011999.1
ENSG00000214071	0	0	0	0	ENSG00000214071	BX842568.1
ENSG00000214073	0.208492	0	0	0	ENSG00000214073	RPL21P17
ENSG00000214074	0	0.400502	0.18081	0.221859	ENSG00000214074	RPL23AP39
ENSG00000214076	0	0.0280394	0.02533	0.0640365	ENSG00000214076	CPSF1P1
ENSG00000214077	0	0	0	0	ENSG00000214077	GNAQP1
ENSG00000214078	60.5126	79.6944	96.1803	68.3036	ENSG00000214078	CPNE1
ENSG00000214081	0.533288	0.531963	0.503393	0.311473	ENSG00000214081	CYP4F30P
ENSG00000214087	14.8556	15.782	13.5788	12.9647	ENSG00000214087	ARL16
ENSG00000214089	0	0.144039	0	0.160464	ENSG00000214089	RPL9P21
ENSG00000214093	0.347524	0.665475	0.312236	1.6675	ENSG00000214093	AL096701.1
ENSG00000214097	1.35549	3.0548	2.73349	4.74027	ENSG00000214097	SMCO1
ENSG00000214100	0	0	0	0	ENSG00000214100	PLAC9P1
ENSG00000214102	0.0178741	0.331303	0.241532	0.247742	ENSG00000214102	WEE2
ENSG00000214106	3.21713	4.78832	5.34838	6.66324	ENSG00000214106	PAXIP1-AS2
ENSG00000214107	0	0.0645518	0.0875302	0.100008	ENSG00000214107	MAGEB1
ENSG00000214108	0.286756	1.37645	0.621119	1.84141	ENSG00000214108	TPT1P5
ENSG00000214109	11.4862	31.0958	31.3977	50.7655	ENSG00000214109	AC008686.1
ENSG00000214110	0.569029	0.318829	0.62857	0.692667	ENSG00000214110	LDHAP4
ENSG00000214111	0.0975511	0	0	0	ENSG00000214111	AC002504.1

ENSG00000214113	20.7062	21.3671	18.8191	21.8159	ENSG00000214113	LYRM4
ENSG00000214114	18.4878	11.26	8.41839	10.382	ENSG00000214114	MYCBP
ENSG00000214121	0.23808	0.228409	0.413046	0.383735	ENSG00000214121	PRDX1P1
ENSG00000214124	0	0.512685	0.457612	1.10322	ENSG00000214124	SNRPEP9
ENSG00000214125	0	0	0.0863517	0	ENSG00000214125	AC005005.1
ENSG00000214128	1.92274	3.40124	3.23797	5.36647	ENSG00000214128	TMEM213
ENSG00000214132	0	0.169671	0	0.390486	ENSG00000214132	AC094103.1
ENSG00000214135	26.8148	39.9154	40.8451	48.0822	ENSG00000214135	AC132008.2
ENSG00000214140	4.67007	6.01816	5.67978	3.826	ENSG00000214140	PRCD
ENSG00000214141	0	0	0	0	ENSG00000214141	ACTN4P2
ENSG00000214142	0.0901826	0.0866267	0	0	ENSG00000214142	RPL7P60
ENSG00000214144	0.0291247	0.0561538	0.101701	0.159719	ENSG00000214144	AL390728.1
ENSG00000214147	0.148727	0.047594	0.215086	0.269939	ENSG00000214147	AC092952.1
ENSG00000214160	27.703	28.5299	22.3724	14.4711	ENSG00000214160	ALG3
ENSG00000214161	0	0	0	0	ENSG00000214161	SDC4P
ENSG00000214164	2.26596	8.07216	1.58971	1.11849	ENSG00000214164	AC08696.5
ENSG00000214167	0	0	0	0.109666	ENSG00000214167	AC005544.1
ENSG00000214174	0.733186	2.85768	0.883477	1.32858	ENSG00000214174	AMZ2P1
ENSG00000214176	38.9532	40.364	52.6071	39.5758	ENSG00000214176	PLEKHM1P1
ENSG00000214178	0	0	0	0	ENSG00000214178	PPIAP23
ENSG00000214179	0	0	0	0	ENSG00000214179	AC112200.1
ENSG00000214181	0	0.0387188	0.0350902	0.0883539	ENSG00000214181	DDX6P2
ENSG00000214182	0.411006	0.345773	0.15422	1.01768	ENSG00000214182	PTMAP5
ENSG00000214185	0.0244215	0.117713	0.0847972	0.080436	ENSG00000214185	XPOTP1
ENSG00000214188	4.80744	13.7019	8.39738	17.7718	ENSG00000214188	ST7-OT4
ENSG00000214189	7.52373	14.8079	12.228	18.4506	ENSG00000214189	ZNF788
ENSG00000214190	0.353321	2.21247	0.828636	1.6464	ENSG00000214190	RNF152P1
ENSG00000214192	0.223656	0	0.20547	0.239204	ENSG00000214192	UBE2V1P2
ENSG00000214193	30.8107	28.7759	38.1192	27.4259	ENSG00000214193	SH3D21
ENSG00000214194	27.4169	24.8639	20.1725	14.2631	ENSG00000214194	SMIM30
ENSG00000214195	0	0	0	0	ENSG00000214195	HMGN2P31
ENSG00000214198	0.702242	1.35529	0.722193	1.37762	ENSG00000214198	TTC41P
ENSG00000214199	0.223465	0.258532	0.311861	0.0490889	ENSG00000214199	EEF1A1P12
ENSG00000214200	0	0	0	0	ENSG00000214200	TPM3P2
ENSG00000214203	0.165487	0.398803	0.28835	0.627309	ENSG00000214203	RPS4XP1
ENSG00000214204	0	0	0	0	ENSG00000214204	HNRNPA1P43
ENSG00000214207	0	0	0	0	ENSG00000214207	KRT18P10
ENSG00000214210	1.37762	2.77795	1.98815	6.59007	ENSG00000214210	AC084017.1
ENSG00000214211	0	0	0	0.0563078	ENSG00000214211	CTAGE14P
ENSG00000214212	0.207376	0.154156	0.177951	0.332191	ENSG00000214212	C19orf38
ENSG00000214215	0.0307565	0.123472	0.0892997	0.337536	ENSG00000214215	C12orf74
ENSG00000214216	0.292833	0.644432	0.598855	1.15892	ENSG00000214216	IQCJ
ENSG00000214222	0	0	0	0.225311	ENSG00000214222	TUBBP2
ENSG00000214223	0.173261	0.468645	0.266641	1.29695	ENSG00000214223	HNRNPA1P10
ENSG00000214226	1.41762	3.01382	4.2072	2.66981	ENSG00000214226	C17orf67
ENSG00000214237	0.235996	0.151246	0.136646	0	ENSG00000214237	MINDY4B
ENSG00000214239	10.5661	0	0	13.8419	ENSG00000214239	AL591025.1
ENSG00000214243	2.01742	2.17499	2.19856	2.09766	ENSG00000214243	AC004980.2
ENSG00000214244	0.071283	0.0685572	0.0620693	0	ENSG00000214244	SETP21
ENSG00000214245	0.108776	0	0	0	ENSG00000214245	PUDPP3
ENSG00000214248	2.0014	3.41258	3.61489	3.87078	ENSG00000214248	AC010336.1
ENSG00000214249	0.0247549	0	0.0210346	0	ENSG00000214249	CTAGE11P
ENSG00000214252	0	0	0	0	ENSG00000214252	AZGP1P2
ENSG00000214253	61.795	44.7048	43.454	39.7506	ENSG00000214253	FIS1

ENSG00000214254	0	0	0	0.430124	ENSG00000214254	AC136896.1
ENSG00000214255	0	0	0	0	ENSG00000214255	AC091305.1
ENSG00000214259	0	0	0.178597	0.110945	ENSG00000214259	AC018695.1
ENSG00000214262	0.344315	0.243125	0.725281	0.369899	ENSG00000214262	ANKRD36BP1
ENSG00000214263	0.62018	0	0	0.433204	ENSG00000214263	RPSAP53
ENSG00000214264	0.0545201	0.0545452	0.196049	0.183804	ENSG00000214264	KCTD9P4
ENSG00000214265	4.88217	7.26765	10.5027	10.5218	ENSG00000214265	AC124312.1
ENSG00000214266	0	0.0703168	0.190618	0	ENSG00000214266	STARP1
ENSG00000214268	0	0	0	0	ENSG00000214268	AF228730.1
ENSG00000214269	0	0.0453088	0	0	ENSG00000214269	LGMNP1
ENSG00000214273	0.242314	0.248497	0.437108	0.169862	ENSG00000214273	AGGF1P1
ENSG00000214274	1.33212	6.03601	3.15674	1.44594	ENSG00000214274	ANG
ENSG00000214278	0.0809519	0.345066	0.352826	2.49871	ENSG00000214278	AC010442.1
ENSG00000214279	3.93897	7.1309	4.78005	8.12802	ENSG00000214279	SCART1
ENSG00000214280	0.118371	0.230306	0.435177	0.884478	ENSG00000214280	AC046134.1
ENSG00000214281	0	0	0	0	ENSG00000214281	HMGN2P39
ENSG00000214282	0.040655	0.469472	0	0.76251	ENSG00000214282	KRT8P14
ENSG00000214283	0.55995	2.40389	2.41573	3.41454	ENSG00000214283	RAD51AP1P1
ENSG00000214285	0	0	0.264967	0	ENSG00000214285	NPS
ENSG00000214286	0	0	0	0	ENSG00000214286	PDCL3P3
ENSG00000214288	0	0	0	0	ENSG00000214288	HMGB3P13
ENSG00000214289	1.4905	2.76867	1.2084	1.70042	ENSG00000214289	RPL39P5
ENSG00000214290	0.0781907	0.0751684	0	0.150035	ENSG00000214290	COLCA2
ENSG00000214295	0	0.0365419	0.165158	0.207669	ENSG00000214295	FOXO1B
ENSG00000214297	0	0.0545229	0.0492575	0.370376	ENSG00000214297	ALDOAP2
ENSG00000214298	0	0	0	0	ENSG00000214298	MRPS21P6
ENSG00000214300	2.59076	7.47742	7.30483	12.3395	ENSG00000214300	SPDYE3
ENSG00000214301	0.0992213	0.095337	0.0861149	0	ENSG00000214301	AC022296.1
ENSG00000214305	9.45519	18.7672	27.4074	36.5031	ENSG00000214305	AP001024.1
ENSG00000214306	16.8022	33.046	32.5022	57.6474	ENSG00000214306	AP001024.2
ENSG00000214309	1.49624	1.35309	1.66504	1.42284	ENSG00000214309	MBLAC1
ENSG00000214313	1.41244	1.51921	1.44852	0.243177	ENSG00000214313	AZGP1P1
ENSG00000214314	0	0	0	0	ENSG00000214314	AC073063.1
ENSG00000214318	17.8561	18.4377	20.7463	17.9172	ENSG00000214318	ATP5G1P6
ENSG00000214319	0	0.0543666	0	0	ENSG00000214319	CXADRP1
ENSG00000214321	0	0.504498	0	0.554649	ENSG00000214321	CBX1P4
ENSG00000214322	0	0	0	0	ENSG00000214322	CBX1P2
ENSG00000214324	0	0	0.086159	0.0852879	ENSG00000214324	C3orf56
ENSG00000214325	0.696952	0.667336	0.768427	1.54445	ENSG00000214325	AC025287.1
ENSG00000214326	0	0	0.4004	0.413629	ENSG00000214326	RPL31P1
ENSG00000214329	0	0	0	0	ENSG00000214329	SLC9B1P2
ENSG00000214330	0.959889	1.12136	1.43941	0.793546	ENSG00000214330	ABCD1P5
ENSG00000214331	10.689	15.7439	17.5512	23.4457	ENSG00000214331	AC009053.1
ENSG00000214335	0.0925173	0.0445452	0.0528517	0.232108	ENSG00000214335	CTAGE16P
ENSG00000214338	0.648419	0.481296	0.758568	2.00182	ENSG00000214338	SOGA3
ENSG00000214342	0.106242	0	0	0	ENSG00000214342	ATP5F1P2
ENSG00000214344	0.380533	0.536685	0.607827	0.644102	ENSG00000214344	OR4F13P
ENSG00000214351	0	0.135874	0.0613846	0.307099	ENSG00000214351	OR1X5P
ENSG00000214354	0.344722	0.321066	0	2.59796	ENSG00000214354	AC133644.1
ENSG00000214357	1.1547	3.83187	0.512162	0.984194	ENSG00000214357	NEURL1B
ENSG00000214359	0.684201	1.19824	1.30345	1.02666	ENSG00000214359	RPL18P10
ENSG00000214360	0.191184	0.0918558	0.248921	0.516728	ENSG00000214360	EFCAB9
ENSG00000214362	0	0	0	0	ENSG00000214362	RPS3AP36
ENSG00000214366	0	0	0	0	ENSG00000214366	EIF4EP5

ENSG00000214367	5.68812	8.1257	8.71028	8.85391	ENSG00000214367	HAUS3
ENSG00000214369	2.15807	4.84126	6.66208	8.85021	ENSG00000214369	AC009967.1
ENSG00000214374	0.561264	0	0	0	ENSG00000214374	AL133267.1
ENSG00000214376	0.44726	0.542355	0.432486	0.919659	ENSG00000214376	VSTM5
ENSG00000214380	0	0.110449	0	0.134979	ENSG00000214380	AC068781.1
ENSG00000214389	1.27075	1.48413	1.66525	1.53828	ENSG00000214389	RPS3AP26
ENSG00000214391	0.0384111	0.0727135	0	0	ENSG00000214391	TUBAP2
ENSG00000214397	0	0.195886	0	0	ENSG00000214397	DKFZP779J2370
ENSG00000214402	1.19994	1.68601	1.69904	3.6959	ENSG00000214402	LCNL1
ENSG00000214405	0.269414	0.129248	0	1.15556	ENSG00000214405	RAP1BP2
ENSG00000214413	11.4645	27.0971	20.0909	20.1568	ENSG00000214413	BBIP1
ENSG00000214414	0	0	0	0	ENSG00000214414	TRIM77
ENSG00000214415	0.311463	0.249852	0.104343	0.169977	ENSG00000214415	GNAT3
ENSG00000214417	0	0	0	0	ENSG00000214417	KRT18P13
ENSG00000214424	0	0	0	0	ENSG00000214424	FAM149B1P1
ENSG00000214425	5.36884	11.3955	13.75	9.19714	ENSG00000214425	LRRC37A4P
ENSG00000214428	0.0735333	0.141429	0.0761268	0.0827713	ENSG00000214428	NPM1P10
ENSG00000214429	0	0	0	0	ENSG00000214429	CYCSP6
ENSG00000214433	0	0.0804882	0.480231	0.365714	ENSG00000214433	GOLGA2P8
ENSG00000214434	0.429957	1.15665	0.424977	1.9445	ENSG00000214434	NIFKP1
ENSG00000214435	4.68727	6.26155	4.64169	8.43435	ENSG00000214435	AS3MT
ENSG00000214439	2.28925	3.68036	4.26568	3.32559	ENSG00000214439	FAM185BP
ENSG00000214447	0.308925	0.231792	0.233999	0.150316	ENSG00000214447	FAM187A
ENSG00000214455	9.06717	20.308	24.4631	22.2887	ENSG00000214455	RCN1P2
ENSG00000214456	2.91505	7.51894	6.44482	9.4245	ENSG00000214456	PLIN5
ENSG00000214457	0.0917242	0.175343	0.079198	0.987129	ENSG00000214457	RPL7P29
ENSG00000214460	0	0.141342	0	0	ENSG00000214460	TPT1P6
ENSG00000214465	0.0984391	0.0472792	0.0855674	0	ENSG00000214465	SMARCE1P6
ENSG00000214479	9.43476	82.5495	55.1522	103.188	ENSG00000214479	AL139333.1
ENSG00000214484	0	0	0.0630965	0	ENSG00000214484	RPSAP28
ENSG00000214485	0.630833	0.313785	0.535794	0	ENSG00000214485	RPL7P1
ENSG00000214487	0.329159	0.208326	0.517937	0.180131	ENSG00000214487	AC092865.2
ENSG00000214491	1.00882	1.67076	1.9904	3.32774	ENSG00000214491	SEC14L6
ENSG00000214510	0.424145	0.529746	0.72665	1.08792	ENSG00000214510	SPINK13
ENSG00000214511	0.483272	0.230499	0.833433	1.0188	ENSG00000214511	HIGD1C
ENSG00000214513	0.784521	1.80679	1.80272	2.77875	ENSG00000214513	NOTO
ENSG00000214514	2.19421	4.88605	5.69264	5.71733	ENSG00000214514	KRT42P
ENSG00000214517	27.0124	20.2459	21.1346	23.3566	ENSG00000214517	PPME1
ENSG00000214518	0	0	0	0.000164447	ENSG00000214518	KRTAP2-2
ENSG00000214525	0.343608	1.35689	1.05836	4.90058	ENSG00000214525	AC130709.1
ENSG00000214526	0	0.217245	0	0	ENSG00000214526	AP000343.1
ENSG00000214530	30.703	43.3176	37.6498	34.0424	ENSG00000214530	STARD10
ENSG00000214533	0	0.0589145	0.10271	0	ENSG00000214533	KRT18P33
ENSG00000214534	0.0885378	0.180977	0.18546	0.13543	ENSG00000214534	ZNF705E
ENSG00000214535	0.230371	1.31762	2.09118	0.999276	ENSG00000214535	RPS15AP1
ENSG00000214541	0	0	0	0	ENSG00000214541	RPS4XP3
ENSG00000214544	0	0.0916124	0.253519	0.317962	ENSG00000214544	GTF2IRD2P1
ENSG00000214549	0	0	0.264858	0.163748	ENSG00000214549	SDHCP2
ENSG00000214552	0	0	0	0	ENSG00000214552	COPS8P2
ENSG00000214553	0.210745	0.30949	0.341837	0.478306	ENSG00000214553	LRRC37A11P
ENSG00000214556	0.34404	0.108317	0.28539	0.118254	ENSG00000214556	C17orf98
ENSG00000214558	0.03735	0.0635051	0	0	ENSG00000214558	AL365217.1
ENSG00000214560	0	0	0	0	ENSG00000214560	RPL21P41
ENSG00000214561	0	0	0	0	ENSG00000214561	RBBP4P4

ENSG00000214562	6.11282	6.5094	9.40148	8.93619	ENSG00000214562	NUTM2D
ENSG00000214563	0	0	0	0.0692656	ENSG00000214563	GAPDHP15
ENSG00000214566	0	0	0	0	ENSG00000214566	GAPDHP41
ENSG00000214575	2.20462	3.82887	4.13725	5.50526	ENSG00000214575	CPEB1
ENSG00000214578	0	0	0.396587	0	ENSG00000214578	HMGN2P15
ENSG00000214581	0	0.142511	0.257613	0.161659	ENSG00000214581	ZNF971P
ENSG00000214584	0	0	0	0	ENSG00000214584	PGGT1BP2
ENSG00000214593	2.01499	1.94651	3.52403	2.0936	ENSG00000214593	AL354710.1
ENSG00000214595	3.67951	5.98281	7.01338	6.31033	ENSG00000214595	EML6
ENSG00000214597	0	0.194541	0.536918	0.563011	ENSG00000214597	TMEM249
ENSG00000214602	0.0940938	0.271368	0.245279	0.0514276	ENSG00000214602	CTBP2P5
ENSG00000214604	0	0.221561	0.133166	0.214393	ENSG00000214604	NPM1P36
ENSG00000214607	0.0268682	0	0	0	ENSG00000214607	ADAM24P
ENSG00000214612	0.251474	0.200957	0	0.290242	ENSG00000214612	RPS19P1
ENSG00000214617	1.1065	1.95315	1.28989	0.939717	ENSG00000214617	SLC6A10P
ENSG00000214626	0.255209	1.78082	1.97471	2.01303	ENSG00000214626	POLR3DP1
ENSG00000214628	0.127461	1.34542	0.441775	0.821337	ENSG00000214628	NDUFB5P2
ENSG00000214629	1.15795	3.63018	3.3607	4.19468	ENSG00000214629	RPSAP6
ENSG00000214641	0	0	0	0	ENSG00000214641	AL445529.1
ENSG00000214642	0	0	0	0	ENSG00000214642	DEFB113
ENSG00000214643	0	0	0	0	ENSG00000214643	DEFB133
ENSG00000214645	30.1136	44.5928	60.9262	94.3181	ENSG00000214645	AL162389.1
ENSG00000214646	0.117131	0.738706	0.545459	0.635326	ENSG00000214646	AC104758.1
ENSG00000214651	0.0797346	0.306668	0.207903	0.130668	ENSG00000214651	AL513122.1
ENSG00000214652	1.85062	2.14117	0.62778	0.943465	ENSG00000214652	ZNF727
ENSG00000214653	0	0.0555126	0.0995569	0	ENSG00000214653	HNRNPA3P3
ENSG00000214654	5.17654	5.798	7.10218	3.075	ENSG00000214654	AL161911.1
ENSG00000214655	55.9404	35.7913	63.2282	57.5677	ENSG00000214655	ZSWIM8
ENSG00000214657	0	0	0	0.357694	ENSG00000214657	AC113608.1
ENSG00000214659	0.0467329	0.0447447	0.20221	0.152769	ENSG00000214659	KRT8P26
ENSG00000214660	0	0	0.0979186	0.122791	ENSG00000214660	SLC29A4P2
ENSG00000214668	0	0	0	0	ENSG00000214668	SLC29A4P1
ENSG00000214669	0	0.370202	0	0	ENSG00000214669	AL157702.1
ENSG00000214670	0	0.0709774	0	1.77051	ENSG00000214670	AC007956.1
ENSG00000214671	0.226709	0.800363	1.248	1.723	ENSG00000214671	AC096741.1
ENSG00000214676	0.508593	1.09811	2.53402	1.50219	ENSG00000214676	AC080188.1
ENSG00000214681	0.14683	0	0	0	ENSG00000214681	IQCF5
ENSG00000214684	0	0	0	0	ENSG00000214684	AC003045.1
ENSG00000214686	0	0	0	0	ENSG00000214686	IQCF6
ENSG00000214688	0.184355	0.351589	0.302789	0.441886	ENSG00000214688	C10orf105
ENSG00000214694	0.6114	1.44866	2.67345	3.28865	ENSG00000214694	ARHGEF33
ENSG00000214695	0.234067	0.550363	0.728933	1.40774	ENSG00000214695	NPAP1P2
ENSG00000214696	1.16862	3.35681	5.8164	5.40792	ENSG00000214696	AC007347.1
ENSG00000214700	0.578174	1.39582	1.15887	2.38371	ENSG00000214700	C12orf71
ENSG00000214702	0.348522	0.174573	0.817105	0.382561	ENSG00000214702	AC010931.1
ENSG00000214706	29.3895	31.2208	36.5244	15.0924	ENSG00000214706	IFRD2
ENSG00000214708	0.626535	0.190449	0.313498	0.383173	ENSG00000214708	AC116407.1
ENSG00000214711	12.8469	1.11867	1.18938	1.78841	ENSG00000214711	CAPN14
ENSG00000214717	12.3469	11.3934	16.3771	10.2139	ENSG00000214717	ZBED1
ENSG00000214720	0	0.148526	0	0	ENSG00000214720	KRT18P49
ENSG00000214727	0	0.535524	0.275975	0.257292	ENSG00000214727	RPL5P35
ENSG00000214732	0	0	0	0	ENSG00000214732	AL096814.1
ENSG00000214736	59.237	26.0059	25.728	26.5951	ENSG00000214736	TOMM6
ENSG00000214743	0	0	0	0	ENSG00000214743	MRPS5P3

ENSG00000214745	0.102679	0.341357	0.291139	0.660723	ENSG00000214745	AL391419.1
ENSG00000214748	0	0	0	0	ENSG00000214748	AL355309.1
ENSG00000214753	6.17631	10.4478	11.456	13.2072	ENSG00000214753	HNRNPUL2
ENSG00000214754	0	0	0.124801	0	ENSG00000214754	AC004870.1
ENSG00000214756	64.5117	73.2804	90.2054	37.1227	ENSG00000214756	METTL12
ENSG00000214759	0.854293	0.806637	0.725023	1.31593	ENSG00000214759	AL355076.1
ENSG00000214760	0.497141	0	0.130408	0.344804	ENSG00000214760	RPL21P1
ENSG00000214761	0.547683	2.12197	0.908693	1.45894	ENSG00000214761	HNRNPA1P15
ENSG00000214765	12.3696	20.9044	22.327	27.5836	ENSG00000214765	SEPT7P2
ENSG00000214776	1.24027	2.62857	3.44158	3.39393	ENSG00000214776	AC092821.1
ENSG00000214782	0	0.127237	0.114971	0.143929	ENSG00000214782	AP004243.1
ENSG00000214784	0.0876891	0.105463	0	0.193486	ENSG00000214784	AC010468.1
ENSG00000214787	3.79205	6.09073	7.59059	8.32195	ENSG00000214787	MS4A4E
ENSG00000214788	0.731728	0	0	0	ENSG00000214788	OOSP1
ENSG00000214794	0	0	0	0	ENSG00000214794	KRT18P42
ENSG00000214796	1.27616	1.47386	1.35748	3.38463	ENSG00000214796	AC098934.1
ENSG00000214807	0	0	0.0752368	0	ENSG00000214807	NPM1P31
ENSG00000214810	0	0	0	0	ENSG00000214810	CYCSP55
ENSG00000214812	0	0	0	0.297329	ENSG00000214812	AL137792.1
ENSG00000214814	0.357149	0.916793	0.360698	0.848336	ENSG00000214814	FER1L6
ENSG00000214815	0	0	0	0	ENSG00000214815	IMPDH1P3
ENSG00000214819	0	0	0.152372	0.132959	ENSG00000214819	CDRT15L2
ENSG00000214820	0.387612	0.711294	0.502509	0.547286	ENSG00000214820	MPRIPP1
ENSG00000214821	0.132858	0	0.114485	0.422252	ENSG00000214821	HMGB1P4
ENSG00000214822	6.98044	8.19	6.34446	3.14712	ENSG00000214822	KRT16P3
ENSG00000214823	0	0	0	0	ENSG00000214823	NXT1P1
ENSG00000214825	0	0	0	0	ENSG00000214825	EI24P3
ENSG00000214826	1.29127	4.26048	1.65362	2.73312	ENSG00000214826	DDX12P
ENSG00000214827	1.87862	3.59487	3.46408	1.91412	ENSG00000214827	MTCP1
ENSG00000214832	0	0.174096	0.464711	0.250488	ENSG00000214832	UPF3AP2
ENSG00000214835	0	0.316987	0.297313	1.05836	ENSG00000214835	RPL23AP6
ENSG00000214841	4.94884	0	0	0	ENSG00000214841	AC005493.1
ENSG00000214842	0.0727442	0.617403	0.596256	0.224183	ENSG00000214842	RAD51AP2
ENSG00000214843	0	0.447665	0.508008	0.1255	ENSG00000214843	ZFYVE9P2
ENSG00000214844	24.1256	63.524	42.064	63.0057	ENSG00000214844	AC007952.1
ENSG00000214846	0.204711	0.294973	0.0888227	0.663686	ENSG00000214846	AC114744.1
ENSG00000214853	1.42229	0.792214	0.611433	0.500392	ENSG00000214853	AC113412.1
ENSG00000214854	0	0	0	0	ENSG00000214854	AL031590.1
ENSG00000214855	2.3735	3.36083	3.60263	6.87063	ENSG00000214855	APOC1P1
ENSG00000214856	1.62538	6.81236	2.75581	2.00512	ENSG00000214856	KRT16P1
ENSG00000214857	0	0.664385	0	0	ENSG00000214857	SEM1P1
ENSG00000214860	0.136346	1.93831	1.62448	0.328625	ENSG00000214860	EVPLL
ENSG00000214866	0	0.157399	0.0613015	0.153344	ENSG00000214866	DCDC2C
ENSG00000214867	0.139749	0.268167	0.242535	0.598875	ENSG00000214867	SRSF9P1
ENSG00000214869	0.266987	0.760747	0.756316	1.05947	ENSG00000214869	TPM3P4
ENSG00000214871	18.4143	24.1647	23.1814	45.9131	ENSG00000214871	AC005082.1
ENSG00000214872	0.272631	0.604356	0.579773	0.748034	ENSG00000214872	SMTNL1
ENSG00000214875	0.377739	0.857312	0.785759	1.08218	ENSG00000214875	MED28P1
ENSG00000214878	0.109005	0	0	0.127004	ENSG00000214878	RPL5P31
ENSG00000214880	0.190261	0.722577	1.11849	1.23135	ENSG00000214880	OR7E5P
ENSG00000214881	0	0	0	0	ENSG00000214881	TMEM14DP
ENSG00000214883	0	0.80264	0.635443	1.10719	ENSG00000214883	AC024405.1
ENSG00000214886	0	0.157993	0.142633	0	ENSG00000214886	FAM177A1P1
ENSG00000214889	0.734775	0.910913	1.69203	0.954512	ENSG00000214889	RPS9P1

ENSG00000214890	0	0.0584991	0.370076	0.397367	ENSG00000214890	AC020937.1
ENSG00000214891	0.0437983	0	0	0	ENSG00000214891	TRIM64C
ENSG00000214892	0	0	0	0.0757496	ENSG00000214892	USP8P1
ENSG00000214896	0	0	0	0.0812834	ENSG00000214896	RPSAP55
ENSG00000214897	0.0481952	0.0464024	0	0.0735551	ENSG00000214897	PNMA6E
ENSG00000214900	2.64555	3.8057	4.11466	5.5255	ENSG00000214900	LINC01588
ENSG00000214903	0	0	0	0	ENSG00000214903	AL358832.1
ENSG00000214904	0	0.150454	0	0.167663	ENSG00000214904	DUTP8
ENSG00000214908	0.0892281	0.171958	0	0.579351	ENSG00000214908	AL353678.1
ENSG00000214914	0	0.169421	0	0	ENSG00000214914	RPL23AP3
ENSG00000214917	0	0	0	0.23811	ENSG00000214917	AC011825.1
ENSG00000214919	0.580586	1.58094	1.51598	4.51348	ENSG00000214919	AC104472.1
ENSG00000214921	2.24729	6.31921	4.51359	10.2111	ENSG00000214921	AC003102.1
ENSG00000214925	0	0	0	0	ENSG00000214925	AC234778.1
ENSG00000214929	0	0.0428121	0	0.0940525	ENSG00000214929	SPATA31D1
ENSG00000214930	0	0	0.0430991	0.16227	ENSG00000214930	KRT8P6
ENSG00000214940	0.523984	1.57029	1.85637	0.867551	ENSG00000214940	NPIPA8
ENSG00000214941	10.0535	17.8449	18.4838	18.7942	ENSG00000214941	ZSWIM7
ENSG00000214943	0	0	0.107494	0.0673179	ENSG00000214943	GPR33
ENSG00000214944	83.6003	98.1542	53.6403	114.532	ENSG00000214944	ARHGEF28
ENSG00000214946	0.371958	1.66222	1.74638	1.41933	ENSG00000214946	TBC1D26
ENSG00000214954	8.8268	17.6011	21.9454	22.4939	ENSG00000214954	LRRC69
ENSG00000214960	1.28296	1.27785	1.15572	1.99339	ENSG00000214960	ISPD
ENSG00000214961	0	0	0	0	ENSG00000214961	FO393409.1
ENSG00000214967	32.2405	59.1632	72.104	13.1474	ENSG00000214967	NPIPA7
ENSG00000214973	0	0	0	0	ENSG00000214973	CHCHD3P3
ENSG00000214975	0	0	0	0	ENSG00000214975	PPIAP29
ENSG00000214976	0	0	0	0.14144	ENSG00000214976	VDAC2P1
ENSG00000214978	0.0718093	0.0766611	0	0	ENSG00000214978	GSG1L2
ENSG00000214980	0	0	0.0746417	0	ENSG00000214980	AC025538.1
ENSG00000214982	16.5935	17.4848	16.556	17.9944	ENSG00000214982	PARGP1
ENSG00000214985	16.9532	38.167	21.9664	44.3058	ENSG00000214985	AL591516.5
ENSG00000214988	0.476457	0.16059	0.458371	0.0861113	ENSG00000214988	RPL7AP26
ENSG00000214992	0.406774	0.659828	0.687313	1.5009	ENSG00000214992	AKAP17BP
ENSG00000214998	0.211324	0.556699	0.227866	0.285841	ENSG00000214998	CCNB2P1
ENSG00000214999	0.19945	0.675145	0.665307	0.341867	ENSG00000214999	AC129492.1
ENSG00000215000	0	0	0.0621433	0	ENSG00000215000	AL034403.1
ENSG00000215002	0	0	0	0	ENSG00000215002	RPL23AP59
ENSG00000215003	0	0	0	0	ENSG00000215003	AC130651.1
ENSG00000215004	0	0	0	0	ENSG00000215004	MESTP4
ENSG00000215005	0	0	0	0	ENSG00000215005	HSPD1P7
ENSG00000215006	0.157858	0	0	0	ENSG00000215006	CHCHD2P2
ENSG00000215007	0	0	0	0	ENSG00000215007	DNAJA1P3
ENSG00000215009	0.0942121	0.403473	0.364757	0.533187	ENSG00000215009	ACSM4
ENSG00000215012	8.74551	9.32173	15.0033	8.44758	ENSG00000215012	RTL10
ENSG00000215014	1.57674	1.81962	4.38576	4.86472	ENSG00000215014	AL645728.1
ENSG00000215016	0	0.168755	0	0	ENSG00000215016	RPL24P7
ENSG00000215018	6.04442	12.2944	14.6238	19.5661	ENSG00000215018	COL28A1
ENSG00000215020	0	0	0	0	ENSG00000215020	AL591684.1
ENSG00000215021	80.9921	89.3107	73.9614	37.5676	ENSG00000215021	PHB2
ENSG00000215024	0	0	0	0	ENSG00000215024	DUSP8P1
ENSG00000215029	0	0	0	0.0089544	ENSG00000215029	TCP11X2
ENSG00000215030	0.69571	0.669538	5.25417	11.8124	ENSG00000215030	AC073621.1
ENSG00000215032	0.332355	0.414685	0.782033	0.219968	ENSG00000215032	GNL3LP1

ENSG00000215033	12.339	4.26149	18.0392	6.44407	ENSG00000215033	AL603965.1
ENSG00000215034	0	0.172558	0	0.350626	ENSG00000215034	DSTNP4
ENSG00000215035	0.149982	0.395033	0	0.0949702	ENSG00000215035	FDPSP5
ENSG00000215037	0	0.661187	0.695694	0.34337	ENSG00000215037	VENTXP2
ENSG00000215041	14.9724	20.177	27.1723	14.9215	ENSG00000215041	NEURL4
ENSG00000215043	0	0	0	0	ENSG00000215043	GLULP6
ENSG00000215044	0	0	0.020275	0	ENSG00000215044	AHCYP1
ENSG00000215045	0.3332	0.312463	0.444989	0.253697	ENSG00000215045	GRID2IP
ENSG00000215046	0	0	0	0.0089544	ENSG00000215046	TCP11X1
ENSG00000215048	1.10981	1.12457	0.827989	0.205747	ENSG00000215048	HLA-DPB1
ENSG00000215049	0.846249	0.928506	1.57352	3.26737	ENSG00000215049	PRDX2P1
ENSG00000215054	0.035809	0	0.150633	0.0389052	ENSG00000215054	HNRNPCP10
ENSG00000215057	0	0.0693553	0.0313481	0	ENSG00000215057	PKMP5
ENSG00000215063	0	0	0	0.174279	ENSG00000215063	RPL21P2
ENSG00000215065	0	0.061488	0	0	ENSG00000215065	DUSP8P4
ENSG00000215066	1.57902	3.7725	2.89251	9.71487	ENSG00000215066	C9orf38
ENSG00000215067	8.93629	15.4014	16.0208	18.5754	ENSG00000215067	ALOX12-AS1
ENSG00000215070	0	0.0841439	0.0380283	0.238858	ENSG00000215070	XRCC6P5
ENSG00000215077	17.4127	30.5954	28.4925	17.8458	ENSG00000215077	BRD2
ENSG00000215085	0.110679	0	0	0	ENSG00000215085	AL365400.1
ENSG00000215086	0.148233	0.254579	0.250489	0.561708	ENSG00000215086	NPM1P24
ENSG00000215088	0.11354	0.0545193	0.0492386	0.0870349	ENSG00000215088	RPS5P3
ENSG00000215089	0	0.0450455	0	0	ENSG00000215089	KRT18P11
ENSG00000215093	0.0554966	0.0533869	0.144742	0	ENSG00000215093	EEF1A1P29
ENSG00000215094	0	0	0	0	ENSG00000215094	AL583835.1
ENSG00000215096	0	0.209255	0.188947	0.694496	ENSG00000215096	IFITM8P
ENSG00000215097	0	0	0.27838	0.140863	ENSG00000215097	DUSP8P3
ENSG00000215102	0	0	0	0.0665556	ENSG00000215102	TERF1P4
ENSG00000215104	0.151964	1.16533	1.1837	0.974683	ENSG00000215104	CHPM1B2P
ENSG00000215105	0.388136	0.357036	1.05097	0.87774	ENSG00000215105	TTC3P1
ENSG00000215110	0	0	0	0	ENSG00000215110	UGT2B25P
ENSG00000215114	6.51497	11.9618	13.0365	9.62304	ENSG00000215114	UBXN2B
ENSG00000215120	0	0	0	0	ENSG00000215120	AL590763.1
ENSG00000215124	1.20373	3.02242	1.70796	3.92655	ENSG00000215124	AMD1P4
ENSG00000215126	10.5827	16.9997	23.2599	14.1336	ENSG00000215126	CBWD6
ENSG00000215127	0.561436	0.25227	0.171497	0.178446	ENSG00000215127	SYT14P1
ENSG00000215131	0.518435	0.140164	0.241284	0.230115	ENSG00000215131	C16orf90
ENSG00000215142	1.91827	5.78521	1.91943	2.27726	ENSG00000215142	RP11-292B8.1
ENSG00000215146	5.72759	20.1232	2.43635	9.27156	ENSG00000215146	BX322639.1
ENSG00000215148	0.072671	0	0	0.073623	ENSG00000215148	PRSS41
ENSG00000215149	0	0	0	0	ENSG00000215149	KRT18P32
ENSG00000215151	0	0	0	0.0394178	ENSG00000215151	ABCD1P2
ENSG00000215154	7.82682	4.82707	9.40893	7.99885	ENSG00000215154	AC141586.1
ENSG00000215156	0.615258	2.41958	1.54517	5.18884	ENSG00000215156	AC138409.1
ENSG00000215158	6.59835	33.045	16.4808	23.5657	ENSG00000215158	AC138409.2
ENSG00000215160	0	0.0604044	0	0.156095	ENSG00000215160	OR7E122P
ENSG00000215165	0	0	0	0	ENSG00000215165	TCEA1P3
ENSG00000215168	0.12333	0	0.0536194	0.3358	ENSG00000215168	AL139276.1
ENSG00000215174	0.0683813	0.148323	0.238574	0.229677	ENSG00000215174	NLRP2B
ENSG00000215177	0.280835	0.776699	2.503	0.832197	ENSG00000215177	IGLV8OR8-1
ENSG00000215179	0.0262398	0.0252787	0	0.289558	ENSG00000215179	AC026241.1
ENSG00000215182	0.138191	0.129828	0.190912	0.0889164	ENSG00000215182	MUC5AC
ENSG00000215183	0	0	0	0	ENSG00000215183	MSMP
ENSG00000215184	1.66338	5.52325	3.43265	9.44272	ENSG00000215184	RPS12P16

ENSG00000215186	0	0.936213	0	0	ENSG00000215186	GOLGA6B
ENSG00000215187	0.848522	2.67622	2.04181	2.21111	ENSG00000215187	FAM166B
ENSG00000215193	9.57497	9.59914	13.4587	11.9722	ENSG00000215193	PEX26
ENSG00000215197	0	0	0	0	ENSG00000215197	PGAM4P1
ENSG00000215198	0	0.102904	0.0293437	0.155598	ENSG00000215198	AL353795.1
ENSG00000215199	0	0	0.160804	0.255269	ENSG00000215199	YWHAZP6
ENSG00000215203	0	0.259453	0.0542624	0.420594	ENSG00000215203	GRXCR1
ENSG00000215206	0	0	0	0	ENSG00000215206	TRBV24OR9-2
ENSG00000215208	0.187925	0.307505	0.718168	2.54434	ENSG00000215208	KRT18P60
ENSG00000215210	0.0540933	0	0	0.0582785	ENSG00000215210	RBMXP2
ENSG00000215217	0.0734326	0.0452108	0.0406216	0.131392	ENSG00000215217	C5orf49
ENSG00000215218	0.10106	0.111162	0.163504	1.39239	ENSG00000215218	UBE2QL1
ENSG00000215221	0	0.220423	1.19176	2.43847	ENSG00000215221	UBA52P6
ENSG00000215223	0.122689	0.236337	0.0712094	1.43388	ENSG00000215223	CYP51A1P3
ENSG00000215227	0	0.44554	0.201174	0.984855	ENSG00000215227	NUTF2P5
ENSG00000215236	0	0	0	0	ENSG00000215236	RPL7P33
ENSG00000215237	0.212998	0.45981	0.143097	0.452477	ENSG00000215237	AL592293.1
ENSG00000215251	8.46502	6.89311	6.35706	5.87429	ENSG00000215251	FASTKD5
ENSG00000215252	36.2377	84.6012	88.3902	94.5321	ENSG00000215252	GOLGA8B
ENSG00000215262	0.646844	0.124119	0.191696	0.555527	ENSG00000215262	KCNU1
ENSG00000215263	0.233305	0.446432	0.201174	0.246621	ENSG00000215263	AC025750.1
ENSG00000215264	0	0.1013	0	0	ENSG00000215264	RPL10AP3
ENSG00000215267	0	0	0.166574	0.0940824	ENSG00000215267	AKR1C7P
ENSG00000215268	0	0	0	0	ENSG00000215268	AP000533.2
ENSG00000215269	0	0	0	0	ENSG00000215269	GAGE12G
ENSG00000215270	0	0.0630468	0	0	ENSG00000215270	AP000523.1
ENSG00000215271	17.4396	17.192	16.9583	8.11059	ENSG00000215271	HOMEZ
ENSG00000215274	0	0	0	0	ENSG00000215274	GAGE10
ENSG00000215277	1.27318	0.879534	3.17902	2.41611	ENSG00000215277	RNF212B
ENSG00000215278	0	0	0	0	ENSG00000215278	RPS7P6
ENSG00000215283	0.455457	0.33782	0.502046	0.507842	ENSG00000215283	HMGB3P24
ENSG00000215284	0.105647	0.834434	0.393924	1.88683	ENSG00000215284	AL512633.1
ENSG00000215286	0	0	0	0	ENSG00000215286	AL031584.1
ENSG00000215288	0	0.462946	0.631461	1.32669	ENSG00000215288	AC067904.1
ENSG00000215296	0.795378	1.29625	1.36303	2.46479	ENSG00000215296	TMCO5B
ENSG00000215297	0.16971	0.812821	0.146738	0.361664	ENSG00000215297	AL354941.1
ENSG00000215298	0	1.67771	2.78881	4.66671	ENSG00000215298	FP15737
ENSG00000215301	60.7572	27.8532	55.5992	67.0771	ENSG00000215301	DDX3X
ENSG00000215302	0.666265	2.72482	1.94492	3.63108	ENSG00000215302	AC127502.1
ENSG00000215305	16.013	19.8858	16.9121	16.3959	ENSG00000215305	VPS16
ENSG00000215306	15.3647	23.7528	19.8947	26.6126	ENSG00000215306	AL135998.1
ENSG00000215307	0	0	0	0	ENSG00000215307	RBBP4P3
ENSG00000215310	0.0484655	0.046662	0.0421752	0.158819	ENSG00000215310	AL050305.1
ENSG00000215311	0	0.0764766	0.0670486	0	ENSG00000215311	NPM1P12
ENSG00000215313	0	0	0	0	ENSG00000215313	RPL6P30
ENSG00000215317	0.0588648	0.0570191	0	0.0654428	ENSG00000215317	THUMPD1P1
ENSG00000215319	0.049152	0.431918	0.231507	0.649852	ENSG00000215319	EIF5P1
ENSG00000215323	0.0714173	0.211923	0.144983	1.24252	ENSG00000215323	OR7E84P
ENSG00000215325	0	0.232358	0.167419	0.26398	ENSG00000215325	ASS1P10
ENSG00000215326	0	0	0	0.126449	ENSG00000215326	GPX1P2
ENSG00000215328	0	0	2.72323	31.6172	ENSG00000215328	HSPA1A
ENSG00000215333	0	0	0.0404344	0.0509117	ENSG00000215333	KRT18P23
ENSG00000215339	0	0	0	0	ENSG00000215339	ZNF705CP
ENSG00000215343	0	0	0	0	ENSG00000215343	ZNF705D

ENSG00000215346	0.903035	3.90666	2.88444	4.8504	ENSG00000215346	AF131215.5
ENSG00000215347	0	0.293316	0.607397	0.405778	ENSG00000215347	SLC25A5P1
ENSG00000215349	0	0	0	0	ENSG00000215349	MRPL3P1
ENSG00000215351	0	0	0	0	ENSG00000215351	PPIAP1
ENSG00000215353	0	0.0816704	0	0	ENSG00000215353	C1QBPP1
ENSG00000215354	0.0506676	0.107056	0.584625	0.0824359	ENSG00000215354	FAM90A24P
ENSG00000215356	0	0	0	0.0540898	ENSG00000215356	ZNF705B
ENSG00000215357	0	0	0	0	ENSG00000215357	HSPD1P8
ENSG00000215365	0.0383417	0	0	0	ENSG00000215365	FAM90A22P
ENSG00000215367	0	0.18783	0.6733	0.148553	ENSG00000215367	TMED11P
ENSG00000215368	0.202309	0.387001	0.699023	0.428891	ENSG00000215368	BOD1P2
ENSG00000215369	0	0	0.312793	0.37956	ENSG00000215369	RPL37P3
ENSG00000215371	0	0	0	0	ENSG00000215371	DEFB108C
ENSG00000215372	0	0	0	0	ENSG00000215372	ZNF705G
ENSG00000215373	0.0383417	0	0.0439405	0.0508184	ENSG00000215373	FAM90A5P
ENSG00000215375	11.5853	9.97877	21.2602	11.2322	ENSG00000215375	MYL5
ENSG00000215378	0	0	0	0	ENSG00000215378	DEFT1P
ENSG00000215380	0	0	0	0	ENSG00000215380	AC090625.1
ENSG00000215381	0	0	0	0	ENSG00000215381	AL109936.1
ENSG00000215388	0.761085	2.19795	1.98608	1.9569	ENSG00000215388	ACTG1P3
ENSG00000215397	0.168186	0.178125	0.242408	0.425496	ENSG00000215397	SCRT2
ENSG00000215398	0	0	0	0	ENSG00000215398	CR383658.1
ENSG00000215399	0	0.550955	0.67436	0.494414	ENSG00000215399	HMGB3P7
ENSG00000215405	0.107184	0.315999	0.193056	0.545752	ENSG00000215405	GOLGA6L6
ENSG00000215409	0.0400002	0.0769011	0.0694771	0.0867638	ENSG00000215409	AL355493.1
ENSG00000215414	0.985389	2.44349	2.46214	0	ENSG00000215414	PSMA6P1
ENSG00000215418	0	0	0	0.0636508	ENSG00000215418	PEX12P1
ENSG00000215421	4.94386	7.79295	6.59579	11.1859	ENSG00000215421	ZNF407
ENSG00000215425	24.7126	21.9868	22.2472	18.3304	ENSG00000215425	DDX39B
ENSG00000215428	0.10195	0.115887	0.17949	0.229171	ENSG00000215428	AL354898.1
ENSG00000215430	0	0	0	0	ENSG00000215430	OR7E156P
ENSG00000215431	0	24.3667	4.17889	11.8823	ENSG00000215431	AC015989.1
ENSG00000215432	0	0	0	0	ENSG00000215432	OR7E104P
ENSG00000215440	11.413	10.6348	16.1463	6.88917	ENSG00000215440	NPEPL1
ENSG00000215441	0.0472462	0.0684829	0.0411738	0.287803	ENSG00000215441	CTAGE12P
ENSG00000215444	0	0.330397	0.149156	0.183715	ENSG00000215444	AL138807.1
ENSG00000215448	0.0715193	0.357234	0.18643	0.631077	ENSG00000215448	SRMP1
ENSG00000215450	0	0	0	0	ENSG00000215450	AL022342.1
ENSG00000215452	0.547059	1.35335	0.923031	1.08905	ENSG00000215452	ZNF663P
ENSG00000215454	0	0.0440913	0	0	ENSG00000215454	KRTAP10-4
ENSG00000215455	0.073732	0.023662	0.0215792	0.0820157	ENSG00000215455	KRTAP10-1
ENSG00000215456	0	0	0	0	ENSG00000215456	BCRP4
ENSG00000215457	0	0	0	0	ENSG00000215457	AC022701.1
ENSG00000215462	4.3111	6.15873	1.39176	2.97928	ENSG00000215462	AL136218.1
ENSG00000215464	0	0.167267	0	0	ENSG00000215464	AP000354.1
ENSG00000215467	0	0.179226	0	0	ENSG00000215467	AL121886.1
ENSG00000215472	2.66597	1.5074	0.610805	0.944572	ENSG00000215472	RPL17-C18orf32
ENSG00000215474	0	0.232374	0.270311	0.770298	ENSG00000215474	SKOR2
ENSG00000215475	0.468071	0.874146	0.82565	1.06722	ENSG00000215475	SIAH3
ENSG00000215477	0.124068	0.179215	0	0.135438	ENSG00000215477	RCN1P1
ENSG00000215478	0.127422	0	0.314674	0.0693495	ENSG00000215478	CES5AP1
ENSG00000215480	0	0	0	0	ENSG00000215480	OR7E37P
ENSG00000215481	0.146248	0.926495	0.911442	0.47233	ENSG00000215481	BCRP3

ENSG00000215482	0.180963	2.23539	3.14878	0.387157	ENSG00000215482	CALM2P3
ENSG00000215486	0	0	0	0.419589	ENSG00000215486	ARL2BPP3
ENSG00000215492	6.19231	4.45391	8.91721	7.93634	ENSG00000215492	HNRNPA1P7
ENSG00000215493	0.795378	0.790757	1.5887	1.82577	ENSG00000215493	AC007731.2
ENSG00000215504	4.20291	7.45633	7.94619	14.7122	ENSG00000215504	AP000974.1
ENSG00000215506	0	0.153004	0.189047	0.0441144	ENSG00000215506	TPTE2P4
ENSG00000215507	0	0	0	0	ENSG00000215507	RBMY2DP
ENSG00000215512	1.18147	3.30711	2.09265	2.61314	ENSG00000215512	AP005901.1
ENSG00000215513	12.0329	7.53729	8.20657	13.0325	ENSG00000215513	PI4KAP1
ENSG00000215515	0	0.077498	0	0.264149	ENSG00000215515	IFIT1P1
ENSG00000215520	0	0	0	0.186356	ENSG00000215520	RPS4XP4
ENSG00000215522	39.6632	10.3894	18.1959	9.14113	ENSG00000215522	DDR1
ENSG00000215527	1.19967	2.37192	2.21669	2.03049	ENSG00000215527	AP005482.1
ENSG00000215529	0.346877	2.01203	0.979047	0.101287	ENSG00000215529	EFCAB8
ENSG00000215537	0.0492481	0.0474136	0.128563	0	ENSG00000215537	ZNF736P11Y
ENSG00000215540	0	0	0	0	ENSG00000215540	RBMY2CP
ENSG00000215544	0	0	0	0	ENSG00000215544	BCRP7
ENSG00000215545	0	0	0	0	ENSG00000215545	DEFB116
ENSG00000215546	0	0	0	0.104097	ENSG00000215546	DKKL1P1
ENSG00000215547	0	0	0	0	ENSG00000215547	DEFB115
ENSG00000215548	0.942185	1.01628	0.372897	0.538587	ENSG00000215548	FRG1JP
ENSG00000215549	0	0	0	0	ENSG00000215549	AL138815.1
ENSG00000215553	0.137993	0.312078	0.0804424	0	ENSG00000215553	KRT18P3
ENSG00000215559	0.760299	1.0689	0.89589	1.56805	ENSG00000215559	ANKRD20A11P
ENSG00000215562	0	0	0	0	ENSG00000215562	CNN2P7
ENSG00000215565	36.786	90.1774	86.6215	165.158	ENSG00000215565	AP003041.1
ENSG00000215567	0	0.117708	0.106293	0	ENSG00000215567	AC138701.1
ENSG00000215568	0.104966	0.362149	0.426338	0.346353	ENSG00000215568	GAB4
ENSG00000215571	0.0774002	0.19605	0.207291	0.168433	ENSG00000215571	GRK6P1
ENSG00000215572	0.0479173	0	0	0	ENSG00000215572	ESRRAP1
ENSG00000215580	0.258668	0.648307	0.869267	0.74153	ENSG00000215580	BCORP1
ENSG00000215583	0	0	0	0	ENSG00000215583	ASS1P6
ENSG00000215586	0	0.135877	0	0	ENSG00000215586	AL031679.1
ENSG00000215589	0	0.0464886	0.0420186	0.105772	ENSG00000215589	KANK1P1
ENSG00000215595	0.107734	0.0345966	0.0625477	0	ENSG00000215595	C20orf202
ENSG00000215601	0	0	0	0	ENSG00000215601	TSPY24P
ENSG00000215603	0.0502991	0.147116	0.131666	0.27651	ENSG00000215603	ZNF92P1Y
ENSG00000215604	0.0610044	0.146296	0.157023	0.125192	ENSG00000215604	ZNF962P
ENSG00000215606	0	0	0	0	ENSG00000215606	KRT18P35
ENSG00000215608	0.300799	0.79	0.246141	0.313579	ENSG00000215608	AL356585.2
ENSG00000215611	0	0	0.0522867	0.129767	ENSG00000215611	AC002321.1
ENSG00000215612	0.029922	0	0	0.06564	ENSG00000215612	HMX1
ENSG00000215615	2.86082	2.11664	1.54203	0	ENSG00000215615	AL354822.1
ENSG00000215616	0	0	0	0	ENSG00000215616	AC002321.2
ENSG00000215621	1.49633	0.621141	2.35259	4.49536	ENSG00000215621	AC174470.1
ENSG00000215630	4.19929	14.7615	16.6823	26.9859	ENSG00000215630	GUSBP9
ENSG00000215635	0.020881	0.321028	0.166351	0.468089	ENSG00000215635	AC145205.1
ENSG00000215641	2.91456	7.02801	4.17031	4.60156	ENSG00000215641	TRIM27
ENSG00000215642	0.112609	0.0969925	0.0789754	0.19091	ENSG00000215642	AL360154.1
ENSG00000215644	0.0303147	0.245824	0.370995	0.095123	ENSG00000215644	GCGR
ENSG00000215689	0.167826	0.556914	0.925032	0.120658	ENSG00000215689	MGC39584
ENSG00000215695	3.63208	3.39561	3.06733	0.409635	ENSG00000215695	RSC1A1
ENSG00000215699	9.09264	12.8282	13.2121	10.1795	ENSG00000215699	SRSF10
ENSG00000215700	0	15.5745	20.233	9.7285	ENSG00000215700	PNRC2

ENSG00000215704	0.419313	0.752905	0.158991	0	ENSG00000215704	CELA2B
ENSG00000215705	0	0	0.447628	0	ENSG00000215705	AC011841.2
ENSG00000215712	3.84836	4.9837	4.23204	3.57993	ENSG00000215712	TMEM242
ENSG00000215713	0	0	0	0	ENSG00000215713	CU179654.1
ENSG00000215717	15.567	15.5914	21.2032	19.8745	ENSG00000215717	TMEM167B
ENSG00000215719	0	0	0	0	ENSG00000215719	AL356585.3
ENSG00000215720	0.477252	1.18888	0.998428	1.83374	ENSG00000215720	AL035405.1
ENSG00000215734	0	0	0	0	ENSG00000215734	MRPL20P1
ENSG00000215749	0.751845	0.785229	1.68785	1.94949	ENSG00000215749	GOLGA6L18
ENSG00000215750	1.70318	1.78229	2.68554	0	ENSG00000215750	AC145212.1
ENSG00000215760	0	0	0.395716	0.162893	ENSG00000215760	TAF9BP2
ENSG00000215764	0	0	0	0	ENSG00000215764	KIR2DL2
ENSG00000215771	0	0.327255	0.295392	0.366366	ENSG00000215771	LRRC37A14P
ENSG00000215781	9.92612	17.0543	11.6734	19.1466	ENSG00000215781	AC011043.1
ENSG00000215784	0.125451	1.72278	0.0821945	0.45449	ENSG00000215784	FAM72D
ENSG00000215785	0	0	0	0.330487	ENSG00000215785	CFL1P6
ENSG00000215788	68.0184	129.52	76.9539	45.0631	ENSG00000215788	TNFRSF25
ENSG00000215790	6.63773	11.5593	12.0381	18.153	ENSG00000215790	SLC35E2
ENSG00000215791	0	1.59731	9.25E-09	1.15027	ENSG00000215791	AL645728.2
ENSG00000215795	0.274732	0.397042	0.300179	0.301042	ENSG00000215795	AL390728.2
ENSG00000215796	0.193681	0.606041	0.379223	0.370235	ENSG00000215796	AL512637.1
ENSG00000215800	0	0.152735	0	0	ENSG00000215800	RSL24D1P4
ENSG00000215802	0	0	0	0	ENSG00000215802	RFKP1
ENSG00000215805	0.0399667	0.160231	0.0696356	0.0437321	ENSG00000215805	AL356361.1
ENSG00000215807	0	0	0	0	ENSG00000215807	KRT18P65
ENSG00000215811	0.60266	0.351266	1.77294	0.251552	ENSG00000215811	BTNL10
ENSG00000215812	0.0565534	0.108854	0.0983793	2.66561	ENSG00000215812	ZNF847P
ENSG00000215817	0.47763	0.379249	0.418788	0.814776	ENSG00000215817	ZC3H11B
ENSG00000215819	0.175755	0.636506	0.778991	0.900144	ENSG00000215819	KRT18P12
ENSG00000215833	0.0375769	0	0	0.0425674	ENSG00000215833	QRSL1P1
ENSG00000215834	0.483359	1.16515	1.22874	2.54141	ENSG00000215834	FMO9P
ENSG00000215835	0.0299744	0	0	0.032792	ENSG00000215835	AL596087.1
ENSG00000215837	7.44268	6.09996	10.1247	9.6529	ENSG00000215837	SDHAP2
ENSG00000215838	0.707334	0.780647	1.28068	0.779375	ENSG00000215838	AL451074.1
ENSG00000215840	0.365026	1.75137	1.31288	5.29545	ENSG00000215840	AL592295.1
ENSG00000215845	49.1732	44.6725	26.9486	15.2621	ENSG00000215845	TSTD1
ENSG00000215846	0	0	0	0	ENSG00000215846	MPTX1
ENSG00000215853	0.547574	0.176025	0.968171	0.569116	ENSG00000215853	RPTN
ENSG00000215860	0.507563	1.34637	1.37514	0.828091	ENSG00000215860	PDZK1P1
ENSG00000215861	0	0	0	0	ENSG00000215861	AC245297.1
ENSG00000215864	1.80612	2.67788	3.79247	3.13681	ENSG00000215864	NBPF7
ENSG00000215867	0.39092	1.41556	1.54847	2.02215	ENSG00000215867	KRT18P57
ENSG00000215871	0	0.0767038	0	0.0870201	ENSG00000215871	AC104457.1
ENSG00000215873	0	0	0	0.11491	ENSG00000215873	FEN1P1
ENSG00000215874	0.218931	1.15793	0.0949305	0.236021	ENSG00000215874	CAPNS1P1
ENSG00000215875	0.808557	0.111957	0.250386	0.425765	ENSG00000215875	ST13P20
ENSG00000215878	1.75169	3.82473	3.21633	4.63377	ENSG00000215878	MARCKSL1P2
ENSG00000215883	3.18759	5.90542	5.39547	10.1859	ENSG00000215883	CYB5RL
ENSG00000215887	0	0.0557887	0	0	ENSG00000215887	ZNF859P
ENSG00000215893	0	0.584367	0	1.62893	ENSG00000215893	RPL23AP17
ENSG00000215895	0	0.0281939	0	0	ENSG00000215895	AL354702.1
ENSG00000215899	0	0	0	0	ENSG00000215899	AC209007.1
ENSG00000215900	0	0	0	0	ENSG00000215900	SELENOWP1
ENSG00000215902	0	0	0	0	ENSG00000215902	AL353354.1

ENSG00000215905	0	0	0	0	ENSG00000215905	AL590609.1
ENSG00000215906	0.140056	0.101201	0.15247	0.153446	ENSG00000215906	LACTBL1
ENSG00000215909	0	0	0	0	ENSG00000215909	BRWD1P1
ENSG00000215910	0.726448	1.60275	1.49976	2.19806	ENSG00000215910	C1orf167
ENSG00000215912	2.96744	6.73848	6.43496	10.2515	ENSG00000215912	TTC34
ENSG00000215914	0.192482	0.450872	0.353202	0.563599	ENSG00000215914	MMP23A
ENSG00000215915	2.32287	2.82139	4.20913	4.83307	ENSG00000215915	ATAD3C
ENSG00000216265	0	0	0	0	ENSG00000216265	FABP12P1
ENSG00000216285	0	0	0	0	ENSG00000216285	AC078819.1
ENSG00000216306	0	0.119678	0.216146	0.40207	ENSG00000216306	KRT19P2
ENSG00000216307	0	0	0	0.105439	ENSG00000216307	AL136309.1
ENSG00000216316	0.122649	0.588538	0.850488	1.84602	ENSG00000216316	AL022722.1
ENSG00000216324	0	0.689776	0.310968	0.754661	ENSG00000216324	AL049697.2
ENSG00000216331	8.0303	1.37012	1.21379	3.65763	ENSG00000216331	HIST1H1PS1
ENSG00000216347	0.639566	0.798945	0.624058	0.802012	ENSG00000216347	RPL10P10
ENSG00000216352	0.0436141	0.0420013	0.113894	0.190768	ENSG00000216352	AL590824.1
ENSG00000216359	0.194736	0.093564	0	0.105245	ENSG00000216359	AL139039.1
ENSG00000216360	0.0659811	1.71E-07	0	0.0717841	ENSG00000216360	AL136968.1
ENSG00000216364	0	0	0	0	ENSG00000216364	MRPL42P2
ENSG00000216365	0	0	0.648636	1.57219	ENSG00000216365	AL133388.1
ENSG00000216368	0	0	0	0	ENSG00000216368	AL136226.1
ENSG00000216378	0	0.0605519	0	0	ENSG00000216378	AL080285.1
ENSG00000216412	0	0	0	0	ENSG00000216412	RPL12P2
ENSG00000216425	0.0807479	0	0	0	ENSG00000216425	AC004066.1
ENSG00000216436	0	0	0	0	ENSG00000216436	AL512384.1
ENSG00000216439	0.166994	0	0	0	ENSG00000216439	DUTP5
ENSG00000216444	0	0	0.102909	0	ENSG00000216444	RAET1M
ENSG00000216471	0	0	0	0.239978	ENSG00000216471	RPSAP43
ENSG00000216475	0	0.115267	0	0.904268	ENSG00000216475	AL024474.1
ENSG00000216480	0	0	0	0	ENSG00000216480	AL078604.1
ENSG00000216490	6.84335	18.6248	14.1742	4.00349	ENSG00000216490	IFI30
ENSG00000216516	0	0	1.09656	0.660364	ENSG00000216516	AL645733.1
ENSG00000216518	0	0.200812	0	0.151332	ENSG00000216518	EEF1GP6
ENSG00000216519	0	0	0	0	ENSG00000216519	AL023284.1
ENSG00000216522	0	0	0.0809018	0	ENSG00000216522	AC011718.1
ENSG00000216523	0	0	0	0	ENSG00000216523	AL109941.1
ENSG00000216548	0	0	0	0	ENSG00000216548	AL357084.1
ENSG00000216560	0.717655	1.73179	1.98569	2.55214	ENSG00000216560	LINC00955
ENSG00000216588	0.385406	0.213318	0.165185	0.397773	ENSG00000216588	IGSF23
ENSG00000216613	0.494103	0.371155	0.428189	0.265552	ENSG00000216613	AL023284.2
ENSG00000216616	0	0	0	0	ENSG00000216616	AL356421.1
ENSG00000216621	1.40831	1.17178	1.37835	1.3443	ENSG00000216621	AL583835.2
ENSG00000216624	0	0.0587545	0	0	ENSG00000216624	GAPDHP72
ENSG00000216629	0.0677043	0	0.117662	0	ENSG00000216629	OR2W4P
ENSG00000216636	0.36963	1.33298	0.613918	1.3009	ENSG00000216636	RPL7P25
ENSG00000216639	1.32476	1.4424	2.23912	2.1986	ENSG00000216639	AL133406.1
ENSG00000216642	0.231315	1.76661	0.604881	0.741161	ENSG00000216642	AL136116.1
ENSG00000216649	0	0	0	0	ENSG00000216649	GAGE12E
ENSG00000216657	0.181323	0.237781	0.375479	0.414605	ENSG00000216657	GLRX3P2
ENSG00000216663	0	0	0	0.0674766	ENSG00000216663	AL365214.1
ENSG00000216671	0.0573035	0.113493	0.318408	0.258244	ENSG00000216671	CCNYL3
ENSG00000216676	0	0	0	0	ENSG00000216676	AL031229.1
ENSG00000216687	0.12396	0.120489	0.156395	0.501113	ENSG00000216687	AL390237.1
ENSG00000216708	0.323661	0.319981	0.420006	1.4088	ENSG00000216708	CIR1P3

ENSG00000216710	0	0	0	0	ENSG00000216710	COX6A1P3
ENSG00000216713	0.0686114	0.262966	0.331253	0.351416	ENSG00000216713	MTND4P13
ENSG00000216718	0.324064	0.594665	0.837754	0.516605	ENSG00000216718	AL024509.2
ENSG00000216721	0	0	0	0	ENSG00000216721	AC093850.1
ENSG00000216723	0	0	0.113467	0.563148	ENSG00000216723	NUDT19P3
ENSG00000216740	0.0611768	0	0	0	ENSG00000216740	ANXA2P3
ENSG00000216753	0	0	0	0	ENSG00000216753	HMGA1P7
ENSG00000216754	0.231635	0.637681	0.14355	1.01958	ENSG00000216754	AL050335.1
ENSG00000216762	0	0	0	0	ENSG00000216762	VN1R13P
ENSG00000216775	0.373316	0.541185	0.429784	2.87214	ENSG00000216775	AL109918.1
ENSG00000216777	0	0	0	0	ENSG00000216777	PRRC2CP1
ENSG00000216781	0.100734	0	0	0	ENSG00000216781	AL138885.1
ENSG00000216802	1.33561	8.91126	3.31139	4.57207	ENSG00000216802	AL590617.1
ENSG00000216809	0.175477	0.317394	0.191181	0.819473	ENSG00000216809	AL589993.1
ENSG00000216811	0	0.246216	0.672245	1.10038	ENSG00000216811	AL035698.1
ENSG00000216813	1.08205	2.06874	2.42756	5.48993	ENSG00000216813	AL358178.1
ENSG00000216817	0	0	0.0467557	0.146778	ENSG00000216817	R3HDM2P2
ENSG00000216819	0.580901	0.327604	0.222161	0.288647	ENSG00000216819	TUBB2BP1
ENSG00000216824	0.110779	0.262706	0.332403	0.423699	ENSG00000216824	ZNF736P10Y
ENSG00000216829	0	0	0	0	ENSG00000216829	FGF7P4
ENSG00000216835	0	0	0.0438318	0	ENSG00000216835	RBMXP1
ENSG00000216844	0	0	0	0.00169038	ENSG00000216844	AC009494.1
ENSG00000216853	0.384319	2.39789	2.77983	2.18127	ENSG00000216853	MTCYBP36
ENSG00000216854	0.792796	0.381885	0.919046	1.41949	ENSG00000216854	AL512422.1
ENSG00000216859	0	0.245824	0.449924	0.96283	ENSG00000216859	DHFRP5
ENSG00000216866	0.0842764	0.825186	0.264105	0.166775	ENSG00000216866	RPS2P55
ENSG00000216867	0	3.24557	0	0.991334	ENSG00000216867	AC226101.1
ENSG00000216895	10.702	18.141	20.5259	32.5327	ENSG00000216895	AC009403.1
ENSG00000216901	0	0.151364	0.160822	0.168651	ENSG00000216901	ZNF603P
ENSG00000216902	0.246201	0	0	0	ENSG00000216902	AL122016.1
ENSG00000216904	0	0.0700652	0	0.0802929	ENSG00000216904	SOCS5P5
ENSG00000216906	0.0771638	0.148754	0.22557	0.0283531	ENSG00000216906	AL355312.1
ENSG00000216913	0	0	0	0	ENSG00000216913	AL049693.1
ENSG00000216915	0.0388437	0.30028	0.203219	0.128636	ENSG00000216915	GPR89P
ENSG00000216917	0	0	0	0	ENSG00000216917	AC005587.1
ENSG00000216921	0.297878	0.981969	0.571733	0.608421	ENSG00000216921	AC131097.2
ENSG00000216937	3.11535	11.7962	11.1224	15.031	ENSG00000216937	CCDC7
ENSG00000216938	0	0	0	0	ENSG00000216938	RPL7P58
ENSG00000216966	0	0	0	0	ENSG00000216966	AL353747.1
ENSG00000216977	1.02664	0.324681	1.2165	1.91198	ENSG00000216977	RPL21P65
ENSG00000216990	0.102617	0.0659342	0.0896125	0.112515	ENSG00000216990	HSPD1P10
ENSG00000216998	0.051193	0.197125	0.0445415	0.0558849	ENSG00000216998	CYP2AC1P
ENSG00000217004	0	0.283962	0	0.62482	ENSG00000217004	Z97832.1
ENSG00000217026	0.107026	0	0	0	ENSG00000217026	RPL10P1
ENSG00000217027	0	0	0	0	ENSG00000217027	TPT1P4
ENSG00000217030	0	0	0	0	ENSG00000217030	AL359643.1
ENSG00000217041	0	0.536312	0.726716	2.36146	ENSG00000217041	AL512430.2
ENSG00000217044	0	0	0	0	ENSG00000217044	MTCO3P31
ENSG00000217060	0	0	0	0	ENSG00000217060	AL135903.1
ENSG00000217067	0	0	0	0	ENSG00000217067	AL355375.1
ENSG00000217075	2.63813	4.04236	1.97455	9.99344	ENSG00000217075	AC007401.2
ENSG00000217078	0.833032	0	0	0	ENSG00000217078	AL021407.1
ENSG00000217083	0	0	0.162639	0	ENSG00000217083	MTCO2P33
ENSG00000217085	0	0.124119	0	0	ENSG00000217085	HMGB3P19

ENSG00000217089	0	0	0	0	ENSG00000217089	RPS29P13
ENSG00000217094	0	0.173143	0.622087	0.205279	ENSG00000217094	PPIAP31
ENSG00000217120	2.63615	9.15979	6.8509	15.042	ENSG00000217120	Z98755.1
ENSG00000217128	18.1955	15.1172	14.5127	14.2984	ENSG00000217128	FNIP1
ENSG00000217130	0	0.299107	0	0.165874	ENSG00000217130	AL139100.1
ENSG00000217135	0	0	0	0	ENSG00000217135	AL590004.1
ENSG00000217139	0.0442291	0	0	0	ENSG00000217139	AL603865.1
ENSG00000217159	1.49412	0.69832	0	0	ENSG00000217159	LARP1P1
ENSG00000217160	0	0	0	0	ENSG00000217160	MTCO2P31
ENSG00000217165	1.14651	1.09263	1.2433	1.08265	ENSG00000217165	ANKRD18EP
ENSG00000217169	0	0	0	0	ENSG00000217169	MTHFD2P2
ENSG00000217178	0	0	0	0	ENSG00000217178	AL357563.1
ENSG00000217179	0	1.04294	0	0	ENSG00000217179	MTCYBP2
ENSG00000217181	0.323815	0	0.147326	0.346585	ENSG00000217181	AL139039.2
ENSG00000217195	1.2844	1.21853	0.275371	3.01177	ENSG00000217195	AL513475.1
ENSG00000217227	0.148756	0.190739	0.345607	0.216359	ENSG00000217227	AL079341.1
ENSG00000217228	0.148512	0	0	0	ENSG00000217228	GSTA12P
ENSG00000217231	0	0	0.183713	0.114254	ENSG00000217231	AL109755.1
ENSG00000217236	0.519833	0.125357	0.189459	0.28954	ENSG00000217236	SP9
ENSG00000217239	0.261845	0	0	0.669283	ENSG00000217239	AL136968.2
ENSG00000217241	0	0	0.2895	0.363457	ENSG00000217241	CBX3P9
ENSG00000217261	0	0	0	0	ENSG00000217261	POM121L4P
ENSG00000217268	0	0	0	0	ENSG00000217268	TXNP7
ENSG00000217272	0	0	0	0	ENSG00000217272	AL049545.1
ENSG00000217275	4.53759	0.146418	0	0.489885	ENSG00000217275	AL031777.1
ENSG00000217281	0	0	0	0	ENSG00000217281	LYPLA2P1
ENSG00000217289	0	0	0	0	ENSG00000217289	AC079776.1
ENSG00000217314	0	0	0.196103	0	ENSG00000217314	UQCRFS1P3
ENSG00000217315	0	0.0665812	0	0	ENSG00000217315	OR2W2P
ENSG00000217325	3.35836	1.8361	1.80269	0.328866	ENSG00000217325	PRELID1P1
ENSG00000217327	0	0	0	0	ENSG00000217327	RPS7P5
ENSG00000217330	0.317825	1.76711	1.37677	1.44557	ENSG00000217330	SSXP10
ENSG00000217331	0.116481	0.283476	0.0919998	0.385182	ENSG00000217331	AL355143.1
ENSG00000217334	0	0.103393	0	0.85313	ENSG00000217334	AL355615.1
ENSG00000217372	0	0	0	0.0527445	ENSG00000217372	TUBB4BP7
ENSG00000217377	0	0	0	0	ENSG00000217377	AK4P5
ENSG00000217379	0	0	0	0	ENSG00000217379	AL589647.1
ENSG00000217385	0	0.0870029	0	0	ENSG00000217385	PSMC1P11
ENSG00000217404	0	0	0	0	ENSG00000217404	RPS4XP9
ENSG00000217408	0	0	0	0	ENSG00000217408	PRELID1P2
ENSG00000217414	0.0318707	0.193187	0.169101	0.146778	ENSG00000217414	DDX18P3
ENSG00000217416	0.815827	0	0.732942	0	ENSG00000217416	ISCA1P1
ENSG00000217442	0	0	0	0.290891	ENSG00000217442	SYCE3
ENSG00000217447	0	0	0	0	ENSG00000217447	AL021331.1
ENSG00000217455	0.422621	2.70077	1.41854	2.22293	ENSG00000217455	AC073316.1
ENSG00000217477	0	0	0	0	ENSG00000217477	AL450346.1
ENSG00000217482	0	0.424901	0.514386	0.740302	ENSG00000217482	HMGB1P17
ENSG00000217483	0	0.226877	0	0	ENSG00000217483	FO393414.2
ENSG00000217488	1.19836	2.45765	3.96778	2.89567	ENSG00000217488	AL356057.1
ENSG00000217495	0.687108	2.17956	2.13337	1.34846	ENSG00000217495	AL136116.2
ENSG00000217512	0.359272	0.85971	0.954727	1.71929	ENSG00000217512	AL356776.1
ENSG00000217514	0	0	0	0	ENSG00000217514	AL031121.1
ENSG00000217527	1.68263	4.82485	3.99378	6.23622	ENSG00000217527	RPS16P5
ENSG00000217539	0.181019	0.173645	0.0949961	0.161048	ENSG00000217539	IQCB2P

ENSG00000217555	15.7871	24.2968	9.52801	10.5389	ENSG00000217555	CKLF
ENSG00000217557	0	0	0.316514	0.383906	ENSG00000217557	AL590286.1
ENSG00000217566	0	0	0	0	ENSG00000217566	TDGF1P4
ENSG00000217585	0	0	0	0	ENSG00000217585	AL021407.2
ENSG00000217612	0	0	0.0263416	0.0997854	ENSG00000217612	AL031119.1
ENSG00000217624	0.204456	0.681364	0.53498	0.219384	ENSG00000217624	AL627402.1
ENSG00000217631	0	0	0	0	ENSG00000217631	FO393413.1
ENSG00000217643	0.482916	1.26395	0.704075	2.5876	ENSG00000217643	PTGES3P2
ENSG00000217644	0.141272	0	0.36702	0.151301	ENSG00000217644	AL355864.1
ENSG00000217646	0	0	0	0	ENSG00000217646	HIST1H2BPS2
ENSG00000217648	2.60811	3.74714	2.63512	1.3239	ENSG00000217648	AL136116.3
ENSG00000217653	0.43558	1.36948	1.80678	1.49673	ENSG00000217653	AL353692.1
ENSG00000217680	0	0	0	0	ENSG00000217680	UBE2V1P15
ENSG00000217684	0	0.35367	0.241652	0.495542	ENSG00000217684	RPS3AP24
ENSG00000217686	0.121785	0.116883	0	0.130954	ENSG00000217686	NUS1P4
ENSG00000217702	0.543764	0.392182	0	0.591265	ENSG00000217702	AC073263.1
ENSG00000217707	0	0	0	0.24825	ENSG00000217707	SERPINB8P1
ENSG00000217716	0	0	0	0	ENSG00000217716	RPS10P3
ENSG00000217718	0	0	0	0	ENSG00000217718	NDUFB4P4
ENSG00000217733	0.35738	0.654709	0.655393	0.313804	ENSG00000217733	CCT7P1
ENSG00000217746	0.072111	0.145494	0.199396	0.277926	ENSG00000217746	AL096800.1
ENSG00000217767	0.515883	0.987929	0.743331	1.64815	ENSG00000217767	NDUFAB1P1
ENSG00000217769	0	0	0	0	ENSG00000217769	AL157777.1
ENSG00000217770	0	0	0	0.0361705	ENSG00000217770	FEM1AP3
ENSG00000217776	0	0	0	0	ENSG00000217776	AL138827.1
ENSG00000217783	0.224987	0.293343	0.330485	0.856166	ENSG00000217783	LDHAL6FP
ENSG00000217786	0	0	0	0	ENSG00000217786	AL355379.1
ENSG00000217791	0	0	0	0	ENSG00000217791	ASS1P9
ENSG00000217792	0	0	0	0	ENSG00000217792	KIR3DL2
ENSG00000217801	13.8221	22.3209	26.935	22.7664	ENSG00000217801	AL390719.1
ENSG00000217805	0	0.215323	0	0.476288	ENSG00000217805	AL590084.1
ENSG00000217809	0	0	0	0	ENSG00000217809	FAT1P1
ENSG00000217811	0.162337	0.311106	0.28084	0.346418	ENSG00000217811	HNRNPDP2
ENSG00000217824	0	0	0	0	ENSG00000217824	SNRPEP6
ENSG00000217825	0.177513	0.353123	0.0770481	0.38429	ENSG00000217825	AC099552.1
ENSG00000217835	0.0743186	0	0.130168	0.163041	ENSG00000217835	AL034397.1
ENSG00000217862	1.35569	0.417579	0.748457	0	ENSG00000217862	AL009179.1
ENSG00000217874	0	0	0	0	ENSG00000217874	OR4F7P
ENSG00000217878	0	0.280889	0	0	ENSG00000217878	AL136100.1
ENSG00000217889	0	0	0.032812	0	ENSG00000217889	KRT18P48
ENSG00000217896	0.301907	1.37241	2.31223	1.72716	ENSG00000217896	ZNF839P1
ENSG00000217897	1.16527	1.44158	2.41078	4.39656	ENSG00000217897	HSPE1P8
ENSG00000217929	0.599205	1.46067	1.10574	1.1099	ENSG00000217929	CICP18
ENSG00000217930	20.1875	21.1965	23.3794	22.3421	ENSG00000217930	PAM16
ENSG00000217950	0	0	0.154677	0	ENSG00000217950	NOC2LP2
ENSG00000218014	0.153044	0.0488134	0.0443386	0	ENSG00000218014	KRT19P1
ENSG00000218016	0	0.081672	0.0738232	0.0463785	ENSG00000218016	ZNF192P2
ENSG00000218020	0.0245172	0.0472662	0.170968	0.269243	ENSG00000218020	THAP12P5
ENSG00000218027	0	0.0703467	0.031633	0	ENSG00000218027	AL512329.1
ENSG00000218029	0	0	0	0	ENSG00000218029	AL078601.1
ENSG00000218048	0.0644207	0	0.0561175	0.069938	ENSG00000218048	AL121949.1
ENSG00000218049	0	0	0	0	ENSG00000218049	AL591034.1
ENSG00000218052	7.69659	5.35362	5.55796	16.8513	ENSG00000218052	ADAMTS7P4
ENSG00000218069	0	0	0	0	ENSG00000218069	RSL24D1P1

ENSG00000218073	0	0.305129	0.281455	0.354219	ENSG00000218073	AL021407.3
ENSG00000218089	0	0.0496234	0	0	ENSG00000218089	DNAJA1P4
ENSG00000218107	0	0.23249	0.140029	0.174852	ENSG00000218107	AL136131.1
ENSG00000218125	0	0	0	0	ENSG00000218125	AP000567.1
ENSG00000218143	0.352998	0	0.301653	0	ENSG00000218143	ERHP2
ENSG00000218153	0.0436876	0.0850682	0.152113	0.0955431	ENSG00000218153	KRT18P22
ENSG00000218173	0.190002	0	0.164133	0.201765	ENSG00000218173	AL356967.1
ENSG00000218175	0.706601	0.367115	0	0	ENSG00000218175	AC016739.1
ENSG00000218180	0	0	0.0612186	0.307797	ENSG00000218180	SLC25A5P7
ENSG00000218186	0	0	0.0347836	0	ENSG00000218186	KRT8P43
ENSG00000218187	0.625194	0.999352	1.32169	1.95872	ENSG00000218187	AL356432.1
ENSG00000218189	0.101191	0.465597	0.273929	0.43218	ENSG00000218189	POM121L14P
ENSG00000218194	0.152411	0.146092	0.263811	0	ENSG00000218194	HLFP1
ENSG00000218198	0	0.326609	0	0.357694	ENSG00000218198	RPS20P32
ENSG00000218208	0	0	0.159593	0	ENSG00000218208	RPS27AP11
ENSG00000218213	0	0	0	0	ENSG00000218213	FTH1P26
ENSG00000218226	8.27063	7.68489	6.18314	6.04488	ENSG00000218226	TATDN2P2
ENSG00000218227	0.127139	0	0	0.134181	ENSG00000218227	AC136632.1
ENSG00000218233	0.128465	0.247439	0.298212	0.140501	ENSG00000218233	NEPNP
ENSG00000218261	0	0	0	0	ENSG00000218261	AL591034.2
ENSG00000218265	0	0	0	0	ENSG00000218265	RPS4XP7
ENSG00000218274	0	0.144421	0.032533	0.0409106	ENSG00000218274	AL121949.2
ENSG00000218281	3.84102	0	1.5128	1.83671	ENSG00000218281	HIST1H2APS3
ENSG00000218283	0.449595	1.20398	1.51668	1.76558	ENSG00000218283	MORF4L1P1
ENSG00000218297	0	0.0275452	0	0.0234623	ENSG00000218297	AL935156.1
ENSG00000218300	0	0	0	0	ENSG00000218300	AL353692.2
ENSG00000218305	0	0	0	0	ENSG00000218305	CDC14C
ENSG00000218313	1.63652	3.41055	2.05231	5.07542	ENSG00000218313	AL139274.1
ENSG00000218336	22.9886	30.8543	23.466	32.2185	ENSG00000218336	TENM3
ENSG00000218337	0.561264	0	0	0	ENSG00000218337	AL589994.1
ENSG00000218346	0.0696583	0.0325235	0.0297489	0.07334	ENSG00000218346	VN1R14P
ENSG00000218347	0	0	0	0	ENSG00000218347	HNRNPA1P1
ENSG00000218350	0.127088	0.227431	0	0.126993	ENSG00000218350	LYPLA1P3
ENSG00000218351	0.196935	0.476149	0.602336	1.27828	ENSG00000218351	RPS3AP23
ENSG00000218357	0.0629376	0.0605519	0	0.142302	ENSG00000218357	LINC01644
ENSG00000218358	1.04864	1.92544	1.51987	1.08172	ENSG00000218358	RAET1K
ENSG00000218359	0	0	0	0	ENSG00000218359	SUMO2P13
ENSG00000218363	0	0	0	0	ENSG00000218363	SLC25A20P1
ENSG00000218410	0	0.0673226	0.0607833	0.1147	ENSG00000218410	AC012078.1
ENSG00000218416	5.48981	11.5333	14.7773	15.4802	ENSG00000218416	PP14571
ENSG00000218418	0.0565995	0.0996042	0.0790798	0.22204	ENSG00000218418	AL591135.1
ENSG00000218422	0.766591	2.71817	0.746806	1.89545	ENSG00000218422	AC016773.1
ENSG00000218424	0.375626	1.77787	0.961397	0.388439	ENSG00000218424	NDUFS5P1
ENSG00000218426	0	0	0.696955	0	ENSG00000218426	AL590867.2
ENSG00000218428	1.16475	1.97628	1.26077	2.98624	ENSG00000218428	NIP7P3
ENSG00000218454	0	0	0	0	ENSG00000218454	HNRNPA1P19
ENSG00000218459	0	0	0	1.49724	ENSG00000218459	AL121972.1
ENSG00000218472	0	0	0	0	ENSG00000218472	AL590004.2
ENSG00000218475	0.0527557	0	0.183587	0.345424	ENSG00000218475	ACTG1P18
ENSG00000218476	0	0	0	0	ENSG00000218476	AL591416.1
ENSG00000218483	0	0.412159	0.738867	0	ENSG00000218483	AL356277.1
ENSG00000218490	0	0	0.14	0	ENSG00000218490	FCF1P10
ENSG00000218497	0.320926	0.168457	0.0678645	0.0167152	ENSG00000218497	ZNF84
ENSG00000218499	0	0	0	0	ENSG00000218499	AL031003.1

ENSG00000218502	0.228212	1.5231	0.826329	1.44355	ENSG00000218502	H2AFZP3
ENSG00000218512	0	0	0	0	ENSG00000218512	SPTLC1P2
ENSG00000218520	0.32407	0	0.428149	0.746107	ENSG00000218520	AL450346.2
ENSG00000218521	0.961975	1.84408	3.65895	5.81985	ENSG00000218521	AL589655.1
ENSG00000218536	0	0	0	0	ENSG00000218536	AP002530.1
ENSG00000218537	2.31033	2.36564	5.28651	3.63738	ENSG00000218537	MIF-AS1
ENSG00000218549	0	0	0	0	ENSG00000218549	OR4K12P
ENSG00000218561	0	0	0	0	ENSG00000218561	AL353133.1
ENSG00000218565	0	0.038042	0.0344277	0.216502	ENSG00000218565	AL592429.1
ENSG00000218574	0	0.252297	0.112077	0.431973	ENSG00000218574	HNRNPA1P37
ENSG00000218577	0	0.272071	0	0.102056	ENSG00000218577	AL035696.2
ENSG00000218582	0.122756	0	0.0533152	0	ENSG00000218582	GAPDHP63
ENSG00000218586	0.0610843	0.0709688	0.139106	0.163511	ENSG00000218586	AC006971.1
ENSG00000218596	0.936938	4.57546	4.73472	2.45504	ENSG00000218596	AL162578.1
ENSG00000218617	0	0	0	0	ENSG00000218617	AL121949.3
ENSG00000218631	0	0.109002	0.0984413	0	ENSG00000218631	AL117344.1
ENSG00000218632	0	0.094244	0.079783	0.716817	ENSG00000218632	RPL7P28
ENSG00000218643	0	0	0	0	ENSG00000218643	RPL5P20
ENSG00000218672	0.188954	0.340143	0.363605	0.881289	ENSG00000218672	AC008060.1
ENSG00000218676	0.221155	0.602124	0.369229	0.727553	ENSG00000218676	BRD7P4
ENSG00000218682	0.4741	0.315169	0.786282	0.353664	ENSG00000218682	AC064847.1
ENSG00000218689	0	0.152165	0	0	ENSG00000218689	RPL5P21
ENSG00000218690	0.538937	0.256685	0	0.282708	ENSG00000218690	HIST1H2APS4
ENSG00000218698	0	0	0	0.271918	ENSG00000218698	ST13P16
ENSG00000218713	0.707033	1.24537	1.63811	2.51445	ENSG00000218713	AL512378.1
ENSG00000218716	0	0	0.406295	0.167174	ENSG00000218716	RPL12P23
ENSG00000218725	0	0	0	0	ENSG00000218725	B3GALNT2P1
ENSG00000218728	0	0.0443856	0	0	ENSG00000218728	KRT18P44
ENSG00000218730	0	0.204426	0.540488	0.663008	ENSG00000218730	AL117342.1
ENSG00000218732	0	0.220558	0.0696629	0.170645	ENSG00000218732	AL035633.1
ENSG00000218739	22.6788	34.101	35.2304	37.3769	ENSG00000218739	CEBPZOS
ENSG00000218748	0	0	0	0	ENSG00000218748	DBIP1
ENSG00000218749	1.00925	4.14547	0.584397	2.79799	ENSG00000218749	AL033519.1
ENSG00000218754	0	0	0	0	ENSG00000218754	RPL18AP8
ENSG00000218757	1.33692	2.95425	2.08813	3.03666	ENSG00000218757	AL121952.1
ENSG00000218766	0	0	0	0.157114	ENSG00000218766	AL450338.1
ENSG00000218772	0.0531886	0	0.140545	0.0603322	ENSG00000218772	FAM8A6P
ENSG00000218776	0	0	0	0	ENSG00000218776	MTATP6P31
ENSG00000218792	0.219676	0.418511	0	0.464719	ENSG00000218792	HSPD1P16
ENSG00000218793	0	0.0606927	0.109912	0.137815	ENSG00000218793	AL049697.3
ENSG00000218803	0	0	0	0	ENSG00000218803	GSTM2P1
ENSG00000218806	0	0	0	0	ENSG00000218806	AL133264.1
ENSG00000218809	0	0	0	0	ENSG00000218809	AL391903.1
ENSG00000218813	0	0	0	0	ENSG00000218813	AL354719.1
ENSG00000218819	0.017356	0.125878	0.0302788	0.09564	ENSG00000218819	TDRD15
ENSG00000218823	0.0126627	0.0977873	0.0662501	0.167599	ENSG00000218823	PAPOLB
ENSG00000218834	0	0.820057	0	0	ENSG00000218834	AL606923.1
ENSG00000218857	0.0517551	0	0.0915176	0.169474	ENSG00000218857	AL137222.1
ENSG00000218868	0	0	0	0	ENSG00000218868	CNN3P1
ENSG00000218870	0	0	0	0	ENSG00000218870	SLC25A6P6
ENSG00000218872	0	0	0.243493	0.296713	ENSG00000218872	AL445189.1
ENSG00000218890	0	0	0	0	ENSG00000218890	AL049842.1
ENSG00000218891	7.31524	6.47402	8.68057	9.05507	ENSG00000218891	ZNF579
ENSG00000218893	1.75871	1.62358	1.38745	0	ENSG00000218893	SUMO2P12

ENSG00000218896	1.6963	1.47788	2.00192	1.31815	ENSG00000218896	TUBB8P2
ENSG00000218902	0.297794	0.855551	0.512196	0	ENSG00000218902	PTMAP3
ENSG00000218965	0	0	0	0	ENSG00000218965	NACAP7
ENSG00000218976	0.0899783	0.0941638	0	0.0990296	ENSG00000218976	AL138725.1
ENSG00000218980	0	0	0.347786	0.842753	ENSG00000218980	FTH1P15
ENSG00000218986	0	0	0	0.410685	ENSG00000218986	AL136087.1
ENSG00000218991	0	0	0	0	ENSG00000218991	CCNG1P1
ENSG00000218996	0.417915	2.47578	2.66902	1.4877	ENSG00000218996	ARL4AP5
ENSG00000219016	0.102154	0.151044	0.11021	0.376065	ENSG00000219016	CTA-299D3.8
ENSG00000219023	0	0	0	0	ENSG00000219023	AL033519.2
ENSG00000219027	0.174525	0.167721	0.378793	0	ENSG00000219027	RPS3AP2
ENSG00000219039	0	0	0	0	ENSG00000219039	AC005102.1
ENSG00000219041	0	0	0	0	ENSG00000219041	IGKV1OR2-118
ENSG00000219061	0	0.0419762	0	0.0539314	ENSG00000219061	TRIM51FP
ENSG00000219073	1.39427	2.93259	3.60929	6.87576	ENSG00000219073	CELA3B
ENSG00000219074	0	0	0	0	ENSG00000219074	SOD1P1
ENSG00000219085	0.421291	2.00277	0.961317	2.12876	ENSG00000219085	NPM1P37
ENSG00000219087	0	0	1.96415	1.33033	ENSG00000219087	MTND4LP19
ENSG00000219088	0.0342733	0.132085	0.0298504	0.0751123	ENSG00000219088	Z97206.1
ENSG00000219095	0	0	0	0	ENSG00000219095	DHFRP6
ENSG00000219102	0	0.112315	0.102303	0	ENSG00000219102	HNRNPA3P12
ENSG00000219133	0.189869	0	0	0.423499	ENSG00000219133	AL592114.1
ENSG00000219135	0.170143	0.666397	0.388857	1.85243	ENSG00000219135	RPL23AP48
ENSG00000219139	0.0731185	0	0.0635395	0.0794296	ENSG00000219139	TYMSP1
ENSG00000219146	0	0	0	0	ENSG00000219146	RPS4XP8
ENSG00000219149	0.161776	0	0	0	ENSG00000219149	AL161626.1
ENSG00000219150	0.745544	0.699043	1.85687	0	ENSG00000219150	AL603914.1
ENSG00000219163	0.405995	0.199535	0.0878247	0.109153	ENSG00000219163	HMGB1P20
ENSG00000219186	0	0	0.060841	0.232082	ENSG00000219186	FTH1P19
ENSG00000219188	0	0.106906	0.289653	0.239978	ENSG00000219188	CACYBPP3
ENSG00000219190	0	0	0	0	ENSG00000219190	AL353133.2
ENSG00000219200	71.2233	30.1649	28.1067	24.2425	ENSG00000219200	RNASEK
ENSG00000219201	0.106838	0.210496	0.186282	0.570879	ENSG00000219201	AC138392.1
ENSG00000219222	0	1.81719	0	0	ENSG00000219222	RPL12P47
ENSG00000219240	0.0419554	0	0	0	ENSG00000219240	AL353692.3
ENSG00000219249	0	0.168645	0.0565982	0.0630203	ENSG00000219249	AMZ2P2
ENSG00000219253	0.561399	2.1349	2.76295	3.43408	ENSG00000219253	AL390316.1
ENSG00000219257	0.0736617	0.213354	0	0.480306	ENSG00000219257	NPM1P38
ENSG00000219262	0	0	0	0	ENSG00000219262	Z98745.1
ENSG00000219273	0.810868	1.68737	1.52897	2.38994	ENSG00000219273	AL035555.1
ENSG00000219274	0.224096	0	0	0	ENSG00000219274	RPS20P2
ENSG00000219280	0.0732724	0.325183	0.146169	0.412945	ENSG00000219280	VN1R8P
ENSG00000219284	0	0	0.227546	0	ENSG00000219284	AL592291.1
ENSG00000219294	0.0365897	0.31808	0.256406	0.361258	ENSG00000219294	PIP5K1P1
ENSG00000219297	0	0	0	0.315729	ENSG00000219297	MRPL42P3
ENSG00000219298	0	0	0	0	ENSG00000219298	AL355497.1
ENSG00000219302	0	0	0	0	ENSG00000219302	AL451046.1
ENSG00000219314	0	0	0	0	ENSG00000219314	AL034372.1
ENSG00000219329	0	0	0	0	ENSG00000219329	AL357515.1
ENSG00000219355	1.72341	1.40823	2.36309	2.69641	ENSG00000219355	RPL31P52
ENSG00000219361	0	1.71233	0.885021	0	ENSG00000219361	RPSAP72
ENSG00000219368	0.031542	0.370134	0.247284	0.490312	ENSG00000219368	ZNF299P
ENSG00000219374	0.0886464	0.173708	0.231486	0.0969178	ENSG00000219374	EEF1A1P42
ENSG00000219375	0	0	0.2011	0	ENSG00000219375	AL139095.1

ENSG00000219384	0.107435	0.722259	0.745371	2.31746	ENSG00000219384	AL138880.1
ENSG00000219387	0.067616	0.195072	0.176263	0.294114	ENSG00000219387	ATF1P1
ENSG00000219391	0	0	0	0	ENSG00000219391	AC019129.1
ENSG00000219392	0.346263	0.456948	0.596216	0.369064	ENSG00000219392	ZNF602P
ENSG00000219395	0.414057	1.0347	1.65384	1.97463	ENSG00000219395	HSPA8P15
ENSG00000219404	0	0.335748	0.5054	1.8825	ENSG00000219404	AL359694.1
ENSG00000219409	0.0817666	0.314368	0.142397	0.620511	ENSG00000219409	AL590704.1
ENSG00000219430	0	0.126561	0	0	ENSG00000219430	MBL3P
ENSG00000219433	0.602243	0.678629	1.04521	2.09695	ENSG00000219433	BTBD10P2
ENSG00000219435	0.0889086	0	0.154359	0.192468	ENSG00000219435	CATSPERZ
ENSG00000219438	0.0210642	0.0942305	0.112924	0.362054	ENSG00000219438	FAM19A5
ENSG00000219448	13.7024	31.9317	29.8177	64.6135	ENSG00000219448	RP11-193H22.2
ENSG00000219451	0	0.18636	0	0	ENSG00000219451	RPL23P8
ENSG00000219453	0	0	0	0	ENSG00000219453	AL133270.1
ENSG00000219463	0	0	0	0	ENSG00000219463	RPSAP42
ENSG00000219470	1.1973	1.99077	4.18193	1.81561	ENSG00000219470	AL355802.2
ENSG00000219481	27.9799	57.8696	56.1519	50.0304	ENSG00000219481	NBPF1
ENSG00000219487	0	0.209238	0.0946302	0.355453	ENSG00000219487	AL603766.1
ENSG00000219491	0.65495	0.507742	1.13467	0.562347	ENSG00000219491	TPT1P8
ENSG00000219492	0	0	0	0	ENSG00000219492	AC116655.1
ENSG00000219500	0	0	0.167114	0	ENSG00000219500	AL391417.1
ENSG00000219507	0	0	0	0.0849338	ENSG00000219507	FTH1P8
ENSG00000219529	2.75449	3.86098	2.51699	2.88192	ENSG00000219529	AP000580.1
ENSG00000219532	0.433776	0	0.347956	0.794509	ENSG00000219532	AL139805.1
ENSG00000219545	8.43254	11.2967	6.64591	9.48779	ENSG00000219545	UMAD1
ENSG00000219547	0.262121	0.889706	0.908707	0.984529	ENSG00000219547	AL359715.1
ENSG00000219549	0	0	0	0	ENSG00000219549	AL607077.1
ENSG00000219553	0	0.0897292	0.0858165	0	ENSG00000219553	AL031133.1
ENSG00000219559	0	0	0	0	ENSG00000219559	AL512430.3
ENSG00000219565	0.0656796	0.204884	0.150635	0.573652	ENSG00000219565	ZNF259P1
ENSG00000219575	0	0	0	0.106419	ENSG00000219575	AL035467.1
ENSG00000219582	0	0	0	0	ENSG00000219582	HNRNPA1P58
ENSG00000219592	0	0	0	0	ENSG00000219592	NCSTNP1
ENSG00000219604	0	0	0	1.73273	ENSG00000219604	AL590143.1
ENSG00000219607	0.52645	0.253743	0.211802	0.61405	ENSG00000219607	PPP1R3G
ENSG00000219608	1.40084	1.31778	3.19563	5.70476	ENSG00000219608	HIGD1AP16
ENSG00000219619	0	0	0	0.485812	ENSG00000219619	AL606845.1
ENSG00000219622	0	0	0	0	ENSG00000219622	AL451061.1
ENSG00000219626	36.5898	77.7563	73.7939	129.633	ENSG00000219626	FAM228B
ENSG00000219627	0	0.304633	0	0	ENSG00000219627	CYCSP17
ENSG00000219642	0.149385	0	0	0.230217	ENSG00000219642	BMPR1APS1
ENSG00000219653	0	0	0	0	ENSG00000219653	GCNT1P4
ENSG00000219666	0.406903	0	1.03852	1.31253	ENSG00000219666	AL451046.2
ENSG00000219669	0	0.152863	0.069053	0.086241	ENSG00000219669	BECN1P2
ENSG00000219681	0	0	0	0	ENSG00000219681	AL590084.2
ENSG00000219682	0	0	0	0	ENSG00000219682	AL133268.1
ENSG00000219693	4.03851	2.76521	3.03327	1.93066	ENSG00000219693	FGF7P8
ENSG00000219699	0	0.382731	0.170529	0	ENSG00000219699	AL356432.2
ENSG00000219700	0	0	0	0	ENSG00000219700	PTCHD3P3
ENSG00000219702	0	0	0	0	ENSG00000219702	AL078599.1
ENSG00000219703	0.401485	0.639866	0.924262	1.14128	ENSG00000219703	RAP1BP3
ENSG00000219712	0.437416	1.45058	1.44315	0.902476	ENSG00000219712	AL357054.1
ENSG00000219722	0	0	0	0	ENSG00000219722	AL356057.2
ENSG00000219736	0.0415789	0.440215	0.397913	0.509959	ENSG00000219736	AL356473.1

ENSG00000219738	0	0	0	0	ENSG00000219738	CD83P1
ENSG00000219747	0.450284	0.644212	0.967313	0.253732	ENSG00000219747	AL133260.1
ENSG00000219755	0.0886236	0.0851751	0.230751	0.0961364	ENSG00000219755	AL137784.1
ENSG00000219757	0.19345	0	0	0.205342	ENSG00000219757	AL357139.1
ENSG00000219758	0	0.262793	0.237542	0	ENSG00000219758	FO393415.2
ENSG00000219770	0.219665	0.0704158	0	0.0795399	ENSG00000219770	VN1R11P
ENSG00000219773	0	0	0	0	ENSG00000219773	RPSAP45
ENSG00000219776	0	0	1.0034	0.696172	ENSG00000219776	RPL21P67
ENSG00000219784	0.312385	0	0.180154	0	ENSG00000219784	AL138729.1
ENSG00000219790	0.348846	0	0.15072	0.924438	ENSG00000219790	OSTCP6
ENSG00000219797	0.0579419	0.0677367	0.106788	0.0857336	ENSG00000219797	PPIAP9
ENSG00000219806	0	0	0	0	ENSG00000219806	ATP5F1P6
ENSG00000219807	0	0	0	0	ENSG00000219807	ARF1P1
ENSG00000219814	0	0	0	0	ENSG00000219814	RPL23AP47
ENSG00000219863	0	0	0	0	ENSG00000219863	AL034374.1
ENSG00000219867	0	0	0	0	ENSG00000219867	AL590635.1
ENSG00000219870	0	0	0	0	ENSG00000219870	AC119618.1
ENSG00000219881	0.252671	1.15456	0.778736	1.71962	ENSG00000219881	GAPDHP42
ENSG00000219891	1.38947	2.08918	0.730514	1.2634	ENSG00000219891	ZSCAN12P1
ENSG00000219902	1.20855	1.64671	4.74316	5.35815	ENSG00000219902	RPL35P3
ENSG00000219928	0	0	0	0	ENSG00000219928	AL161787.1
ENSG00000219930	0	0	0	0	ENSG00000219930	GAPDHP67
ENSG00000219932	0	0	0.140803	0	ENSG00000219932	RPL12P8
ENSG00000219940	0	0	0	0	ENSG00000219940	SPTLC1P3
ENSG00000219941	0	0.046444	0	0.0523108	ENSG00000219941	KRT18P50
ENSG00000219951	0.623064	1.91574	1.89435	1.89704	ENSG00000219951	AL391416.1
ENSG00000219986	0.629823	0.60832	0.136559	0.168486	ENSG00000219986	BTF3P7
ENSG00000219992	0.373316	0.714344	0.322482	0.198311	ENSG00000219992	AL391422.1
ENSG00000219993	0.270794	0.262205	0	0	ENSG00000219993	AL138878.1
ENSG00000220008	0.0781758	0.50116	0.363773	1.00555	ENSG00000220008	LINGO3
ENSG00000220023	16.802	14.525	16.1637	25.6362	ENSG00000220023	AL592183.1
ENSG00000220030	0	0	0	0	ENSG00000220030	AL356131.1
ENSG00000220032	1.67932	3.41073	3.06923	4.95199	ENSG00000220032	RP11-17M16.1
ENSG00000220069	0	0.0889179	0	0.200297	ENSG00000220069	RPL7P27
ENSG00000220076	0	0	0	0	ENSG00000220076	AL034345.1
ENSG00000220091	0.728334	0	1.24387	0	ENSG00000220091	LAP3P1
ENSG00000220105	0	0.111916	0	0	ENSG00000220105	AL353151.1
ENSG00000220110	0	0.161515	0	0.179697	ENSG00000220110	AL080315.1
ENSG00000220113	0	0.413203	0.420343	1.01512	ENSG00000220113	MTCYBP4
ENSG00000220125	0	0	0	0	ENSG00000220125	MRPL32P1
ENSG00000220130	0.43656	0	0	0	ENSG00000220130	AL079342.1
ENSG00000220131	0	0	0	0	ENSG00000220131	AL121835.1
ENSG00000220132	0	0	0	0	ENSG00000220132	AC236430.1
ENSG00000220139	0	0	0	0	ENSG00000220139	AL022722.2
ENSG00000220154	1.2289	0	1.58135	0	ENSG00000220154	AL355796.1
ENSG00000220157	0.0677484	0	0.0702937	0.0767097	ENSG00000220157	HNRNPA1P12
ENSG00000220181	0	0.715545	0.159006	0.495273	ENSG00000220181	AL357075.1
ENSG00000220184	0	0	0.104332	0	ENSG00000220184	HMGB3P18
ENSG00000220201	1.59577	1.7671	2.93448	2.45716	ENSG00000220201	ZGLP1
ENSG00000220204	0	0	0	0	ENSG00000220204	AL035079.1
ENSG00000220205	5.52704	11.318	8.72811	7.23721	ENSG00000220205	VAMP2
ENSG00000220212	0	0	0	0	ENSG00000220212	OR4F1P
ENSG00000220237	1.09487	0.418511	0.755789	3.209	ENSG00000220237	RPS24P12
ENSG00000220240	0	0	1.44991	1.81142	ENSG00000220240	AL157777.2

ENSG00000220248	0.0181631	0	0	0.0216851	ENSG00000220248	ZNF402P
ENSG00000220256	0.495413	1.28799	1.06092	1.68987	ENSG00000220256	AC093802.1
ENSG00000220267	0	0	0	0	ENSG00000220267	ACTBP8
ENSG00000220291	0.0615919	0.53335	0.275784	0.872057	ENSG00000220291	AL139806.1
ENSG00000220305	0.152005	0.194823	0.308151	0.832371	ENSG00000220305	HNRNPH1P1
ENSG00000220311	0	0	0	0	ENSG00000220311	AL133475.1
ENSG00000220323	0.532681	1.15916	1.00461	0.768747	ENSG00000220323	AC239868.1
ENSG00000220326	0	0	0	0	ENSG00000220326	AL603865.2
ENSG00000220340	0	0	0	0	ENSG00000220340	MTCO1P56
ENSG00000220343	0	0.164416	0.159865	0.509107	ENSG00000220343	AC092965.1
ENSG00000220347	0	0	0	0	ENSG00000220347	AL355297.1
ENSG00000220349	0	0	0.116359	0	ENSG00000220349	Z85996.1
ENSG00000220370	0.742835	1.37771	0.565787	2.44256	ENSG00000220370	AL078595.1
ENSG00000220377	0	0.312764	0.376562	0.351137	ENSG00000220377	GSTA8P
ENSG00000220378	0	0	0	0	ENSG00000220378	KRT8P42
ENSG00000220379	0	0.0275452	0	0.0234623	ENSG00000220379	CR759834.1
ENSG00000220391	0.234692	0.279645	0.864192	0.50177	ENSG00000220391	HCG4B
ENSG00000220392	0.320658	1.38306	1.66488	2.90992	ENSG00000220392	FCF1P5
ENSG00000220412	0.128443	0.062103	0.0281141	0.035393	ENSG00000220412	AL356234.1
ENSG00000220418	0	0	0	0	ENSG00000220418	TUBB3P1
ENSG00000220446	0.766267	0.750719	0.660669	1.07469	ENSG00000220446	AL121978.1
ENSG00000220447	0	0	0	0	ENSG00000220447	AL139098.1
ENSG00000220472	0	0	0.0794974	0	ENSG00000220472	AL139095.2
ENSG00000220483	0	0	0	0	ENSG00000220483	SLC25A51P1
ENSG00000220494	0.0421424	0.0406369	0.219992	0.18454	ENSG00000220494	YAP1P1
ENSG00000220505	0	0	0	0	ENSG00000220505	EIF4EBP2P3
ENSG00000220506	0.104839	0.506593	0.6366	1.58376	ENSG00000220506	AL136310.1
ENSG00000220514	0	0	0	0	ENSG00000220514	MTND4LP20
ENSG00000220515	0	1.00426	0.144903	0.594969	ENSG00000220515	PGAM1P10
ENSG00000220517	0	0	0	0	ENSG00000220517	ASS1P1
ENSG00000220522	0	0	0	0.435385	ENSG00000220522	AL590002.1
ENSG00000220537	0	0	0	0.206796	ENSG00000220537	AL121977.1
ENSG00000220540	0	0	0	0	ENSG00000220540	AL359511.1
ENSG00000220541	0	0	0	0	ENSG00000220541	AC233289.1
ENSG00000220548	0.0914596	0.308239	0.159204	0.349873	ENSG00000220548	VIM2P
ENSG00000220550	0	0.00838819	0.0181864	0	ENSG00000220550	OR10C1
ENSG00000220553	0.141491	0	0.122936	0	ENSG00000220553	RPL5P19
ENSG00000220556	0	0	0	0	ENSG00000220556	AL035690.1
ENSG00000220557	0	0.20636	0.199181	0.115873	ENSG00000220557	HMGB1P13
ENSG00000220563	0	0.448575	0.89146	0.504881	ENSG00000220563	PKMP3
ENSG00000220575	1.22352	2.35944	2.17255	3.80101	ENSG00000220575	HTR5A-AS1
ENSG00000220581	0	0	0.125842	0.0786656	ENSG00000220581	VN1R12P
ENSG00000220583	2.61174	1.35948	0.44047	0.278825	ENSG00000220583	RPL35P2
ENSG00000220585	0.288331	0.0480646	0.793464	2.03531	ENSG00000220585	DDX18P6
ENSG00000220586	0	0.0531645	0	0	ENSG00000220586	TUBBP9
ENSG00000220598	0.2378	0.457191	0.206529	0.86561	ENSG00000220598	SSR1P1
ENSG00000220600	0.148088	0.769072	0.769167	0.158764	ENSG00000220600	AL121834.1
ENSG00000220614	0.552519	0.525586	0.475083	1.15792	ENSG00000220614	AL583834.1
ENSG00000220635	3.17847	4.27348	4.48105	5.4157	ENSG00000220635	KRASP1
ENSG00000220643	2.39424	0.377164	2.03904	0.41087	ENSG00000220643	AL031577.2
ENSG00000220660	0.583428	2.21418	2.34288	0.738394	ENSG00000220660	AL023284.3
ENSG00000220666	0.0470099	0.0453448	0	0.0516078	ENSG00000220666	RCC2P7
ENSG00000220685	0	0.39587	0.39817	0.456304	ENSG00000220685	AL139094.1
ENSG00000220693	1.77308	3.79378	3.31959	4.7206	ENSG00000220693	AC011498.1

ENSG00000220694	0	0	0.113753	0.140933	ENSG00000220694	AL096711.1
ENSG00000220695	0.702603	1.18337	1.1185	2.18598	ENSG00000220695	Z86062.1
ENSG00000220702	1.33522	2.48498	2.1609	6.89736	ENSG00000220702	Z85994.1
ENSG00000220721	0	0.0657933	0.178348	0.148776	ENSG00000220721	OR1F12
ENSG00000220725	0	0	0	0	ENSG00000220725	AL590290.1
ENSG00000220730	0	0	0	0.293728	ENSG00000220730	AL356057.3
ENSG00000220733	0	0.860725	3.77757	0.914483	ENSG00000220733	MTND3P20
ENSG00000220734	0	0	0	0	ENSG00000220734	AL157823.1
ENSG00000220739	0.662386	0.632996	0.205878	1.40003	ENSG00000220739	AL513475.2
ENSG00000220744	0.0709855	0.409877	0.925977	0.831635	ENSG00000220744	RPL5P18
ENSG00000220745	0	0	0	0	ENSG00000220745	AL080276.1
ENSG00000220748	0	0	0	0.125214	ENSG00000220748	AL032822.1
ENSG00000220749	3.82134	3.86711	3.48572	4.84432	ENSG00000220749	RPL21P28
ENSG00000220758	0.168444	0.637996	0.184378	0.809595	ENSG00000220758	VN1R10P
ENSG00000220771	0	1.33769	0.822136	2.44185	ENSG00000220771	BOLA2P3
ENSG00000220773	0	0	0.311503	0	ENSG00000220773	RPSAP44
ENSG00000220785	0.455654	1.44111	0.982891	1.78448	ENSG00000220785	MTMR9LP
ENSG00000220793	0	0	0.345774	0.591443	ENSG00000220793	AC087190.1
ENSG00000220804	5.04899	9.96464	9.6717	11.2445	ENSG00000220804	LINC01881
ENSG00000220823	2.84538	8.69829	34.3952	8.60823	ENSG00000220823	AC018692.1
ENSG00000220831	0	0	0	0	ENSG00000220831	NDUFA5P9
ENSG00000220842	421.532	299.311	224.69	169.338	ENSG00000220842	RPL21P16
ENSG00000220848	6.6806	9.62543	6.09236	5.71905	ENSG00000220848	RPS18P9
ENSG00000220867	4.84573	5.76362	2.80615	13.9061	ENSG00000220867	HSPE1P26
ENSG00000220868	0	0	0	0.135904	ENSG00000220868	MRPL35P1
ENSG00000220871	0.39866	3.01731	4.00434	2.47437	ENSG00000220871	DNAJC19P6
ENSG00000220875	0.40623	0	0	0	ENSG00000220875	HIST1H3PS1
ENSG00000220884	0	0	0	0.279046	ENSG00000220884	MESTP1
ENSG00000220891	1.11487	1.8506	1.48886	3.28133	ENSG00000220891	LL22NC03-63E9.3
ENSG00000220903	0	0.882685	0	0	ENSG00000220903	FRG2C
ENSG00000220913	0	0	0	0	ENSG00000220913	AL391361.1
ENSG00000220918	0	0	0	0.0715151	ENSG00000220918	AL132875.1
ENSG00000220920	7.7291	3.9029	5.94602	6.98551	ENSG00000220920	AL023807.1
ENSG00000220924	0	0.358455	0	0.191489	ENSG00000220924	OSTCP4
ENSG00000220937	0.0678292	0.0659197	0.0589638	0.0861614	ENSG00000220937	HNRNPA1P41
ENSG00000220948	0	0.316426	0.0379327	0.216337	ENSG00000220948	TRIM51GP
ENSG00000220949	0	0	0.0746062	0.185514	ENSG00000220949	AC008543.2
ENSG00000220960	0	0	0	0	ENSG00000220960	AL079342.2
ENSG00000221813	0	0	0.0508478	0	ENSG00000221813	OR6B1
ENSG00000221818	0.559435	1.04239	1.0902	2.37511	ENSG00000221818	EBF2
ENSG00000221819	1.80889	2.99276	3.5887	3.66758	ENSG00000221819	GAS8-AS1
ENSG00000221821	2.12265	1.90914	2.72409	1.4232	ENSG00000221821	C6orf226
ENSG00000221823	14.8532	14.8139	17.5887	21.4035	ENSG00000221823	PPP3R1
ENSG00000221826	0.627243	1.46727	1.67988	3.17647	ENSG00000221826	PSG3
ENSG00000221829	11.6378	27.1021	10.9761	15.1806	ENSG00000221829	FANCG
ENSG00000221836	0	0.0584991	0	0.0662278	ENSG00000221836	OR2A5
ENSG00000221837	0	0	0	0	ENSG00000221837	KRTAP10-9
ENSG00000221838	18.8434	14.6756	16.512	18.6601	ENSG00000221838	AP4M1
ENSG00000221840	0	0	0	0	ENSG00000221840	OR4A5
ENSG00000221843	0.206031	0.372674	0.47925	0.435263	ENSG00000221843	C2orf16
ENSG00000221844	0	0	0	0	ENSG00000221844	DPP3P2
ENSG00000221845	0.225767	1.00806	0.752645	1.00491	ENSG00000221845	C7orf65
ENSG00000221849	0	0	0	0.0489143	ENSG00000221849	AC018880.1

ENSG00000221852	0	0	0.0221834	0.501008	ENSG00000221852	KRTAP1-5
ENSG00000221855	0.135763	0.326392	0.353905	0.295251	ENSG00000221855	TAS2R41
ENSG00000221858	0.0585326	0.0722663	0	0.0637927	ENSG00000221858	OR2A12
ENSG00000221859	0.110574	0.239452	0.0961836	0.211263	ENSG00000221859	KRTAP10-10
ENSG00000221864	0.0447613	0.129021	0.0777097	0.145328	ENSG00000221864	KRTAP12-2
ENSG00000221866	0.122543	0.287914	0.360472	0.715968	ENSG00000221866	PLXNA4
ENSG00000221867	0.0748064	0.0437099	0.0726767	0.0936253	ENSG00000221867	MAGEA3
ENSG00000221869	20.3311	24.1472	49.1537	10.7099	ENSG00000221869	CEBPD
ENSG00000221870	0.238738	0.285045	0.247772	0.337296	ENSG00000221870	TMEM257
ENSG00000221874	0.108643	0	0	0	ENSG00000221874	ZNF816-ZNF321P
ENSG00000221878	2.69054	1.80611	2.24674	5.10078	ENSG00000221878	PSG7
ENSG00000221879	0	0	0	0	ENSG00000221879	MRPS21P3
ENSG00000221880	0.128687	0	0	0.140056	ENSG00000221880	KRTAP1-3
ENSG00000221882	0.11323	0.0544863	0.196973	0.0617293	ENSG00000221882	OR3A2
ENSG00000221883	1.72924	4.18598	6.51103	4.23504	ENSG00000221883	ARIH2OS
ENSG00000221886	1.76111	2.34961	1.32394	2.11834	ENSG00000221886	ZBED8
ENSG00000221887	0.299383	2.12627	0.461677	0.468276	ENSG00000221887	HMSD
ENSG00000221888	0.142658	0.250389	0	0.228585	ENSG00000221888	OR1C1
ENSG00000221890	0.283077	0.588412	0.655876	1.26313	ENSG00000221890	NPTXR
ENSG00000221891	0	0	0	0	ENSG00000221891	FAM218BP
ENSG00000221900	0	0	0	0	ENSG00000221900	POM121L12
ENSG00000221909	4.7379	4.03897	4.57157	3.23388	ENSG00000221909	FAM200A
ENSG00000221910	0	0.104643	0.0472877	0.355799	ENSG00000221910	OR2F2
ENSG00000221914	41.6802	54.5607	46.0607	65.4826	ENSG00000221914	PPP2R2A
ENSG00000221916	0.444543	1.59051	0.944979	1.00996	ENSG00000221916	C19orf73
ENSG00000221923	14.8365	19.3777	17.2989	21.7456	ENSG00000221923	ZNF880
ENSG00000221926	59.4031	32.7693	34.2013	35.3999	ENSG00000221926	TRIM16
ENSG00000221930	0.642869	1.0902	1.00119	1.08051	ENSG00000221930	FAM45BP
ENSG00000221931	0	0.166726	0.100454	0.062951	ENSG00000221931	OR6X1
ENSG00000221932	0	0	0	0	ENSG00000221932	HEPN1
ENSG00000221933	0	0	0.158418	0.0661512	ENSG00000221933	OR2A25
ENSG00000221937	0.0594043	0.114325	0.112137	0.140928	ENSG00000221937	TAS2R40
ENSG00000221938	0.0608688	0.292838	0.159762	0.266293	ENSG00000221938	OR2A14
ENSG00000221944	50.2592	117.311	107.388	169.442	ENSG00000221944	TIGD1
ENSG00000221946	0.577446	1.35923	0.331519	0.679526	ENSG00000221946	FXYD7
ENSG00000221947	2.31654	7.83485	5.30199	9.7423	ENSG00000221947	XKR9
ENSG00000221949	2.72847	2.91928	2.48011	4.91923	ENSG00000221949	LINC01465
ENSG00000221953	1.13111	1.71412	1.91935	2.91037	ENSG00000221953	C1orf229
ENSG00000221954	0	0	0	0.0626068	ENSG00000221954	OR4C12
ENSG00000221955	18.0278	28.1731	22.957	27.3103	ENSG00000221955	SLC12A8
ENSG00000221957	0	0	0	0	ENSG00000221957	KIR2DS4
ENSG00000221961	0	0	0	0	ENSG00000221961	PRR21
ENSG00000221962	2.22104	6.14327	4.58589	7.4753	ENSG00000221962	TMEM14EP
ENSG00000221963	7.5662	21.4238	16.047	17.5826	ENSG00000221963	APOL6
ENSG00000221968	30.7219	22.912	93.3738	35.8473	ENSG00000221968	FADS3
ENSG00000221970	0.382846	0.425753	0.355468	1.67515	ENSG00000221970	OR2A1
ENSG00000221971	0.157372	0.203446	0.231405	0.526011	ENSG00000221971	TTC4P1
ENSG00000221972	0.0689111	0.0331966	0	0.755086	ENSG00000221972	C3orf36
ENSG00000221974	2.42888	0.280746	2.20319	1.37523	ENSG00000221974	GTF2H4
ENSG00000221977	0.0663187	0	0.057632	0	ENSG00000221977	OR4E2
ENSG00000221978	106.241	114.892	190.372	129.311	ENSG00000221978	CCNL2
ENSG00000221983	374.269	253.361	185.595	125.346	ENSG00000221983	UBA52
ENSG00000221986	1.01518	0.848139	1.14354	2.12201	ENSG00000221986	MYBPHL
ENSG00000221988	0.0409104	0.251919	0.351314	0.267143	ENSG00000221988	PPT2

ENSG00000221989	0.174612	0.168033	0.101241	0.190318	ENSG00000221989	OR2A2
ENSG00000221990	2.26342	3.13594	3.51792	4.36666	ENSG00000221990	EXOC3-AS1
ENSG00000221994	0.775126	1.33868	1.41447	2.38528	ENSG00000221994	ZNF630
ENSG00000221995	1.92583	4.61229	3.27688	3.66777	ENSG00000221995	TIAF1
ENSG00000221996	0	0	0	0	ENSG00000221996	OR52B4
ENSG00000222000	0.515398	0.83459	0.854012	1.26156	ENSG00000222000	AC092675.1
ENSG00000222001	0.414776	1.30504	0.598749	1.31778	ENSG00000222001	AC106876.1
ENSG00000222004	0.789576	1.42521	1.13847	1.68979	ENSG00000222004	C7orf71
ENSG00000222005	0.437143	1.05478	0.68459	2.60761	ENSG00000222005	LINC01118
ENSG00000222007	1.52219	4.56233	3.67731	7.27914	ENSG00000222007	AC064874.1
ENSG00000222009	10.6196	17.672	28.21	20.1992	ENSG00000222009	BTBD19
ENSG00000222011	6.35986	11.7363	13.1204	8.11646	ENSG00000222011	FAM185A
ENSG00000222012	0.0472007	0.0151833	0.041205	0.155796	ENSG00000222012	AC005481.1
ENSG00000222014	0.0400089	0.0792895	0.084624	0.0659924	ENSG00000222014	RAB6C
ENSG00000222017	0	0	0.232269	0.151586	ENSG00000222017	AC011997.1
ENSG00000222018	0.434849	0.668641	1.28359	1.60099	ENSG00000222018	C21orf140
ENSG00000222019	1.41348	1.94516	2.85935	0.883659	ENSG00000222019	URAHP
ENSG00000222020	2.27273	2.84538	2.52058	0.857783	ENSG00000222020	AC062017.1
ENSG00000222022	0.765146	3.46663	3.14916	10.2308	ENSG00000222022	AC112721.1
ENSG00000222024	0.315071	1.41198	0.839406	1.92085	ENSG00000222024	AC004945.1
ENSG00000222028	0.0299047	0.0288186	0.0260523	0.0984036	ENSG00000222028	PSMB11
ENSG00000222031	0.166994	0	0.288851	0.181504	ENSG00000222031	AC023469.1
ENSG00000222033	0.0265456	0	0.0461762	0.145427	ENSG00000222033	LINC01124
ENSG00000222036	0.614834	1.84314	1.80447	2.63033	ENSG00000222036	POTEM
ENSG00000222037	0	0	0	0	ENSG00000222037	IGLC6
ENSG00000222038	0	0	0	0.077384	ENSG00000222038	POTEJ
ENSG00000222040	0.0831502	0.0962201	0.0727726	0.0182952	ENSG00000222040	ADRA2B
ENSG00000222046	1.28597	3.12874	3.03837	2.86442	ENSG00000222046	DCDC2B
ENSG00000222047	17.0139	15.9722	8.96461	9.28397	ENSG00000222047	C10orf55
ENSG00000223345	0.952332	11.3127	1.55654	4.53182	ENSG00000223345	HIST2H2BA
ENSG00000223349	0.0792913	0	0.118489	0	ENSG00000223349	KLF2P3
ENSG00000223350	0	0	0.356321	0	ENSG00000223350	IGLV9-49
ENSG00000223352	15.3181	8.48971	0.293017	0	ENSG00000223352	HLA-U
ENSG00000223353	0	0	0.0751002	0.0946753	ENSG00000223353	AL589763.1
ENSG00000223355	0.202364	0.611621	0.465939	0.84093	ENSG00000223355	NOTCH4
ENSG00000223359	0	0	0	0	ENSG00000223359	CR354545.1
ENSG00000223361	0	0.072276	0.13952	0	ENSG00000223361	FTH1P10
ENSG00000223362	0	0	0	0	ENSG00000223362	CDY15P
ENSG00000223367	249.329	186.853	166.574	87.6578	ENSG00000223367	RPS18
ENSG00000223368	0	0	0.0988714	0	ENSG00000223368	AL513124.1
ENSG00000223372	0	0	0	0	ENSG00000223372	HLA-DPB2
ENSG00000223375	0	0.621358	1.1071	0.667074	ENSG00000223375	AC096638.1
ENSG00000223376	0	0.0341391	0.030885	0	ENSG00000223376	CR759768.1
ENSG00000223377	0	0	0	0	ENSG00000223377	AC244098.1
ENSG00000223383	0	0	0.457115	0	ENSG00000223383	HIST1H2APS6
ENSG00000223389	0	0.219699	0	0.633878	ENSG00000223389	SDCBP2P1
ENSG00000223391	0	0	0	0	ENSG00000223391	AC006210.1
ENSG00000223394	1.05603	1.23204	1.1927	4.39307	ENSG00000223394	TRBV29OR9-2
ENSG00000223395	0	0	0	0	ENSG00000223395	RBM22P7
ENSG00000223398	0	0	0	0	ENSG00000223398	AC027124.1
ENSG00000223402	0	0	0	0	ENSG00000223402	AC074121.1
ENSG00000223406	0	0.0766014	0	0.0853309	ENSG00000223406	XKRYP5
ENSG00000223407	0	0	0	0	ENSG00000223407	USP9YP18
ENSG00000223409	0.782067	2.12584	2.37093	2.3783	ENSG00000223409	RPL17P17

ENSG00000223412	0	0	0	0	ENSG00000223412	SUCLA2P1
ENSG00000223416	0	0	0	0	ENSG00000223416	RPS26P15
ENSG00000223417	0.0368541	0.0349414	0.0287418	0.0366548	ENSG00000223417	TRIM49D1
ENSG00000223418	0	0	0.0345183	0	ENSG00000223418	AC004554.1
ENSG00000223419	0	0	0	0	ENSG00000223419	AC006022.1
ENSG00000223421	0	0.0415135	0.0375238	0	ENSG00000223421	AL354854.1
ENSG00000223422	0	0	0.268512	0.111365	ENSG00000223422	AC007274.1
ENSG00000223427	0	0	0	0	ENSG00000223427	AC016716.1
ENSG00000223428	0	0.76262	0.459388	0	ENSG00000223428	AC010997.1
ENSG00000223429	0.304497	1.46394	1.26059	1.23959	ENSG00000223429	AL139156.1
ENSG00000223431	0.165173	0.153673	0.6937	0.684688	ENSG00000223431	MTND6P21
ENSG00000223433	0	0	0	0	ENSG00000223433	RPS29P9
ENSG00000223437	0	2.60682	2.1285	2.62575	ENSG00000223437	TMSB4XP3
ENSG00000223439	0.111634	0.322334	0.119037	0.102342	ENSG00000223439	HLA-J
ENSG00000223441	0	0	0.016343	0	ENSG00000223441	OR2I1P
ENSG00000223443	0.10223	0.716575	0.536933	0.335846	ENSG00000223443	USP17L2
ENSG00000223445	0.478981	0.471827	0.552763	1.05432	ENSG00000223445	RPL6P21
ENSG00000223447	0	0	0	0	ENSG00000223447	HLA-DPA3
ENSG00000223448	0.013508	0	0.0359938	0.0362078	ENSG00000223448	LTB
ENSG00000223449	0	0.0491177	0.0443564	0.164295	ENSG00000223449	RP11-93P10.2
ENSG00000223450	1.74082	3.68798	3.1266	2.29229	ENSG00000223450	AL590632.1
ENSG00000223452	0	0.410361	0	0	ENSG00000223452	HMGN2P18
ENSG00000223455	0	0	0	0	ENSG00000223455	AL355298.1
ENSG00000223457	0	0.0288995	0.0208992	0	ENSG00000223457	HTATSF1P1
ENSG00000223459	4.70834	4.16165	2.8789	6.27503	ENSG00000223459	TCAF1P1
ENSG00000223460	0	0	0	0	ENSG00000223460	GAPDHP69
ENSG00000223463	0.103196	2.2871	0	0.202559	ENSG00000223463	HLA-H
ENSG00000223465	0.808594	2.33727	1.58026	1.40974	ENSG00000223465	LST1
ENSG00000223467	0	0	0	0	ENSG00000223467	CALM1P1
ENSG00000223474	1.14403	1.606	1.67373	1.71303	ENSG00000223474	AL020996.1
ENSG00000223476	1.06331	2.61632	1.89098	2.62477	ENSG00000223476	VN1R42P
ENSG00000223481	0.212806	12.8813	1.77078	3.08992	ENSG00000223481	TAP2
ENSG00000223484	0	0	0	0.0782357	ENSG00000223484	TRPC6P
ENSG00000223488	0.0818753	0.157917	0.0952187	0.213146	ENSG00000223488	MAPK6PS2
ENSG00000223489	0	0	0.036612	0	ENSG00000223489	NEFHP1
ENSG00000223490	0.213855	1.4295	0.829685	0	ENSG00000223490	CHCHD2P5
ENSG00000223491	1.17946	0.980124	0	0.604206	ENSG00000223491	RP3-328E19.4
ENSG00000223493	1.98078	2.02494	2.8233	2.14355	ENSG00000223493	SKIV2L
ENSG00000223494	3.93218	1.13555	0.597917	4.77349	ENSG00000223494	VARS2
ENSG00000223495	0	0.149859	0.270845	0.987716	ENSG00000223495	AC239859.2
ENSG00000223496	23.4338	32.1507	40.9247	33.6294	ENSG00000223496	EXOSC6
ENSG00000223497	0	0	0	0	ENSG00000223497	AC063979.1
ENSG00000223498	0.0729129	0.0704465	0.126723	0.0796371	ENSG00000223498	AL929302.1
ENSG00000223500	0.097574	0	0	0.26323	ENSG00000223500	AC083862.1
ENSG00000223501	0.948011	0.562313	1.51113	2.85005	ENSG00000223501	VPS52
ENSG00000223503	0.10317	0.469209	0.558581	0.222731	ENSG00000223503	AL353807.1
ENSG00000223505	1.79479	4.54339	3.85001	6.47107	ENSG00000223505	AC114402.1
ENSG00000223506	0	0	0.028314	0	ENSG00000223506	SLC20A1P1
ENSG00000223508	8.71528	12.8387	13.4332	18.5811	ENSG00000223508	RPL23AP53
ENSG00000223509	7.75337	13.5655	10.3141	15.8369	ENSG00000223509	AC135983.2
ENSG00000223510	1.27115	0.949138	0.902759	1.36298	ENSG00000223510	CDRT15
ENSG00000223512	0	0	0	0	ENSG00000223512	BX649597.3
ENSG00000223513	0	0	0.43339	1.56797	ENSG00000223513	ATP6V0E1P2

ENSG00000223514	0	0	0	0	ENSG00000223514	AC004866.1
ENSG00000223518	0.309226	0.648332	0.696114	0.631226	ENSG00000223518	CSNK1A1P1
ENSG00000223519	0.0469727	0.135684	0.566188	0.833407	ENSG00000223519	KIF28P
ENSG00000223524	0	0	0	0	ENSG00000223524	REXO1L11P
ENSG00000223529	0.0846059	0.122209	0	0.0462636	ENSG00000223529	EEF1A1P8
ENSG00000223531	0.437028	1.72013	0.630594	1.84647	ENSG00000223531	TRIM31
ENSG00000223532	12.3659	87.5971	48.1525	78.2846	ENSG00000223532	HLA-B
ENSG00000223533	0.0538926	1.59682	0.816886	2.53553	ENSG00000223533	CCHCR1
ENSG00000223535	0	0	0	0	ENSG00000223535	FAM90A17P
ENSG00000223538	0	0	0	0	ENSG00000223538	AC079602.1
ENSG00000223539	0	0	0	0	ENSG00000223539	AC011431.1
ENSG00000223540	0	0	0	0	ENSG00000223540	RPS15AP5
ENSG00000223543	0	0.11607	0	0.260123	ENSG00000223543	TCEAL4P1
ENSG00000223544	0	0	0.536625	0.744626	ENSG00000223544	AC005838.1
ENSG00000223547	6.32123	4.36064	3.45465	5.40117	ENSG00000223547	ZNF844
ENSG00000223549	0.108485	0.209025	0.103077	0.237719	ENSG00000223549	MTND5P28
ENSG00000223550	0	0	0	0	ENSG00000223550	SNRPBP1
ENSG00000223551	0.686783	1.25216	1.24064	1.14596	ENSG00000223551	TMSB4XP4
ENSG00000223553	0.621879	1.11727	0.780398	2.09	ENSG00000223553	SMPD4P1
ENSG00000223555	0	0	0	0	ENSG00000223555	USP9YP23
ENSG00000223558	0.303185	0.801685	0.161096	1.10296	ENSG00000223558	TRIM60P17
ENSG00000223559	0	0	0	0	ENSG00000223559	AC073136.1
ENSG00000223560	0	0.00827178	0.059801	0.0281478	ENSG00000223560	UBQLN1P1
ENSG00000223564	0.0890375	0.079306	0	0	ENSG00000223564	CYP4F32P
ENSG00000223565	0	0	0.0544583	0.1364	ENSG00000223565	AC069540.1
ENSG00000223566	0	0.0200621	0.0362813	0	ENSG00000223566	TNRC18P2
ENSG00000223568	0	0	0	0	ENSG00000223568	RPL3P11
ENSG00000223569	0	0	0	0	ENSG00000223569	USP17L15
ENSG00000223570	0.264464	0.251752	0.455092	0.277399	ENSG00000223570	AL592045.1
ENSG00000223572	31.1292	57.8793	54.6851	21.3355	ENSG00000223572	CKMT1A
ENSG00000223574	0	0.192119	0.173534	0.108025	ENSG00000223574	TPMTP4
ENSG00000223575	0	0.238464	0.0656097	0.885005	ENSG00000223575	RBMX2P3
ENSG00000223583	0.69057	0.434765	1.0183	2.31489	ENSG00000223583	AL513365.1
ENSG00000223584	0.648577	0.311466	0.656253	2.79766	ENSG00000223584	TVP23CP1
ENSG00000223588	0	0.163627	0	0	ENSG00000223588	AC103564.9
ENSG00000223589	0	0.266808	2.03471	0.587456	ENSG00000223589	AL139158.1
ENSG00000223590	0.165177	0.311692	0.142505	0.454979	ENSG00000223590	MUC21
ENSG00000223591	0	0	0	0	ENSG00000223591	CENPVL1
ENSG00000223592	0	0	0	0	ENSG00000223592	FNDC3CP
ENSG00000223593	0.144552	0.805655	0.545443	1.07986	ENSG00000223593	AL356806.1
ENSG00000223595	0	0	0	0	ENSG00000223595	LYPLA1P1
ENSG00000223599	0.24823	0.614718	0.808002	1.24343	ENSG00000223599	AL513523.1
ENSG00000223600	0.723704	0	0	0	ENSG00000223600	EEF1A1P41
ENSG00000223601	0	0	0	0	ENSG00000223601	EBLN1
ENSG00000223602	0.0858217	0.245049	0.451119	0.503065	ENSG00000223602	AC125634.1
ENSG00000223603	0	0	0	0	ENSG00000223603	CRPP1
ENSG00000223604	0.139374	0.401176	0.362125	1.34396	ENSG00000223604	AC007394.1
ENSG00000223605	0.442703	0.835158	0.772155	0.453635	ENSG00000223605	AC107399.1
ENSG00000223606	1.3861	2.54058	3.35E-06	0.221237	ENSG00000223606	HLA-V
ENSG00000223609	0	0	0	0.303707	ENSG00000223609	HBD
ENSG00000223611	0.0931753	0.0827538	0.0970633	0.0867073	ENSG00000223611	SUPT20HL2
ENSG00000223612	0	0	0	0	ENSG00000223612	AC241585.1
ENSG00000223614	0	0	0	0	ENSG00000223614	ZNF735

ENSG00000223615	0	0	0.920175	0	ENSG00000223615	AL807761.1
ENSG00000223618	0	0	0	0	ENSG00000223618	VPS52
ENSG00000223619	0	0	0	0	ENSG00000223619	MTCO1P17
ENSG00000223620	0	0.0531433	0.0479711	0.433198	ENSG00000223620	RBM48P1
ENSG00000223621	0	0.21155	0.184821	0.229885	ENSG00000223621	AK4P4
ENSG00000223622	0	0.119109	0	0.266789	ENSG00000223622	GSTA6P
ENSG00000223624	0	0	0	1.69203	ENSG00000223624	AL033528.1
ENSG00000223625	0	0	0	0	ENSG00000223625	CYCSP32
ENSG00000223628	0	0	1.16063	0	ENSG00000223628	AC023449.1
ENSG00000223629	1.15622	0.41503	0	1.35724	ENSG00000223629	DEFA8P
ENSG00000223636	0.208591	0	0	0	ENSG00000223636	UBE2Q2P5Y
ENSG00000223637	0	0	0	0.148169	ENSG00000223637	RBMY2EP
ENSG00000223638	0	0	0	0	ENSG00000223638	RFPL4A
ENSG00000223639	47.8587	52.6287	21.8263	21.5159	ENSG00000223639	CLIC1
ENSG00000223640	0	0	0	0	ENSG00000223640	RPL30P3
ENSG00000223648	0	0	0	0	ENSG00000223648	IGHV3-64
ENSG00000223650	0.398381	1.72061	2.19184	1.91245	ENSG00000223650	UHRF2P1
ENSG00000223651	0	0	0	0.027026	ENSG00000223651	AL049812.1
ENSG00000223654	1.15791	1.96272	3.80558	0	ENSG00000223654	FLOT1
ENSG00000223655	0	0	0	0	ENSG00000223655	RAB9AP3
ENSG00000223656	0.376862	0.588411	0.623308	0.328387	ENSG00000223656	HMGB3P10
ENSG00000223657	0	0	0	0	ENSG00000223657	KRT8P51
ENSG00000223658	0.559235	1.24855	0.926431	1.81001	ENSG00000223658	C1GALT1C1L
ENSG00000223663	0	0	0	0	ENSG00000223663	NDUFB4P8
ENSG00000223664	0	0.0491177	0.0443564	0.164295	ENSG00000223664	AL162415.4
ENSG00000223666	2.57528	0	1.42846	0	ENSG00000223666	FKBPL
ENSG00000223668	0	0	0.0370964	0.0466131	ENSG00000223668	EEF1A1P24
ENSG00000223671	0	0	0.243493	1.18685	ENSG00000223671	RPL34P3
ENSG00000223672	0	0	0	0	ENSG00000223672	AL162386.1
ENSG00000223676	0	0	0	0	ENSG00000223676	RPL34P26
ENSG00000223677	0	0	0	0	ENSG00000223677	AL662791.1
ENSG00000223679	0	0	0	0	ENSG00000223679	AC245054.1
ENSG00000223680	13.6227	16.0691	7.82144	4.28832	ENSG00000223680	DDR1
ENSG00000223683	0.833094	1.26942	0.934477	0.51645	ENSG00000223683	RPSAP65
ENSG00000223684	0	0.116213	0.156138	0	ENSG00000223684	IFNWP18
ENSG00000223687	0.0832886	1.40351	0	1.16063	ENSG00000223687	ZNF311
ENSG00000223688	0	0	0	0	ENSG00000223688	AC127526.1
ENSG00000223691	0.339937	0.662867	0.742038	0.915408	ENSG00000223691	AC068044.1
ENSG00000223693	0	0	0	0	ENSG00000223693	SUCLA2P1
ENSG00000223694	0	0	0	0.406391	ENSG00000223694	ADH5P3
ENSG00000223696	0	0	0	0	ENSG00000223696	HLA-DPA3
ENSG00000223698	0	0	0	0.0474905	ENSG00000223698	GOLGA6L11P
ENSG00000223699	0	0.0476721	0.0752155	0	ENSG00000223699	COL11A2
ENSG00000223700	0.13099	1.00542	0.226935	0.843521	ENSG00000223700	AC104395.1
ENSG00000223702	0.191366	0.114275	0.165316	0.406353	ENSG00000223702	ZDHHC20P2
ENSG00000223703	0.16916	0.281916	0.403144	0.267294	ENSG00000223703	AC027612.1
ENSG00000223705	11.4357	15.5809	17.8081	13.8231	ENSG00000223705	NSUN5P1
ENSG00000223707	0.181835	0.349462	0.246691	0.196747	ENSG00000223707	SFR1P2
ENSG00000223708	0.0289227	0	0	0	ENSG00000223708	AL645935.1
ENSG00000223709	0.368999	0.591066	0.723707	1.63973	ENSG00000223709	TRIM64EP
ENSG00000223710	0	0	0	0	ENSG00000223710	CRYGGP
ENSG00000223717	0	0	0	0	ENSG00000223717	DNAJA1P1
ENSG00000223718	0.11551	0.110679	0	0.12414	ENSG00000223718	AC093107.1
ENSG00000223719	0.757309	0.543462	0.654158	0.804226	ENSG00000223719	AC069277.2

ENSG00000223721	0	0	0	0	ENSG00000223721	UQCRFS1P2
ENSG00000223722	0	0.20379	0.18428	0.226122	ENSG00000223722	AC023157.1
ENSG00000223723	0	0	0	0.0276344	ENSG00000223723	BX842568.2
ENSG00000223724	0.180761	0.780775	0.616965	1.17334	ENSG00000223724	RAD17P2
ENSG00000223728	0	0	0.0182327	0	ENSG00000223728	AC239801.1
ENSG00000223730	0.0677928	0.0651933	0	0.0828789	ENSG00000223730	Z83838.1
ENSG00000223731	0.0865805	0.149113	0.02199	0.130539	ENSG00000223731	SUPT20HL1
ENSG00000223733	0	0	0	0.151301	ENSG00000223733	RPL18AP14
ENSG00000223735	0	0	0.359054	0.149749	ENSG00000223735	OR51B3P
ENSG00000223738	0.0263256	0.0832202	0.111248	0.144706	ENSG00000223738	AC016930.1
ENSG00000223739	0	0.320861	0	0.703292	ENSG00000223739	AC007389.2
ENSG00000223740	0.0984676	0	0	0	ENSG00000223740	AC092447.3
ENSG00000223741	0	0	0	0	ENSG00000223741	PSMD4P1
ENSG00000223744	0	0	0	0	ENSG00000223744	RBMY2GP
ENSG00000223746	0	0.334661	0	0	ENSG00000223746	ELOCP30
ENSG00000223750	0.0491081	0	0.0427328	0.107268	ENSG00000223750	SIRPB3P
ENSG00000223752	0.324103	0.639154	0.80941	0.973813	ENSG00000223752	ATAT1
ENSG00000223753	0.0507767	0	0	0	ENSG00000223753	AC234775.1
ENSG00000223756	5.79221	12.2877	15.8303	34.4685	ENSG00000223756	TSSC2
ENSG00000223757	1.02425	1.71745	2.89525	2.54589	ENSG00000223757	VWA7
ENSG00000223758	0	0	0	0	ENSG00000223758	RP11-347J14.4
ENSG00000223760	0.739555	0.996652	1.44193	2.3727	ENSG00000223760	MED15P9
ENSG00000223766	0.546796	1.39487	0.984671	1.40641	ENSG00000223766	PRR3
ENSG00000223767	1.35259	0.556113	1.36117	0.483865	ENSG00000223767	RNF5
ENSG00000223769	0	0.0341391	0.030885	0	ENSG00000223769	CR388393.1
ENSG00000223771	0	0	0	0	ENSG00000223771	SUMO2P1
ENSG00000223772	0.09254	0.0889179	0.401613	0.108224	ENSG00000223772	GEMIN8P3
ENSG00000223773	12.4314	21.7838	8.65115	15.5796	ENSG00000223773	CD99P1
ENSG00000223775	3.6819	4.08555	4.50723	3.12515	ENSG00000223775	MRPS18B
ENSG00000223777	0	0	0	0	ENSG00000223777	AC092162.1
ENSG00000223780	0.0326956	0.0631299	0.319327	0.264028	ENSG00000223780	MEP1AP2
ENSG00000223782	0	0	0	0	ENSG00000223782	RPS21P8
ENSG00000223787	2.44969	7.25575	4.21242	9.41479	ENSG00000223787	AL354890.1
ENSG00000223788	0	0	0.224681	0.139219	ENSG00000223788	DIS3L2P1
ENSG00000223793	0	0	0	0.334679	ENSG00000223793	HLA-DQA2
ENSG00000223794	0	0	0	0	ENSG00000223794	COX5BP8
ENSG00000223798	0	0	0	0	ENSG00000223798	CR759960.1
ENSG00000223802	0.63767	0.546793	0.255154	0.526755	ENSG00000223802	CERS1
ENSG00000223803	0	0	0	0.715352	ENSG00000223803	RPS20P14
ENSG00000223807	0.427509	0	0	0	ENSG00000223807	BOLA3P4
ENSG00000223810	0.0421601	0	0.220212	0.737872	ENSG00000223810	KRT8P28
ENSG00000223816	3.01E-06	0	0.224367	0	ENSG00000223816	IGKV1OR2-2
ENSG00000223819	0	0.389277	0	0.685646	ENSG00000223819	Z95327.1
ENSG00000223820	5.47643	9.28432	8.91181	13.5187	ENSG00000223820	CFL1P1
ENSG00000223822	0	0.0861014	0	0	ENSG00000223822	EEF1A1P1
ENSG00000223824	0	0	0	0	ENSG00000223824	AC019178.2
ENSG00000223825	0	0.291449	0.917066	0.483228	ENSG00000223825	DAZAP2P1
ENSG00000223828	0.427147	2.01659	0.819563	4.45218	ENSG00000223828	BANF1P4
ENSG00000223833	0	0	0	0	ENSG00000223833	NCR3
ENSG00000223836	0.780189	1.36462	1.30893	1.85559	ENSG00000223836	AC023141.1
ENSG00000223840	0	0	0	0	ENSG00000223840	TRIM26BP
ENSG00000223841	0	0	0	0.0329902	ENSG00000223841	AC006484.1
ENSG00000223844	0.188139	0	0.163327	0.156317	ENSG00000223844	CR933540.1
ENSG00000223845	0	0.127724	0	0.0722369	ENSG00000223845	VN1R40P

ENSG00000223847	0	0.148666	0.26848	0	ENSG00000223847	AL645474.1
ENSG00000223849	0.538937	1.15037	5.16996	1.13083	ENSG00000223849	AL354893.1
ENSG00000223851	0.087419	0.412726	0	0.298453	ENSG00000223851	PTMAP1
ENSG00000223852	0.597048	0.883221	0.053838	0.24367	ENSG00000223852	ZFP57
ENSG00000223853	0	0	0	0.0734341	ENSG00000223853	CR759766.1
ENSG00000223856	0	0.0568481	0	0.127456	ENSG00000223856	RAB9AP2
ENSG00000223858	0.597048	0.883221	0.053838	0.24367	ENSG00000223858	ZFP57
ENSG00000223860	0	0	0	0	ENSG00000223860	MCCD1P1
ENSG00000223861	2.94943	2.25207	2.68482	3.77475	ENSG00000223861	AL365436.1
ENSG00000223864	0.223726	0.937206	1.14692	2.07695	ENSG00000223864	NPM1P19
ENSG00000223865	0.132978	0.351802	0.211819	2.49313	ENSG00000223865	HLA-DPB1
ENSG00000223866	0	0	0	0	ENSG00000223866	AC002486.1
ENSG00000223867	0	0.553035	0.999862	0.912884	ENSG00000223867	AC098592.1
ENSG00000223869	0	0	0	0	ENSG00000223869	AC099563.1
ENSG00000223873	0.17358	0	0	0.36743	ENSG00000223873	SAP18P2
ENSG00000223874	0	0	0	0	ENSG00000223874	LINC01921
ENSG00000223875	0	0	0	0	ENSG00000223875	NBEAP3
ENSG00000223876	0	0	0	0	ENSG00000223876	RPS27P1
ENSG00000223877	0.112248	0	0	0	ENSG00000223877	RPS8P10
ENSG00000223878	3.51542	9.0602	10.7117	6.91724	ENSG00000223878	AC005517.1
ENSG00000223885	0.0383417	0.0557239	0.199643	0	ENSG00000223885	FAM90A13P
ENSG00000223886	0.681068	0.489282	0.591076	0.181405	ENSG00000223886	AC073073.1
ENSG00000223887	1.24177	1.79606	3.14341	2.86624	ENSG00000223887	PRR3
ENSG00000223889	2.63858	2.83576	5.27499	0	ENSG00000223889	AC073188.1
ENSG00000223890	0	0	0.644707	2.33634	ENSG00000223890	AC008171.1
ENSG00000223892	0.0596122	0	0.467426	0.31596	ENSG00000223892	CR759763.1
ENSG00000223893	0	0.246215	0.022259	0.479227	ENSG00000223893	GNL2P1
ENSG00000223894	0.00091433	0	0.000798201	0.000801615	ENSG00000223894	HLA-DPA2
ENSG00000223896	0.413628	0.746572	0.674764	3.58421	ENSG00000223896	CCNJP2
ENSG00000223897	0	1.70999	0	0	ENSG00000223897	AC069157.1
ENSG00000223898	0.21123	0.457168	0.423707	0.844127	ENSG00000223898	OR11A1
ENSG00000223899	0.462693	1.20499	0.82972	1.19886	ENSG00000223899	SEC13P1
ENSG00000223903	0.200762	0	0.520301	0.425745	ENSG00000223903	RPL23P4
ENSG00000223904	0	0	0.102443	0	ENSG00000223904	HMGB1P12
ENSG00000223905	0	0	0.0891512	0.22189	ENSG00000223905	AC103592.1
ENSG00000223908	1.88326	2.00745	2.31904	3.04676	ENSG00000223908	AC068657.1
ENSG00000223912	0.0435502	0	0	0.04762	ENSG00000223912	EEF1A1P36
ENSG00000223915	0.150157	1.50634	0.905469	0	ENSG00000223915	DPPA2P1
ENSG00000223916	0	0.152353	0.126619	2.29026	ENSG00000223916	AC097638.1
ENSG00000223917	0.455308	0.286446	0.421993	0	ENSG00000223917	AC009237.1
ENSG00000223918	0.615517	0.575895	0.515716	0.621582	ENSG00000223918	AL513328.1
ENSG00000223919	0.0274983	0.0159269	0.0264951	0.0206416	ENSG00000223919	LTA
ENSG00000223920	0	0	0	0.100982	ENSG00000223920	AC099791.1
ENSG00000223921	0.0698875	0	0	0	ENSG00000223921	MTND1P27
ENSG00000223922	0.391066	0.422717	0.63723	0.643295	ENSG00000223922	ASS1P2
ENSG00000223925	0	0	0	0	ENSG00000223925	SLC25A15P4
ENSG00000223927	0	0	0	0	ENSG00000223927	RPL3P2
ENSG00000223928	0.0658973	0	0	0	ENSG00000223928	NUP35P1
ENSG00000223931	0	0	0	0	ENSG00000223931	AC142381.1
ENSG00000223932	2.24011	1.64312	1.48252	0.448828	ENSG00000223932	GPANK1
ENSG00000223933	0.0161927	0.00793847	0.00709454	0.0446566	ENSG00000223933	TMPOP1
ENSG00000223939	0	0	0	0	ENSG00000223939	PPP1R2P1
ENSG00000223940	0.0476746	0	0	0	ENSG00000223940	KRT8P8
ENSG00000223945	0.268595	0.461995	0.498962	0.52463	ENSG00000223945	AC244033.1

ENSG00000223948	0	0.374318	0.513041	0.837142	ENSG00000223948	AC092648.1
ENSG00000223951	0	0	0	1.19489	ENSG00000223951	AL133244.1
ENSG00000223952	0.222879	0.099013	0.196978	0.0453146	ENSG00000223952	TNF
ENSG00000223953	0.0609404	0.0248291	0.264957	1.48085	ENSG00000223953	C1QTNF5
ENSG00000223955	0	0.186462	0.336714	0.82722	ENSG00000223955	MTND6P1
ENSG00000223957	4.65105	3.54583	2.17492	1.03442	ENSG00000223957	NEU1
ENSG00000223958	0	0	0	0	ENSG00000223958	AC244505.2
ENSG00000223959	10.8643	19.6429	20.0832	20.5387	ENSG00000223959	AFG3L1P
ENSG00000223962	0	0	0	0	ENSG00000223962	UBBP3
ENSG00000223963	0	0	0.0349326	0	ENSG00000223963	THAP12P8
ENSG00000223965	0.768464	2.58026	1.5852	2.93085	ENSG00000223965	ZNF587P1
ENSG00000223967	0	0	0	0	ENSG00000223967	AL603910.2
ENSG00000223968	0	0.449963	0	0	ENSG00000223968	AC098614.2
ENSG00000223970	0	0	0.106107	0.0664584	ENSG00000223970	AC074397.1
ENSG00000223971	0	0	0	0	ENSG00000223971	AL669854.1
ENSG00000223972	0.746828	1.18431	1.17482	1.45296	ENSG00000223972	DDX11L1
ENSG00000223973	0.871609	0.977926	0.303068	2.59903	ENSG00000223973	AC068491.1
ENSG00000223974	1.18735	2.47611	0.884332	3.01486	ENSG00000223974	BNIP3P42
ENSG00000223976	0	0.192035	0.346868	0	ENSG00000223976	EXTL2P1
ENSG00000223977	0.483656	0.664731	0.584279	1.42536	ENSG00000223977	AC138623.1
ENSG00000223978	0	0	0	0	ENSG00000223978	ZNF736P1Y
ENSG00000223980	9.24097	181.818	0.125156	0.191796	ENSG00000223980	HLA-A
ENSG00000223981	0.755734	1.3254	1.66948	3.03874	ENSG00000223981	PHBP6
ENSG00000223982	0	0	0	0	ENSG00000223982	SNRPD2P2
ENSG00000223983	0	0.461006	2.77761	0.760791	ENSG00000223983	RP11-12A20.8
ENSG00000223984	0.821395	1.26059	1.53163	1.77338	ENSG00000223984	HNRNPRP1
ENSG00000223986	0	0	0	0	ENSG00000223986	AC069421.1
ENSG00000223987	0	0	0.161818	0	ENSG00000223987	RPL26P28
ENSG00000223990	0.00091433	0	0.000798201	0.000801615	ENSG00000223990	HLA-DPA2
ENSG00000223995	0	0.209255	0	0	ENSG00000223995	RPL32P35
ENSG00000223996	0.00219419	0.195312	0.00203041	0.0715276	ENSG00000223996	ETF1P1
ENSG00000223997	0	0	0	0	ENSG00000223997	TRDD1
ENSG00000224001	2.52493	2.43521	1.64842	3.16559	ENSG00000224001	AL360081.1
ENSG00000224002	0	0.0455491	0.0265533	0.307368	ENSG00000224002	AC090099.2
ENSG00000224003	0.212246	0.835667	0.943693	0.668861	ENSG00000224003	YES1P1
ENSG00000224004	0	0	0	0	ENSG00000224004	ATP5C1P1
ENSG00000224005	12.6094	12.4114	19.2063	20.3569	ENSG00000224005	AC022400.1
ENSG00000224006	0.174034	1.31219	0	0	ENSG00000224006	AL645935.2
ENSG00000224007	0.540209	1.03961	1.25272	1.89647	ENSG00000224007	AC019070.1
ENSG00000224011	0	0.304812	0.2787	0	ENSG00000224011	AC110602.1
ENSG00000224012	0	0	0	0	ENSG00000224012	AC116917.1
ENSG00000224014	0	1.20995	0.725023	0	ENSG00000224014	AL390728.3
ENSG00000224016	0.597403	0	1.29611	1.46304	ENSG00000224016	AC092681.1
ENSG00000224019	0.162847	1.09227	2.67629	3.5516	ENSG00000224019	RPL21P32
ENSG00000224025	0.0385388	0.055693	0.0336299	0	ENSG00000224025	AL353616.1
ENSG00000224033	0	0	0.0201666	0.0253225	ENSG00000224033	CDY8P
ENSG00000224035	0	0.0307299	0	0.0349645	ENSG00000224035	SFPQP1
ENSG00000224036	0	0	0	0	ENSG00000224036	CTSLP2
ENSG00000224039	0.0410615	0.28081	0.253576	0.576499	ENSG00000224039	CDYLP1
ENSG00000224040	0	0	0	0	ENSG00000224040	HMGN1P4
ENSG00000224041	0	0	0	0	ENSG00000224041	IGKV3D-15
ENSG00000224042	0	0.158493	0	0	ENSG00000224042	MTND4P6
ENSG00000224044	0	0	0	3.56E-07	ENSG00000224044	UBDP1
ENSG00000224045	0	0	0	0	ENSG00000224045	AL354761.1

ENSG00000224051	26.5569	15.7338	22.0495	7.70355	ENSG00000224051	CPTP
ENSG00000224052	0	0.0288995	0.0208992	0	ENSG00000224052	HTATSF1P1
ENSG00000224053	0	0.0197876	0.0178653	0	ENSG00000224053	CR788300.1
ENSG00000224054	0	0.0371295	0.0329437	0.207035	ENSG00000224054	AL022163.1
ENSG00000224055	0.41543	1.70533	0.420087	1.09763	ENSG00000224055	GAPDHP55
ENSG00000224058	5.01453	10.7975	13.1408	15.1989	ENSG00000224058	AC006509.1
ENSG00000224059	0.0305957	0.0300964	0.0281239	0.0336078	ENSG00000224059	HSPA8P16
ENSG00000224060	0.304822	0.495159	1.04768	0	ENSG00000224060	ARSEP1
ENSG00000224061	0	0	0	0	ENSG00000224061	AC092106.2
ENSG00000224062	0	0	0	0	ENSG00000224062	TUBB4BP5
ENSG00000224064	0.648965	0.413367	0.186647	0.457494	ENSG00000224064	AL356390.1
ENSG00000224065	0	0	0	0	ENSG00000224065	SRIP2
ENSG00000224067	0	0.582696	0.701733	1.72202	ENSG00000224067	AL354877.1
ENSG00000224069	0	0	0	0	ENSG00000224069	BX842559.1
ENSG00000224070	0.741673	0.356563	0	0.38967	ENSG00000224070	HMGN1P6
ENSG00000224071	0	0	0	0	ENSG00000224071	AC009474.1
ENSG00000224072	0.510358	0.923103	0.887752	0.801673	ENSG00000224072	AL139811.1
ENSG00000224080	8.87199	2.0633	2.01787	7.38183	ENSG00000224080	UBE2FP1
ENSG00000224082	0.192693	0.407191	0.335733	0.369018	ENSG00000224082	UBTFL8
ENSG00000224083	0.189534	0.45952	0.165039	0.78857	ENSG00000224083	MTCO1P11
ENSG00000224085	0	0	0	0	ENSG00000224085	RPL23AP41
ENSG00000224089	0	0.0219476	0.0109151	0.0319741	ENSG00000224089	CT47A10
ENSG00000224092	0	0	0	0	ENSG00000224092	AL591644.1
ENSG00000224094	0	0	0.19128	0.235043	ENSG00000224094	RPS24P8
ENSG00000224097	0.257663	0.600186	0.665103	0.620165	ENSG00000224097	AC021148.1
ENSG00000224098	0	0.0858021	0.0808883	0.0707639	ENSG00000224098	BX120009.1
ENSG00000224103	0.0861485	0.0143133	0.111636	0.051048	ENSG00000224103	HLA-DPA1
ENSG00000224104	0	0	0	0	ENSG00000224104	AC079809.1
ENSG00000224105	0.357191	0.0509367	0.0789204	0.332033	ENSG00000224105	C6orf15
ENSG00000224106	0.239247	0	0	0	ENSG00000224106	CYP4F25P
ENSG00000224108	0.00219419	0.195312	0.0547187	0.0715276	ENSG00000224108	ETF1P1
ENSG00000224109	0	0	0	0	ENSG00000224109	CENPVL3
ENSG00000224110	0.862794	1.11927	1.60394	1.17313	ENSG00000224110	MTRF1LP2
ENSG00000224114	0.284643	1.09089	2.06495	1.01267	ENSG00000224114	AL591846.1
ENSG00000224117	0.18007	0.231025	0.470899	0.988242	ENSG00000224117	PTPN2P2
ENSG00000224118	0	0	0	0	ENSG00000224118	MICF
ENSG00000224120	0.461121	0.704371	0.620046	0.33653	ENSG00000224120	C6orf136
ENSG00000224121	2.20838	3.64866	3.14396	7.45054	ENSG00000224121	ATG12P2
ENSG00000224124	0.85683	1.654	1.33035	2.2071	ENSG00000224124	POM121L10P
ENSG00000224126	0	0.243075	1.20609	0.992098	ENSG00000224126	AC026271.2
ENSG00000224129	0.0969342	0.270646	0	0.152949	ENSG00000224129	DPPA2P2
ENSG00000224130	0.174805	0.290747	0.177963	0.662857	ENSG00000224130	AP001652.1
ENSG00000224131	0.468525	0.798622	0.813675	0.756316	ENSG00000224131	CR318637.1
ENSG00000224132	0.266831	0.254207	0	0.839999	ENSG00000224132	AC112715.1
ENSG00000224134	0	0.154147	0.139139	0.171685	ENSG00000224134	AC004866.2
ENSG00000224136	0	0	0.145579	0	ENSG00000224136	AC007568.1
ENSG00000224140	0	0.0103777	0.17011	0.0956457	ENSG00000224140	TNXA
ENSG00000224143	0.596717	0.8323	0.962411	1.69301	ENSG00000224143	EHMT2
ENSG00000224144	0	0	0.0546556	0.0684377	ENSG00000224144	ASH2LP1
ENSG00000224145	0.208044	0.749081	0.160154	0.231175	ENSG00000224145	TRIM15
ENSG00000224146	0.0288811	0.0197876	0.0178653	0	ENSG00000224146	BX927223.1
ENSG00000224151	0	0	0	0	ENSG00000224151	USP9YP28
ENSG00000224153	0	0	0	0	ENSG00000224153	LINC02054

ENSG00000224155	0	0	0	0	ENSG00000224155	AC073136.2
ENSG00000224156	20.0144	27.9814	5.53441	0.46487	ENSG00000224156	TUBB
ENSG00000224158	0	0	0	0	ENSG00000224158	CR753651.1
ENSG00000224159	0.106669	0.103037	0.377667	0.230076	ENSG00000224159	HMGB1P9
ENSG00000224160	0.397008	0	0	0.605267	ENSG00000224160	CICP10
ENSG00000224161	0	0	0	0	ENSG00000224161	AC098847.1
ENSG00000224162	0	0	0	0	ENSG00000224162	UQCRHP3
ENSG00000224163	0	0	0	0	ENSG00000224163	AC025594.1
ENSG00000224166	0.180889	0	0	0	ENSG00000224166	PRYP1
ENSG00000224168	0.437028	1.14643	0.536075	1.93888	ENSG00000224168	TRIM31
ENSG00000224169	0	0	0	0	ENSG00000224169	HSFY6P
ENSG00000224172	0.0834498	0	0	0	ENSG00000224172	AC091799.1
ENSG00000224180	0.0538926	1.59682	0.816886	2.53553	ENSG00000224180	CCHCR1
ENSG00000224183	0	0	0	1.71E-08	ENSG00000224183	SDHDP6
ENSG00000224185	0.249661	0	0	0	ENSG00000224185	SNX18P9
ENSG00000224186	5.5173	12.7425	10.2998	10.7174	ENSG00000224186	C5orf66
ENSG00000224188	0	0	0	0	ENSG00000224188	UBE2D3P4
ENSG00000224196	0	0	0	7.46247	ENSG00000224196	OR5AK4P
ENSG00000224197	0	0	0	0	ENSG00000224197	HLA-DQB3
ENSG00000224199	0.0200683	0	0	0.0219617	ENSG00000224199	WI2-2994D6.1
ENSG00000224200	0	0	0.476154	0.430663	ENSG00000224200	FKBPL
ENSG00000224201	0	0	0	0.0985457	ENSG00000224201	PNMA6A
ENSG00000224203	0	0	0.411218	0.680084	ENSG00000224203	RPS23P10
ENSG00000224205	0	0	0	0	ENSG00000224205	AC253536.1
ENSG00000224207	0.955223	0.89893	0.873002	0.571419	ENSG00000224207	AC018797.1
ENSG00000224208	0.450326	1.18528	0.531132	0.939438	ENSG00000224208	AL590762.3
ENSG00000224210	0.262669	0.370789	0.678177	1.24368	ENSG00000224210	TRIM60P5Y
ENSG00000224212	0.191537	16.5088	0.637794	0.237786	ENSG00000224212	TAP1
ENSG00000224217	0.144119	0.444797	0.496854	0.144856	ENSG00000224217	BX119904.1
ENSG00000224219	0	0	0	0	ENSG00000224219	AC074290.1
ENSG00000224221	0.272752	0.0873655	0.157859	0.0983737	ENSG00000224221	AC019205.1
ENSG00000224224	0	0	0	0	ENSG00000224224	HAUS1P2
ENSG00000224226	0.624437	2.6833	2.04421	0.648232	ENSG00000224226	TBC1D3B
ENSG00000224227	0.0666597	0	0	0	ENSG00000224227	OR2L1P
ENSG00000224230	0	0	0	0	ENSG00000224230	BX927235.1
ENSG00000224232	0.399947	0.288179	1.13592	0.219094	ENSG00000224232	AC005104.2
ENSG00000224233	0	0.0275452	0	0.0234623	ENSG00000224233	AL645937.3
ENSG00000224234	0	0.00838819	0.0181864	0	ENSG00000224234	OR10C1
ENSG00000224236	0	0.0662931	0.0624798	0.0387224	ENSG00000224236	MRRFP1
ENSG00000224237	0	0	0	1.57719	ENSG00000224237	MINOS1P3
ENSG00000224240	0	0.894346	0	0	ENSG00000224240	CYCSP49
ENSG00000224241	0	0	0	0	ENSG00000224241	TMEM183AP1
ENSG00000224242	0.0140136	0.0646215	0.0389217	0.0176708	ENSG00000224242	BTNL2
ENSG00000224244	0	0	0	0	ENSG00000224244	AC073508.1
ENSG00000224245	0	0	0	0	ENSG00000224245	AL358232.1
ENSG00000224246	0	0	0	0	ENSG00000224246	SFTA2
ENSG00000224252	0	0	0	4.96416	ENSG00000224252	AC113618.1
ENSG00000224253	2.13296	1.99934	1.44905	2.25545	ENSG00000224253	AL669813.1
ENSG00000224254	0	0	0	0	ENSG00000224254	MTCO1P39
ENSG00000224255	0.199336	0.567073	0.845402	1.92156	ENSG00000224255	PDCL3P6
ENSG00000224256	0.515407	3.08187	1.83799	1.04532	ENSG00000224256	Z93930.1
ENSG00000224261	0.171048	0.181204	0.189769	0.158983	ENSG00000224261	RPSAP18
ENSG00000224263	0	0	0	0	ENSG00000224263	CYCSP12
ENSG00000224264	14.1863	11.6285	12.687	3.36147	ENSG00000224264	VARS

ENSG00000224273	0.0710347	0.549948	0.160148	0.877621	ENSG00000224273	AC005077.2
ENSG00000224274	0.604331	0	0	0	ENSG00000224274	ENSAP1
ENSG00000224278	0	0	0	0	ENSG00000224278	AL592447.1
ENSG00000224279	2.45495	2.29735	0	0	ENSG00000224279	RPS29P31
ENSG00000224280	0.0241846	0.0378583	0.0484511	0.0203401	ENSG00000224280	AC005014.1
ENSG00000224282	0	0.119647	0.108088	0	ENSG00000224282	AC010469.1
ENSG00000224287	2.44178	3.04747	3.95451	2.17771	ENSG00000224287	MSL3P1
ENSG00000224288	0.0546461	0	0.0475361	0	ENSG00000224288	MTCYBP11
ENSG00000224289	0.213978	0.627676	0.480996	0.876198	ENSG00000224289	IFIT6P
ENSG00000224290	0.164783	0.252772	0.0998859	0.157885	ENSG00000224290	APOM
ENSG00000224291	0	0	0	0	ENSG00000224291	AC012671.1
ENSG00000224293	0	0	0	0	ENSG00000224293	TMEM183AP1
ENSG00000224295	0.472138	0.492674	0.274056	0.605919	ENSG00000224295	OLFM5P
ENSG00000224296	0.284174	0.478584	0.12706	0.481505	ENSG00000224296	MRPL49P1
ENSG00000224297	0.601775	0.613196	0.774371	1.08769	ENSG00000224297	AL158825.1
ENSG00000224299	0	0.813054	0.36702	0.453904	ENSG00000224299	MTATP6P16
ENSG00000224300	0	0.255123	0.057632	0.216438	ENSG00000224300	OR51P1P
ENSG00000224302	0.477611	0.449465	0.804231	0.485812	ENSG00000224302	AL500527.1
ENSG00000224305	0.0425612	0	0.145953	0.0990776	ENSG00000224305	HLA-DQB2
ENSG00000224309	0.378613	0.998937	0.748161	1.24764	ENSG00000224309	ANKRD30BP2
ENSG00000224312	0	0	0.165242	0.129105	ENSG00000224312	MCCD1P2
ENSG00000224313	1.69617	2.37247	1.46123	0.0777383	ENSG00000224313	DXO
ENSG00000224314	0	0	0.117878	0	ENSG00000224314	AC005002.1
ENSG00000224315	0.653255	2.4824	1.55192	1.69713	ENSG00000224315	RPL7P7
ENSG00000224316	0.407195	0.313898	0.748127	0.20931	ENSG00000224316	GTF2IP5
ENSG00000224319	0.0330719	0	0.0385538	0.0189047	ENSG00000224319	OR2H2
ENSG00000224320	53.9091	7.08621	0.189178	0.132326	ENSG00000224320	HLA-A
ENSG00000224321	0.318776	0.152313	0.146354	0.177259	ENSG00000224321	RPL12P14
ENSG00000224323	1.71961	4.79857	3.12199	4.0288	ENSG00000224323	DPRXP1
ENSG00000224324	0	0.445391	0	1.852	ENSG00000224324	THAP5P1
ENSG00000224331	1.98583	5.64196	5.66929	0.344651	ENSG00000224331	AC019181.1
ENSG00000224333	0.431139	0.294561	0.479168	0.333453	ENSG00000224333	GAPDHP20
ENSG00000224334	0	0.0499713	0	0	ENSG00000224334	AP000357.1
ENSG00000224335	0	0	0	0	ENSG00000224335	AC239809.1
ENSG00000224336	0	0.0807479	0.0729492	0.182081	ENSG00000224336	FAM197Y1
ENSG00000224337	0	0	0	0	ENSG00000224337	FAM8A3P
ENSG00000224338	0	0	0	0	ENSG00000224338	MTCYBP45
ENSG00000224339	0.212527	0.136244	0.123103	0.384906	ENSG00000224339	AL121578.1
ENSG00000224340	0.28503	0.273956	1.54471	1.49966	ENSG00000224340	AL590639.1
ENSG00000224341	0	0.0624281	0	0.0710307	ENSG00000224341	AC006965.1
ENSG00000224344	0.19345	0.185101	0.334227	0.205342	ENSG00000224344	KNOP1P3
ENSG00000224346	0	0.0470127	0	0	ENSG00000224346	BICD1P1
ENSG00000224348	0	0	0	0	ENSG00000224348	AL592076.1
ENSG00000224351	0	0	0	0	ENSG00000224351	CDKN2AIPNLP3
ENSG00000224352	0	0	0	0	ENSG00000224352	AC132479.1
ENSG00000224353	0	0	0	0	ENSG00000224353	ACE3P
ENSG00000224354	0	0.412872	0.426429	0.335543	ENSG00000224354	MTND2P5
ENSG00000224355	0	0	0	0	ENSG00000224355	MICG
ENSG00000224357	0	0.132809	0.300005	0.675638	ENSG00000224357	ATG3P1
ENSG00000224361	0.854501	1.05441	1.26955	1.05003	ENSG00000224361	AC011239.1
ENSG00000224362	0.233474	0.0627516	0.0983601	0.475397	ENSG00000224362	DDX39BP2
ENSG00000224365	3.08336	0	0	2.89354	ENSG00000224365	AC073261.1
ENSG00000224366	0.456067	0.430217	1.15525	0.932264	ENSG00000224366	AC243964.1

ENSG00000224367	0	0.437189	0.235961	1.41261	ENSG00000224367	OACYLP
ENSG00000224368	0	0	0	0	ENSG00000224368	ARAFP2
ENSG00000224370	3.03067	5.21857	11.3823	9.83179	ENSG00000224370	AC093392.2
ENSG00000224372	0	0	0	0	ENSG00000224372	HLA-N
ENSG00000224373	0.249975	0.437288	0.679821	0.841474	ENSG00000224373	IGHV4-59
ENSG00000224378	0.238434	0.898692	1.75628	0.927638	ENSG00000224378	MICB
ENSG00000224379	0	0	0.0255424	0	ENSG00000224379	TCF19
ENSG00000224383	0.383325	0.395387	0.237404	0.659634	ENSG00000224383	PRR29
ENSG00000224389	0.312399	2.6995	1.83901	0.616794	ENSG00000224389	C4B
ENSG00000224392	0	0	0	0	ENSG00000224392	AL935156.2
ENSG00000224393	0.181329	0.151186	0.308192	0.303335	ENSG00000224393	MPIG6B
ENSG00000224395	0.0440785	0.10084	0.119165	0.128925	ENSG00000224395	OR2H1
ENSG00000224396	0.0488767	0.0964815	0.0432118	0.216689	ENSG00000224396	METTL15P3
ENSG00000224398	64.0057	17.2922	32.8538	1.13045	ENSG00000224398	CSNK2B
ENSG00000224399	8.10034	7.04224	6.12923	6.51393	ENSG00000224399	SLC39A7
ENSG00000224401	0.22754	0.798009	0.788226	0.864693	ENSG00000224401	RPL7P57
ENSG00000224402	0	0.0320128	0.0876673	0.0362098	ENSG00000224402	OR6D1P
ENSG00000224403	0	0.100486	0	0	ENSG00000224403	DPPA2P3
ENSG00000224408	0	0	0	0	ENSG00000224408	USP9YP22
ENSG00000224410	0	0	0	0	ENSG00000224410	AC097499.1
ENSG00000224411	0.0682854	0	0	0.144144	ENSG00000224411	HSP90AA2P
ENSG00000224412	0	4.36557	2.5111	9.3162	ENSG00000224412	AC022022.1
ENSG00000224414	0.34422	0.712762	0.528131	0.796324	ENSG00000224414	AC010886.1
ENSG00000224415	0.240734	0.462371	0.730268	1.03451	ENSG00000224415	AC007683.1
ENSG00000224416	0.253096	0	0	0	ENSG00000224416	IFNA22P
ENSG00000224419	0	0.0905649	0.039863	0.149294	ENSG00000224419	KRT18P27
ENSG00000224420	0.573572	1.65074	1.47615	0.632198	ENSG00000224420	ADM5
ENSG00000224421	0.557799	2.62492	0.468273	1.12889	ENSG00000224421	ATP5J2LP
ENSG00000224425	0	0	0	0	ENSG00000224425	AC073869.2
ENSG00000224426	0	0	0.111175	0.138148	ENSG00000224426	SLC31A1P1
ENSG00000224427	0	0.303552	0	0.333183	ENSG00000224427	AP000281.1
ENSG00000224430	0.437019	2.00147	3.20803	3.59823	ENSG00000224430	MKRN5P
ENSG00000224431	1.08549	1.98364	2.46376	3.7778	ENSG00000224431	AC063976.2
ENSG00000224435	0	0	0.0614369	0.0384297	ENSG00000224435	NF1P6
ENSG00000224436	0	0.516946	0.4614	1.1126	ENSG00000224436	BX323014.1
ENSG00000224437	0.158858	0	0	0.200258	ENSG00000224437	PIGUP1
ENSG00000224438	0	0	0	0	ENSG00000224438	RPL23AP14
ENSG00000224439	0	0.139534	0.128377	0.397925	ENSG00000224439	RPSAP10
ENSG00000224442	0	0	0	0	ENSG00000224442	AC017035.1
ENSG00000224443	0.218076	0	0.18818	0	ENSG00000224443	AC006509.2
ENSG00000224444	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000224444	MAS1LP1
ENSG00000224447	0	0	0	0	ENSG00000224447	U91328.1
ENSG00000224448	0.426898	1.50831	1.11081	0.760126	ENSG00000224448	AC005020.1
ENSG00000224451	2.99904	6.88428	4.76583	6.1775	ENSG00000224451	ATP5F1P1
ENSG00000224452	2.00515	1.85841	1.12701	1.57683	ENSG00000224452	RSL24D1P6
ENSG00000224455	5.41159	9.51597	9.77761	4.93757	ENSG00000224455	VPS52
ENSG00000224458	0.100281	0.0482446	0.181005	0.389521	ENSG00000224458	GUSBP6
ENSG00000224462	0	0.0288352	0.104269	0.09846	ENSG00000224462	C4BPAP1
ENSG00000224463	1.41802	6.85806	3.84478	6.12502	ENSG00000224463	AC079354.2
ENSG00000224464	0	0.44121	0.537071	0.860321	ENSG00000224464	PGAM1P6
ENSG00000224465	0.125015	0	0.108329	0.134334	ENSG00000224465	SOCS2P2
ENSG00000224466	0	0	0.0811382	0	ENSG00000224466	CDCA4P2
ENSG00000224469	0	0	0	0	ENSG00000224469	AC009517.1

ENSG00000224470	9.2974	8.11499	12.2585	7.71527	ENSG00000224470	ATXN1L
ENSG00000224471	0	0.294845	0.532783	1.53598	ENSG00000224471	MTCO3P19
ENSG00000224472	0.10729	0	0.54126	1.51871	ENSG00000224472	TCF19
ENSG00000224473	0.123232	0.118264	0	0	ENSG00000224473	CCND3P1
ENSG00000224474	9.00767	12.2287	7.16455	10.9765	ENSG00000224474	AL355490.1
ENSG00000224475	0	0	0.073067	0.0911856	ENSG00000224475	AC073900.1
ENSG00000224476	0.338473	0	0	0.351646	ENSG00000224476	RPL36P16
ENSG00000224479	1.06073	2.18497	2.71259	5.49638	ENSG00000224479	AC104162.1
ENSG00000224482	0.0507918	0.146688	0.0441935	0.166356	ENSG00000224482	HSFY4P
ENSG00000224484	0	0.990013	1.50418	0.581867	ENSG00000224484	AC023141.2
ENSG00000224485	0	0	0	0	ENSG00000224485	USP9YP7
ENSG00000224486	0	0.0149857	0	0	ENSG00000224486	AL662795.1
ENSG00000224487	0.0151711	0.0536059	0.0442655	0.0942871	ENSG00000224487	OR12D3
ENSG00000224488	0.0419775	0.241858	0.255781	0.640991	ENSG00000224488	SAMM50P1
ENSG00000224493	0	0	0	0.109681	ENSG00000224493	AC093156.1
ENSG00000224494	0	0	0	0	ENSG00000224494	HNRNPA3P14
ENSG00000224496	0.0435963	0.0729458	0.0165025	0	ENSG00000224496	TRIM40
ENSG00000224497	0	0	0	0	ENSG00000224497	RPL36P4
ENSG00000224498	0	0	0	0.0466595	ENSG00000224498	MAPKAPK5P1
ENSG00000224501	0	0	0.539944	19.3561	ENSG00000224501	HSPA1B
ENSG00000224503	5.37496	8.62784	11.305	18.8649	ENSG00000224503	AC104438.1
ENSG00000224510	0	0.961255	0.849129	0	ENSG00000224510	POLR2KP2
ENSG00000224512	0.755982	1.14101	0.152357	1.1792	ENSG00000224512	AC021593.1
ENSG00000224518	0	0	0	0	ENSG00000224518	AC006989.1
ENSG00000224519	0	0.290632	0.264329	0.912884	ENSG00000224519	HMGN1P19
ENSG00000224520	0	0	0	0.045327	ENSG00000224520	KRT8P45
ENSG00000224523	0.176606	0.0848472	0	0.191182	ENSG00000224523	AL445213.1
ENSG00000224524	0	0	0	0	ENSG00000224524	CYCSP42
ENSG00000224526	0	0.0596028	0	0.0788231	ENSG00000224526	HLA-K
ENSG00000224529	0.0564918	0	0.0491362	0	ENSG00000224529	AC093698.2
ENSG00000224530	0	0.165792	0.897897	0.921532	ENSG00000224530	PPIAP10
ENSG00000224531	5.70389	5.58713	7.41173	4.62211	ENSG00000224531	SMIM13
ENSG00000224537	0	0	0	0.0610058	ENSG00000224537	MEP1AP4
ENSG00000224538	0	0	0.241007	0	ENSG00000224538	MCCD1P1
ENSG00000224539	0	0	0.007018	0	ENSG00000224539	SAGE4P
ENSG00000224540	0.0489459	0.0942954	0.0424124	0.053877	ENSG00000224540	AC092810.1
ENSG00000224542	0.0843416	1.72277	0.425854	1.98519	ENSG00000224542	TRIM31
ENSG00000224543	8.17147	12.0159	14.6365	15.7211	ENSG00000224543	SNRPGP15
ENSG00000224544	0	0	0.0232283	3.18E-06	ENSG00000224544	PSORS1C2
ENSG00000224545	0	0	0.212181	0	ENSG00000224545	AC008264.1
ENSG00000224546	0.0354514	0	0.0319304	0	ENSG00000224546	EIF4BP3
ENSG00000224547	0	0.084187	0.0760127	0.663599	ENSG00000224547	ZNF619P1
ENSG00000224548	0	0	0	0	ENSG00000224548	Z75741.1
ENSG00000224550	0.758203	0	0	0	ENSG00000224550	AC114491.1
ENSG00000224551	0.688334	1.19319	1.54676	2.07847	ENSG00000224551	HMGB3P21
ENSG00000224552	0.875271	0.813988	1.17844	0.651601	ENSG00000224552	ABHD16A
ENSG00000224553	1.11978	1.28803	1.39412	1.99274	ENSG00000224553	AC008065.1
ENSG00000224554	0.051091	0	0.0451445	0.0287014	ENSG00000224554	RANP1
ENSG00000224555	0.708962	1.65845	2.40494	1.1152	ENSG00000224555	AC087441.1
ENSG00000224556	0	0	0	0	ENSG00000224556	BX510359.1
ENSG00000224557	3.99596	6.14621	5.3641	7.63265	ENSG00000224557	HLA-DPB2
ENSG00000224560	0	0	0	0	ENSG00000224560	AC108043.1
ENSG00000224564	1.86909	1.3845	0.332359	0.329597	ENSG00000224564	HCG4
ENSG00000224566	2.99063	8.71786	2.67129	3.97502	ENSG00000224566	FAM96AP2

ENSG00000224567	0	0	0	0	ENSG00000224567	AC134879.1
ENSG00000224569	0.0737425	0.0709147	0.0640793	0.160193	ENSG00000224569	AC095052.1
ENSG00000224570	0.126708	0.640998	0.33114	0.972505	ENSG00000224570	AC097063.1
ENSG00000224571	0	0.463822	0.42475	0.895008	ENSG00000224571	USP9YP13
ENSG00000224573	0	0	0	0	ENSG00000224573	AC083863.1
ENSG00000224578	1.00231	2.65088	0.987071	1.51615	ENSG00000224578	HNRNPA1P48
ENSG00000224579	0	0.0570873	0.328356	0.0814314	ENSG00000224579	AC245052.2
ENSG00000224581	0	0	0	0	ENSG00000224581	XX-FW84067D5.2
ENSG00000224584	0	1.06027	0	0.196272	ENSG00000224584	UBE2V1P13
ENSG00000224585	0	0	0	0	ENSG00000224585	AC103563.1
ENSG00000224586	0	0.297583	0.246895	0.287314	ENSG00000224586	GPX5
ENSG00000224587	0.600581	2.71671	1.21032	1.35815	ENSG00000224587	MDC1
ENSG00000224589	0	0	0	0	ENSG00000224589	AC112492.1
ENSG00000224590	0.274879	0.523264	0	0.576161	ENSG00000224590	MTND3P16
ENSG00000224593	0	0	0.413764	1.66716	ENSG00000224593	AC092427.1
ENSG00000224594	0.344058	0.494424	1.2546	3.75053	ENSG00000224594	AC041040.1
ENSG00000224598	0.905047	0.828857	0.688916	0.975353	ENSG00000224598	RPS5P2
ENSG00000224599	0	0	1.04711	0	ENSG00000224599	BMS1P12
ENSG00000224600	0	0	0	0	ENSG00000224600	AL031864.2
ENSG00000224602	0	0	0	0	ENSG00000224602	RPS26P5
ENSG00000224603	0	0	0	0	ENSG00000224603	BX664725.1
ENSG00000224604	0	0	0.171169	0	ENSG00000224604	AC008069.1
ENSG00000224607	0	0	0	0	ENSG00000224607	IGKV1D-27
ENSG00000224608	8.99231	17.0547	24.7539	42.9405	ENSG00000224608	HLA-B
ENSG00000224611	1.31695	0.837137	6.00013	0.660364	ENSG00000224611	AC007919.1
ENSG00000224615	0	0	1.24166	0	ENSG00000224615	RP11-34H11.1
ENSG00000224617	0	0	0	0	ENSG00000224617	BX276092.1
ENSG00000224618	10.6821	13.3694	4.50322	15.5214	ENSG00000224618	AC096921.1
ENSG00000224620	0	0.14522	0	0.249324	ENSG00000224620	MEF2AP1
ENSG00000224622	0	0.0695421	0.251335	0	ENSG00000224622	OR9R1P
ENSG00000224625	0	0	0	0	ENSG00000224625	TUBB8P6
ENSG00000224627	0	0	0	0	ENSG00000224627	RPL37P10
ENSG00000224628	0.0772559	0.222177	0.134611	0.17033	ENSG00000224628	AL121723.1
ENSG00000224629	4.30056	10.0692	18.3509	12.939	ENSG00000224629	AC004975.1
ENSG00000224630	0	0	0	0.257549	ENSG00000224630	AC234064.1
ENSG00000224631	0.729649	0.415729	0.183706	0.226938	ENSG00000224631	RPS27AP16
ENSG00000224632	0	0	0.0993054	0.246675	ENSG00000224632	Z73361.1
ENSG00000224633	0.009462	0.0181999	0.0164453	0.0102936	ENSG00000224633	CR933842.1
ENSG00000224634	0	0.0474136	0	0.10757	ENSG00000224634	ZNF736P6Y
ENSG00000224637	0.101304	0.309314	0.608431	0.221511	ENSG00000224637	PDSS1P2
ENSG00000224640	0	0	0	0	ENSG00000224640	SRSF1P1
ENSG00000224646	0	0	0	0	ENSG00000224646	AC007387.1
ENSG00000224647	0.0915403	0.132219	0.0796722	0.100051	ENSG00000224647	AC026954.1
ENSG00000224650	0.0606138	0	0	0	ENSG00000224650	IGHV3-74
ENSG00000224653	0	0	0	0.257235	ENSG00000224653	AC023141.3
ENSG00000224654	0	0	0	0	ENSG00000224654	UBD
ENSG00000224656	0	0	0	0.0602991	ENSG00000224656	AL009172.1
ENSG00000224657	0	0	0	0	ENSG00000224657	RBMY2BP
ENSG00000224659	0	0	0	0	ENSG00000224659	GAGE12J
ENSG00000224662	0	0.377164	1.0184	1.66184	ENSG00000224662	ATP6V1G1P3
ENSG00000224664	0	0	0	0	ENSG00000224664	RPL36AP53
ENSG00000224667	0.968062	1.95342	1.38222	4.0127	ENSG00000224667	AC013470.1
ENSG00000224668	0.0182035	0.0523408	0.0472665	0.139574	ENSG00000224668	IPO8P1
ENSG00000224669	0.169854	0	0	0.17928	ENSG00000224669	AC016769.2

ENSG00000224670	0	0	0	0	ENSG00000224670	AC068135.1
ENSG00000224672	0.65495	1.00542	0.718896	0.984108	ENSG00000224672	RPL17P10
ENSG00000224674	0.650852	1.78638	1.31355	2.4743	ENSG00000224674	EIF3EP2
ENSG00000224676	0	0.29911	0.675138	1.00012	ENSG00000224676	AP000351.8
ENSG00000224677	4.98774	7.96734	3.37634	5.36249	ENSG00000224677	PDIA3P2
ENSG00000224678	0.124372	0.299154	0.109488	0.346685	ENSG00000224678	GAPDHP46
ENSG00000224679	0	0	0	0	ENSG00000224679	MED15P4
ENSG00000224680	0.149154	0.711268	0.139791	0.147516	ENSG00000224680	PLA2G12AP1
ENSG00000224681	0	0	0	0	ENSG00000224681	BX664727.1
ENSG00000224682	0	0.0416517	0	0.094596	ENSG00000224682	SOCS5P2
ENSG00000224683	0	0.58969	1.33196	0.974076	ENSG00000224683	RPL36AP29
ENSG00000224685	0	0	0	0	ENSG00000224685	AC099670.2
ENSG00000224686	0	0	0.251303	0	ENSG00000224686	ELOCP23
ENSG00000224688	0	0.292881	0	0	ENSG00000224688	E2F6P2
ENSG00000224689	7.66015	8.40891	4.38752	8.48278	ENSG00000224689	ZNF812P
ENSG00000224690	0	0.557308	0.670933	1.23987	ENSG00000224690	UBE2D3P3
ENSG00000224692	0.0761243	0.0731968	0	0.165279	ENSG00000224692	Z68694.1
ENSG00000224693	0	0	0	0	ENSG00000224693	HLA-T
ENSG00000224695	0.142046	0	0	0.783042	ENSG00000224695	MTND6P7
ENSG00000224697	0.061654	0.412872	0.533036	0.468331	ENSG00000224697	NEFMP1
ENSG00000224701	0	0.122506	0.522328	0.681598	ENSG00000224701	MED28P4
ENSG00000224706	0	0	0	0	ENSG00000224706	RPS17P13
ENSG00000224708	0.0327523	0	0	0	ENSG00000224708	LY6G6E
ENSG00000224709	0	0	0	0	ENSG00000224709	OR11M1P
ENSG00000224710	0	0	0	0	ENSG00000224710	FAM90A8P
ENSG00000224712	1.06415	2.91238	3.84934	0.655226	ENSG00000224712	NPIPA3
ENSG00000224719	0	0	0.660996	0.400223	ENSG00000224719	AC009237.2
ENSG00000224722	0.159928	0.264223	0.470639	0.0617175	ENSG00000224722	AC020688.1
ENSG00000224723	0	0	0	0	ENSG00000224723	GUSBP10
ENSG00000224725	0	0	0	0	ENSG00000224725	CEP57L1P1
ENSG00000224727	0.657862	3.46768	3.77435	5.60697	ENSG00000224727	FCF1P7
ENSG00000224728	0.18995	0.919152	0.997704	0.59173	ENSG00000224728	IMPDH1P8
ENSG00000224730	0.23394	0.38731	0.32465	0.694744	ENSG00000224730	LILRB1-AS1
ENSG00000224732	0.0331593	0.0956711	0	0.0721459	ENSG00000224732	MAGEA7P
ENSG00000224735	0	0	0	0	ENSG00000224735	BX323845.1
ENSG00000224736	3.27029	2.94532	0.97788	2.22002	ENSG00000224736	HLA-V
ENSG00000224740	8.17875	12.1814	9.6525	4.98079	ENSG00000224740	FLOT1
ENSG00000224747	0	0.422451	0.047668	0.609067	ENSG00000224747	MTCYBP21
ENSG00000224748	0.191537	0.320675	0.637794	0.237786	ENSG00000224748	TAP1
ENSG00000224751	0.368251	1.28468	0.892603	2.26048	ENSG00000224751	SHMT1P1
ENSG00000224752	0.604878	0	0.297553	0.185623	ENSG00000224752	VN1R21P
ENSG00000224755	0	0	0	0	ENSG00000224755	HMGN1P34
ENSG00000224760	0	0	0	0	ENSG00000224760	C1DP3
ENSG00000224762	1.64275	0.840973	0.915578	1.41601	ENSG00000224762	CR769776.1
ENSG00000224763	0.0669674	0.13152	0.130863	0.199315	ENSG00000224763	FDPSP8
ENSG00000224769	3.17376	0.349285	0.152021	0.173579	ENSG00000224769	MUC20P1
ENSG00000224770	0.0140136	0	0	0	ENSG00000224770	BTNL2
ENSG00000224773	0	0.014036	0.000353627	0.0478109	ENSG00000224773	HSPA8P7
ENSG00000224774	1.81705	13.5204	4.77528	7.07669	ENSG00000224774	CSNK2B
ENSG00000224775	0.144592	0.202846	0.185264	0.20783	ENSG00000224775	BRAFP1
ENSG00000224776	0.0749145	0	0	0.0813481	ENSG00000224776	RPSAP50
ENSG00000224777	0	0	0	0	ENSG00000224777	OR4F2P
ENSG00000224778	0	0.0676951	0.126187	0.227902	ENSG00000224778	CENPIP1
ENSG00000224781	0	0	0	0	ENSG00000224781	EIF4A2P4

ENSG00000224782	5.71416	2.89829	3.53188	3.21515	ENSG00000224782	PFDN6
ENSG00000224783	0.0312568	0.0602391	0.108912	0.102822	ENSG00000224783	MIPEPP2
ENSG00000224784	0	0	0	0.969422	ENSG00000224784	AL591704.2
ENSG00000224785	0.0638735	0	0	0.20983	ENSG00000224785	AC006026.1
ENSG00000224786	0.166994	1.11987	0.866553	0.890104	ENSG00000224786	CETN4P
ENSG00000224791	0.0456035	0.0878403	0	0	ENSG00000224791	KRT18P39
ENSG00000224792	0.202317	0	0.108329	0	ENSG00000224792	IQCF4
ENSG00000224793	0	0	0	0	ENSG00000224793	HLA-DQB3
ENSG00000224796	0	0.0858021	0.0808883	0.0707639	ENSG00000224796	AL645931.1
ENSG00000224797	0.886245	2.1998	3.37163	2.80453	ENSG00000224797	AL359092.1
ENSG00000224800	0	0	0	0	ENSG00000224800	RPS27AP6
ENSG00000224801	0	0.0936022	0	0	ENSG00000224801	HCG4P8
ENSG00000224802	0.40627	0.468608	0.211681	0.176198	ENSG00000224802	TUBB4BP2
ENSG00000224806	0	0	0	0	ENSG00000224806	ARL5AP4
ENSG00000224807	0	0	0	0	ENSG00000224807	DUX4L9
ENSG00000224809	0.0516966	0.0494734	0.115657	0.170702	ENSG00000224809	BEND3P2
ENSG00000224813	0	7.44247	11.3152	9.56741	ENSG00000224813	RP4-669L17.4
ENSG00000224815	0	0.691879	0	2.99155	ENSG00000224815	AL691447.1
ENSG00000224816	0	0	0	0	ENSG00000224816	NAP1L4P2
ENSG00000224820	0	0	0.133462	0.498871	ENSG00000224820	BTF3P4
ENSG00000224826	1.0134	1.41233	1.86011	2.4293	ENSG00000224826	AC019109.1
ENSG00000224827	0.192575	0.0873611	0	0	ENSG00000224827	LINC00265-2P
ENSG00000224828	0	0	0	0	ENSG00000224828	RP11-186G6.5
ENSG00000224829	0.199747	0.57541	0.174024	0.210642	ENSG00000224829	TOMM20P1
ENSG00000224830	0.098281	0	0.0853118	0.212443	ENSG00000224830	OR2X1P
ENSG00000224831	0	0.413039	0.229888	0	ENSG00000224831	AC117395.2
ENSG00000224834	0	0.372597	0	0.898078	ENSG00000224834	BTF3P9
ENSG00000224836	0	0.275026	0.248592	2.11944	ENSG00000224836	AL356498.1
ENSG00000224837	7.96599	5.75933	1.27746	3.6014	ENSG00000224837	GCSHP5
ENSG00000224838	57.1737	133.672	136.822	164.646	ENSG00000224838	FKSG52
ENSG00000224839	0.154761	0	0	0	ENSG00000224839	RPL12P17
ENSG00000224841	5.86561	7.28875	5.7293	4.35313	ENSG00000224841	RGL2
ENSG00000224852	0.0322683	0.118144	0.136012	0.415335	ENSG00000224852	MTND5P24
ENSG00000224854	0.234263	0.112419	0.30457	0	ENSG00000224854	CDKN2A-AS1
ENSG00000224856	0.618779	0.293178	1.06102	1.00664	ENSG00000224856	AL035398.1
ENSG00000224858	0.819146	2.30732	2.98428	3.04449	ENSG00000224858	RPL29P11
ENSG00000224859	0	0	0	0	ENSG00000224859	ZNRD1
ENSG00000224860	0.0484655	0.0939917	0.0424877	0.317637	ENSG00000224860	GXYLT1P2
ENSG00000224861	0	0	0.168324	0	ENSG00000224861	YBX1P1
ENSG00000224864	0	0	0	0	ENSG00000224864	AC011447.1
ENSG00000224866	0	0	0	0	ENSG00000224866	USP9YP25
ENSG00000224867	20.8419	37.776	42.583	74.5751	ENSG00000224867	AC096644.1
ENSG00000224869	0	0	0	0	ENSG00000224869	AC062016.1
ENSG00000224870	10.2601	7.52055	12.4299	5.69871	ENSG00000224870	AL391244.1
ENSG00000224873	0	0	0.00240944	0.00769717	ENSG00000224873	CDY13P
ENSG00000224874	0	0	0	0	ENSG00000224874	MYL8P
ENSG00000224877	49.901	42.1267	48.8884	38.0388	ENSG00000224877	NDUFAF8
ENSG00000224880	0	0.0848462	0	0	ENSG00000224880	MTCYBP29
ENSG00000224881	3.60901	5.00986	11.4321	5.32681	ENSG00000224881	AC068279.1
ENSG00000224882	1.10543	0.789327	0.0576924	2.37248	ENSG00000224882	IKBKGP1
ENSG00000224886	4.2873	3.0391	6.41419	10.0851	ENSG00000224886	AL132656.1
ENSG00000224887	0	0	0.163313	0.205524	ENSG00000224887	AL513318.1
ENSG00000224889	0.087419	0.412726	0	0.298453	ENSG00000224889	PTMAP1
ENSG00000224891	0.429231	3.0598	1.71167	2.13607	ENSG00000224891	AC007899.1

ENSG00000224892	0.893421	2.29664	4.46589	1.20859	ENSG00000224892	RPS4XP16
ENSG00000224894	0	0	0	0.0890581	ENSG00000224894	GPR53P
ENSG00000224895	1.21962	2.80116	3.20659	6.3501	ENSG00000224895	VPS26BP1
ENSG00000224896	0.0664036	0.447035	0.174516	0.442508	ENSG00000224896	SIGLEC30P
ENSG00000224902	0	0	0	0	ENSG00000224902	GAGE12H
ENSG00000224904	0.0209691	0	0	0	ENSG00000224904	AL021155.1
ENSG00000224906	0	6.74135	1.27117	3.70994	ENSG00000224906	AC005840.2
ENSG00000224907	0	0	0	0	ENSG00000224907	RPL21P91
ENSG00000224908	0	0	0	0	ENSG00000224908	TIMM8BP2
ENSG00000224916	0	0.0765732	0	0	ENSG00000224916	APOC4-APOC2
ENSG00000224917	0	0	0	0.10372	ENSG00000224917	AC016694.1
ENSG00000224920	0	0.116	0	0	ENSG00000224920	TACC1P1
ENSG00000224921	0	0	0.0540797	0.179459	ENSG00000224921	AL844851.1
ENSG00000224925	0	0	0.00828591	0	ENSG00000224925	AL662852.1
ENSG00000224927	0	0	0	0	ENSG00000224927	NDUFA5P10
ENSG00000224928	0	0.101737	0	0	ENSG00000224928	KRT8P30
ENSG00000224929	0	0	0	0	ENSG00000224929	HLA-DPA3
ENSG00000224931	0	0.0111776	0.131832	0.114254	ENSG00000224931	AC152010.1
ENSG00000224936	0	0	0	0	ENSG00000224936	SUCLA2P1
ENSG00000224937	0	3.26589	2.35048	1.32073	ENSG00000224937	RP11-34H11.6
ENSG00000224940	0.397999	0.304794	0.504793	0.687856	ENSG00000224940	PRRT4
ENSG00000224941	0.10729	0	0.54126	1.51871	ENSG00000224941	TCF19
ENSG00000224942	0.0486474	0.0468367	0	0.0531361	ENSG00000224942	AL137014.1
ENSG00000224946	0	0.878522	0.39344	1.42619	ENSG00000224946	AC007312.1
ENSG00000224947	0	0	0	0	ENSG00000224947	VN1R25P
ENSG00000224948	0	0	0	0	ENSG00000224948	ATP5G1P8
ENSG00000224949	0	0.17889	0	0.390809	ENSG00000224949	AL589872.1
ENSG00000224952	4.24207	4.8778	6.62556	4.5143	ENSG00000224952	PBX2
ENSG00000224953	0	0	0	0	ENSG00000224953	SRIP3
ENSG00000224954	0	0.159557	0	0.193505	ENSG00000224954	BX248419.1
ENSG00000224955	0	0	0	0	ENSG00000224955	KCTD10P1
ENSG00000224956	0	0.466318	0.300924	1.0733	ENSG00000224956	RP11-206L10.1
ENSG00000224960	0.0222261	0.0433705	0.0774871	0.0244208	ENSG00000224960	PPP4R3CP
ENSG00000224962	0	0	0	0	ENSG00000224962	PSAT1P4
ENSG00000224963	0.0479682	0.0460971	0.291477	0.15558	ENSG00000224963	U82695.1
ENSG00000224964	0	0	0	0	ENSG00000224964	TRAPPC2P3
ENSG00000224966	0	0	0	0	ENSG00000224966	TBC1D3P6
ENSG00000224967	1.32149	2.10362	0.910184	3.94756	ENSG00000224967	AC009303.1
ENSG00000224971	0	0	0	0	ENSG00000224971	SUMO2P3
ENSG00000224976	0.0351302	0.0861747	0.015372	0.050457	ENSG00000224976	PARP4P2
ENSG00000224978	0	0	0	0	ENSG00000224978	BX682237.1
ENSG00000224979	2.05115	3.2431	2.47841	1.71742	ENSG00000224979	LSM2
ENSG00000224980	0	0	0.325967	0.400746	ENSG00000224980	RPL23AP85
ENSG00000224981	8.70092	21.4344	20.1399	33.8561	ENSG00000224981	AC000367.1
ENSG00000224982	0.115918	0.288758	0.434024	0.761849	ENSG00000224982	TMEM233
ENSG00000224986	0	0.16936	0.255099	0.447546	ENSG00000224986	PPP1R8P1
ENSG00000224987	0.830849	0	0	0	ENSG00000224987	AL024507.1
ENSG00000224988	0	0.273423	0.479781	0.584634	ENSG00000224988	AL158207.1
ENSG00000224990	0	0	0	0	ENSG00000224990	CR753509.1
ENSG00000224993	0	0.561702	0.367575	0.413801	ENSG00000224993	RPL29P12
ENSG00000224994	1.40869	1.16201	0.860284	0.269129	ENSG00000224994	TRIM39
ENSG00000224997	1.43164	2.55676	2.38255	2.77449	ENSG00000224997	AC049840.1
ENSG00000224999	0	0.0706145	0.191425	0.0797615	ENSG00000224999	VTA1P1

ENSG00000225003	0	0	0.057632	0	ENSG00000225003	OR51A5P
ENSG00000225005	0.462329	0.801689	0.971503	1.40246	ENSG00000225005	AC211485.1
ENSG00000225008	0	0.0301048	0	0.0340585	ENSG00000225008	AC234781.2
ENSG00000225010	0	0	0	0	ENSG00000225010	RP11-435B5.1
ENSG00000225011	0	0	0.230843	0	ENSG00000225011	AL671862.1
ENSG00000225014	0	0	0	0.115209	ENSG00000225014	KCTD9P1
ENSG00000225015	1.23316	3.51315	1.97675	2.13357	ENSG00000225015	SNX18P15
ENSG00000225016	0.645454	5.0204	4.97094	6.48746	ENSG00000225016	LINC00328-2P
ENSG00000225017	0.309624	0.984147	0.50823	1.3642	ENSG00000225017	AP004289.1
ENSG00000225018	0	0	0	0.17564	ENSG00000225018	AC092647.1
ENSG00000225022	0	0	0	0	ENSG00000225022	UBE2D3P1
ENSG00000225023	0	0	0.157902	0.133016	ENSG00000225023	HCG4P8
ENSG00000225024	0	1.04887	0.315769	0	ENSG00000225024	AC015977.1
ENSG00000225025	0.0464989	0.0895445	0.121	0.102229	ENSG00000225025	KIF4CP
ENSG00000225026	0	0	0	0.967005	ENSG00000225026	AC091492.1
ENSG00000225027	0.364167	0	0.310968	0	ENSG00000225027	IFNWP4
ENSG00000225029	0.0174175	0.000999815	0	0.0522935	ENSG00000225029	USP8P1
ENSG00000225031	1.63123	1.08388	1.04825	1.09371	ENSG00000225031	EIF4BP7
ENSG00000225034	0	0	0	0.0734341	ENSG00000225034	BX927223.2
ENSG00000225036	0.88801	2.86784	1.60822	4.2126	ENSG00000225036	CDK4P1
ENSG00000225043	0.320658	1.38306	1.94236	1.88289	ENSG00000225043	RPL18AP2
ENSG00000225045	0	0.0960841	0.055951	0.12027	ENSG00000225045	MTND5P27
ENSG00000225046	0	0	0	0	ENSG00000225046	AL035423.1
ENSG00000225048	0	0	0	0	ENSG00000225048	CR759835.1
ENSG00000225049	8.33174	20.6642	29.0853	38.9766	ENSG00000225049	AC068279.2
ENSG00000225051	0.677773	0.245552	0.899561	0.538063	ENSG00000225051	HMGB3P22
ENSG00000225053	0	0	0	0	ENSG00000225053	PRPF38AP1
ENSG00000225055	0	0	0	0	ENSG00000225055	AL606490.1
ENSG00000225060	11.0877	13.2953	9.93908	10.5618	ENSG00000225060	PPP1R18
ENSG00000225066	1.01563	1.06522	1.02683	1.94534	ENSG00000225066	Z93929.1
ENSG00000225067	0	0	0	0	ENSG00000225067	RPL23AP2
ENSG00000225069	0	0.0750557	0.271245	0.0847099	ENSG00000225069	AL080312.1
ENSG00000225071	0	0	0.352785	0	ENSG00000225071	AC004552.1
ENSG00000225072	0	0	0	0	ENSG00000225072	OR7E116P
ENSG00000225073	32.7092	46.6972	36.987	9.0436	ENSG00000225073	DDX39B
ENSG00000225078	0.080508	0.857049	0.560044	1.04859	ENSG00000225078	AL365338.1
ENSG00000225079	0	0	0	0	ENSG00000225079	FTH1P22
ENSG00000225080	0	0	0	0	ENSG00000225080	PFN1P4
ENSG00000225082	1.21273	0	1.03172	0	ENSG00000225082	DAP3P1
ENSG00000225086	0.0596122	0	0.467426	0.31596	ENSG00000225086	BX927229.1
ENSG00000225093	0.0498662	0.23823	0.129275	0.278467	ENSG00000225093	RPL3P7
ENSG00000225094	0.0756973	0.195928	0.472559	0.409629	ENSG00000225094	SETP20
ENSG00000225098	0	0	0	0	ENSG00000225098	BCRP1
ENSG00000225099	0.0999635	0	0	0	ENSG00000225099	ATP6V1E1P1
ENSG00000225100	0	0.279378	0	0	ENSG00000225100	DPY19L2P5
ENSG00000225101	0.314516	0.100689	0.665338	0	ENSG00000225101	OR52K3P
ENSG00000225103	0	0	0	0.0829926	ENSG00000225103	HLA-DQA2
ENSG00000225108	3.98113	5.57226	3.8511	2.29802	ENSG00000225108	ZBTB45P1
ENSG00000225109	0.0999439	0.239336	0.563214	0.38701	ENSG00000225109	CR388382.1
ENSG00000225110	0	0	0.0376479	0.0190546	ENSG00000225110	PNMA6F
ENSG00000225114	0	0	0.22521	1.75835	ENSG00000225114	CR388220.1
ENSG00000225116	0.433512	0.409182	0.36695	0	ENSG00000225116	AL353193.1
ENSG00000225117	0.367559	0.571682	0.848984	0	ENSG00000225117	ARSDP1
ENSG00000225118	0	1.49364	0	0	ENSG00000225118	AL392103.1

ENSG00000225119	22.0452	49.5333	61.8389	58.0917	ENSG00000225119	LINC00999
ENSG00000225120	0.0859609	0.200014	0.994099	0.315769	ENSG00000225120	CT009517.1
ENSG00000225121	0	0	0	0	ENSG00000225121	EEF1B2P5
ENSG00000225122	0.119751	0.296107	0.267453	0.349407	ENSG00000225122	AL603841.1
ENSG00000225123	1.77763	3.33537	3.47913	7.18017	ENSG00000225123	AL139008.1
ENSG00000225124	1.73109	1.65851	2.29305	1.84306	ENSG00000225124	RPL23AP36
ENSG00000225125	0	0.200973	0.908275	0.225805	ENSG00000225125	RANP4
ENSG00000225130	0.383012	0.333286	0.333678	0.561387	ENSG00000225130	TRIM31
ENSG00000225131	0	0	0	0	ENSG00000225131	PSME2P2
ENSG00000225132	0	1.3374	0.0273378	0.10145	ENSG00000225132	HLA-DPB2
ENSG00000225133	0.190664	0.366826	0.663075	0.691819	ENSG00000225133	MORF4L1P4
ENSG00000225136	0	0	0	0	ENSG00000225136	PGBD4P5
ENSG00000225137	0	0.0822338	0	0.0468844	ENSG00000225137	DYNC1I2P1
ENSG00000225141	0.0315493	0.0750009	0.205173	0.116243	ENSG00000225141	PRRT1
ENSG00000225142	0	0	0	0	ENSG00000225142	AC114495.1
ENSG00000225145	0	0	0	0	ENSG00000225145	HLA-S
ENSG00000225147	0	0	0.202938	1.24125	ENSG00000225147	RPS12P10
ENSG00000225150	0	0	0	0	ENSG00000225150	AL662857.1
ENSG00000225151	24.002	34.5949	41.0866	25.3656	ENSG00000225151	GOLGA2P7
ENSG00000225154	0	0	0.128711	0	ENSG00000225154	AL450996.1
ENSG00000225155	0.189327	0	0	0	ENSG00000225155	TOMM22P5
ENSG00000225157	26.9223	37.7762	43.0508	59.4407	ENSG00000225157	AC005779.1
ENSG00000225158	1.10926	0.512685	0	1.10322	ENSG00000225158	HSPE1P24
ENSG00000225159	0	0.285777	0.143604	0.807799	ENSG00000225159	NPM1P39
ENSG00000225164	1.25018	6.12417	6.79696	8.50462	ENSG00000225164	PRRC2A
ENSG00000225165	0	0	0.281922	0.115824	ENSG00000225165	AC090071.1
ENSG00000225167	0	0	0.309101	0	ENSG00000225167	TXNP2
ENSG00000225169	0.239031	1.13223	1.24305	2.52726	ENSG00000225169	BRI3P1
ENSG00000225170	0.128619	0.21207	0.299572	0.330956	ENSG00000225170	AL049737.1
ENSG00000225171	0.85414	2.45723	1.32926	1.45571	ENSG00000225171	DUTP6
ENSG00000225175	0.0437983	0.0421784	0.0381244	0	ENSG00000225175	AC109780.1
ENSG00000225176	0	0	0	0	ENSG00000225176	ATP5LP4
ENSG00000225178	0.143929	0	0.475518	0.31302	ENSG00000225178	RPSAP58
ENSG00000225182	0	0	0	0	ENSG00000225182	AC092601.1
ENSG00000225183	1.09115	1.28859	0	0	ENSG00000225183	AL353898.1
ENSG00000225185	0	0.191687	0	0.173298	ENSG00000225185	AC013283.1
ENSG00000225189	0	0	0	0	ENSG00000225189	REREP1Y
ENSG00000225190	56.3089	65.8546	62.3938	73.2157	ENSG00000225190	PLEKHM1
ENSG00000225191	0	0.0463556	0.0417857	0.210747	ENSG00000225191	AL136455.1
ENSG00000225192	0.247823	0.537301	0.708654	0.441595	ENSG00000225192	ZNF33BP1
ENSG00000225193	4.15278	24.9344	12.1009	23.1813	ENSG00000225193	AC091167.1
ENSG00000225196	0	0	0.273873	0	ENSG00000225196	RPL10P17
ENSG00000225198	0.157818	0.231327	0.0800459	0.606284	ENSG00000225198	SSXP3
ENSG00000225200	0.171238	0.0549481	0.0998003	0.0552403	ENSG00000225200	AC246787.1
ENSG00000225201	19.219	6.72749	2.56494	0.358481	ENSG00000225201	HLA-E
ENSG00000225211	0.072505	0	0	0	ENSG00000225211	NCR3
ENSG00000225212	0	0.23574	0.214728	0	ENSG00000225212	AP001793.1
ENSG00000225215	0.253018	0.486584	0.564433	0.995564	ENSG00000225215	SMARCE1P1
ENSG00000225217	0.812141	0	0.03508	0.315875	ENSG00000225217	HSPA7
ENSG00000225221	0	0	0	0	ENSG00000225221	PLA2G12AP2
ENSG00000225222	0.771079	4.64763	1.17566	8.98453	ENSG00000225222	CHCHD4P5
ENSG00000225224	3.57079	8.11072	6.77344	14.1773	ENSG00000225224	RPS27AP12
ENSG00000225225	0	0	0	0	ENSG00000225225	ARL2BPP10
ENSG00000225228	0.0916753	0	0	0	ENSG00000225228	MCCD1

ENSG00000225236	0.0994116	0	0	0	ENSG00000225236	AP000936.2
ENSG00000225237	0	0	0	0	ENSG00000225237	HNRNPA1P2
ENSG00000225238	0	0	0	0.705769	ENSG00000225238	Z93015.1
ENSG00000225239	0	0	0	0	ENSG00000225239	RPL21P107
ENSG00000225240	0	0	0	0	ENSG00000225240	AC117490.1
ENSG00000225241	65.1227	130.595	98.3277	159.161	ENSG00000225241	RP11-640M9.2
ENSG00000225242	0	0	0	0	ENSG00000225242	COX6B1P7
ENSG00000225244	0	0.0646241	0	0	ENSG00000225244	AC069152.1
ENSG00000225246	0	0	0.0696608	0	ENSG00000225246	RPS2P1
ENSG00000225247	0	0.0114325	0.0103321	0.0258921	ENSG00000225247	OR12D2
ENSG00000225248	0	0	0	0	ENSG00000225248	TMEM183AP1
ENSG00000225251	0	0	0	0	ENSG00000225251	RPL5P25
ENSG00000225253	0	0.232571	0	0.770723	ENSG00000225253	AC011225.1
ENSG00000225254	0	0	0	0	ENSG00000225254	ARMC8P1
ENSG00000225256	0	0	0	0	ENSG00000225256	TRAPPC2P5
ENSG00000225259	0	0	0	0	ENSG00000225259	ST13P6
ENSG00000225264	0.563512	1.45067	0.996607	1.80128	ENSG00000225264	ZNRF2P2
ENSG00000225267	0	0	0	0	ENSG00000225267	RPL8P2
ENSG00000225270	0.249895	0.50116	0.434358	0.986518	ENSG00000225270	CICP12
ENSG00000225271	0.108164	0.289949	0.223202	0.513201	ENSG00000225271	AC074281.1
ENSG00000225272	0.496452	0.952592	0.534777	0.176602	ENSG00000225272	AL451074.3
ENSG00000225273	6.54631	12.6879	10.2823	25.9937	ENSG00000225273	UBE2Q2P2
ENSG00000225274	0	0	0	0	ENSG00000225274	GPR53P
ENSG00000225275	0	0	0	0	ENSG00000225275	NUP210P2
ENSG00000225276	0.125317	0.240507	0.217177	0.870995	ENSG00000225276	MTND1P18
ENSG00000225282	0.262535	0.187511	1.27277	1.56809	ENSG00000225282	AP000350.2
ENSG00000225286	0	0.0788397	0.21368	0.355679	ENSG00000225286	AC005105.1
ENSG00000225287	0	0	0	0	ENSG00000225287	OFD1P13Y
ENSG00000225289	0	0.561477	0.506958	3.11332	ENSG00000225289	RPL29P29
ENSG00000225291	0	0	0	0	ENSG00000225291	OR14J1
ENSG00000225293	0.0583023	0.167874	0.15162	0.1255	ENSG00000225293	ABCD1P4
ENSG00000225294	0.185049	1.48913	0.476274	0.584383	ENSG00000225294	OSTCP2
ENSG00000225295	0	0	0	0	ENSG00000225295	MTND4P4
ENSG00000225297	2.76968	4.91048	3.82319	5.56123	ENSG00000225297	AC126124.1
ENSG00000225304	0	0	0	0	ENSG00000225304	AC106901.1
ENSG00000225305	0	0	0	0	ENSG00000225305	TMEM183AP1
ENSG00000225308	0	0	0	0	ENSG00000225308	ASS1P11
ENSG00000225310	0	0	0	0	ENSG00000225310	DNAJC19P4
ENSG00000225312	1.5288	1.62628	2.07747	0.55839	ENSG00000225312	HSD17B8
ENSG00000225314	0	0	0	0	ENSG00000225314	AC018634.1
ENSG00000225317	0.0579419	0.0677367	0.106788	0.0857336	ENSG00000225317	PPIAP9
ENSG00000225322	0	0	0	0	ENSG00000225322	RP11-472D17.1
ENSG00000225323	0	0	0	0	ENSG00000225323	Z84721.1
ENSG00000225326	0	0	0	0	ENSG00000225326	USP9YP19
ENSG00000225327	0	0.154649	0	0	ENSG00000225327	USP17L3
ENSG00000225333	0	0	0	0	ENSG00000225333	AL035404.1
ENSG00000225336	0.375951	0.242341	0	0.40508	ENSG00000225336	HMGB3P1
ENSG00000225338	0.90718	3.44394	1.61982	3.82372	ENSG00000225338	RPL23AP18
ENSG00000225343	0	0	0	0.36004	ENSG00000225343	RPL21P66
ENSG00000225344	0	0.0678449	0	0.0777138	ENSG00000225344	AL035252.1
ENSG00000225345	5.50829	11.4013	8.39428	10.3059	ENSG00000225345	SNX18P3
ENSG00000225346	0	0	0	0	ENSG00000225346	HCG4
ENSG00000225347	0	0	0	0	ENSG00000225347	SLC25A5P8
ENSG00000225349	1.69149	3.01441	4.27513	9.23639	ENSG00000225349	AC022080.2

ENSG00000225351	0.281502	0.296324	0.329162	0.107474	ENSG00000225351	ZNF311
ENSG00000225352	0	0	0	0	ENSG00000225352	RPL31P53
ENSG00000225354	0	0	0	0	ENSG00000225354	RPL7AP52
ENSG00000225355	0	0	0	0	ENSG00000225355	ARL6IP1P2
ENSG00000225356	0	0	0	0	ENSG00000225356	AC093840.1
ENSG00000225357	0	0	0	0	ENSG00000225357	RPF2P1
ENSG00000225358	0	0.267683	0.266193	0.27431	ENSG00000225358	MIPEPP1
ENSG00000225360	0	0	0	0	ENSG00000225360	AL772155.2
ENSG00000225362	4.99979	5.94139	5.05682	5.24378	ENSG00000225362	CT62
ENSG00000225364	3.02755	3.42959	6.58335	6.70337	ENSG00000225364	ATP6V0E1P1
ENSG00000225366	0.192548	0.67987	0.65479	1.28914	ENSG00000225366	TDGF1P3
ENSG00000225369	0	0	0	0	ENSG00000225369	AC009506.2
ENSG00000225370	0	0	0	0	ENSG00000225370	AC243962.1
ENSG00000225371	0	0	0.035285	0.0660882	ENSG00000225371	CICP8
ENSG00000225373	74.6419	97.3185	83.0804	74.3837	ENSG00000225373	WASH5P
ENSG00000225380	0	0.496327	0	0	ENSG00000225380	IGKV1OR9-2
ENSG00000225381	0	0	0	0	ENSG00000225381	RPS5P7
ENSG00000225384	0	0	0	0	ENSG00000225384	AL606662.1
ENSG00000225385	0	0	0.172789	0	ENSG00000225385	AL353572.1
ENSG00000225392	0	0	0	0	ENSG00000225392	AC016700.1
ENSG00000225394	0.128727	0	0	0	ENSG00000225394	AC106883.1
ENSG00000225397	0	0	0	0	ENSG00000225397	AC244505.3
ENSG00000225398	0	0	0	0	ENSG00000225398	PGM5P4
ENSG00000225399	1.271	2.19027	1.5053	4.16197	ENSG00000225399	AC121247.1
ENSG00000225400	0.426529	1.5815	2.3968	2.07279	ENSG00000225400	RAB28P5
ENSG00000225401	0.59193	0.568771	0.519583	0.219578	ENSG00000225401	TGIF2P1
ENSG00000225402	0	0	0	0	ENSG00000225402	AC010878.1
ENSG00000225403	0.0533493	0.0644828	0.0698207	0.0879944	ENSG00000225403	WASF5P
ENSG00000225404	0.531647	0	0	1.50813	ENSG00000225404	RPL26P34
ENSG00000225405	0	0	0	0	ENSG00000225405	RPS15AP17
ENSG00000225406	0	0.314355	0	0	ENSG00000225406	AC080125.1
ENSG00000225410	89.1774	189.766	55.7494	62.1271	ENSG00000225410	AC107016.1
ENSG00000225412	0.0140136	0.0646215	0.0389217	0.0176708	ENSG00000225412	BTNL2
ENSG00000225414	0	0.287411	0.864486	0.0641262	ENSG00000225414	RP11-746P2.1
ENSG00000225415	0	0.114835	0	0	ENSG00000225415	CCRL1P1
ENSG00000225416	0	0	0	0	ENSG00000225416	AC104843.1
ENSG00000225418	0	0.0556668	0.254598	0	ENSG00000225418	AKR1C5P
ENSG00000225419	0.174679	0.337937	0.573747	0.330148	ENSG00000225419	RPL21P3
ENSG00000225422	0.126851	6.60617	0.340956	3.52408	ENSG00000225422	RBMS1P1
ENSG00000225423	1.12118	1.96917	1.02676	2.2549	ENSG00000225423	TNPO1P1
ENSG00000225428	0	0	0	0	ENSG00000225428	NDUFB4P7
ENSG00000225429	0	0	0	0.216064	ENSG00000225429	HLA-DPB2
ENSG00000225433	0.316398	0	0	0	ENSG00000225433	MTND1P12
ENSG00000225438	0.838257	0.17339	0.0401656	0.450229	ENSG00000225438	KRT41P
ENSG00000225441	0.0332871	0	0	0.0136277	ENSG00000225441	OR2J1
ENSG00000225443	0	0	0	0	ENSG00000225443	AC004938.1
ENSG00000225447	2.30238	1.76057	6.24378	5.25993	ENSG00000225447	RPS15AP10
ENSG00000225448	1.31695	1.84423	2.19312	1.98109	ENSG00000225448	AC009477.1
ENSG00000225449	0.182904	0.289304	0.220721	0.183337	ENSG00000225449	RAB6C-AS1
ENSG00000225451	0.183036	0	0.0533066	0	ENSG00000225451	AC092634.2
ENSG00000225452	1.35259	0.556113	1.36117	0.483865	ENSG00000225452	RNF5
ENSG00000225453	0.087419	0.412726	0	0.298453	ENSG00000225453	PTMAP1
ENSG00000225454	0	0	0	0	ENSG00000225454	SFTA2
ENSG00000225455	1.32883	0.969904	1.57623	2.29888	ENSG00000225455	TPI1P4

ENSG00000225459	1.93885	0.673681	0.561095	0.695858	ENSG00000225459	HLA-Z
ENSG00000225460	0	0.166834	0	0	ENSG00000225460	AL590233.1
ENSG00000225462	0.128665	0	0.0548807	0.0657736	ENSG00000225462	FDPSP1
ENSG00000225463	0	0.0184226	0	0	ENSG00000225463	ZNF70P1
ENSG00000225466	0	0	0	0	ENSG00000225466	OFD1P10Y
ENSG00000225469	0.161387	0.15534	0.187195	0.058692	ENSG00000225469	AL023773.1
ENSG00000225471	1.5332	4.00805	3.54885	5.40454	ENSG00000225471	BX119917.1
ENSG00000225475	0	0	3.8012	0.0878469	ENSG00000225475	AC099789.1
ENSG00000225476	0	0.0898761	0	0	ENSG00000225476	MTCO3P5
ENSG00000225477	0	0.049088	0	0	ENSG00000225477	AC099730.1
ENSG00000225478	0.62117	0	0.957568	0	ENSG00000225478	AL031737.1
ENSG00000225480	17.0466	15.6446	1.3995	5.88414	ENSG00000225480	AC006548.1
ENSG00000225482	0.130793	0.717493	0.449252	0.973788	ENSG00000225482	RPS6P14
ENSG00000225483	0	0	0	0	ENSG00000225483	AC244035.1
ENSG00000225485	24.2017	28.943	23.7473	30.4119	ENSG00000225485	ARGGAP23
ENSG00000225486	0.277008	0	0	0	ENSG00000225486	AL663058.1
ENSG00000225487	0	0	0	0	ENSG00000225487	AL390119.1
ENSG00000225491	0.208591	0	0	0	ENSG00000225491	UBE2Q2P4Y
ENSG00000225492	0.641362	2.15948	1.0286	0.819046	ENSG00000225492	GBP1P1
ENSG00000225496	0	0	0	0	ENSG00000225496	AC104651.1
ENSG00000225499	0	0.0169735	0.0627602	0.0560227	ENSG00000225499	AL663061.1
ENSG00000225501	0	0	0	0	ENSG00000225501	SNRPFP3
ENSG00000225502	0	0.124391	0.168618	0	ENSG00000225502	GAPDHP16
ENSG00000225505	2.42244	3.26189	2.22474	6.80873	ENSG00000225505	AC104332.1
ENSG00000225507	5.70868	8.01363	9.24907	9.72025	ENSG00000225507	AC069282.1
ENSG00000225508	0	0	0	0	ENSG00000225508	SSXP5
ENSG00000225509	0	0	0	0.0694715	ENSG00000225509	AIFM1P1
ENSG00000225510	0	0	0	0	ENSG00000225510	PCDH8P1
ENSG00000225513	0	0.170282	0.686044	0.189322	ENSG00000225513	AL158824.1
ENSG00000225514	0	0.0973679	0.263815	0.109471	ENSG00000225514	MTND1P34
ENSG00000225516	0.701099	0.773432	0.331841	0.896984	ENSG00000225516	FAM197Y5
ENSG00000225522	0.139	0.400107	0.373479	0.468102	ENSG00000225522	AL592114.2
ENSG00000225523	0	0.197155	0	0	ENSG00000225523	IGKV6D-21
ENSG00000225526	4.30542	5.37018	3.34681	3.01144	ENSG00000225526	MKRN2OS
ENSG00000225529	0.518491	0	0	0	ENSG00000225529	BX088645.3
ENSG00000225530	0	0	0	0	ENSG00000225530	SP3P
ENSG00000225531	0.100318	0	0.0865513	0.112835	ENSG00000225531	AL807761.2
ENSG00000225533	0.127775	0.245221	0.222134	0.137904	ENSG00000225533	PAWRP1
ENSG00000225536	0	0.0343406	0	0.0390004	ENSG00000225536	STIP1P3
ENSG00000225538	0	0	0	0	ENSG00000225538	OR5BE1P
ENSG00000225543	0.357191	0.0509367	0.0789204	0.332033	ENSG00000225543	C6orf15
ENSG00000225544	0	0	0	0.374757	ENSG00000225544	AC245452.2
ENSG00000225549	0.101783	0.367185	0.2214	0.111119	ENSG00000225549	AL359634.1
ENSG00000225550	0	0	0	0	ENSG00000225550	OR2J2
ENSG00000225551	0	0	3.1251	0	ENSG00000225551	AL157827.1
ENSG00000225553	11.966	17.8013	11.6883	13.9218	ENSG00000225553	PHF1
ENSG00000225556	0.556669	0.563168	0.791928	0.355949	ENSG00000225556	C2CD4D
ENSG00000225557	0	0.0942596	0	0	ENSG00000225557	MTCO3P20
ENSG00000225558	1.46873	1.2477	0.807158	2.95233	ENSG00000225558	UBE2D3P2
ENSG00000225567	0	0	0	0	ENSG00000225567	CR936923.1
ENSG00000225568	0.156071	0.879844	0.488902	0.695377	ENSG00000225568	AC093155.1
ENSG00000225569	0.0373666	0.0726072	0.0981519	0.622139	ENSG00000225569	CCT4P2
ENSG00000225571	0	0.0458373	0.0827353	0.200941	ENSG00000225571	AL845443.1
ENSG00000225573	0.286843	0.927114	0.756598	0.612181	ENSG00000225573	RPL35P5

ENSG00000225574	0	0.253187	0.228803	0.235123	ENSG00000225574	DRAXINP1
ENSG00000225580	0.0531727	0	0	0	ENSG00000225580	AL358942.1
ENSG00000225581	0	0	0	0	ENSG00000225581	TRIM53AP
ENSG00000225583	0	0	0	0	ENSG00000225583	AC004690.1
ENSG00000225585	0	0	0	0	ENSG00000225585	IPPKP1
ENSG00000225589	0.0961644	0.686575	0.460787	0.446605	ENSG00000225589	MDC1
ENSG00000225590	0.948011	0.562313	1.51113	2.85005	ENSG00000225590	VPS52
ENSG00000225591	0.480819	1.36033	1.21435	0.492015	ENSG00000225591	BX248409.1
ENSG00000225592	0	0	0.0584294	0.110658	ENSG00000225592	BX248084.1
ENSG00000225594	0.381175	3.48577	0	1.04902	ENSG00000225594	AC098826.1
ENSG00000225603	0	0.0338616	0	0.0392417	ENSG00000225603	AC244394.1
ENSG00000225609	0	0	0.0201666	0.0253225	ENSG00000225609	CDY20P
ENSG00000225614	0.0514285	0.142907	0.279134	5.47424	ENSG00000225614	ZNF469
ENSG00000225615	0	0.290107	0	0	ENSG00000225615	RBMY2UP
ENSG00000225616	0	0.279812	1.26503	0	ENSG00000225616	AL138785.1
ENSG00000225622	0	0	0	0	ENSG00000225622	PPIAP17
ENSG00000225624	0.119769	0.116568	0.416614	0.409359	ENSG00000225624	TBL1YP1
ENSG00000225625	0	0	0	0	ENSG00000225625	AC090517.1
ENSG00000225630	7.43848	10.6799	18.9831	28.4417	ENSG00000225630	MTND2P28
ENSG00000225635	1.24175	1.01416	2.15986	0.700784	ENSG00000225635	DDAH2
ENSG00000225636	0	0	0	0	ENSG00000225636	HNRNPA3P15
ENSG00000225638	0.0614814	0.0470641	0.0780947	0.271113	ENSG00000225638	PABPC1P12
ENSG00000225639	0.183885	0.140335	0.165565	0.273869	ENSG00000225639	PGAM1P2
ENSG00000225642	0	0	0	0	ENSG00000225642	SNRPEP5
ENSG00000225644	0.898463	0	0	0.335064	ENSG00000225644	RPL35AP4
ENSG00000225646	24.5162	68.368	43.2149	143.752	ENSG00000225646	AC015815.7
ENSG00000225648	22.8651	16.4584	26.4572	5.50138	ENSG00000225648	SBDSP1
ENSG00000225650	0.908307	1.90919	1.89577	3.6754	ENSG00000225650	EIF2S2P5
ENSG00000225653	0.195019	0.508771	0.327442	1.07817	ENSG00000225653	RNF19BPY
ENSG00000225658	0	0.725331	0.652632	0.720861	ENSG00000225658	TAF13P2
ENSG00000225659	0	0	0	0.0189286	ENSG00000225659	TRIM26BP
ENSG00000225660	0	0	0	0	ENSG00000225660	Z99497.1
ENSG00000225661	0	0	0	0	ENSG00000225661	RPL14P5
ENSG00000225662	0	0	0	0	ENSG00000225662	AC012519.1
ENSG00000225663	16.6962	17.2765	9.32857	15.7511	ENSG00000225663	MCRIP1
ENSG00000225664	0	0	0	0	ENSG00000225664	YWHAZP8
ENSG00000225665	0	0.120752	0.434354	0.13465	ENSG00000225665	AC073475.1
ENSG00000225669	0	0.878857	0	3.00023	ENSG00000225669	RPL23AP27
ENSG00000225671	0	0	0	0	ENSG00000225671	FCF1P6
ENSG00000225672	0	0.0864703	0	0.0981641	ENSG00000225672	CCNT2P1
ENSG00000225673	0.24079	0.1733	0.417329	0.517893	ENSG00000225673	AC104164.1
ENSG00000225674	0.0350017	0	0.0615208	0.47261	ENSG00000225674	IPO7P2
ENSG00000225678	1.35562	0.307961	0.468822	0.275677	ENSG00000225678	AP000619.1
ENSG00000225679	0	0	0	0	ENSG00000225679	RP11-216M21.6
ENSG00000225681	0	0	0	0	ENSG00000225681	AC005730.1
ENSG00000225682	1.69617	2.37247	1.46123	0.0777383	ENSG00000225682	DXO
ENSG00000225683	0	0	0	0.0582738	ENSG00000225683	PACRG-AS3
ENSG00000225685	0.135266	0.129468	0.117514	0.145725	ENSG00000225685	TSPY5P
ENSG00000225690	0	0	0.107812	0.133706	ENSG00000225690	TREML5P
ENSG00000225691	14.8238	130.579	54.6301	69.9046	ENSG00000225691	HLA-C
ENSG00000225693	3.52218	6.65232	8.42481	6.89303	ENSG00000225693	LAGE3P1
ENSG00000225695	0.337144	0.584243	0.531908	0.664316	ENSG00000225695	HNRNPA1P35
ENSG00000225696	0	0.0184226	0	0	ENSG00000225696	ZNF70P1
ENSG00000225697	29.9554	52.3237	30.5943	32.6142	ENSG00000225697	SLC26A6

ENSG00000225698	0	0	0	0	ENSG00000225698	IGHV3-72
ENSG00000225701	0	0	0	0.588682	ENSG00000225701	EIF4A1P13
ENSG00000225704	0	1.07616	0	0	ENSG00000225704	AL031274.1
ENSG00000225705	0	0	0	0	ENSG00000225705	AC004899.1
ENSG00000225710	0.0801794	0.380002	0.281701	0.439658	ENSG00000225710	AL355149.1
ENSG00000225711	0.461878	0.809301	1.3295	1.94517	ENSG00000225711	AL512326.1
ENSG00000225712	0	0	0.334227	0	ENSG00000225712	ATP5G2P1
ENSG00000225713	0.295639	0	0	0.927486	ENSG00000225713	RPL30P1
ENSG00000225714	0	0	0	0	ENSG00000225714	POLR2LP1
ENSG00000225715	0.251649	0.889542	1.01964	1.09312	ENSG00000225715	AL512504.1
ENSG00000225716	0	0	0	0	ENSG00000225716	ELOCP13
ENSG00000225719	0.148117	0	0	0	ENSG00000225719	NMNAT1P2
ENSG00000225720	0	1.17871	0.623121	0.902232	ENSG00000225720	AL031846.1
ENSG00000225722	0	0	0	0	ENSG00000225722	BX890604.2
ENSG00000225723	0	0	0	0	ENSG00000225723	MTND6P15
ENSG00000225724	0	0	0	0.0383357	ENSG00000225724	ASH2LP3
ENSG00000225726	1.26336	2.72456	3.96311	3.72387	ENSG00000225726	AC007000.2
ENSG00000225727	0.641481	4.70057	4.16713	6.98831	ENSG00000225727	AL139184.1
ENSG00000225728	3.9527	9.3271	4.8073	6.12899	ENSG00000225728	AL034399.1
ENSG00000225735	0	0	0	0	ENSG00000225735	NEK4P1
ENSG00000225736	0	0.0131907	0.0059608	0	ENSG00000225736	OR2B3
ENSG00000225737	1.64907	1.54557	2.04994	1.19061	ENSG00000225737	SKIV2L
ENSG00000225739	0.107536	0	0	0	ENSG00000225739	NPM1P18
ENSG00000225740	0	0	0	0	ENSG00000225740	ELOCP6
ENSG00000225741	0.47137	0.4531	0	0.514182	ENSG00000225741	AC245517.1
ENSG00000225748	46.648	33.9472	51.5273	3.91314	ENSG00000225748	PRRC2A
ENSG00000225755	0.106596	0.256511	0.463671	0.407088	ENSG00000225755	AL451063.1
ENSG00000225758	0	0.197155	0.178161	0	ENSG00000225758	RPS17P17
ENSG00000225763	0	0	0	0	ENSG00000225763	MICG
ENSG00000225766	2.15811	2.68053	3.43312	2.76454	ENSG00000225766	DHRS4L1
ENSG00000225769	0.0360882	0.074055	0.114847	0.134785	ENSG00000225769	CROCCP1
ENSG00000225770	1.52273	0	0	0	ENSG00000225770	RPS29P3
ENSG00000225774	0.0984555	0.0334131	0.149674	0.110772	ENSG00000225774	SIRPAP1
ENSG00000225777	0	0	0	0	ENSG00000225777	DDX39AP1
ENSG00000225779	0	0	0.420932	0	ENSG00000225779	AL122001.1
ENSG00000225781	0	0	0	0.0325491	ENSG00000225781	OR6V1
ENSG00000225784	0.212042	1.58133	3.78038	0	ENSG00000225784	RP11-592B15.4
ENSG00000225786	21.1172	38.8366	26.2972	71.6983	ENSG00000225786	AL590639.1
ENSG00000225787	0.338473	1.92683	0.484866	1.13817	ENSG00000225787	LSM3P3
ENSG00000225795	0	0	0	0	ENSG00000225795	AC006463.1
ENSG00000225796	0.0923821	0.223466	0.225143	0.341089	ENSG00000225796	MTND4P23
ENSG00000225797	0	0	0	3.56E-07	ENSG00000225797	UBDP1
ENSG00000225801	0	0.403363	0.260384	0	ENSG00000225801	RABEPKP1
ENSG00000225802	0.350834	0	0	0	ENSG00000225802	WARSP1
ENSG00000225803	0	0	0	0	ENSG00000225803	MRPS11P1
ENSG00000225805	1.69746	3.72815	2.51113	2.53074	ENSG00000225805	DEFB131B
ENSG00000225808	4.47046	11.4264	6.84682	7.902	ENSG00000225808	DNAJC19P5
ENSG00000225809	0	0	0	0	ENSG00000225809	RBMY2KP
ENSG00000225812	0	0	0	0	ENSG00000225812	RP11-157L3.3
ENSG00000225813	0.0930288	0	0.0809357	0.301864	ENSG00000225813	AC009299.1
ENSG00000225814	0	0	0	0.122934	ENSG00000225814	GRPEL2P2
ENSG00000225816	0.0964622	0.243519	0.252596	0.842638	ENSG00000225816	GTF3AP5
ENSG00000225823	0	0	0	0	ENSG00000225823	RPL7P45
ENSG00000225824	0.301984	0.391043	1.14421	2.55354	ENSG00000225824	HLA-DQB1

ENSG00000225825	0	0	0	0	ENSG00000225825	IGHD6-25
ENSG00000225827	0	0	0	0	ENSG00000225827	SFTPA3P
ENSG00000225828	1.74984	2.75577	2.73707	1.68087	ENSG00000225828	FAM229A
ENSG00000225830	18.5665	25.1585	12.6679	22.377	ENSG00000225830	ERCC6
ENSG00000225831	0.173109	0.497236	0.299299	0	ENSG00000225831	RPS18P1
ENSG00000225832	1.17029	1.18592	1.25754	1.83552	ENSG00000225832	AL035090.1
ENSG00000225838	0	0	0	0	ENSG00000225838	AL662852.2
ENSG00000225840	8641.53	2080.25	1311.25	1743.48	ENSG00000225840	AC010970.1
ENSG00000225842	0	0	0.252473	0.295183	ENSG00000225842	AC139712.2
ENSG00000225843	0	0	0.110513	0.0691819	ENSG00000225843	NIPA2P1
ENSG00000225845	0.0140136	0	0	0.0176708	ENSG00000225845	BTNL2
ENSG00000225846	0	0.304948	0	0.334641	ENSG00000225846	AC112719.1
ENSG00000225849	0.0975694	0.422717	0.297165	0.267843	ENSG00000225849	MKRN7P
ENSG00000225851	0	0	0	0	ENSG00000225851	HLA-S
ENSG00000225854	6.79879	3.61023	6.78668	1.14119	ENSG00000225854	AL451139.1
ENSG00000225856	0	0	0	0	ENSG00000225856	PCNPP2
ENSG00000225858	0	0.233448	0	0	ENSG00000225858	BX295541.1
ENSG00000225859	11.4947	10.8787	13.6749	27.3451	ENSG00000225859	DDX39B
ENSG00000225864	0	0	0	0	ENSG00000225864	AL645939.2
ENSG00000225869	0.116601	0	0	0	ENSG00000225869	AC008696.1
ENSG00000225871	0	0	0	0.513751	ENSG00000225871	AC245100.2
ENSG00000225876	1.24234	1.74272	1.55988	7.51195	ENSG00000225876	AC024067.1
ENSG00000225878	0	0	0	0	ENSG00000225878	SERBP1P2
ENSG00000225883	1.3718	1.29988	2.47542	0.405275	ENSG00000225883	BMS1P11
ENSG00000225885	2.9816	11.8592	9.05085	20.9675	ENSG00000225885	AC023590.1
ENSG00000225890	1.70741	0.322211	5.83751	1.184	ENSG00000225890	HLA-DQA1
ENSG00000225892	1.49493	1.44421	3.58746	2.9817	ENSG00000225892	RP11-384K6.2
ENSG00000225893	0.363669	0.613604	2.27872	1.0291	ENSG00000225893	AL136231.1
ENSG00000225894	0.0301905	0.0145578	0	0	ENSG00000225894	PPP1R26P2
ENSG00000225895	0	0	0	0	ENSG00000225895	TRAPPC2P8
ENSG00000225896	0	0	0	0	ENSG00000225896	AC007742.1
ENSG00000225898	0	0.0964297	0.0871008	0.759041	ENSG00000225898	AC002075.1
ENSG00000225899	0.227561	0.285896	0.412718	0.80267	ENSG00000225899	FRG2B
ENSG00000225900	0.360181	3.13432	4.94921	4.13304	ENSG00000225900	HSPE1P13
ENSG00000225901	0	0.389923	0.176307	0.3658	ENSG00000225901	MTND2P9
ENSG00000225904	0	0.183375	2.54858	0.618956	ENSG00000225904	MORF4L1P7
ENSG00000225906	0.333281	0.721628	0.400335	1.57508	ENSG00000225906	AP000949.1
ENSG00000225907	1.53833	5.76893	4.46564	3.6122	ENSG00000225907	RPS27P16
ENSG00000225911	0.444473	0.169628	0.459541	0.188517	ENSG00000225911	AC009310.1
ENSG00000225912	0	0	0	0	ENSG00000225912	AL121871.1
ENSG00000225918	0	0	0	0	ENSG00000225918	RPL7P59
ENSG00000225920	2.65094	7.75522	6.50829	4.90023	ENSG00000225920	RIMKLBP2
ENSG00000225921	22.1672	17.1461	21.4602	14.3039	ENSG00000225921	NOL7
ENSG00000225922	0	0	0	0	ENSG00000225922	RPL21P92
ENSG00000225923	0	0	0	0	ENSG00000225923	AC092393.1
ENSG00000225925	0	0.175088	0.0527444	0	ENSG00000225925	AL672138.1
ENSG00000225926	0	0	0	0	ENSG00000225926	DDX39BP1
ENSG00000225927	0	0	0	0.00316142	ENSG00000225927	DDX6P1
ENSG00000225928	0.704987	1.57765	1.38666	2.99556	ENSG00000225928	CACYBPP1
ENSG00000225932	7.92E-09	0	3.38764	4.67576	ENSG00000225932	CTAGE4
ENSG00000225933	1.90228	3.12456	0	1.24113	ENSG00000225933	AC133965.1
ENSG00000225934	1.01744	1.58739	1.34494	1.87123	ENSG00000225934	AL592310.1
ENSG00000225935	0	0.873214	1.17141	1.41639	ENSG00000225935	BANF1P5
ENSG00000225939	0	0.0458373	0.0827353	0.200941	ENSG00000225939	AL662833.1

ENSG00000225940	0	0	0	0	ENSG00000225940	C5orf67
ENSG00000225943	0	0.358451	0.323635	0.397961	ENSG00000225943	AC016907.1
ENSG00000225944	0.0758132	0	0.0330076	0.124511	ENSG00000225944	RIOK3P1
ENSG00000225947	0	0	0	0	ENSG00000225947	AL596448.1
ENSG00000225949	0	0.0983689	0.133362	0.27888	ENSG00000225949	Z77249.1
ENSG00000225950	24.152	45.2748	31.2783	17.6335	ENSG00000225950	NTF4
ENSG00000225954	0.0533493	0.0644828	0.0698207	0.0879944	ENSG00000225954	WASF5P
ENSG00000225955	0	0.0207547	0.0239362	0	ENSG00000225955	CR759770.1
ENSG00000225957	0	0	0	0	ENSG00000225957	AC231532.1
ENSG00000225959	0	0	0	0	ENSG00000225959	MTND4P3
ENSG00000225962	10.0585	25.6405	36.6072	42.094	ENSG00000225962	RP11-459A10.2
ENSG00000225965	0	0.924467	0	2.28461	ENSG00000225965	AL117339.2
ENSG00000225967	0.212806	12.8813	1.77078	3.08992	ENSG00000225967	TAP2
ENSG00000225968	0.417273	0.450718	0.89958	1.89042	ENSG00000225968	ELFN1
ENSG00000225971	0	0	0	0	ENSG00000225971	AC003071.1
ENSG00000225972	3.37265	7.43288	1.72595	14.4957	ENSG00000225972	MTND1P23
ENSG00000225976	0	1.98388	2.01255	3.1714	ENSG00000225976	CKS1BP2
ENSG00000225980	0	0	0	0.52918	ENSG00000225980	OR7E19P
ENSG00000225984	0	0	0	0	ENSG00000225984	HMGB1P26
ENSG00000225987	2.19759	2.21931	2.69887	2.12724	ENSG00000225987	PBX2
ENSG00000225989	2.82599	3.55352	4.48725	10.0877	ENSG00000225989	ABCF1
ENSG00000225990	0	0	0	0	ENSG00000225990	SNRPEP7
ENSG00000225991	0.616299	0.695109	2.87888	3.19098	ENSG00000225991	RPL23AP34
ENSG00000225992	0	0	0	0	ENSG00000225992	TRGVA
ENSG00000225993	0.0302896	0.0578806	0	0.032054	ENSG00000225993	LY6G6D
ENSG00000225995	0	0	0	0	ENSG00000225995	ATP5A1P9
ENSG00000225996	3.10098	3.05723	2.86915	1.49572	ENSG00000225996	AL356356.1
ENSG00000225997	0.13213	0	0	0	ENSG00000225997	OR4A8
ENSG00000225998	2.05115	3.2431	2.47841	1.71742	ENSG00000225998	LSM2
ENSG00000225999	0	0	0	0	ENSG00000225999	NDUFA12P1
ENSG00000226000	0	0	0	0	ENSG00000226000	OR2J2
ENSG00000226002	1.7235	2.68739	4.55241	1.21021	ENSG00000226002	GTF2IP14
ENSG00000226003	0	0	0	0	ENSG00000226003	AL354714.3
ENSG00000226008	0	0	0	0	ENSG00000226008	SEPT14P3
ENSG00000226010	0.0643764	0.186094	0.336553	0.494094	ENSG00000226010	AL355852.1
ENSG00000226011	0	0	0	0	ENSG00000226011	OFD1P1Y
ENSG00000226013	0	0	0	0	ENSG00000226013	MRPS18BP1
ENSG00000226014	0	0	0	0	ENSG00000226014	AL358176.2
ENSG00000226015	0	0	0	0	ENSG00000226015	CCT8P1
ENSG00000226016	0	0	0	0	ENSG00000226016	RPL36AP55
ENSG00000226020	0	0	0	0	ENSG00000226020	CDK2AP2P3
ENSG00000226023	0	0.0219476	0.0109151	0.0319741	ENSG00000226023	CT47A6
ENSG00000226024	0	0	0	0	ENSG00000226024	COX5BP7
ENSG00000226025	0.387177	0.449788	0.546304	0.955027	ENSG00000226025	LGALS17A
ENSG00000226027	0	0	0	0	ENSG00000226027	HLA-S
ENSG00000226028	0.35915	0.687164	0.629361	1.02678	ENSG00000226028	PFN1P12
ENSG00000226030	0	0	0	0	ENSG00000226030	HLA-DQB3
ENSG00000226033	2.07367	2.232	2.56416	2.01413	ENSG00000226033	STK19
ENSG00000226034	0.166664	1.38306	1.60492	0.799649	ENSG00000226034	NANOGNBP1
ENSG00000226035	0.0394657	0.0375419	0	0	ENSG00000226035	HLA-DRB9
ENSG00000226036	0	0	0	0	ENSG00000226036	AL590648.1
ENSG00000226038	0	0.149196	0	0	ENSG00000226038	PPIAP21
ENSG00000226040	0.317112	1.0002	2.00222	1.78326	ENSG00000226040	AC005740.1
ENSG00000226042	0.0737115	0.142019	0	0.0807252	ENSG00000226042	CDY10P

ENSG00000226045	0.485534	0.694556	0	0	ENSG00000226045	AC234644.1
ENSG00000226046	0	0	0	0	ENSG00000226046	AP1S2P1
ENSG00000226048	0.066234	0.828094	0.230235	0.936716	ENSG00000226048	YBX1P8
ENSG00000226049	0	0.0244056	0	0	ENSG00000226049	AC123769.1
ENSG00000226050	0.0174175	0.000999815	0	0.0522935	ENSG00000226050	USP8P1
ENSG00000226054	0.248608	0.307175	0.0780343	0.291977	ENSG00000226054	MEMO1P1
ENSG00000226055	0.400505	0.947169	0.74231	0.805399	ENSG00000226055	PAICSP1
ENSG00000226056	0.144451	0.463695	0.377116	0.539667	ENSG00000226056	MTND4P32
ENSG00000226057	0.038443	0.0739319	0.134989	0.10624	ENSG00000226057	PHF2P2
ENSG00000226058	0	0	0	0	ENSG00000226058	AC092570.1
ENSG00000226059	0	0.225853	0	0.381699	ENSG00000226059	HMGB3P20
ENSG00000226060	1.82591	0.98202	3.18287	0.727701	ENSG00000226060	TRIM26
ENSG00000226061	0	0	0	0	ENSG00000226061	PCMTD1P1
ENSG00000226064	0	0	0	0	ENSG00000226064	PGBD4P6
ENSG00000226065	1.45072	1.75488	2.63272	0.983428	ENSG00000226065	ZBTB45P2
ENSG00000226066	0.269421	0.380443	0.289373	0.250567	ENSG00000226066	AC009541.1
ENSG00000226068	0	0	0	0	ENSG00000226068	HNRNPA3P4
ENSG00000226071	0	0	0.342347	1.46938	ENSG00000226071	HLA-DPB2
ENSG00000226072	0.141302	0.181404	0.205251	0.154514	ENSG00000226072	AC016772.1
ENSG00000226074	0	0	0	0.250151	ENSG00000226074	PRSS44
ENSG00000226075	0	0	0.255925	0	ENSG00000226075	PHKG1P1
ENSG00000226080	0	0	0	0	ENSG00000226080	AC062028.2
ENSG00000226081	0	0	0	0	ENSG00000226081	USP12PX
ENSG00000226082	0	0.141079	0.130989	0	ENSG00000226082	AC096915.1
ENSG00000226084	0.344519	0	0.702953	1.70609	ENSG00000226084	AC113935.1
ENSG00000226085	4.25195	2.63307	2.7244	1.43872	ENSG00000226085	UQCRFS1P1
ENSG00000226086	0.157234	0	0.0686381	0	ENSG00000226086	EIF3LP3
ENSG00000226092	0	0	0	0	ENSG00000226092	RBMY2AP
ENSG00000226093	0	0	0	0	ENSG00000226093	RPS28P8
ENSG00000226094	0.0467661	0	0	0.0505773	ENSG00000226094	RPL7P3
ENSG00000226096	0	0	0	0	ENSG00000226096	AC087499.2
ENSG00000226098	0	0	0	0	ENSG00000226098	SEC11B
ENSG00000226102	0	0.124998	0	0.295805	ENSG00000226102	SEPT7P3
ENSG00000226103	2.36123	2.70737	3.73633	0	ENSG00000226103	C6orf47
ENSG00000226104	60.5984	194.686	148.538	222.583	ENSG00000226104	AC011475.1
ENSG00000226107	0	1.06672	0.64162	0.776877	ENSG00000226107	AC004383.1
ENSG00000226108	0	0	0	0	ENSG00000226108	RAB28P1
ENSG00000226109	0	0.23484	0	0	ENSG00000226109	CR382333.1
ENSG00000226110	0	0	0	0	ENSG00000226110	BX323845.2
ENSG00000226111	3.6819	4.08555	4.50723	3.12515	ENSG00000226111	MRPS18B
ENSG00000226112	0	0	0	0.948027	ENSG00000226112	FCF1P4
ENSG00000226114	0	0	0	0	ENSG00000226114	NDUFB4P5
ENSG00000226116	0	0.144339	0.132071	0.162235	ENSG00000226116	USP9YP6
ENSG00000226117	0	0	0	0	ENSG00000226117	AC090844.1
ENSG00000226118	0	2.39266	0	0	ENSG00000226118	MTND3P1
ENSG00000226119	0.203879	0.210211	0.359138	0	ENSG00000226119	Z80107.1
ENSG00000226121	0.238511	0.174679	0.0659206	0.240288	ENSG00000226121	AC009487.2
ENSG00000226124	0.61677	0.598658	0.748876	0.458851	ENSG00000226124	FTCDNL1
ENSG00000226126	0	0.0873474	0.0410555	0	ENSG00000226126	PSMC1P12
ENSG00000226127	0.0140136	0	0	0.0176708	ENSG00000226127	BTNL2
ENSG00000226128	0	0	0.162983	0.601119	ENSG00000226128	RPL26P9
ENSG00000226129	2.57193	4.74896	3.51075	6.73928	ENSG00000226129	RP11-157L3.5
ENSG00000226131	0	0	0	0	ENSG00000226131	AC073465.2
ENSG00000226132	0.472857	0.821051	0.750806	1.38555	ENSG00000226132	RPS3AP46

ENSG00000226138	0.508545	2.31125	0.444173	1.01439	ENSG00000226138	AC004801.1
ENSG00000226141	0	0	0	0	ENSG00000226141	AC244107.1
ENSG00000226142	0	0	0	0	ENSG00000226142	RPL35P8
ENSG00000226144	0	1.07806	0.340508	0.969215	ENSG00000226144	RPS27AP3
ENSG00000226145	215.755	560.453	335.214	539.733	ENSG00000226145	KRT16P6
ENSG00000226147	0.0909275	0.301792	0.27431	0.523873	ENSG00000226147	TUBBP10
ENSG00000226148	1.31798	2.76068	3.77075	2.76768	ENSG00000226148	SLC25A39P1
ENSG00000226152	0	0	0	0	ENSG00000226152	AL671561.1
ENSG00000226153	0.788955	0.501033	1.58549	1.93262	ENSG00000226153	Z93242.1
ENSG00000226156	0	0	0	0	ENSG00000226156	RPL23AP76
ENSG00000226157	0	0	0	0	ENSG00000226157	OR52E3P
ENSG00000226158	0.202241	0.188551	0.51067	0.20905	ENSG00000226158	CLCP2
ENSG00000226160	0	0	0	0	ENSG00000226160	AC137499.1
ENSG00000226161	0.0554953	0.0534352	0	0.0605335	ENSG00000226161	EIF4A1P5
ENSG00000226164	0	0.77304	0.199486	1.48645	ENSG00000226164	FGFR3P6
ENSG00000226165	0	0.130285	0	0.0988326	ENSG00000226165	HLA-DQB2
ENSG00000226166	0	0	0	0	ENSG00000226166	AC244670.1
ENSG00000226168	0	0	0	0	ENSG00000226168	AL589794.1
ENSG00000226170	0.0263015	0.025284	0.0228434	0.0285321	ENSG00000226170	U82671.12
ENSG00000226171	2.76168	2.47104	2.17439	1.77552	ENSG00000226171	DHX16
ENSG00000226173	3.97772	4.76897	4.68948	3.88382	ENSG00000226173	TAP1
ENSG00000226174	1.38616	1.0988	1.77314	0.224528	ENSG00000226174	TEX22
ENSG00000226175	0	0.159557	0	0.193505	ENSG00000226175	BX927221.1
ENSG00000226180	0.723631	0.949924	1.09144	0.882673	ENSG00000226180	AC010536.1
ENSG00000226182	0.306091	0.145015	0.112516	0	ENSG00000226182	LST1
ENSG00000226183	0.213983	0.411024	0.185674	0.230812	ENSG00000226183	RANP7
ENSG00000226185	0	0.0849294	0	0.674997	ENSG00000226185	TRIM64FP
ENSG00000226186	0	0.136101	0.24594	0.14988	ENSG00000226186	ELOCP21
ENSG00000226187	0.0327523	0	0	0	ENSG00000226187	LY6G6E
ENSG00000226188	0	1.49259	1.56078	4.75608	ENSG00000226188	HNRNPA1P3
ENSG00000226191	0	0	0	0	ENSG00000226191	CLK3P2
ENSG00000226192	0.0332871	0	0	0.0136277	ENSG00000226192	OR2J1
ENSG00000226196	0	0	0	0	ENSG00000226196	GAPDHP75
ENSG00000226199	0	0	0	0	ENSG00000226199	AC112492.2
ENSG00000226201	1.10486	0.54819	1.3866	1.30105	ENSG00000226201	PSMB8
ENSG00000226205	0.166688	2.41963	1.7548	2.44164	ENSG00000226205	AC007790.1
ENSG00000226209	0	0	0	0	ENSG00000226209	C8orf59P1
ENSG00000226210	2.02392	4.79055	3.1705	2.69189	ENSG00000226210	AC215219.1
ENSG00000226211	0	0.24582	0	0	ENSG00000226211	AL445466.1
ENSG00000226212	0	0	0	0	ENSG00000226212	TRGV6
ENSG00000226213	0	0	0	0.532137	ENSG00000226213	UBQLN4P2
ENSG00000226215	0.164783	0.252772	0.0998859	0.157885	ENSG00000226215	APOM
ENSG00000226216	0.483493	1.84399	0.833433	3.06349	ENSG00000226216	RPS12P5
ENSG00000226217	0	0	0	0	ENSG00000226217	RPL19P1
ENSG00000226220	0.0840026	0.202014	0.0403656	0.0527658	ENSG00000226220	CICP22
ENSG00000226221	0	0	0.254496	0	ENSG00000226221	AC022431.1
ENSG00000226222	0	0	0	0	ENSG00000226222	AC079168.1
ENSG00000226223	0	0	0	0	ENSG00000226223	TSPY16P
ENSG00000226225	249.329	186.853	166.574	87.6578	ENSG00000226225	RPS18
ENSG00000226226	0	0.130597	0	0	ENSG00000226226	PRELID3BP1
ENSG00000226227	0	0	0	0	ENSG00000226227	BX120007.1
ENSG00000226229	0	0	0	0	ENSG00000226229	RPLP0P1
ENSG00000226230	0	0.292184	0.131905	0.651572	ENSG00000226230	AC007237.1
ENSG00000226232	11.2032	18.4772	23.3161	11.6368	ENSG00000226232	NPIPB14P

ENSG00000226233	0	1.32115	1.2338	0	ENSG00000226233	Z82188.1
ENSG00000226234	0	0	0.181198	0	ENSG00000226234	KRT18P24
ENSG00000226241	0.0272765	0	0.0478094	0.06027	ENSG00000226241	Z75746.1
ENSG00000226242	0	0	0	0	ENSG00000226242	RPS17P8
ENSG00000226243	0.803745	0	0.684616	0	ENSG00000226243	RPL37AP1
ENSG00000226246	0	0	0	0	ENSG00000226246	KRT18P36
ENSG00000226247	1.12253	1.60085	1.20523	1.17491	ENSG00000226247	SUPT4H1P1
ENSG00000226248	47.8587	52.6287	21.8263	21.5159	ENSG00000226248	CLIC1
ENSG00000226253	1.73556	4.72755	5.95569	4.39496	ENSG00000226253	MRPL35P3
ENSG00000226254	0.218237	0.567791	1.19606	1.46856	ENSG00000226254	PTP4A1P3
ENSG00000226255	0	0	0	0	ENSG00000226255	UBE2V2P1
ENSG00000226257	2.51661	2.6234	2.61714	2.27233	ENSG00000226257	STK19
ENSG00000226259	3.69976	2.23531	2.6309	2.75075	ENSG00000226259	GTF2H2B
ENSG00000226260	0.132708	0.0207335	0.166196	0.116951	ENSG00000226260	HLA-DRA
ENSG00000226261	0.392554	0.377176	0.578693	0.531315	ENSG00000226261	AC064836.1
ENSG00000226262	0.0289529	0.0558054	0.100898	0.190584	ENSG00000226262	PHKBP1
ENSG00000226264	0	0.00799456	0.00913478	0.00910544	ENSG00000226264	HLA-DMB
ENSG00000226267	8.53183	0	0	0	ENSG00000226267	BX005428.1
ENSG00000226268	0	0	0	0	ENSG00000226268	AC135977.1
ENSG00000226270	0	0	0	0	ENSG00000226270	ZNF736P2Y
ENSG00000226271	0	0	0.00605942	0	ENSG00000226271	OR2J3
ENSG00000226273	0	0.123824	0	0	ENSG00000226273	AC079305.2
ENSG00000226275	0.0274983	0.0159269	0.0264951	0.0206416	ENSG00000226275	LTA
ENSG00000226278	7.75707	7.61007	14.9289	0	ENSG00000226278	PSPHP1
ENSG00000226279	0	0	0	0.163473	ENSG00000226279	RPL12P10
ENSG00000226280	0	0.0838483	0.0510658	0.0318169	ENSG00000226280	AL049641.1
ENSG00000226284	0.830297	2.31145	1.60492	1.84227	ENSG00000226284	ARPC3P1
ENSG00000226285	0.066234	0	0.174089	0.43233	ENSG00000226285	NUP35P2
ENSG00000226288	0	0.118425	0	0	ENSG00000226288	OR52I2
ENSG00000226289	0	0.0940823	0.0849913	0	ENSG00000226289	CDCA4P3
ENSG00000226292	0.158825	0	0	0	ENSG00000226292	AL606495.1
ENSG00000226297	0	0	0.334685	0.155831	ENSG00000226297	AC007677.1
ENSG00000226298	0	0	0	0.171163	ENSG00000226298	RAD23BP3
ENSG00000226299	0	0	0	0	ENSG00000226299	RPSAP62
ENSG00000226301	0	0	0	0.097712	ENSG00000226301	PDCL3P1
ENSG00000226303	0.0558802	0	0.0241408	0.0296507	ENSG00000226303	ZDHHC20P1
ENSG00000226306	0.257594	0.687432	1.07409	1.01528	ENSG00000226306	NPY6R
ENSG00000226307	0.265332	0.127276	0	0	ENSG00000226307	HNRNPDLP1
ENSG00000226309	0.197983	0.164887	0.200213	0.108249	ENSG00000226309	SMARCE1P2
ENSG00000226313	0	0.102499	0	0.0580964	ENSG00000226313	MTCYBP12
ENSG00000226314	2.32992	4.65399	3.92357	2.857	ENSG00000226314	ZNF192P1
ENSG00000226318	1.3756	3.50628	3.34227	5.27861	ENSG00000226318	RPS3AP38
ENSG00000226321	2.53324	4.28775	3.07502	5.66273	ENSG00000226321	CROCC2
ENSG00000226324	0	0.466896	0	2.51738	ENSG00000226324	AL358453.1
ENSG00000226327	0	0	0	0	ENSG00000226327	RPSAP49
ENSG00000226329	0.439149	1.44982	1.6471	2.45586	ENSG00000226329	AC005682.1
ENSG00000226331	0	0	0	0	ENSG00000226331	RPL23AP28
ENSG00000226336	0	0.227539	0.822488	0.50284	ENSG00000226336	MRPS16P3
ENSG00000226338	2.01303	0	0	1.57354	ENSG00000226338	AC079150.2
ENSG00000226339	0.537051	0	0	0.54282	ENSG00000226339	RPS26P56
ENSG00000226340	0	0	0	0.288164	ENSG00000226340	AC105402.1
ENSG00000226341	0	0.170527	0	0	ENSG00000226341	MTCYBP39
ENSG00000226342	0.0784317	0.151887	0.13627	0.258506	ENSG00000226342	NMD3P1
ENSG00000226343	0	0	0	0	ENSG00000226343	HLA-DQB3

ENSG00000226344	0	0	0	0	ENSG00000226344	CST12P
ENSG00000226345	3.07666	5.04781	5.74154	5.39999	ENSG00000226345	AC083822.1
ENSG00000226347	0	0	0	0	ENSG00000226347	OR2J2
ENSG00000226348	0	0.217048	0.587523	0.243698	ENSG00000226348	VN2R10P
ENSG00000226353	0	0	0	0	ENSG00000226353	TAF9P1
ENSG00000226354	15.3181	8.48971	0.293017	0	ENSG00000226354	HLA-U
ENSG00000226356	0.891501	3.46797	1.79144	4.18989	ENSG00000226356	AC092850.1
ENSG00000226358	0.244992	0.0786776	0.183029	0.17871	ENSG00000226358	KRT8P38
ENSG00000226359	0.22207	0.208664	0.314168	0.157115	ENSG00000226359	ACTG1P24
ENSG00000226360	0.242279	0.465541	0.212769	0.663805	ENSG00000226360	AC096919.1
ENSG00000226361	0	0.111641	0.107045	0.122277	ENSG00000226361	TERF1P5
ENSG00000226364	2.96529	5.18618	5.72877	5.73992	ENSG00000226364	LINC02089
ENSG00000226365	0	0	0	0.0488226	ENSG00000226365	UBDP1
ENSG00000226366	0	0	0	0	ENSG00000226366	AC097463.1
ENSG00000226368	0	0	0	0	ENSG00000226368	BX088645.2
ENSG00000226369	7.98E-06	5.37E-05	2.18E-05	1.73E-05	ENSG00000226369	USP9YP11
ENSG00000226372	0.0953746	0.0919159	0.0829629	0.300143	ENSG00000226372	DCAF8L1
ENSG00000226379	1.86909	1.3845	0.332359	0.329597	ENSG00000226379	HCG4
ENSG00000226384	0.272781	15.3611	9.31042	5.82394	ENSG00000226384	GTF2H4
ENSG00000226388	0	0	0	0	ENSG00000226388	ELL2P4
ENSG00000226389	0.175185	0.170621	0.102442	0.258712	ENSG00000226389	MAPK6PS6
ENSG00000226392	0	0	2.90775	2.64261	ENSG00000226392	MTATP6P21
ENSG00000226393	0.702533	0.673962	0.486728	0.602024	ENSG00000226393	IFNA20P
ENSG00000226394	0	1.57289	0	8.80605	ENSG00000226394	AC093423.1
ENSG00000226395	0	0	0.484479	0	ENSG00000226395	MRPS21P5
ENSG00000226396	1.05059	2.14336	1.76103	2.15716	ENSG00000226396	AL031727.1
ENSG00000226397	3.71302	7.39603	6.3734	13.48	ENSG00000226397	C12orf77
ENSG00000226400	0	0	0	0	ENSG00000226400	AC010385.1
ENSG00000226401	0.252439	0	0	0	ENSG00000226401	AC006015.1
ENSG00000226402	0.233694	1.34104	0.325348	0.561387	ENSG00000226402	TRIM31
ENSG00000226404	0.0973281	0.0758412	0.0529561	0.0644326	ENSG00000226404	LY6G5C
ENSG00000226405	0	0	0	0	ENSG00000226405	AL133325.1
ENSG00000226406	0.230062	0.368643	0.402135	0.249721	ENSG00000226406	RBMX2P1
ENSG00000226407	0	0	0	0	ENSG00000226407	RPL23P11
ENSG00000226410	0.714623	4.06232	3.66262	4.81752	ENSG00000226410	AC104058.1
ENSG00000226411	0	0	0	0	ENSG00000226411	AC079355.1
ENSG00000226413	0.0684121	0.19738	0.118898	0	ENSG00000226413	OR8T1P
ENSG00000226414	0.0661157	0.129701	0.198304	0	ENSG00000226414	MTCYBP38
ENSG00000226415	0	0	0.190181	0	ENSG00000226415	TPI1P1
ENSG00000226417	47.8587	52.6287	21.8263	21.5159	ENSG00000226417	CLIC1
ENSG00000226420	0	0	0	0	ENSG00000226420	IGLV3-4
ENSG00000226421	0	0	0.0614734	0.0766672	ENSG00000226421	SLC25A5P5
ENSG00000226427	0	0	0	0	ENSG00000226427	HMGN2P7
ENSG00000226428	0.747604	0.102546	0.0925994	0.460695	ENSG00000226428	RPL15P13
ENSG00000226429	0.997542	0.315353	0.8541	2.42212	ENSG00000226429	AL590399.2
ENSG00000226430	0.197756	0.628162	0.811286	0.519154	ENSG00000226430	USP17L7
ENSG00000226432	0.112217	0.198232	0	0	ENSG00000226432	AC010342.1
ENSG00000226435	0.664561	1.10034	0.926398	0.926183	ENSG00000226435	ANKRD18DP
ENSG00000226436	0	0	0	0	ENSG00000226436	AC002367.1
ENSG00000226437	4.24243	5.23432	7.06466	0.269057	ENSG00000226437	TRIM39
ENSG00000226439	0	0	0.942361	0	ENSG00000226439	AC108161.1
ENSG00000226443	0.123772	0.535889	0.322893	0.67406	ENSG00000226443	GAPDHP32
ENSG00000226444	0	0	0	0	ENSG00000226444	ACTR3BP6
ENSG00000226446	1.04922	1.6852	0.39777	1.60276	ENSG00000226446	NOTCH2P1

ENSG00000226448	0	0	0.0750047	0.280682	ENSG00000226448	RPL7AP51
ENSG00000226449	0.0182591	0.0175902	0.0318013	0.120396	ENSG00000226449	CDY5P
ENSG00000226450	0.316627	0.991074	1.93025	1.04916	ENSG00000226450	CYP2D8P
ENSG00000226457	0.940705	3.15633	3.55996	4.32757	ENSG00000226457	AL358794.1
ENSG00000226461	0	0	0	0	ENSG00000226461	OR10G5P
ENSG00000226462	0	0.00880756	0.00776227	0	ENSG00000226462	KRT18P1
ENSG00000226463	0	0	0	0	ENSG00000226463	OR2W1
ENSG00000226466	0	0	0.0716993	0	ENSG00000226466	RPA2P2
ENSG00000226467	4.49328	0	0.758657	3.4111	ENSG00000226467	AGPAT1
ENSG00000226468	0.0815095	0	0.141562	0	ENSG00000226468	AC018641.1
ENSG00000226469	0.398565	0.746794	0.72629	0.919684	ENSG00000226469	ADAM1B
ENSG00000226470	0	0	0	0	ENSG00000226470	RPS29P33
ENSG00000226473	0	0	0	0	ENSG00000226473	AC079807.1
ENSG00000226474	0	0	0	0	ENSG00000226474	AP000532.1
ENSG00000226477	0	0	0	0	ENSG00000226477	AC245028.1
ENSG00000226478	0.155199	1.34611	0.833925	1.59052	ENSG00000226478	UPF3AP1
ENSG00000226479	14.5486	19.0943	18.4202	9.38599	ENSG00000226479	TMEM185B
ENSG00000226480	0	0	0	0	ENSG00000226480	OR7H1P
ENSG00000226481	0	0	0.0383181	0	ENSG00000226481	ACTR3BP2
ENSG00000226483	0.311444	0.100209	0.741615	1.12857	ENSG00000226483	AL392088.1
ENSG00000226485	0	0.0638148	0.0567701	0.0710712	ENSG00000226485	RBM22P3
ENSG00000226489	0	0	0	0	ENSG00000226489	AC104308.1
ENSG00000226490	0.106116	0.407676	0	0.343448	ENSG00000226490	AC138647.1
ENSG00000226491	0.0796155	0.213349	0.129352	0.321284	ENSG00000226491	FTOP1
ENSG00000226492	6.74161	5.95613	6.52695	6.01454	ENSG00000226492	CUTA
ENSG00000226493	0.37224	1.30954	1.28607	1.8529	ENSG00000226493	RPL26P27
ENSG00000226494	0.0259809	0.0124808	0.033827	0	ENSG00000226494	RPL7P4
ENSG00000226498	0.25183	0.481845	1.05763	1.08787	ENSG00000226498	RPSAP21
ENSG00000226499	1.27005	1.49689	2.4339	2.33648	ENSG00000226499	AL136380.1
ENSG00000226500	0	0	0.0887399	0.108843	ENSG00000226500	AC243772.1
ENSG00000226501	0.425164	0.684762	0.6117	1.36171	ENSG00000226501	USF1P1
ENSG00000226502	0	0.0385104	0	0	ENSG00000226502	KRT8P27
ENSG00000226504	0	0	0	0	ENSG00000226504	TMEM167AP1
ENSG00000226507	0	0	0	0	ENSG00000226507	IPMKP1
ENSG00000226509	0	1.18201	0	0	ENSG00000226509	AC005588.1
ENSG00000226513	0	0	0	0	ENSG00000226513	COL11A2P1
ENSG00000226515	0	0	0	0	ENSG00000226515	AC004386.2
ENSG00000226517	0.0859609	0.200014	0.994099	0.315769	ENSG00000226517	CR388220.2
ENSG00000226521	0	0.0541071	0.0492869	0.123614	ENSG00000226521	AC087499.3
ENSG00000226523	0	4.00142	2.80968	5.10389	ENSG00000226523	AC074375.1
ENSG00000226524	2.76579	4.20015	5.11841	8.2741	ENSG00000226524	RP1-102H19.8
ENSG00000226525	0.14283	0	0.123667	0	ENSG00000226525	RPS7P10
ENSG00000226529	0	0	0	0	ENSG00000226529	MTND1P1
ENSG00000226531	2.36123	2.70737	3.73633	0	ENSG00000226531	C6orf47
ENSG00000226532	0	0	0	0	ENSG00000226532	AL022718.1
ENSG00000226534	0	0	0	0	ENSG00000226534	AP000552.2
ENSG00000226535	0.292883	0.105761	0.287199	0.200404	ENSG00000226535	AL445487.1
ENSG00000226536	0	0.270729	0	0.298228	ENSG00000226536	SETP15
ENSG00000226537	0	0.149076	0	0.168813	ENSG00000226537	OR7E33P
ENSG00000226538	0.898463	0	0	0.335064	ENSG00000226538	RPL35AP4
ENSG00000226539	0.464311	0.267705	0.241826	0.100445	ENSG00000226539	AC012512.1
ENSG00000226540	0	0.0589447	0	0	ENSG00000226540	GAPDHP73
ENSG00000226541	0	0	0	0	ENSG00000226541	AL359633.1
ENSG00000226543	0.176143	0	0.15215	0.187283	ENSG00000226543	MYL6P1

ENSG00000226544	0	0.192321	0	0	ENSG00000226544	RPL7P22
ENSG00000226545	1.38739	0.97591	1.30705	3.18926	ENSG00000226545	AL357552.1
ENSG00000226546	0.0571755	2.57486	5.20658	1.91158	ENSG00000226546	RP11-34H11.5
ENSG00000226547	0	0	0	0	ENSG00000226547	SSU72P1
ENSG00000226549	0.0569241	0.115689	0.396261	0.190962	ENSG00000226549	SCDP1
ENSG00000226552	0	0	0.0609881	0.0767228	ENSG00000226552	BX284613.1
ENSG00000226553	0	0.14963	0.202374	0.0424792	ENSG00000226553	AC018735.1
ENSG00000226554	0.0820253	0.315359	0.142454	0	ENSG00000226554	MTCL1P1
ENSG00000226555	0.517168	1.85603	1.59575	0	ENSG00000226555	AGKP1
ENSG00000226556	0	0	0	0.101211	ENSG00000226556	NPM1P49
ENSG00000226557	0	0.0738338	0.0997761	0	ENSG00000226557	TRAF6P1
ENSG00000226558	0	0	0	0	ENSG00000226558	AL590383.1
ENSG00000226560	0.446933	0.631435	0.339268	0.149681	ENSG00000226560	C2
ENSG00000226563	0	0	0	0	ENSG00000226563	HCG4B
ENSG00000226564	0	0	0	0	ENSG00000226564	FTH1P20
ENSG00000226565	0	0	0	0	ENSG00000226565	AL445493.1
ENSG00000226570	0	0	0	0	ENSG00000226570	AL450304.1
ENSG00000226573	0	0	0	0	ENSG00000226573	AC003071.2
ENSG00000226575	0	0	0	0	ENSG00000226575	MYL8P
ENSG00000226577	0.00724298	0	0	0.00789492	ENSG00000226577	MICC
ENSG00000226579	0	0	0	0.135653	ENSG00000226579	MTCYBP31
ENSG00000226580	0	1.47588	0	0	ENSG00000226580	RPL39P40
ENSG00000226582	0	0	0.182501	0.221859	ENSG00000226582	UBE2V1P5
ENSG00000226586	0.111634	0.322334	0.119037	0.102342	ENSG00000226586	HLA-J
ENSG00000226589	2.55148	6.56435	5.10324	8.23062	ENSG00000226589	VARS
ENSG00000226590	0	0	0	0.441613	ENSG00000226590	UBE2V1P10
ENSG00000226591	0	0	0	0	ENSG00000226591	COL11A2P1
ENSG00000226592	0.0729129	0.14024	0.253446	0.479861	ENSG00000226592	AC004911.1
ENSG00000226595	0	0	0	0.31241	ENSG00000226595	AC245291.1
ENSG00000226597	0	0.116213	0.156138	0	ENSG00000226597	IFNWP9
ENSG00000226600	0	0.0219476	0.0109151	0.0319741	ENSG00000226600	CT47A9
ENSG00000226603	0.0302896	0.0578806	0	0.032054	ENSG00000226603	LY6G6D
ENSG00000226608	0.494958	0.145081	0	0	ENSG00000226608	FTLP3
ENSG00000226610	0	0.0275452	0	0.0234623	ENSG00000226610	AL662852.3
ENSG00000226611	0.0998199	0.0856461	0.147576	0	ENSG00000226611	OFD1P2Y
ENSG00000226613	0	0	0	0	ENSG00000226613	Ghc-1077H7.2
ENSG00000226614	8.10034	7.04224	6.12923	6.51393	ENSG00000226614	SLC39A7
ENSG00000226615	0	0	0.538806	0	ENSG00000226615	AC018696.1
ENSG00000226616	0	0.0624281	0	0.0706328	ENSG00000226616	OR52M2P
ENSG00000226617	0.190746	0.345392	0.156062	0	ENSG00000226617	RPL21P110
ENSG00000226618	6.13844	4.31529	8.72247	4.15843	ENSG00000226618	PRRC2A
ENSG00000226621	1.40084	0	1.9672	0	ENSG00000226621	AC083855.1
ENSG00000226624	0.230333	0.553502	0.89899	1.23959	ENSG00000226624	AC005099.1
ENSG00000226625	0.27032	0.812512	0	0.34007	ENSG00000226625	RBM17P1
ENSG00000226626	0	0.693903	0.295955	0.645495	ENSG00000226626	NOP56P2
ENSG00000226631	0.0503901	0.140843	0.0159481	0.0685824	ENSG00000226631	SLC9A3P3
ENSG00000226632	2.00058	2.53253	2.59034	5.38615	ENSG00000226632	UBE2V1P1
ENSG00000226633	0	0.9139	0.137563	0.508951	ENSG00000226633	PPIAP28
ENSG00000226634	0.365304	2.25855	0.892104	1.57402	ENSG00000226634	DDAH2
ENSG00000226636	0.0306109	0.147491	0	0.201423	ENSG00000226636	AC006020.1
ENSG00000226641	0	0	0	0.315093	ENSG00000226641	AL391647.1
ENSG00000226642	0	0.0992575	0.224296	0.0562694	ENSG00000226642	ACTG1P12
ENSG00000226646	0	0	0	0.0971028	ENSG00000226646	RPL7P37
ENSG00000226650	0.0122854	0.0727518	0.0934741	0.0561424	ENSG00000226650	KIF4B

ENSG00000226651	47.8587	52.6287	21.8263	21.5159	ENSG00000226651	CLIC1
ENSG00000226652	1.33774	0.986315	0.175536	0.112966	ENSG00000226652	PSMD10P2
ENSG00000226653	0.0769148	0.628546	0.134782	0.251845	ENSG00000226653	OR13Z1P
ENSG00000226657	0	0	0	0	ENSG00000226657	AL662852.4
ENSG00000226658	0.606237	1.01681	1.0502	1.61988	ENSG00000226658	RPL23AP30
ENSG00000226660	0	0	0	0	ENSG00000226660	TRBV2
ENSG00000226662	0	0	0	0	ENSG00000226662	CHMP1AP1
ENSG00000226663	0.131173	0.150448	0.187619	0.35383	ENSG00000226663	MTND4P10
ENSG00000226665	0	0	0.0717918	0.179231	ENSG00000226665	SSR1P2
ENSG00000226666	0.0283705	0	0.0490352	0.0625356	ENSG00000226666	HSPA9P1
ENSG00000226668	0.37978	0.986923	0.423335	2.31518	ENSG00000226668	AL136981.1
ENSG00000226670	0	0	0	0	ENSG00000226670	BCAS2P3
ENSG00000226671	0	0	0	0	ENSG00000226671	AC005008.1
ENSG00000226675	0	0.231626	0.697308	0.313895	ENSG00000226675	RP11-666A1.3
ENSG00000226677	0.257069	0.789856	0	1.13646	ENSG00000226677	IGBP1P1
ENSG00000226683	0	0.0711788	0.0213859	0.350346	ENSG00000226683	PWWP2AP1
ENSG00000226685	0	6.95E-08	2.23E-08	2.92E-08	ENSG00000226685	CT47A12
ENSG00000226691	1.93885	0.673681	0.561095	0.695858	ENSG00000226691	HLA-Z
ENSG00000226693	0	0	0.0506203	0	ENSG00000226693	NXNP1
ENSG00000226695	0.0792037	0.0378872	0.0667724	0.173941	ENSG00000226695	ANKRD20A10P
ENSG00000226700	0.170284	0.0584101	0.203527	0	ENSG00000226700	MTND4P25
ENSG00000226701	0.217736	0.628396	0.756316	0.946836	ENSG00000226701	RPL15P14
ENSG00000226703	0.16356	0.15363	0.145117	0.165802	ENSG00000226703	NPM1P4
ENSG00000226704	0.232265	0.119065	0.0689541	0.135567	ENSG00000226704	HSPA1L
ENSG00000226705	0	0.136745	0.0625275	1.0105	ENSG00000226705	SDCBPP1
ENSG00000226710	15.4939	19.3381	37.5121	13.313	ENSG00000226710	C6orf48
ENSG00000226713	0	0.0431034	0	0	ENSG00000226713	MICD
ENSG00000226714	0	0	0	0	ENSG00000226714	AL669978.1
ENSG00000226718	0	0	0	0	ENSG00000226718	SNRPGP8
ENSG00000226721	0	0	1.64E-05	0	ENSG00000226721	EEF1DP2
ENSG00000226723	0	0	0	0	ENSG00000226723	AL513175.1
ENSG00000226724	0	0.145542	0	0	ENSG00000226724	AC109780.2
ENSG00000226726	0.27915	0	0.239891	0.292317	ENSG00000226726	TMEM256P2
ENSG00000226727	0	0	0.117234	0	ENSG00000226727	HLA-T
ENSG00000226729	0	0	0.252577	0.954974	ENSG00000226729	AC004815.1
ENSG00000226732	0.191366	0.114275	0.165316	0.406353	ENSG00000226732	ZDHHC20P2
ENSG00000226734	0	3.19754	0	0.684899	ENSG00000226734	SNRPGP12
ENSG00000226736	0	4.34957	0	0	ENSG00000226736	BX284699.1
ENSG00000226742	38.291	29.9305	33.1659	24.502	ENSG00000226742	HSBP1L1
ENSG00000226744	0	64.3939	37.6449	5.35622	ENSG00000226744	AC005326.1
ENSG00000226745	0	0	0	0	ENSG00000226745	AL512599.1
ENSG00000226750	7.38799	1.60871	0	2.53294	ENSG00000226750	AL360271.2
ENSG00000226753	0	0	0	0	ENSG00000226753	AL451105.1
ENSG00000226755	0	0	0	0	ENSG00000226755	VPS25P1
ENSG00000226757	0.201082	0.314965	0.197499	0.413988	ENSG00000226757	PP12613
ENSG00000226761	0.094057	0.748871	0.222503	0.556636	ENSG00000226761	TAS2R46
ENSG00000226763	0.45058	0.553398	0.948783	0.8148	ENSG00000226763	SRRM5
ENSG00000226765	0	0.0707143	0	0.0943564	ENSG00000226765	RPSAP33
ENSG00000226766	0.221717	1.23668	0.382456	2.15763	ENSG00000226766	FABP7P1
ENSG00000226767	0	0	0	0	ENSG00000226767	AC114501.1
ENSG00000226769	0.282983	0.0680294	0	0.153756	ENSG00000226769	GAPDHP54
ENSG00000226773	0	0.072877	0	0.24685	ENSG00000226773	AL663109.1
ENSG00000226774	0	0.177338	0	0.393893	ENSG00000226774	AC073910.1

ENSG00000226776	0	0	0	0	ENSG00000226776	KRTAP3-4P
ENSG00000226777	0.701671	1.24301	2.04036	3.57445	ENSG00000226777	FAM30A
ENSG00000226781	0	0	0	0	ENSG00000226781	TBCAP1
ENSG00000226783	0.0685916	0.0444117	0.0201251	0.0505807	ENSG00000226783	TLK1P1
ENSG00000226784	0.11222	0.0631192	0.109461	0.125562	ENSG00000226784	PGAM4
ENSG00000226788	5.04E-10	0.383319	0.39664	7.80729	ENSG00000226788	RING1
ENSG00000226789	0.941945	1.95279	2.36938	3.82113	ENSG00000226789	AC110926.1
ENSG00000226790	0.0875264	0.209431	0.124384	0.195475	ENSG00000226790	HNRNPA3P1
ENSG00000226794	0	0	0	0	ENSG00000226794	MTND1P20
ENSG00000226795	0	0	0	0	ENSG00000226795	AL929561.2
ENSG00000226796	0	0.0207547	0.0239362	0	ENSG00000226796	AL662826.1
ENSG00000226801	1.79813	4.07751	3.62137	3.90585	ENSG00000226801	OSTCP8
ENSG00000226802	0	0	0	0.0807743	ENSG00000226802	AL442647.2
ENSG00000226804	0.0562749	0.382288	0.146196	0.544589	ENSG00000226804	AL359839.1
ENSG00000226807	0.156822	0.0953835	0.30924	0.186624	ENSG00000226807	MROH5
ENSG00000226810	0	0	0.0427354	0	ENSG00000226810	AC112198.1
ENSG00000226814	0.591592	1.07931	1.11038	1.8998	ENSG00000226814	AL035407.1
ENSG00000226818	0	0.0297262	0.161258	0.0678814	ENSG00000226818	SLC6A6P1
ENSG00000226820	0	0	0	0	ENSG00000226820	AL592049.1
ENSG00000226823	1.98558	2.17712	3.29221	1.95582	ENSG00000226823	SUGT1P1
ENSG00000226826	0	0.223915	0.211819	2.4135	ENSG00000226826	HLA-DPB1
ENSG00000226827	1.19208	1.80041	2.66882	4.01914	ENSG00000226827	NPM1P11
ENSG00000226831	0	0	0.261498	0	ENSG00000226831	MED15P3
ENSG00000226832	0	0.0131907	0.0059608	0	ENSG00000226832	OR2B3
ENSG00000226834	0	0.0458373	0.0827353	0.200941	ENSG00000226834	BX248310.1
ENSG00000226836	0	0	0.370258	0	ENSG00000226836	AC018437.1
ENSG00000226837	0.127775	0	0.110703	0.274435	ENSG00000226837	HMGB1P32
ENSG00000226838	0	0	0	0	ENSG00000226838	AC096582.1
ENSG00000226839	0	0	0	0	ENSG00000226839	MTND6P11
ENSG00000226840	0	0	0.134285	0	ENSG00000226840	PAICSP3
ENSG00000226841	0.0916753	0	0	0	ENSG00000226841	MCCD1
ENSG00000226843	0	0	0	4.96407	ENSG00000226843	AL606753.1
ENSG00000226844	0	0.0415668	0.00939099	0.0470305	ENSG00000226844	AL662857.2
ENSG00000226845	0	0	0	0	ENSG00000226845	EEF1GP3
ENSG00000226847	0	0	0	0	ENSG00000226847	PRPS1P1
ENSG00000226850	0.00314444	0.0186652	0.023055	0.174972	ENSG00000226850	ATP6V1G2
ENSG00000226855	0.0870213	0	0	0	ENSG00000226855	RPSAP17
ENSG00000226857	0	0	0	0	ENSG00000226857	DUTP3
ENSG00000226858	0.474928	9.80456	0.246307	0.24367	ENSG00000226858	ZFP57
ENSG00000226860	0	0	0	0	ENSG00000226860	AC109638.1
ENSG00000226863	0.0470062	0.134857	0.0609598	0.0512231	ENSG00000226863	SHROOM2P1
ENSG00000226867	0	0	0	0	ENSG00000226867	AC244505.4
ENSG00000226870	0	0	0	0	ENSG00000226870	BX276092.2
ENSG00000226873	0	0	0.0503937	0.190748	ENSG00000226873	CDY14P
ENSG00000226874	0.466456	0.89108	1.40822	2.21592	ENSG00000226874	AC005154.2
ENSG00000226875	0	0	0.198611	0	ENSG00000226875	ZNF877P
ENSG00000226878	0.183412	1.77108	1.10926	2.37289	ENSG00000226878	GSTM3P2
ENSG00000226879	0	0.0858021	0.0808883	0.0707639	ENSG00000226879	CR762479.1
ENSG00000226880	1.25446	4.79818	4.0008	3.89784	ENSG00000226880	XX-213648.7
ENSG00000226881	0.104457	0	0	0	ENSG00000226881	H3F3AP5
ENSG00000226882	2.29229	6.13227	10.9194	4.42371	ENSG00000226882	GNL1
ENSG00000226884	0	0	0	0	ENSG00000226884	RPS29P10
ENSG00000226885	0	6.48E-09	0	0.521158	ENSG00000226885	E2F6P3
ENSG00000226886	0	0	0	0	ENSG00000226886	AC093787.1

ENSG00000226887	3.73425	4.67239	3.92409	2.52839	ENSG00000226887	ERVMER34-1
ENSG00000226888	0	0	0	0	ENSG00000226888	RPLP1P10
ENSG00000226892	0	0	0	0	ENSG00000226892	C6orf10
ENSG00000226893	0	0	0	0	ENSG00000226893	HLA-H
ENSG00000226894	0.200794	0.21053	0.296982	0.445734	ENSG00000226894	TMPRSS11BNL
ENSG00000226896	0	0	0.016343	0	ENSG00000226896	OR2I1P
ENSG00000226898	0	0	0	0	ENSG00000226898	UBD
ENSG00000226902	0	0	0	0	ENSG00000226902	CHCHD2P1
ENSG00000226905	0	0	0	0	ENSG00000226905	AC005040.1
ENSG00000226907	0	0	0.128044	0.170561	ENSG00000226907	CT45A6
ENSG00000226908	0	0	0	0	ENSG00000226908	HIST1H2BPS3
ENSG00000226912	0.179034	0	0.309411	0	ENSG00000226912	ISCA2P1
ENSG00000226914	0	0	0	0	ENSG00000226914	PPP1R2P1
ENSG00000226915	0	0	0	0	ENSG00000226915	AC068137.1
ENSG00000226916	3.55765	5.32633	4.7322	6.88796	ENSG00000226916	WDR46
ENSG00000226918	0	0.223793	0.0505638	0.126738	ENSG00000226918	AC010086.1
ENSG00000226923	0.0916753	0.264657	0.272079	0.660025	ENSG00000226923	MCCD1
ENSG00000226926	0	0.0307866	0	0.0997448	ENSG00000226926	PDZPH1P
ENSG00000226928	4.84307	12.8816	7.47459	28.2301	ENSG00000226928	RPS14P4
ENSG00000226929	0	0.0219476	0.0109151	0.0319741	ENSG00000226929	CT47A11
ENSG00000226930	0	0.370827	0.168076	0.213026	ENSG00000226930	GTF2IP2
ENSG00000226931	0	0.0224316	0.118574	0.193776	ENSG00000226931	OR2J1
ENSG00000226932	0	0.0415668	0.00939099	0.0470305	ENSG00000226932	BX005432.1
ENSG00000226933	0	0	0	0	ENSG00000226933	NRBF2P2
ENSG00000226936	0.310039	0.93125	0	0	ENSG00000226936	B3GALT4
ENSG00000226937	2.50462	6.90991	5.67575	9.73256	ENSG00000226937	CEP164P1
ENSG00000226940	0	0	0	0	ENSG00000226940	MCCD1P1
ENSG00000226941	0	0	0	0.0311953	ENSG00000226941	RBMY1J
ENSG00000226942	0.143155	0.358474	0.206615	0.400103	ENSG00000226942	IL9RP3
ENSG00000226943	0.0853226	0	0	0	ENSG00000226943	ALG1L5P
ENSG00000226945	0.115026	0	0.29984	0.372566	ENSG00000226945	AC098935.1
ENSG00000226946	0.0340259	0.163917	0.0592707	0.447446	ENSG00000226946	AC062022.1
ENSG00000226947	0	0	0	0	ENSG00000226947	AL139247.1
ENSG00000226948	0	0.158137	0	0.0888973	ENSG00000226948	RPS4XP2
ENSG00000226949	0	0	0	0	ENSG00000226949	OR6K5P
ENSG00000226952	0.975482	3.21778	0.410807	2.97906	ENSG00000226952	AC093019.1
ENSG00000226955	0	0	0	0	ENSG00000226955	AC104306.2
ENSG00000226958	32562.3	3445.44	2109.61	2262.65	ENSG00000226958	CTD-2328D6.1
ENSG00000226960	0	0.231602	0.31372	0.129767	ENSG00000226960	MTCO1P21
ENSG00000226961	0	0	0.314371	0.501283	ENSG00000226961	AC099344.1
ENSG00000226962	0	0.119678	0.10807	0.272581	ENSG00000226962	RAC1P6
ENSG00000226964	0.403672	0.597575	1.13449	0	ENSG00000226964	RHEBP2
ENSG00000226967	0	0	0.0458039	0.11491	ENSG00000226967	HAUS4P1
ENSG00000226970	0	0	0	0	ENSG00000226970	AL450063.1
ENSG00000226971	0.0221909	0.042682	0.0196878	0.169939	ENSG00000226971	AL606490.2
ENSG00000226972	0.160624	0	0	0	ENSG00000226972	RPL12P19
ENSG00000226973	0	0.078592	0	0.0886444	ENSG00000226973	AL512638.1
ENSG00000226974	0	0	0	0	ENSG00000226974	AL445989.1
ENSG00000226975	0.422665	0.859891	0.73206	1.07878	ENSG00000226975	AC006987.1
ENSG00000226976	0.204632	0.569897	0.163327	0	ENSG00000226976	COX6A1P2
ENSG00000226977	1.06526	0.673199	3.04225	4.06847	ENSG00000226977	HMGN1P24
ENSG00000226979	0.0274983	0.0159269	0.0264951	0.0188624	ENSG00000226979	LTA
ENSG00000226981	0.0675854	0	0	0	ENSG00000226981	ABHD17AP6
ENSG00000226982	0.0225272	0.345153	0.323917	0.194332	ENSG00000226982	CENPCP1

ENSG00000226984	0.963849	0.922094	1.49864	3.13045	ENSG00000226984	AL035410.1
ENSG00000226986	0	0.141577	0	0.247726	ENSG00000226986	AC092017.1
ENSG00000226987	0.140233	0.306776	0.590315	1.25545	ENSG00000226987	AL157938.1
ENSG00000226989	1.51425	1.44678	0.590842	2.28747	ENSG00000226989	AL049758.1
ENSG00000226991	0.28503	0.287722	0.124259	0.17279	ENSG00000226991	AC140479.1
ENSG00000226993	0	0	0	0	ENSG00000226993	POLR2LP1
ENSG00000226998	0	0	0.0891512	0	ENSG00000226998	MTATP6P30
ENSG00000226999	0	0	0	0	ENSG00000226999	AC073325.2
ENSG00000227000	0.0355664	0.0685299	0.0619986	0.389983	ENSG00000227000	HSPD1P14
ENSG00000227001	7.49148	12.4088	15.0953	31.1597	ENSG00000227001	NBPF2P
ENSG00000227002	0	0	0	0	ENSG00000227002	SNRPEP10
ENSG00000227004	0	0.678588	3.00492	0	ENSG00000227004	AC108032.1
ENSG00000227008	0	0.219327	0.199521	0	ENSG00000227008	AL009174.1
ENSG00000227009	0	0	0	0.20905	ENSG00000227009	FUNDC2P4
ENSG00000227011	0	0	0	0	ENSG00000227011	C17orf112
ENSG00000227013	0	0	0	0	ENSG00000227013	OR7E96P
ENSG00000227015	1.68643	3.34873	4.8666	6.18342	ENSG00000227015	AC023141.4
ENSG00000227018	0	0	0	0	ENSG00000227018	IL6STP1
ENSG00000227019	0.14886	0.281974	0.325798	0.658973	ENSG00000227019	OR7E101P
ENSG00000227023	0	0	0	0	ENSG00000227023	OR51A3P
ENSG00000227025	0	0	0	0	ENSG00000227025	CR388205.1
ENSG00000227027	0	0	0.117234	0	ENSG00000227027	HLA-T
ENSG00000227030	0.0488289	0.0266211	0	0	ENSG00000227030	CR759769.1
ENSG00000227032	0	0	0	0	ENSG00000227032	RPS2P36
ENSG00000227034	0	0	0	0	ENSG00000227034	AL445433.1
ENSG00000227035	0.100956	0	0	0.109074	ENSG00000227035	MTATP6P18
ENSG00000227038	2.14392	5.05644	4.39013	7.51087	ENSG00000227038	GTF2IP7
ENSG00000227040	0	0	0	0	ENSG00000227040	AC022483.1
ENSG00000227044	0.0330719	0	0.0385538	0.0189047	ENSG00000227044	OR2H2
ENSG00000227046	0.794617	0.498114	1.84831	3.32793	ENSG00000227046	DAXX
ENSG00000227048	0.283974	0.215323	0	1.3269	ENSG00000227048	AC096677.3
ENSG00000227051	2.70791	2.49726	3.125	9.76994	ENSG00000227051	C14orf132
ENSG00000227054	0	0	0	0.751037	ENSG00000227054	FDX1P2
ENSG00000227055	2.10816	3.80311	1.68882	6.51125	ENSG00000227055	AC009961.2
ENSG00000227056	0.416284	0.480898	0.505855	0.72173	ENSG00000227056	RPL6P2
ENSG00000227057	2.40172	2.95127	3.77654	2.43303	ENSG00000227057	WDR46
ENSG00000227058	0	0	0	0	ENSG00000227058	BX510359.2
ENSG00000227059	0.0327774	0.106714	0.0848495	0.138762	ENSG00000227059	ANHX
ENSG00000227062	0	0	0	0	ENSG00000227062	AL596276.1
ENSG00000227063	417.834	354.944	282.884	253.099	ENSG00000227063	RPL41P1
ENSG00000227064	0	0	0	0.370578	ENSG00000227064	Z82205.1
ENSG00000227067	0	0	0	0	ENSG00000227067	DPPA3P1
ENSG00000227069	8.78E-09	0	0	0	ENSG00000227069	CNN2P2
ENSG00000227072	0.154669	0.296452	0.535425	0.665383	ENSG00000227072	AL353706.1
ENSG00000227073	0.371248	0.346586	0.772848	1.73145	ENSG00000227073	SDHDP2
ENSG00000227074	2.89E-08	0.22701	0.346537	0	ENSG00000227074	SAPCD1
ENSG00000227077	0.653752	0.84541	0.370528	1.91588	ENSG00000227077	AC107983.1
ENSG00000227080	1.31184	0.482468	0.271426	1.4442	ENSG00000227080	AC012441.1
ENSG00000227081	0.672828	0.666284	0.633577	4.41208	ENSG00000227081	AC005912.1
ENSG00000227087	0.16443	0	0.198578	0.6633	ENSG00000227087	RBMX2P5
ENSG00000227096	8.53789	11.5496	17.9067	12.464	ENSG00000227096	HMGB3P8
ENSG00000227097	211.318	272.491	175.342	195.502	ENSG00000227097	RPS28P7
ENSG00000227099	0	0	0.0360102	0	ENSG00000227099	HLA-DRB7
ENSG00000227100	0	0.0149857	0	0	ENSG00000227100	AL773535.1

ENSG00000227102	0	0	0	0	ENSG00000227102	OR2AS1P
ENSG00000227104	0	0	0	0	ENSG00000227104	PIGQP1
ENSG00000227105	0	0	0.0158674	0.0399728	ENSG00000227105	PARP1P1
ENSG00000227108	0	0	0	0	ENSG00000227108	IGHD1-14
ENSG00000227109	0.639674	2.99083	2.13807	3.21317	ENSG00000227109	CRIP1P3
ENSG00000227113	4.40924	2.69039	7.05991	5.53582	ENSG00000227113	AC073210.1
ENSG00000227114	0	0	3.46659	5.15837	ENSG00000227114	AC018696.3
ENSG00000227118	0	0	0	0	ENSG00000227118	BTF3P13
ENSG00000227120	0.577124	0.362746	0.670143	0.606866	ENSG00000227120	AC009238.1
ENSG00000227122	0.0315493	0.0750009	0.205173	0.116243	ENSG00000227122	PRRT1
ENSG00000227123	1.51079	1.59322	2.53431	2.29307	ENSG00000227123	RPL12P44
ENSG00000227124	10.0046	17.6373	19.2964	18.844	ENSG00000227124	ZNF717
ENSG00000227129	4.87821	3.55462	1.94829	1.17492	ENSG00000227129	NEU1
ENSG00000227133	0	0	0.162398	0	ENSG00000227133	AC011742.1
ENSG00000227134	0	0	0	0	ENSG00000227134	AC093084.1
ENSG00000227137	0	0	0	0.0254603	ENSG00000227137	OR5V1
ENSG00000227138	0	0	0	0	ENSG00000227138	AL161788.1
ENSG00000227140	0	0	0	0	ENSG00000227140	USP17L5
ENSG00000227141	0.114091	0.0867325	0.0982284	0.0498457	ENSG00000227141	AL160286.1
ENSG00000227144	0.700172	0.386945	0.0915342	1.50586	ENSG00000227144	VWA7
ENSG00000227147	0.208044	0.749081	0.160154	0.231175	ENSG00000227147	TRIM15
ENSG00000227149	0	0	0	0	ENSG00000227149	MTCO1P44
ENSG00000227151	0	0	0	0	ENSG00000227151	PRR20D
ENSG00000227152	0	0	0	0	ENSG00000227152	OR2T7
ENSG00000227154	0.0821576	0.236519	0.129664	0	ENSG00000227154	AL022721.1
ENSG00000227158	0	0	0	0	ENSG00000227158	AC073621.2
ENSG00000227159	0.199688	0.117366	0.271598	0	ENSG00000227159	DDX11L16
ENSG00000227160	0	0	0	0.327786	ENSG00000227160	THEM7P
ENSG00000227163	5.91164	9.42443	8.45205	14.9951	ENSG00000227163	AL139220.1
ENSG00000227164	0	0	0.597101	0	ENSG00000227164	AL354993.1
ENSG00000227166	0	0	0	0	ENSG00000227166	STSP1
ENSG00000227168	0.898463	0	0	0.335064	ENSG00000227168	RPL35AP4
ENSG00000227171	0	0	0	0	ENSG00000227171	RNF39
ENSG00000227173	0	0	0	0.201057	ENSG00000227173	MYL6P3
ENSG00000227176	0.260775	1.01587	0.718045	1.75723	ENSG00000227176	AC092641.1
ENSG00000227177	0	0	0	0.68074	ENSG00000227177	AIMP1P2
ENSG00000227178	0.009462	0.0181999	0.0164453	0.0102936	ENSG00000227178	BX908738.2
ENSG00000227179	0.346695	0	0.0107043	0	ENSG00000227179	PGCP1
ENSG00000227180	0	0	0.051193	0	ENSG00000227180	AC013467.1
ENSG00000227182	0	0	0	0	ENSG00000227182	VN1R28P
ENSG00000227183	0	3.96765	2.41517	1.81056	ENSG00000227183	HDGFP1
ENSG00000227184	9.4197	23.1001	35.0777	5.07976	ENSG00000227184	EPPK1
ENSG00000227187	0	0	0	0.427291	ENSG00000227187	AC007435.1
ENSG00000227191	0	0	0.026671	0.0300785	ENSG00000227191	TRGC2
ENSG00000227194	0	0	0	0	ENSG00000227194	GLUD1P7
ENSG00000227196	0	0	0	0	ENSG00000227196	IGHD4-23
ENSG00000227201	0.208905	0.252615	0.535043	0.22662	ENSG00000227201	CNN2P1
ENSG00000227203	0	0.223354	0	0.486156	ENSG00000227203	SUB1P1
ENSG00000227204	0	0	0	0	ENSG00000227204	RBMY2JP
ENSG00000227205	0.190464	0	0	0	ENSG00000227205	PFN1P9
ENSG00000227207	0.259036	0.745955	0.460534	0.804649	ENSG00000227207	RPL31P12
ENSG00000227208	0.687328	1.17727	1.10225	2.51524	ENSG00000227208	LINC00552
ENSG00000227209	0	0	0	0	ENSG00000227209	WARS2P1
ENSG00000227211	0.269468	0.513371	0.46377	0.848125	ENSG00000227211	AL035551.1

ENSG00000227212	2.22184	5.91584	1.51992	5.10103	ENSG00000227212	PFN1P6
ENSG00000227216	1.17162	3.52805	4.18374	5.02953	ENSG00000227216	PFN1P5
ENSG00000227222	0.365246	0.434357	0.263771	0.530556	ENSG00000227222	DHX16
ENSG00000227224	0	0	0	0.235256	ENSG00000227224	AC092035.1
ENSG00000227225	0	0	0	0	ENSG00000227225	MTND1P14
ENSG00000227228	0	0	0	3.56E-07	ENSG00000227228	UBDP1
ENSG00000227231	4.65E-10	35.1599	5.83678	11.0089	ENSG00000227231	IER3
ENSG00000227232	26.4937	15.0744	15.7755	12.3395	ENSG00000227232	WASH7P
ENSG00000227233	0	0.0344741	0.0424074	0.0260681	ENSG00000227233	CICP17
ENSG00000227234	0	0	0	0	ENSG00000227234	SPANXB1
ENSG00000227236	0.232089	0.638925	1.1339	1.4327	ENSG00000227236	AL583844.1
ENSG00000227238	0	0.163489	0.0591158	0	ENSG00000227238	TTC39DP
ENSG00000227239	0.746781	0.804906	0	0	ENSG00000227239	AL121985.1
ENSG00000227241	0	0	2.12134	0	ENSG00000227241	AC011998.1
ENSG00000227242	0	0.137384	0.409115	0.283127	ENSG00000227242	NBPF13P
ENSG00000227243	0	0	0	0	ENSG00000227243	SLAMF6P1
ENSG00000227246	0	0	0	0.253379	ENSG00000227246	PSORS1C2
ENSG00000227247	0.0461778	0.222323	0	0.0504664	ENSG00000227247	TRIM60P13
ENSG00000227249	0.0327163	0.315236	0.0569938	0.179312	ENSG00000227249	AC000374.1
ENSG00000227251	0	0	0	0	ENSG00000227251	TRIM60P9Y
ENSG00000227254	0	0.0690622	0	0	ENSG00000227254	VDAC1P12
ENSG00000227255	0	0.201147	0	0	ENSG00000227255	CDRT15P2
ENSG00000227257	0.886869	2.629	2.6885	5.25765	ENSG00000227257	AL158827.1
ENSG00000227259	0	0	0	0	ENSG00000227259	HMGN2P22
ENSG00000227261	0	0.154132	0	0.355945	ENSG00000227261	YWHAZP7
ENSG00000227262	0	0	0	0	ENSG00000227262	HCG4B
ENSG00000227264	0	0	0	0	ENSG00000227264	ACTR3BP5
ENSG00000227265	0.00368873	0.00053336	0.00327464	0.022906	ENSG00000227265	AL845331.1
ENSG00000227267	0.125056	1.0911	0.649081	1.34068	ENSG00000227267	AC072039.1
ENSG00000227268	0.704835	0.804659	1.1901	1.70849	ENSG00000227268	KLLN
ENSG00000227270	0	0	0	0	ENSG00000227270	AC009963.1
ENSG00000227271	0	0.663318	0	0	ENSG00000227271	RPL39P25
ENSG00000227275	0	0	0.125378	0.744338	ENSG00000227275	MTND6P10
ENSG00000227277	1.35259	0.556113	1.36117	0.483865	ENSG00000227277	RNF5
ENSG00000227283	0	0	0	0	ENSG00000227283	RPL35AP12
ENSG00000227284	0	0	0.0353543	0	ENSG00000227284	MARK2P10
ENSG00000227286	0.0875574	0	0.0738577	0.0932189	ENSG00000227286	HLA-DPA2
ENSG00000227288	0	0	0	0.117167	ENSG00000227288	AL138799.1
ENSG00000227289	0.251496	0.048423	0.21883	0	ENSG00000227289	HSFY3P
ENSG00000227291	0	0.246959	0.446654	0	ENSG00000227291	AC092170.1
ENSG00000227295	0.199955	0.637033	0.430192	0.660596	ENSG00000227295	ELL2P1
ENSG00000227296	0	0	0	0	ENSG00000227296	HLA-H
ENSG00000227298	0	0	0	0	ENSG00000227298	ARAFP3
ENSG00000227300	3.42942	11.8748	2.87384	1.90731	ENSG00000227300	KRT16P2
ENSG00000227302	0	0	0	0	ENSG00000227302	SSXP9
ENSG00000227304	0.448323	1.25313	1.54528	1.43289	ENSG00000227304	AC067942.1
ENSG00000227309	0.253198	3.13542	1.72256	2.66309	ENSG00000227309	AC140076.1
ENSG00000227311	0.165674	0	0	0	ENSG00000227311	AL031985.2
ENSG00000227312	0.269468	0	0	0.282708	ENSG00000227312	AL445686.1
ENSG00000227314	1.42309	3.45529	2.24397	3.08904	ENSG00000227314	MSH5
ENSG00000227315	0	0.683222	0	2.26075	ENSG00000227315	NEU1
ENSG00000227317	1.24175	1.01415	1.3181	0.700784	ENSG00000227317	DDAH2
ENSG00000227318	0.960169	3.77028	0.189589	0.615688	ENSG00000227318	RP11-282E4.1
ENSG00000227319	0	0	0	0	ENSG00000227319	RBM22P6

ENSG00000227321	0.95047	0.696298	0.723248	1.06431	ENSG00000227321	MTND4P15
ENSG00000227322	1.92051	6.7577	4.59335	5.4819	ENSG00000227322	RXRB
ENSG00000227325	0	0	0	0	ENSG00000227325	AC021106.1
ENSG00000227326	0.0488289	0	0	0	ENSG00000227326	BX005428.2
ENSG00000227329	1.73178	4.28707	2.6825	5.81931	ENSG00000227329	AL139396.1
ENSG00000227331	1.13416	2.9413	2.58884	3.05044	ENSG00000227331	AC005042.1
ENSG00000227333	0.78392	1.11679	1.7764	2.39349	ENSG00000227333	EHMT2
ENSG00000227334	0	0	0	0	ENSG00000227334	HLA-N
ENSG00000227335	0	0	0	0	ENSG00000227335	IGHJ1P
ENSG00000227337	0	0	0	0	ENSG00000227337	RPL23AP43
ENSG00000227339	0.158912	0.095725	0.510199	0.131026	ENSG00000227339	THRAP3P1
ENSG00000227343	0	0	0.101981	0.12661	ENSG00000227343	RPL15P1
ENSG00000227344	0	0	0	0	ENSG00000227344	HAUS6P1
ENSG00000227345	6.2193	8.24655	8.75348	8.18597	ENSG00000227345	PARG
ENSG00000227347	0	0.0414034	0.0372658	0	ENSG00000227347	HNRNPKP2
ENSG00000227348	0.324508	0.704359	0.213694	0.851031	ENSG00000227348	MTND5P25
ENSG00000227349	0.332509	0.82313	0.672943	0.341832	ENSG00000227349	CEACAMP7
ENSG00000227350	0	0	0.291845	0.359572	ENSG00000227350	AL389915.1
ENSG00000227351	0	0	0.13113	0	ENSG00000227351	NANOGP6
ENSG00000227353	0.239853	0	0.410701	0.127456	ENSG00000227353	RAB28P3
ENSG00000227357	0	0	0	0	ENSG00000227357	HLA-DRB4
ENSG00000227358	0.303357	0.270007	0	0.655429	ENSG00000227358	AL354861.1
ENSG00000227361	0	0	0	0	ENSG00000227361	RPS24P7
ENSG00000227366	15.3181	8.48971	0.293017	0	ENSG00000227366	HLA-U
ENSG00000227367	0	0	0	0	ENSG00000227367	SLC9B1P4
ENSG00000227368	0	0.128254	0.301761	0	ENSG00000227368	CDK8P2
ENSG00000227370	0.703141	1.66834	0.75323	0	ENSG00000227370	AC254562.1
ENSG00000227371	0	0	0	0	ENSG00000227371	AC074085.1
ENSG00000227376	0.134787	1.21799	0.581137	1.85712	ENSG00000227376	FTH1P16
ENSG00000227379	0.313348	0.150996	0.54178	0.508668	ENSG00000227379	PPIAP2
ENSG00000227382	0.399751	0.713318	0.743502	0.746407	ENSG00000227382	EIF4A2P2
ENSG00000227383	3.91018	4.56698	6.19198	6.59594	ENSG00000227383	AL353662.1
ENSG00000227384	0.0394657	0.0375419	0	0	ENSG00000227384	HLA-DRB9
ENSG00000227389	0.233474	0.0627516	0.0983601	0.475397	ENSG00000227389	DDX39BP2
ENSG00000227391	0.0172629	0.0339526	0	0	ENSG00000227391	SALL1P1
ENSG00000227393	0.252245	1.30996	1.12706	1.64386	ENSG00000227393	AL031575.1
ENSG00000227394	0.122649	0	0.326782	0.131859	ENSG00000227394	AC007386.1
ENSG00000227395	0	0	0	0.0701433	ENSG00000227395	EIF2AP4
ENSG00000227397	0	0	0	0	ENSG00000227397	AC079355.2
ENSG00000227399	0	0	0	0	ENSG00000227399	AL391219.1
ENSG00000227401	0	0	0	0	ENSG00000227401	RPL37P1
ENSG00000227402	8.10034	7.04224	6.12923	6.51393	ENSG00000227402	SLC39A7
ENSG00000227404	0	0	0	0	ENSG00000227404	KRT8P20
ENSG00000227405	0.0642566	0.230628	0	0.272811	ENSG00000227405	ZDHHC20P2
ENSG00000227406	0.063861	0.123071	0.111734	0.175036	ENSG00000227406	RNF6P1
ENSG00000227408	0	0	0.0597582	0	ENSG00000227408	AMYP1
ENSG00000227411	0.105608	0.0700163	0	0.181156	ENSG00000227411	BAATP1
ENSG00000227412	0.284878	0.230717	0.301191	0.52774	ENSG00000227412	STK33P1
ENSG00000227413	1.80069	3.97013	4.65596	8.47061	ENSG00000227413	AL022238.1
ENSG00000227416	0	0	0	0	ENSG00000227416	AL929472.1
ENSG00000227417	2.36328	5.96071	3.28114	5.66577	ENSG00000227417	AC114402.2
ENSG00000227420	3.6819	4.08555	4.50723	3.12515	ENSG00000227420	MRPS18B
ENSG00000227423	0.069606	0.133875	0	0	ENSG00000227423	OR10U1P
ENSG00000227425	0	0	0	0	ENSG00000227425	MRPS21P2

ENSG00000227426	0	0.0685889	0	0	ENSG00000227426	VN1R33P
ENSG00000227427	0	0.184088	0	0	ENSG00000227427	Z93019.1
ENSG00000227430	0	0	0	0	ENSG00000227430	AC019185.1
ENSG00000227433	0.492402	2.16192	1.48527	1.8689	ENSG00000227433	AC090018.1
ENSG00000227434	0	0	0	0	ENSG00000227434	RNF19BPX
ENSG00000227435	0	0	0	0	ENSG00000227435	PPP1R2P1
ENSG00000227436	0.251826	0.129383	0.893897	0.68892	ENSG00000227436	FCF1P1
ENSG00000227437	0	0	0	0	ENSG00000227437	RPS8P4
ENSG00000227440	0.553383	1.24876	0	0.40048	ENSG00000227440	ATP5G1P4
ENSG00000227442	0	0	0	0	ENSG00000227442	HLA-DRB2
ENSG00000227443	0	0	0.203838	0	ENSG00000227443	AL137022.1
ENSG00000227444	0	0	0	0	ENSG00000227444	AC007322.1
ENSG00000227445	0	0	0	0.253569	ENSG00000227445	OR10R1P
ENSG00000227446	0	0	0	0	ENSG00000227446	OR12D2
ENSG00000227447	0	0.176004	0	0	ENSG00000227447	XGY1
ENSG00000227449	2.88268	5.29422	4.3521	2.88683	ENSG00000227449	FGF7P6
ENSG00000227450	0.319984	0.28474	0.227685	0.152575	ENSG00000227450	CTB-58E17.5
ENSG00000227453	0	0	0	0	ENSG00000227453	HNRNPA1P63
ENSG00000227454	1.05611	2.29038	2.04543	4.97461	ENSG00000227454	MTND4P30
ENSG00000227458	0.00462984	0.00875722	0.0165025	0	ENSG00000227458	TRIM40
ENSG00000227460	2.66035	7.86189	7.91147	7.27039	ENSG00000227460	SYNGAP1
ENSG00000227462	0	0	0	0	ENSG00000227462	PSME2P6
ENSG00000227465	0	0	0	0	ENSG00000227465	GPN3P1
ENSG00000227469	0	0	0	0	ENSG00000227469	RBM22P8
ENSG00000227470	4.31464	4.0165	3.53589	0	ENSG00000227470	AC073415.1
ENSG00000227471	10.3006	24.0834	24.3685	36.0589	ENSG00000227471	AKR1B15
ENSG00000227472	0	0	0	0	ENSG00000227472	TRIM10
ENSG00000227473	1.94375	0.667588	4.22246	1.05653	ENSG00000227473	TSSK5P
ENSG00000227474	0.590166	1.45663	0.65575	1.13648	ENSG00000227474	RPL6P24
ENSG00000227488	0	0	0	0	ENSG00000227488	GAGE12D
ENSG00000227490	3.13632	7.18171	10.6045	7.74983	ENSG00000227490	RP11-157L3.6
ENSG00000227491	0	0	0.0470392	0	ENSG00000227491	CCNJP1
ENSG00000227493	0	0	0	0.0363477	ENSG00000227493	AC239367.1
ENSG00000227494	0.385223	0	0.444944	0.413635	ENSG00000227494	USP9YP14
ENSG00000227497	0	0	0	0	ENSG00000227497	PABPC1P6
ENSG00000227499	0	0	0	0	ENSG00000227499	AC092647.2
ENSG00000227500	34.4945	41.3531	34.6115	30.2179	ENSG00000227500	SCAMP4
ENSG00000227505	0	0	0	0	ENSG00000227505	AC016925.1
ENSG00000227506	0.0874301	0.12896	0.145468	0.26788	ENSG00000227506	MUC21
ENSG00000227507	0	0.0813401	0.59808	0.342007	ENSG00000227507	LTB
ENSG00000227511	0	0	0	0.0802085	ENSG00000227511	AC005297.1
ENSG00000227513	0	0.071214	0	0	ENSG00000227513	AC114755.1
ENSG00000227514	0	0	0	0	ENSG00000227514	AC107890.1
ENSG00000227515	0.783273	0.186462	0	0.207352	ENSG00000227515	C1DP4
ENSG00000227521	0	0	0	0	ENSG00000227521	AL390840.1
ENSG00000227523	2.30023	10.6622	5.24543	21.6119	ENSG00000227523	RPS20P15
ENSG00000227525	0.224615	0	0	0	ENSG00000227525	RPL7P6
ENSG00000227526	0.0394657	0.0375419	0	0	ENSG00000227526	HLA-DRB9
ENSG00000227529	0	0	0	0	ENSG00000227529	CR547123.1
ENSG00000227532	2.51465	0	2.08387	4.31772	ENSG00000227532	AC002542.1
ENSG00000227534	0	0.062819	0	0	ENSG00000227534	Z83841.1
ENSG00000227536	0.335714	0.289226	0.87218	1.01642	ENSG00000227536	SOCS5P4
ENSG00000227537	0	0	0	0.301245	ENSG00000227537	AL139281.1
ENSG00000227538	0	0.0513023	0	0	ENSG00000227538	HNRNPFP1

ENSG00000227541	0.201334	0.0977487	0.13755	0.109889	ENSG00000227541	SFR1P1
ENSG00000227545	0	0	0	0	ENSG00000227545	AC006455.2
ENSG00000227547	0	0	0	0	ENSG00000227547	OR4A2P
ENSG00000227550	0	0	0	0.154764	ENSG00000227550	TRBV7-5
ENSG00000227551	0.0247832	0	0	0	ENSG00000227551	USP17L12
ENSG00000227556	0	0	0	0	ENSG00000227556	AC096531.1
ENSG00000227557	0	0	0	0	ENSG00000227557	MTND3P9
ENSG00000227558	6.15522	13.8515	14.1498	28.4079	ENSG00000227558	PGM5P2
ENSG00000227560	0	0.850657	3.6392	4.70512	ENSG00000227560	RPS15AP30
ENSG00000227563	0	0	0.159897	0	ENSG00000227563	RNF11P2
ENSG00000227565	1.27859	1.68772	2.62759	1.01061	ENSG00000227565	NFKBIL1
ENSG00000227567	0.164783	0.252772	0.0998859	0.157885	ENSG00000227567	APOM
ENSG00000227568	0	0	0	0	ENSG00000227568	SNX18P26
ENSG00000227569	0	0.461006	0	0	ENSG00000227569	RP11-266E16.1
ENSG00000227573	0.233136	0	0	0	ENSG00000227573	AC004986.1
ENSG00000227576	0	0	0	0	ENSG00000227576	GPR53P
ENSG00000227577	0	0	0	0	ENSG00000227577	COL11A2P1
ENSG00000227578	0	0	0.0923649	0	ENSG00000227578	RPS3AP53
ENSG00000227581	0.346598	0.119964	0.514357	0.856468	ENSG00000227581	AL121877.1
ENSG00000227582	1.72919	3.89708	3.4603	6.84806	ENSG00000227582	ADGRF5P1
ENSG00000227583	0	0	0	0.767292	ENSG00000227583	RPS3AP37
ENSG00000227584	0	0.123313	0	0.046681	ENSG00000227584	MTND4P5
ENSG00000227585	0.148541	0	0.193609	0.161321	ENSG00000227585	AL360013.1
ENSG00000227586	0.858405	1.09586	2.84606	0.577632	ENSG00000227586	RPS26P39
ENSG00000227587	0.00314444	0.0186652	0.622337	0.174972	ENSG00000227587	ATP6V1G2
ENSG00000227590	0	0	0	0	ENSG00000227590	ATP5G1P5
ENSG00000227592	0.0922108	0.531618	0.720348	0.19949	ENSG00000227592	PIGFP3
ENSG00000227593	0.393882	0.694506	0.114113	1.0035	ENSG00000227593	PHBP16
ENSG00000227597	0	0.0514077	0.141126	0.233095	ENSG00000227597	WASF1P1
ENSG00000227600	4.08201	4.58467	4.35562	4.1271	ENSG00000227600	PPT2
ENSG00000227604	0	0	0	0.286638	ENSG00000227604	TOMM22P3
ENSG00000227607	0.477611	1.3484	0	0	ENSG00000227607	SUMO2P2
ENSG00000227609	0	0	0	0	ENSG00000227609	TMEM183AP1
ENSG00000227613	0.0645036	0.198399	0.292682	0.0717492	ENSG00000227613	QRSL1P2
ENSG00000227615	0	0	0.211897	0.27592	ENSG00000227615	AP001324.1
ENSG00000227616	0	0.282417	0	0.621555	ENSG00000227616	AC063976.3
ENSG00000227620	0	0	0.170985	0	ENSG00000227620	ALG1L8P
ENSG00000227621	0	0	0	0	ENSG00000227621	PHBP11
ENSG00000227623	0	0	0	0	ENSG00000227623	AC010881.1
ENSG00000227624	0.409731	0	0	0.496201	ENSG00000227624	SNRPEP3
ENSG00000227625	0	0	0	0	ENSG00000227625	AL359510.1
ENSG00000227626	0	0	0	0	ENSG00000227626	AL662865.1
ENSG00000227628	0	0	0	0.891735	ENSG00000227628	RP11-472D17.3
ENSG00000227629	1.64692	1.18244	0.297086	0.319174	ENSG00000227629	SLC25A15P1
ENSG00000227632	0.272378	0.225544	0.446414	0.129967	ENSG00000227632	AC018804.1
ENSG00000227633	0	0	0	0	ENSG00000227633	RBMY2YP
ENSG00000227635	0.406052	1.16451	1.60546	1.91833	ENSG00000227635	USP9YP21
ENSG00000227638	0.949675	2.31043	1.50235	4.40235	ENSG00000227638	HNRNPA1P14
ENSG00000227639	0	0	0	0	ENSG00000227639	OR2W1
ENSG00000227642	0	0	0	0	ENSG00000227642	AGPAT1
ENSG00000227644	0	0	0	0	ENSG00000227644	HIGD1AP11
ENSG00000227645	0	0	0	0	ENSG00000227645	RPL7P54
ENSG00000227649	0	1.17528	0.637545	1.46462	ENSG00000227649	MTND6P32
ENSG00000227650	0	0	0	0	ENSG00000227650	UQCRHP1

ENSG00000227652	0.051091	0	0.0451445	0.0287014	ENSG00000227652	RANP1
ENSG00000227653	0	0.277966	0.258269	0.285849	ENSG00000227653	ISCA1P6
ENSG00000227655	0.087419	0.412726	0	0.298453	ENSG00000227655	PTMAP1
ENSG00000227656	0	0.153882	0.659379	0.334133	ENSG00000227656	RPL3P2
ENSG00000227657	0	0	0	0	ENSG00000227657	SERPINA7P1
ENSG00000227661	0	0	0	0	ENSG00000227661	MTCO3P18
ENSG00000227663	0	0	0	0	ENSG00000227663	RPL7P2
ENSG00000227666	1.99655	3.1956	1.92838	9.13427	ENSG00000227666	CYCSP24
ENSG00000227667	0	0	0	0	ENSG00000227667	AL392003.1
ENSG00000227668	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000227668	MAS1LP1
ENSG00000227669	0.185579	0	0.267742	0.271418	ENSG00000227669	HLA-H
ENSG00000227671	51.0518	79.3645	47.1138	55.0166	ENSG00000227671	AL390728.4
ENSG00000227672	0	0	0	0	ENSG00000227672	RPL3P2
ENSG00000227675	8.0884	20.0775	18.8039	41.2051	ENSG00000227675	GS1-256O22.1
ENSG00000227679	0	0	0	0	ENSG00000227679	AL133173.1
ENSG00000227682	0	0	0	0	ENSG00000227682	ATP5A1P2
ENSG00000227684	0.30569	0.146505	0.133416	0.490074	ENSG00000227684	CROCCP4
ENSG00000227686	0.347115	2.28193	2.33196	6.03321	ENSG00000227686	VARS
ENSG00000227688	0.20634	0	0.0895038	0.334096	ENSG00000227688	HNRNPA3P2
ENSG00000227689	0	0	0	0	ENSG00000227689	SRP68P2
ENSG00000227691	0	0	0	0	ENSG00000227691	CYCSP41
ENSG00000227692	0.58666	1.6047	2.05204	1.79194	ENSG00000227692	MED28P3
ENSG00000227693	0.125015	0.599826	0.866629	0.134334	ENSG00000227693	GSTM3P1
ENSG00000227694	0.197452	0.513281	0	0.753254	ENSG00000227694	RPL23AP74
ENSG00000227700	0.0724045	0.431293	0.125378	0.160749	ENSG00000227700	AC239809.2
ENSG00000227703	0.051091	0	0.0451445	0.0287014	ENSG00000227703	RANP1
ENSG00000227707	0	0	0	0	ENSG00000227707	SDAD1P3
ENSG00000227709	0	0	0	0	ENSG00000227709	AC091607.1
ENSG00000227710	0	0.518268	1.44158	0	ENSG00000227710	AC245517.2
ENSG00000227714	0.146415	0.57907	0.126783	0.313368	ENSG00000227714	MTND6P18
ENSG00000227715	15.5461	21.7163	48.6447	51.3499	ENSG00000227715	HLA-A
ENSG00000227717	0	0	0	0	ENSG00000227717	AC138749.1
ENSG00000227720	3.18119	0.998512	1.14687	1.58835	ENSG00000227720	PPP1R11
ENSG00000227721	0	0	0	0	ENSG00000227721	RPSAP64
ENSG00000227722	0	0	0.115495	0.143017	ENSG00000227722	AL022100.1
ENSG00000227725	0.627181	0.209862	0.27379	0.599436	ENSG00000227725	GCOM2
ENSG00000227728	0.0428217	0.0412398	0	0.0936674	ENSG00000227728	AL356583.1
ENSG00000227729	0.0996317	0.183637	0.173387	0.138531	ENSG00000227729	RD3L
ENSG00000227730	0	0.721013	0.38138	0.314228	ENSG00000227730	MTND6P5
ENSG00000227735	0	0	0	0	ENSG00000227735	CYCSP5
ENSG00000227736	0	0.0838603	0	0.191141	ENSG00000227736	MTCO3P16
ENSG00000227737	0.0684121	0	0	0	ENSG00000227737	OR8B1P
ENSG00000227738	0	0	0	0	ENSG00000227738	AC092646.1
ENSG00000227739	1.69152	0.0743718	0.362998	1.84E-06	ENSG00000227739	TUBB
ENSG00000227742	0.0659811	0.0634572	0.11468	0	ENSG00000227742	CALR4P
ENSG00000227745	0.74509	1.39624	0	0.134998	ENSG00000227745	AC098826.2
ENSG00000227746	1.16734	2.15857	1.44748	0.902349	ENSG00000227746	C4A
ENSG00000227747	0	0.0791262	0	0	ENSG00000227747	AC096631.2
ENSG00000227750	0.181202	0.192808	0.148701	0.226604	ENSG00000227750	HTATSF1P1
ENSG00000227753	0	0.317189	0	0	ENSG00000227753	AC023194.1
ENSG00000227754	0	0	0	0	ENSG00000227754	SUCLA2P1
ENSG00000227755	0	0	0	0	ENSG00000227755	AP000344.1
ENSG00000227758	2.13296	1.99934	1.44905	2.25545	ENSG00000227758	AL645939.3

ENSG00000227759	0	0.810858	0.244628	0.754513	ENSG00000227759	VTI1BP4
ENSG00000227760	0	1.47882	1.3313	0.402831	ENSG00000227760	AC135001.1
ENSG00000227761	16.7354	8.49559	15.0188	8.57231	ENSG00000227761	BAG6
ENSG00000227762	0	0.118837	0.0887575	0	ENSG00000227762	GUSBP8
ENSG00000227765	0.147256	0.141552	0.25562	0	ENSG00000227765	MYL12BP2
ENSG00000227766	0.192534	0	0	0	ENSG00000227766	AL671277.1
ENSG00000227770	0.0878833	0.0845025	0.331928	0.095158	ENSG00000227770	RPL7P12
ENSG00000227772	1.70442	7.06419	2.32283	2.87829	ENSG00000227772	MICB
ENSG00000227775	11.019	15.2774	20.4812	18.647	ENSG00000227775	AL031282.1
ENSG00000227776	0	0	0	0	ENSG00000227776	AKR1D1P1
ENSG00000227777	0.113045	0	0	0	ENSG00000227777	AL031736.1
ENSG00000227778	0	0	0.157116	0.074192	ENSG00000227778	Xxyac-YX155B6.2
ENSG00000227779	0	0	0	0.397773	ENSG00000227779	AC234779.1
ENSG00000227780	0.0773985	0.121619	0.973648	1.17022	ENSG00000227780	ZBTB22
ENSG00000227781	2.94715	7.21358	6.10186	7.6172	ENSG00000227781	GLUD1P2
ENSG00000227782	4.81609	19.4933	10.6924	10.1722	ENSG00000227782	AC002553.1
ENSG00000227784	0	0	0.205926	0.258941	ENSG00000227784	ZNF965P
ENSG00000227785	0	0	0	0	ENSG00000227785	AC092013.1
ENSG00000227788	0	0.163075	0.147323	0.186435	ENSG00000227788	MTCO3P43
ENSG00000227789	0	0.222468	0.185278	0.755254	ENSG00000227789	MTCYBP7
ENSG00000227790	0	0.120543	0	0.299338	ENSG00000227790	AC015922.1
ENSG00000227791	0.17355	0.66411	0	0.554492	ENSG00000227791	AC007365.2
ENSG00000227792	0	0	0.0565918	0	ENSG00000227792	RP13-210D15.6
ENSG00000227794	20.8116	50.2959	44.4017	39.4801	ENSG00000227794	RPS18
ENSG00000227795	0	0	1.76961	2.12559	ENSG00000227795	MTND4LP9
ENSG00000227799	0.857687	2.58139	3.16253	2.0638	ENSG00000227799	AC012358.2
ENSG00000227800	0	0	0	0	ENSG00000227800	IGHD4-17
ENSG00000227801	0	0.02877	0.158621	0.203896	ENSG00000227801	COL11A2
ENSG00000227802	0.143884	0.612434	1.27195	0.256171	ENSG00000227802	DNAJB3
ENSG00000227804	5.55483	9.33778	7.87132	5.90532	ENSG00000227804	PPP1R10
ENSG00000227805	0	0.503006	0.728962	0.805818	ENSG00000227805	RPL21P90
ENSG00000227806	0	0	0	0	ENSG00000227806	OR5W1P
ENSG00000227813	0.347792	1.65004	0.270864	0.334347	ENSG00000227813	Z82190.1
ENSG00000227814	0	0	0	0	ENSG00000227814	MRPS17P9
ENSG00000227815	0.163276	0.470813	1.98498	0.531044	ENSG00000227815	AL359265.1
ENSG00000227816	3.85017	4.43194	4.80779	2.8079	ENSG00000227816	TAP1
ENSG00000227817	0	0	0.0251424	0	ENSG00000227817	ARHGAP42P1
ENSG00000227821	8.50285	6.34106	3.98568	5.7655	ENSG00000227821	AL392086.1
ENSG00000227825	0.316232	0.415472	0.665072	0.617134	ENSG00000227825	SLC9A7P1
ENSG00000227826	0	0	0	0.0559395	ENSG00000227826	HLA-DRB4
ENSG00000227827	0.164071	2.99508	0.551071	0.407024	ENSG00000227827	AC138969.2
ENSG00000227830	0.20192	0.872914	0.265778	0.54527	ENSG00000227830	TRIM60P3Y
ENSG00000227832	0	0	0	0.181415	ENSG00000227832	ST13P21
ENSG00000227834	0	0.340147	0.061468	0.153756	ENSG00000227834	AP003385.1
ENSG00000227835	1.21182	1.19736	2.87974	2.4351	ENSG00000227835	CARM1P1
ENSG00000227836	0	1.28711	1.08798	0.530984	ENSG00000227836	AC008850.1
ENSG00000227837	0	0	0.0702319	0.087694	ENSG00000227837	TRIM60P11Y
ENSG00000227839	3.34291	10.7556	10.556	17.7607	ENSG00000227839	AL645730.2
ENSG00000227840	0	0	0	0	ENSG00000227840	KRTAP8-3P
ENSG00000227841	0	0.123414	0.111554	0.186876	ENSG00000227841	MTND5P31
ENSG00000227842	0.295639	0.280889	0	0.618324	ENSG00000227842	AC093166.1
ENSG00000227843	0	0	0	0.00448499	ENSG00000227843	DDX6P1
ENSG00000227845	0	0.52463	0.947478	0.641364	ENSG00000227845	AL627223.1
ENSG00000227846	0	0	0	0	ENSG00000227846	UGT1A11P

ENSG00000227847	0.478953	0	0.41308	1.51502	ENSG00000227847	AC010099.2
ENSG00000227850	0	0	0	0	ENSG00000227850	SEPT2P1
ENSG00000227852	0	0	0.982073	0	ENSG00000227852	RPS29P17
ENSG00000227854	0	0	0	0	ENSG00000227854	AL590135.1
ENSG00000227855	1.08635	2.396	1.66472	2.25782	ENSG00000227855	DPY19L2P3
ENSG00000227858	0.161933	0.00101078	0	0	ENSG00000227858	ZFP57
ENSG00000227859	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000227859	MAS1LP1
ENSG00000227860	0.0957784	0.0650071	0.0808782	0.271441	ENSG00000227860	MTND5P18
ENSG00000227861	2.89E-08	0.22701	0.346537	0	ENSG00000227861	SAPCD1
ENSG00000227862	0	0.0615891	0	0.139374	ENSG00000227862	HNRNPA1P31
ENSG00000227864	0	0	0.580991	0	ENSG00000227864	ARL5AP1
ENSG00000227867	0	0	0	0	ENSG00000227867	ELOCP11
ENSG00000227868	0.88642	0.861436	0.906736	1.83324	ENSG00000227868	TEX46
ENSG00000227871	0	0	0	0	ENSG00000227871	USP9YP12
ENSG00000227873	0	0	0	0	ENSG00000227873	Z93242.2
ENSG00000227874	0	0	0	0	ENSG00000227874	GRAMD4P1
ENSG00000227875	0	0	0	0.971624	ENSG00000227875	RPL23AP89
ENSG00000227878	0.315793	0.303286	0.182601	0	ENSG00000227878	AC114760.1
ENSG00000227879	0	0.19713	0.390166	0.23814	ENSG00000227879	PSPC1P1
ENSG00000227881	0	0	0	0.0264192	ENSG00000227881	ASS1P5
ENSG00000227882	0	0	0.0210359	0.0267484	ENSG00000227882	THAP12P6
ENSG00000227883	0	0	0	0	ENSG00000227883	ATP6V0E1P4
ENSG00000227887	0	0	0	0	ENSG00000227887	RPS26P13
ENSG00000227890	0.101599	0	0.263217	0	ENSG00000227890	PSMA2P3
ENSG00000227892	0.890532	0.39528	1.01197	0.521395	ENSG00000227892	OR5P4P
ENSG00000227905	0	0	0	0	ENSG00000227905	MED6P1
ENSG00000227910	0.864787	4.86614	6.59045	1.03777	ENSG00000227910	AC092634.4
ENSG00000227913	0.17431	0.0419661	0.189791	0.715498	ENSG00000227913	KRT8P44
ENSG00000227915	0	0	0	0	ENSG00000227915	ELOCP16
ENSG00000227919	0	0	0	14.7897	ENSG00000227919	AL353997.1
ENSG00000227921	1.79059	5.89918	4.04725	4.49182	ENSG00000227921	AL353791.1
ENSG00000227922	0	0	0	0	ENSG00000227922	SPTLC1P5
ENSG00000227923	0	0	0	2.13006	ENSG00000227923	AC006455.3
ENSG00000227924	0	0	0	0	ENSG00000227924	RBPJP6
ENSG00000227934	0.125317	0.602433	0.657409	0.270249	ENSG00000227934	AL732414.1
ENSG00000227936	0	0	0	0	ENSG00000227936	HLA-DPA3
ENSG00000227937	0.920951	0.659569	0.595878	1.11436	ENSG00000227937	MTND2P30
ENSG00000227939	0.0500492	0.0322418	0.0466621	0.142358	ENSG00000227939	RPL3P2
ENSG00000227941	0.714623	0.338527	0	0.741157	ENSG00000227941	UQCRBP2
ENSG00000227942	0.0448134	0.165363	0.284764	0.104581	ENSG00000227942	FRMD8P1
ENSG00000227948	1.72022	5.27226	3.22169	5.90035	ENSG00000227948	AC003989.1
ENSG00000227949	2.23663	2.79617	1.85687	3.73837	ENSG00000227949	CYCSP46
ENSG00000227950	0.766708	6.87465	2.29079	5.86685	ENSG00000227950	AL590128.1
ENSG00000227952	0	0	0	0	ENSG00000227952	RPL18AP17
ENSG00000227956	0	0	0	0	ENSG00000227956	HCG4B
ENSG00000227961	0.0288811	0.0197876	0.0178653	0	ENSG00000227961	CR759870.1
ENSG00000227962	0	2.97778	3.49391	0.810781	ENSG00000227962	AL391994.1
ENSG00000227965	0	0	0	0	ENSG00000227965	AC098592.2
ENSG00000227968	0	0.178772	0	0.203145	ENSG00000227968	BUB3P1
ENSG00000227969	0.0778927	0.131265	0.179905	0.227909	ENSG00000227969	NPM1P22
ENSG00000227970	0.132299	0.251587	0.18577	0.326235	ENSG00000227970	NR1H5P
ENSG00000227971	0	0	0	1.69203	ENSG00000227971	AC078809.1
ENSG00000227972	0.225173	0.0715177	0.0215806	0.0814527	ENSG00000227972	THAP12P3

ENSG00000227973	0.453619	1.39363	0.205419	0.814371	ENSG00000227973	PIN4P1
ENSG00000227974	0.0315037	0.0303571	0.0823281	0.172713	ENSG00000227974	HCG22
ENSG00000227979	0.609416	1.14248	1.53429	0.615122	ENSG00000227979	AC002127.1
ENSG00000227982	0	0	0	0	ENSG00000227982	RPL7P30
ENSG00000227983	0	0	0	0	ENSG00000227983	BRK1P2
ENSG00000227986	1.66585	3.08128	2.56594	2.61082	ENSG00000227986	TRIM60P18
ENSG00000227988	0	0	0	0	ENSG00000227988	TDGF1P1
ENSG00000227989	0	0	0	0	ENSG00000227989	AC010141.1
ENSG00000227992	1.08317	2.07889	1.39748	9.45679	ENSG00000227992	AC108463.1
ENSG00000227993	0.105419	0.0207335	0.142379	0	ENSG00000227993	HLA-DRA
ENSG00000227994	0	0	0	0	ENSG00000227994	AL035417.1
ENSG00000227995	0	0	0	0	ENSG00000227995	RAB11AP1
ENSG00000227997	0	0	0	0	ENSG00000227997	CENPVP2
ENSG00000227999	0.128042	0.0822087	0.18577	0.326767	ENSG00000227999	MTND5P1
ENSG00000228000	0.352611	0.931833	0.956711	1.00749	ENSG00000228000	AC127537.1
ENSG00000228001	0.00462984	0.00875722	0.0165025	0	ENSG00000228001	TRIM40
ENSG00000228002	0	0	0	0.0395995	ENSG00000228002	DHX9P1
ENSG00000228004	0	0	0	0	ENSG00000228004	MYCLP2
ENSG00000228007	0.371531	0.750037	0.324542	3.74075	ENSG00000228007	AC011933.1
ENSG00000228008	1.14501	5.62913	1.46026	1.04558	ENSG00000228008	AC105935.1
ENSG00000228012	10.5457	31.1415	16.715	47.8934	ENSG00000228012	RP11-393M18.1
ENSG00000228014	0.277307	0.153251	0.103476	0.0434969	ENSG00000228014	ZNF680P1
ENSG00000228015	0	2.56363	2.26224	0	ENSG00000228015	AC074338.1
ENSG00000228019	2.81081	2.254	3.12267	0.495167	ENSG00000228019	AC006480.1
ENSG00000228020	0	0	0.0792366	0	ENSG00000228020	HNRNPA1P46
ENSG00000228024	0	0.117705	0	0.222866	ENSG00000228024	CYP1D1P
ENSG00000228025	0	0	0	0	ENSG00000228025	MTCO3P1
ENSG00000228029	0.0843996	0	0.204343	0.21079	ENSG00000228029	HLA-W
ENSG00000228030	0	0	0	0	ENSG00000228030	AC019084.1
ENSG00000228032	2.03391	5.36799	4.91288	9.5663	ENSG00000228032	C14orf144
ENSG00000228034	0	0	0	0	ENSG00000228034	HMGN2P21
ENSG00000228036	0.0351326	0.135391	0.275706	0.0769807	ENSG00000228036	HSPD1P9
ENSG00000228038	0.0660652	0.0635378	0	0	ENSG00000228038	VN1R51P
ENSG00000228039	0.481214	0.226601	0.404967	0	ENSG00000228039	AC253536.2
ENSG00000228040	0	1.2844	0	0	ENSG00000228040	AL390729.2
ENSG00000228041	0	0	0	0	ENSG00000228041	AL031313.1
ENSG00000228042	0	0	0	0	ENSG00000228042	AL512882.1
ENSG00000228045	0.788815	0	0.717483	0.655562	ENSG00000228045	DNAJA1P6
ENSG00000228046	0	0	0.17497	0	ENSG00000228046	MTCO3P40
ENSG00000228049	5.78382	28.2049	8.51569	17.3202	ENSG00000228049	POLR2J2
ENSG00000228050	0.514273	0.4414	0.211433	0	ENSG00000228050	TOP3BP1
ENSG00000228051	0	0	0.0258873	0.0655363	ENSG00000228051	AL512504.2
ENSG00000228053	0	0	0	1.73483	ENSG00000228053	AL158823.1
ENSG00000228054	0	0	0.0907605	0.112903	ENSG00000228054	RANP5
ENSG00000228056	0.430862	0.300006	0.548291	0.338298	ENSG00000228056	CFL1P3
ENSG00000228057	0.0611781	0.173267	0.15695	0.194803	ENSG00000228057	SEC63P1
ENSG00000228069	0.418738	1.60034	0.75865	1.22129	ENSG00000228069	MTCO3P29
ENSG00000228071	0.136859	0.131668	0	0	ENSG00000228071	RPL7P47
ENSG00000228074	0	0	0	0	ENSG00000228074	UBBP5
ENSG00000228075	0.288901	0.587985	0.468948	0.585944	ENSG00000228075	BOD1L2
ENSG00000228076	0.847915	0.938091	1.80451	2.15356	ENSG00000228076	AL591719.1
ENSG00000228078	0	0	0	0	ENSG00000228078	HLA-U
ENSG00000228080	0.967197	1.11993	1.25843	2.45802	ENSG00000228080	HLA-DRB1
ENSG00000228081	0.486519	0	0	0	ENSG00000228081	AC092810.2

ENSG00000228083	0	0	0	0	ENSG00000228083	IFNA14
ENSG00000228085	0	0	0	0	ENSG00000228085	AC009296.1
ENSG00000228089	0	0.18242	0	0	ENSG00000228089	PNKDP1
ENSG00000228090	0.0174484	0.467939	0.198607	0.724551	ENSG00000228090	MPIG6B
ENSG00000228092	0	0.650743	0	0	ENSG00000228092	COX6CP15
ENSG00000228095	1.2844	2.4749	6.22708	6.95327	ENSG00000228095	AL354692.1
ENSG00000228097	0.203107	0.489115	0.387749	0.548404	ENSG00000228097	MTATP6P11
ENSG00000228098	0	0	0.497019	0	ENSG00000228098	AC110620.1
ENSG00000228099	0	0	0	0.367602	ENSG00000228099	RPL12P1
ENSG00000228102	0	0.470711	0.115654	2.13E-05	ENSG00000228102	IFITM4P
ENSG00000228110	0	0	0	0	ENSG00000228110	ST13P19
ENSG00000228111	0.90393	0.43326	0	0.483228	ENSG00000228111	TPT1P2
ENSG00000228112	0	0	0	0	ENSG00000228112	AC112220.1
ENSG00000228116	0.580371	3.82366	3.23733	8.73175	ENSG00000228116	PPT2
ENSG00000228118	0.348589	0	0	0	ENSG00000228118	MYL6P5
ENSG00000228120	0.0581388	0	0	0	ENSG00000228120	AP001631.1
ENSG00000228121	0	0.0756228	0.0685745	0.170682	ENSG00000228121	PHBP3
ENSG00000228122	0	0	0	0	ENSG00000228122	MTND1P17
ENSG00000228123	0.153001	0.286118	0.380499	0.448371	ENSG00000228123	AL162726.2
ENSG00000228125	0.127427	0.614859	0.110687	0.681927	ENSG00000228125	AKIRIN1P2
ENSG00000228128	1.24175	1.01416	2.15986	0.700784	ENSG00000228128	DDAH2
ENSG00000228130	0	0	0	0	ENSG00000228130	SUMO2P1
ENSG00000228131	0	0	0	0	ENSG00000228131	IGHD6-6
ENSG00000228132	0	0	0.247259	0.301245	ENSG00000228132	AL360221.1
ENSG00000228134	0	0	0	0	ENSG00000228134	UBE2V1P14
ENSG00000228143	0	0.118558	0.106543	0.405303	ENSG00000228143	AL512649.1
ENSG00000228144	0	0	0	0	ENSG00000228144	AC078927.1
ENSG00000228146	1.75237	2.98971	3.15529	4.2752	ENSG00000228146	CASP16P
ENSG00000228149	0.0494043	0.237697	0.43007	0.377553	ENSG00000228149	RPL3P1
ENSG00000228154	0	0.28884	0.394839	0	ENSG00000228154	AC092436.1
ENSG00000228155	51.5335	96.0496	65.0586	126.678	ENSG00000228155	AL589685.1
ENSG00000228157	2.68863	3.91839	3.44578	7.18797	ENSG00000228157	AC007952.2
ENSG00000228158	0	0.477982	1.51005	0.468312	ENSG00000228158	TLE1P1
ENSG00000228161	0	0	0	0	ENSG00000228161	AC245452.3
ENSG00000228163	0.015404	0	0.0767526	0.0375628	ENSG00000228163	HLA-DPA1
ENSG00000228164	0	0	0	0	ENSG00000228164	COL11A2P1
ENSG00000228166	0	0.139278	0.251684	0.786656	ENSG00000228166	MTND1P11
ENSG00000228167	0	0	0	0	ENSG00000228167	AL353072.1
ENSG00000228168	0	0.0924791	0	0.0706544	ENSG00000228168	HNRNPA1P21
ENSG00000228169	0.556052	0.304913	1.15649	2.43316	ENSG00000228169	PPIAP19
ENSG00000228171	3.55703	4.42636	6.61712	10.368	ENSG00000228171	AC121251.1
ENSG00000228175	0.364308	0.316067	0.711607	0.117285	ENSG00000228175	GEMIN8P4
ENSG00000228177	0	0	0	0	ENSG00000228177	C6orf47
ENSG00000228179	0	0	0	0	ENSG00000228179	HLA-S
ENSG00000228181	0.524514	0	0	0	ENSG00000228181	AL590365.1
ENSG00000228182	0	0	0	0	ENSG00000228182	MTND2P25
ENSG00000228184	0	0.0750269	0.055346	0.0469612	ENSG00000228184	SNX19P1
ENSG00000228186	1.24177	1.79606	3.14341	2.86624	ENSG00000228186	PRR3
ENSG00000228187	0.385793	1.03832	0.233443	1.73176	ENSG00000228187	AC093433.1
ENSG00000228190	0	0.377235	0.170223	0.20905	ENSG00000228190	RPL23AP16
ENSG00000228191	1.47929	0	0	1.43924	ENSG00000228191	AL512326.2
ENSG00000228193	0	0.139689	0.126289	0.153766	ENSG00000228193	ELOCP14
ENSG00000228194	0	0	0	0	ENSG00000228194	Z83846.1
ENSG00000228195	0	0.0671283	0.425728	0	ENSG00000228195	RPL5P27

ENSG00000228196	0.238452	0	0.104254	1.16406	ENSG00000228196	PTPN2P1
ENSG00000228197	0	0	0	0.00316142	ENSG00000228197	DDX6P1
ENSG00000228198	0	0	0	0	ENSG00000228198	OR2M3
ENSG00000228199	0	0	0	0	ENSG00000228199	AL845450.1
ENSG00000228202	2.13296	1.99934	1.44905	2.25545	ENSG00000228202	CR788234.1
ENSG00000228205	0.0921672	0.0888629	0.160247	0.30069	ENSG00000228205	AC131235.1
ENSG00000228206	0	0	0	0	ENSG00000228206	AC016717.1
ENSG00000228207	0	0	0	0	ENSG00000228207	AC007967.2
ENSG00000228208	0.316328	0.940885	1.41154	2.35054	ENSG00000228208	C1orf143
ENSG00000228209	0	0.141629	0	0.0799844	ENSG00000228209	AC073091.1
ENSG00000228210	0	0	0	0	ENSG00000228210	AL121916.1
ENSG00000228211	0.0463429	0.0446231	0.0806664	0	ENSG00000228211	HYALP1
ENSG00000228212	0.214648	0.513969	0.480499	1.107	ENSG00000228212	OFD1P17
ENSG00000228217	0	0	0	0	ENSG00000228217	PNRC2P1
ENSG00000228218	0.0641938	0	0	0	ENSG00000228218	ATF4P3
ENSG00000228219	0.544468	0.673608	0.509164	1.35091	ENSG00000228219	NPM1P30
ENSG00000228220	0.111634	0.322334	0.119037	0.102342	ENSG00000228220	HLA-J
ENSG00000228224	0.245415	0.484589	0.565348	0.820805	ENSG00000228224	NACAP1
ENSG00000228225	0	0.188582	0.0852241	0.267418	ENSG00000228225	AC016908.1
ENSG00000228227	0.0999439	0.239336	0.563214	0.38701	ENSG00000228227	AL844220.1
ENSG00000228232	0	0.120427	0.109409	0	ENSG00000228232	GAPDHP1
ENSG00000228234	0	0	0	0	ENSG00000228234	GLRXP1
ENSG00000228236	0	0.307357	0.836861	1.34893	ENSG00000228236	TXNP5
ENSG00000228238	0.0602325	0	0.261891	0.328103	ENSG00000228238	AL096803.1
ENSG00000228241	0	0	0	0	ENSG00000228241	MOB1AP1
ENSG00000228243	0.710117	0	1.87439	1.97976	ENSG00000228243	RP11-436G20.1
ENSG00000228247	1.83159	3.69147	2.66025	2.86478	ENSG00000228247	UBBP2
ENSG00000228248	0	0	0	0	ENSG00000228248	NUTF2P3
ENSG00000228250	0.329801	0	0.241696	0	ENSG00000228250	LY6G6C
ENSG00000228252	0.126837	0.121716	0.710403	2.02795	ENSG00000228252	COL6A4P2
ENSG00000228253	1052.11	779.162	1893.02	1784.65	ENSG00000228253	MT-ATP8
ENSG00000228254	0.0674196	0	0	0.153849	ENSG00000228254	HLA-DQB2
ENSG00000228257	0	0	0	0	ENSG00000228257	AC010141.2
ENSG00000228259	0	0	0	0	ENSG00000228259	AC136604.1
ENSG00000228260	0.0394657	0.0375419	0	0	ENSG00000228260	HLA-DRB9
ENSG00000228263	0.0393897	0.290961	0.258819	0.412492	ENSG00000228263	SLC44A4
ENSG00000228264	1.10648	1.31192	0.96073	0.831813	ENSG00000228264	PSMD8P1
ENSG00000228267	0.437181	0.183949	0.55803	0.600656	ENSG00000228267	C4B
ENSG00000228273	0	0	0.0533665	0.0668463	ENSG00000228273	MUC3A
ENSG00000228278	0	0.121681	0	0	ENSG00000228278	ORM2
ENSG00000228283	0	0.0771791	0	0	ENSG00000228283	KATNBL1P6
ENSG00000228284	5.51773	11.6478	10.1333	28.5187	ENSG00000228284	HLA-DQA1
ENSG00000228285	0	0	0	0	ENSG00000228285	LYPLA2P1
ENSG00000228286	0	0.665081	0	0.0891464	ENSG00000228286	AP000593.2
ENSG00000228289	0	0	0	0	ENSG00000228289	AL355862.1
ENSG00000228291	0	0	0	0	ENSG00000228291	ARL4AP3
ENSG00000228292	0.940956	1.77068	3.46186	4.78917	ENSG00000228292	AL512604.1
ENSG00000228299	9.45967	63.1883	40.5061	85.4454	ENSG00000228299	HLA-C
ENSG00000228300	23.4995	15.5099	20.1152	11.9651	ENSG00000228300	C19orf24
ENSG00000228301	0	0.257509	0.31451	0.191502	ENSG00000228301	RPL7P55
ENSG00000228303	0	0	0	0.0428146	ENSG00000228303	AC095038.1
ENSG00000228304	0	0	0	0	ENSG00000228304	OR4K6P
ENSG00000228305	0	0.41876	0.4155	0	ENSG00000228305	AC016734.1
ENSG00000228307	0	0	0	0.0714259	ENSG00000228307	OR2S1P

ENSG00000228312	0.268129	0	0	0.281347	ENSG00000228312	GAPDHP45
ENSG00000228314	0.111586	0.238906	0.0967573	0.287718	ENSG00000228314	CYP4F29P
ENSG00000228316	0.415158	0.199371	0.768552	1.21129	ENSG00000228316	MTATP6P19
ENSG00000228319	0.141844	0.765131	0.736897	1.56613	ENSG00000228319	SPATA2P1
ENSG00000228321	0.222879	0.099013	0.196978	0.0453146	ENSG00000228321	TNF
ENSG00000228325	0	0	0	0	ENSG00000228325	IGKV3D-7
ENSG00000228326	0	0	0.0747919	0	ENSG00000228326	RP11-109G10.2
ENSG00000228328	0.143315	0.321952	0.0833216	0.313619	ENSG00000228328	AL158201.1
ENSG00000228330	1.77636	5.10532	3.84802	7.61808	ENSG00000228330	AL355355.1
ENSG00000228331	0	0	0	0.154621	ENSG00000228331	AC004448.2
ENSG00000228333	0.770594	0.900677	1.42709	0.954922	ENSG00000228333	RXRB
ENSG00000228335	1.6609	1.2535	1.94264	0.779084	ENSG00000228335	AC073063.1
ENSG00000228336	0	0	0	0	ENSG00000228336	OR9H1P
ENSG00000228337	0	0	0	0.538948	ENSG00000228337	AC096920.1
ENSG00000228339	0	0.196971	0.177415	0.14865	ENSG00000228339	AMD1P1
ENSG00000228341	1.59464	9.80627	4.41307	5.75218	ENSG00000228341	AC002381.1
ENSG00000228345	0	0	0	0	ENSG00000228345	AC112492.3
ENSG00000228347	0	0	0	0	ENSG00000228347	FTLP17
ENSG00000228348	0	0	0	0	ENSG00000228348	EFCAB14P1
ENSG00000228349	0	0	0	0	ENSG00000228349	RPS26P4
ENSG00000228354	0	0	0	0	ENSG00000228354	AL450023.1
ENSG00000228357	1.5288	1.62628	2.07747	0.55839	ENSG00000228357	HSD17B8
ENSG00000228360	0	0.389751	0.701538	0.424721	ENSG00000228360	AC009220.1
ENSG00000228364	0	0	0	0	ENSG00000228364	AL662791.2
ENSG00000228366	0.777908	0	0.269279	0.997219	ENSG00000228366	AL592437.1
ENSG00000228367	0.124815	0.0602268	0.213779	0.0679571	ENSG00000228367	AC108120.1
ENSG00000228368	0.690133	3.30397	1.19325	5.87888	ENSG00000228368	AC106873.1
ENSG00000228371	0.0558802	0	0.0241408	0.0296507	ENSG00000228371	ZDHHC20P1
ENSG00000228373	0	0	0	0	ENSG00000228373	AL353752.1
ENSG00000228374	0	0.239356	0.217939	0	ENSG00000228374	AC012497.1
ENSG00000228375	0	0	0	0	ENSG00000228375	RPS20P25
ENSG00000228376	0.176733	0.221091	0.353125	0.509136	ENSG00000228376	GAS2L1P2
ENSG00000228377	0	0	0	0	ENSG00000228377	MAS1L
ENSG00000228380	0.712872	0.764603	1.20416	0.619554	ENSG00000228380	MYL6BP1
ENSG00000228398	0	0	0	0	ENSG00000228398	HMGN2P25
ENSG00000228399	0	0	0	0	ENSG00000228399	AL109741.2
ENSG00000228405	0	4.38503	0.231572	2.54711	ENSG00000228405	RNF5
ENSG00000228407	0.910685	2.14182	2.6208	2.70441	ENSG00000228407	AL139156.2
ENSG00000228409	1.95394	2.26574	3.32935	2.17489	ENSG00000228409	CCT6P1
ENSG00000228410	0	0	0.52762	0	ENSG00000228410	ELOCP24
ENSG00000228411	0.728211	2.58939	1.90804	0	ENSG00000228411	CDY4P
ENSG00000228413	0.274879	0.523264	0.236373	0.585353	ENSG00000228413	AC024937.1
ENSG00000228415	0	0.412722	0	0.298453	ENSG00000228415	PTMAP1
ENSG00000228418	0	0	0.264752	0	ENSG00000228418	CTSLP3
ENSG00000228425	0.948011	0.562313	1.51113	2.85005	ENSG00000228425	VPS52
ENSG00000228429	3.54493	7.77892	6.643	11.7082	ENSG00000228429	AC004910.1
ENSG00000228431	0.452802	0.21621	0.390632	0	ENSG00000228431	ARL5AP3
ENSG00000228432	0	0	0.11579	0	ENSG00000228432	DHFRP2
ENSG00000228433	0.560398	0.113	0	0.320377	ENSG00000228433	OR7E23P
ENSG00000228435	0	0	0.358304	4.07428	ENSG00000228435	C6orf47
ENSG00000228438	0	0	0	0	ENSG00000228438	AL445567.1
ENSG00000228440	0.0316576	0.0666874	0.031735	0.0497575	ENSG00000228440	MTND5P6
ENSG00000228445	0	0.41129	0.531002	0.638092	ENSG00000228445	UGT1A2P
ENSG00000228446	1.12239	3.95455	3.00393	5.86696	ENSG00000228446	AC073052.1

ENSG00000228450	0	0	0	0	ENSG00000228450	AL049734.1
ENSG00000228451	0.410458	0.4443	0.578905	1.04062	ENSG00000228451	SDAD1P1
ENSG00000228453	0	0	0.199461	0.244114	ENSG00000228453	RPS15AP9
ENSG00000228454	0.437181	0.465692	0.303908	0.512031	ENSG00000228454	C4B
ENSG00000228458	0	0.0627516	0	0	ENSG00000228458	DDX39BP2
ENSG00000228459	5.9862	16.4071	11.2033	20.8056	ENSG00000228459	LINC01546
ENSG00000228460	0	0	0	0	ENSG00000228460	CYP2C59P
ENSG00000228461	0	2.92E-05	0	0	ENSG00000228461	RPL3P2
ENSG00000228462	0	0	0	0	ENSG00000228462	RPS19P7
ENSG00000228464	0	0.101505	0.184024	0.228054	ENSG00000228464	AC073614.1
ENSG00000228465	0	0	0	0	ENSG00000228465	TRAPPC2P10
ENSG00000228466	0	0	0	0.0973297	ENSG00000228466	TUBB4AP1
ENSG00000228471	0	0	0	0	ENSG00000228471	AC018865.2
ENSG00000228473	0.519328	0.662982	0.748248	0.737225	ENSG00000228473	LIN28AP2
ENSG00000228474	116.681	79.7737	54.7339	46.0555	ENSG00000228474	OST4
ENSG00000228476	0	0	0	0	ENSG00000228476	CSTP1
ENSG00000228477	5.46834	6.7571	7.73584	6.17634	ENSG00000228477	AL663070.1
ENSG00000228480	0	0.111831	0.0336958	0.0423635	ENSG00000228480	AC130464.1
ENSG00000228483	0	0.0275452	0	0.0234623	ENSG00000228483	CR388415.2
ENSG00000228489	0	0	0.320775	1.02691	ENSG00000228489	RPL21P50
ENSG00000228490	0	0	0	0	ENSG00000228490	CT009496.1
ENSG00000228491	1.7408	4.95173	1.21917	5.02782	ENSG00000228491	MICE
ENSG00000228492	5.66458	9.94677	17.5203	14.0689	ENSG00000228492	RAB11FIP1P1
ENSG00000228498	1.93885	0.673681	0.561095	0.695858	ENSG00000228498	HLA-Z
ENSG00000228499	0	0	1.70561	1.93906	ENSG00000228499	TMSB10P1
ENSG00000228501	0.344877	0.551296	0.596708	0.494858	ENSG00000228501	RPL15P18
ENSG00000228502	0.137033	0.132654	0.31831	0.252042	ENSG00000228502	EEF1A1P11
ENSG00000228507	0.590666	0	0.77658	0.96021	ENSG00000228507	DAP3P2
ENSG00000228510	0.268872	0.160652	0.14425	0.145083	ENSG00000228510	AL359091.1
ENSG00000228513	0.704695	1.52921	1.30987	2.54869	ENSG00000228513	AC023271.1
ENSG00000228515	0	0	0	0	ENSG00000228515	MAS1L
ENSG00000228517	0	0.0219476	0.0109151	0.0319741	ENSG00000228517	CT47A7
ENSG00000228518	0	0	0	0	ENSG00000228518	SURF6P1
ENSG00000228519	0	0.138447	0	0	ENSG00000228519	AC097263.1
ENSG00000228520	0	2.37574	2.34196	0.817843	ENSG00000228520	RING1
ENSG00000228522	0.30743	0.56502	2.23947	3.36325	ENSG00000228522	AL845321.1
ENSG00000228523	0	0.0906218	0.0799876	0.1004	ENSG00000228523	AL389925.1
ENSG00000228524	0.111634	0.322334	0.119037	0.102342	ENSG00000228524	HLA-J
ENSG00000228525	0	2.10046	0	2.98576	ENSG00000228525	AL353689.1
ENSG00000228530	0	0	0	0	ENSG00000228530	AL445687.1
ENSG00000228532	0.144057	0.0930406	0.57493	0.452386	ENSG00000228532	AC005000.1
ENSG00000228537	6.69777	14.0557	12.0261	21.2531	ENSG00000228537	AL353608.1
ENSG00000228546	0.216734	0.405185	0.796981	0.717673	ENSG00000228546	AC091390.2
ENSG00000228547	0.31192	0.457647	0.597486	0.149917	ENSG00000228547	OR7E26P
ENSG00000228550	0.213754	0.612645	0.368805	1.58274	ENSG00000228550	AC073583.1
ENSG00000228551	0	0	0	7.16533	ENSG00000228551	SNRPGP9
ENSG00000228557	0	0	0	0	ENSG00000228557	HSPA8P17
ENSG00000228567	0	0	0.15306	0	ENSG00000228567	VN1R4
ENSG00000228568	0.906496	5.16957	5.72022	4.4202	ENSG00000228568	AC006461.1
ENSG00000228570	0.479262	1.11125	1.09223	1.85041	ENSG00000228570	NUTM2E
ENSG00000228571	0	0	0	0	ENSG00000228571	HSFY7P
ENSG00000228572	0	0	0	0	ENSG00000228572	AL954722.1
ENSG00000228575	0.600581	2.44995	1.16341	1.1447	ENSG00000228575	MDC1
ENSG00000228578	0	0	0	2.64E-08	ENSG00000228578	TUBB1P2

ENSG00000228579	0.224254	1.08508	0.890579	1.9143	ENSG00000228579	AL662824.1
ENSG00000228581	4.7918	2.11576	2.67785	2.50199	ENSG00000228581	GNL1
ENSG00000228582	0.732317	4.24445	0.66121	0.591079	ENSG00000228582	TAP2
ENSG00000228585	0	0.216212	0	0	ENSG00000228585	AC073143.1
ENSG00000228589	0.652568	0.665514	0.418395	0.418814	ENSG00000228589	SPCS2P4
ENSG00000228593	0	0	0	0	ENSG00000228593	CFTRP1
ENSG00000228594	2.31661	0.986586	1.76035	1.93452	ENSG00000228594	FNDC10
ENSG00000228595	0	0	0.0455732	0	ENSG00000228595	PAICSP2
ENSG00000228597	0	0	0.034571	0.0869135	ENSG00000228597	MTND4P1
ENSG00000228599	0.178258	0.599678	0.464369	0.581192	ENSG00000228599	RPL7P52
ENSG00000228600	0	0.0823424	0	0.0928115	ENSG00000228600	POLR2CP1
ENSG00000228601	1.38154	0	0	0	ENSG00000228601	AL121914.1
ENSG00000228605	0	0.74578	0.291819	1.01343	ENSG00000228605	GPANK1
ENSG00000228607	0	0	0	0	ENSG00000228607	CLDN25
ENSG00000228610	0	0.251752	0	0.277399	ENSG00000228610	PDCL2P1
ENSG00000228611	0.0476198	0.230716	0.223207	0.495033	ENSG00000228611	HNF4GP1
ENSG00000228612	0	0	0.0375023	0.045864	ENSG00000228612	HK2P1
ENSG00000228615	0.201283	0.437948	0.344765	0.93777	ENSG00000228615	AC093166.2
ENSG00000228617	0	0	0	0	ENSG00000228617	RP11-157L3.2
ENSG00000228626	0.385406	0	0	0.397773	ENSG00000228626	AC245100.3
ENSG00000228628	30.7619	50.743	27.9301	8.34268	ENSG00000228628	ATF6B
ENSG00000228635	0	0	0	0	ENSG00000228635	CR933783.1
ENSG00000228638	1.8519	3.93729	4.37099	1.77972	ENSG00000228638	FCF1P2
ENSG00000228645	0.553463	0.323217	0.638135	0.48225	ENSG00000228645	PHKG1P2
ENSG00000228646	0	0	0	0	ENSG00000228646	RPL31P13
ENSG00000228652	0	0	0	0	ENSG00000228652	OR2W1
ENSG00000228653	0.905589	1.75842	1.08426	1.0611	ENSG00000228653	HNRNPCP7
ENSG00000228656	0	0	0	0	ENSG00000228656	MYO5BP3
ENSG00000228657	0.681595	0.891542	1.03032	2.1654	ENSG00000228657	RPL23AP58
ENSG00000228660	0	0	0	0	ENSG00000228660	VN1R35P
ENSG00000228662	0.0916753	0.264657	0.272079	0.660025	ENSG00000228662	MCCD1
ENSG00000228663	2.09596	7.10354	6.96398	8.21563	ENSG00000228663	PSMD10P1
ENSG00000228664	0	0	0	0	ENSG00000228664	AL513480.1
ENSG00000228665	0.489423	1.39232	0.833581	0	ENSG00000228665	BX679664.1
ENSG00000228666	0	0.00880756	0.00776227	0	ENSG00000228666	KRT18P1
ENSG00000228667	0	0	0.36695	0	ENSG00000228667	AL157385.1
ENSG00000228668	0	0.498638	0.225439	0.824293	ENSG00000228668	TRGV5P
ENSG00000228670	0.215234	0	0.38438	0	ENSG00000228670	NANOGP2
ENSG00000228672	1.89861	3.78556	2.05131	3.56556	ENSG00000228672	PROB1
ENSG00000228674	1.54543	0.454809	0.355962	0.170502	ENSG00000228674	AC011483.1
ENSG00000228681	22.6634	55.8568	46.6691	77.0423	ENSG00000228681	AC008072.1
ENSG00000228684	0	0	0	0	ENSG00000228684	HLA-DQB3
ENSG00000228685	0	0	0	0	ENSG00000228685	AL365356.2
ENSG00000228687	0	0.449081	0.606157	0.989009	ENSG00000228687	AL035407.2
ENSG00000228688	0	0	0	0	ENSG00000228688	COL11A2P1
ENSG00000228691	4.87821	3.55462	1.94829	1.17492	ENSG00000228691	NEU1
ENSG00000228694	0	0	0	0.180263	ENSG00000228694	MTND4P18
ENSG00000228695	0.111054	0.765571	0.224642	0.409326	ENSG00000228695	CES1P1
ENSG00000228696	5.6781	10.5468	14.8095	10.9149	ENSG00000228696	ARL17B
ENSG00000228698	0	0	0.00828591	0	ENSG00000228698	CR759834.2
ENSG00000228700	0	0.69832	0.944023	0.381896	ENSG00000228700	AC010655.1
ENSG00000228702	0	0	0	0	ENSG00000228702	AL645998.1
ENSG00000228706	1.86909	1.3845	0.332359	0.329597	ENSG00000228706	HCG4
ENSG00000228711	0	0	0	0	ENSG00000228711	AC004006.1

ENSG00000228712	1.5288	1.62628	2.07747	0.55839	ENSG00000228712	HSD17B8
ENSG00000228713	0	0.0458373	0.0827353	0.200941	ENSG00000228713	CR759828.1
ENSG00000228716	7.7266	9.70705	7.8428	14.7108	ENSG00000228716	DHFR
ENSG00000228717	0	0	0	0.0431353	ENSG00000228717	AF013593.1
ENSG00000228721	0	0	1.96415	3.54303	ENSG00000228721	AC016909.1
ENSG00000228725	1.0662	3.09676	2.2278	5.45205	ENSG00000228725	MTND2P12
ENSG00000228727	1.25213	1.47048	2.11575	0.64384	ENSG00000228727	SAPCD1
ENSG00000228728	0.717455	1.11944	1.19754	1.83659	ENSG00000228728	AF274573.1
ENSG00000228729	0.42736	1.53278	0.839384	1.99195	ENSG00000228729	AL627308.1
ENSG00000228733	0	85.1923	55.9612	94.2974	ENSG00000228733	AC015815.8
ENSG00000228736	5.86561	7.28875	5.7293	4.35313	ENSG00000228736	RGL2
ENSG00000228744	0.150944	0.153008	0	0	ENSG00000228744	AF228730.2
ENSG00000228745	0	0	0	0	ENSG00000228745	CTSLP5
ENSG00000228751	1.03032	0.443172	0.597419	0.499217	ENSG00000228751	AC004022.1
ENSG00000228753	0.0319813	0	0.0559714	0.114655	ENSG00000228753	EIF4BP2
ENSG00000228754	0	0	0	0	ENSG00000228754	RPL13AP19
ENSG00000228755	0.104678	0.208467	0.128274	0.0835193	ENSG00000228755	PABPC1P8
ENSG00000228757	0	0	0	0	ENSG00000228757	AC244452.1
ENSG00000228759	0.0456863	0	0.079819	0.0996158	ENSG00000228759	FAF2P1
ENSG00000228760	16.0086	8.37162	12.4059	10.295	ENSG00000228760	BAG6
ENSG00000228764	0.0552871	0.106423	0.0961836	0	ENSG00000228764	ZNF885P
ENSG00000228765	3.98E-06	0	0.109696	2.74E-05	ENSG00000228765	ETF1P1
ENSG00000228766	0	0.0882305	0.079911	0	ENSG00000228766	RPL7L1P8
ENSG00000228767	0	0.038998	0	0	ENSG00000228767	KRT8P18
ENSG00000228768	2.0704	1.65198	5.66794	8.26717	ENSG00000228768	AC003101.1
ENSG00000228769	0	0	1.2284	0	ENSG00000228769	ABCF2P2
ENSG00000228770	0	0	0	0.773909	ENSG00000228770	AC007327.1
ENSG00000228771	0	0	0	0	ENSG00000228771	BX510359.3
ENSG00000228776	0	0	0	0	ENSG00000228776	AC114492.1
ENSG00000228780	0	0	0	0	ENSG00000228780	Z92545.1
ENSG00000228781	0	0	0	0	ENSG00000228781	AL353705.1
ENSG00000228782	10.5008	8.03662	10.5906	13.9191	ENSG00000228782	MRPL45P2
ENSG00000228783	0	0	0	0	ENSG00000228783	AL358976.1
ENSG00000228785	1.93885	0.673681	0.561095	0.695858	ENSG00000228785	HLA-Z
ENSG00000228790	0	0	0	0	ENSG00000228790	AC245128.2
ENSG00000228797	0.214278	0	0	0	ENSG00000228797	FAM207BP
ENSG00000228803	0	0.0514605	0	0.132942	ENSG00000228803	MTCYBP42
ENSG00000228804	0.222676	0.205917	0.47534	1.0776	ENSG00000228804	AC072022.2
ENSG00000228806	0	0	0	0	ENSG00000228806	AC092628.1
ENSG00000228807	0	0	0	0	ENSG00000228807	MRPS18CP6
ENSG00000228808	1.02248	2.3803	1.89644	2.95248	ENSG00000228808	HMGB3P4
ENSG00000228810	0.461174	1.00815	0.81666	2.12249	ENSG00000228810	PABPC1P11
ENSG00000228813	0.0674196	0	0	0.153849	ENSG00000228813	HLA-DQB2
ENSG00000228814	0	0.193735	0.176301	0	ENSG00000228814	AC017007.1
ENSG00000228815	0	0	0.0534905	0.0336692	ENSG00000228815	MARK2P13
ENSG00000228816	7.00698	15.875	5.16975	25.819	ENSG00000228816	AK3P5
ENSG00000228818	0	0.0200041	0	0.205693	ENSG00000228818	AL359918.1
ENSG00000228819	0	0.09062	0	0	ENSG00000228819	AL049792.1
ENSG00000228820	0	0	0	0	ENSG00000228820	RPSAP1
ENSG00000228823	0	0	0	0	ENSG00000228823	AL592309.1
ENSG00000228825	0	0	0	0	ENSG00000228825	LAMTOR3P1
ENSG00000228827	0	0.405913	1.74095	0.595531	ENSG00000228827	AL929410.1
ENSG00000228828	0.224834	0.555706	0.617383	0.648042	ENSG00000228828	TLK2P2
ENSG00000228829	0.350864	0.319754	0	0.556616	ENSG00000228829	AC005077.3

ENSG00000228833	0	0	0	0	ENSG00000228833	AC244098.2
ENSG00000228834	0.93519	0.873214	1.18456	0.96238	ENSG00000228834	AL445189.2
ENSG00000228835	0.553676	0.492984	0.693426	1.19858	ENSG00000228835	AC012123.1
ENSG00000228836	0	0	0	0	ENSG00000228836	CT45A5
ENSG00000228837	0	0	0.198811	0.183488	ENSG00000228837	CBX3P6
ENSG00000228840	0	0.0341391	0.030885	0	ENSG00000228840	BX927133.2
ENSG00000228844	0	0	0	0	ENSG00000228844	AL358176.3
ENSG00000228845	0	0	0	0	ENSG00000228845	MTCO3P1
ENSG00000228846	0	0	0.00828591	0	ENSG00000228846	BX927132.1
ENSG00000228847	0	0	0	0	ENSG00000228847	ATP5G2P4
ENSG00000228848	0	0	0	0	ENSG00000228848	AC105402.2
ENSG00000228849	0.222879	0.099013	0.196978	0.0453146	ENSG00000228849	TNF
ENSG00000228850	0	0	0.00240944	0.00769717	ENSG00000228850	CDY12P
ENSG00000228851	0.0833028	0.240984	0.289835	0.179625	ENSG00000228851	MTCO3P4
ENSG00000228854	0.463793	1.24111	0.515031	0.408103	ENSG00000228854	NRM
ENSG00000228855	0	0	0	0.368346	ENSG00000228855	AL009048.1
ENSG00000228856	0	0	0	0	ENSG00000228856	USP17L30
ENSG00000228859	0.329801	0	0.241696	0	ENSG00000228859	LY6G6C
ENSG00000228860	0	0	0	0	ENSG00000228860	AL731547.1
ENSG00000228861	0	0	0	0	ENSG00000228861	RPL23AP12
ENSG00000228867	0.463793	1.24111	0.515031	0.408103	ENSG00000228867	NRM
ENSG00000228868	0	0.03544	0	0.0412358	ENSG00000228868	MYLKP1
ENSG00000228869	0.45565	1.66279	1.71969	3.3141	ENSG00000228869	COX4I1P2
ENSG00000228871	0	0	0.195055	0	ENSG00000228871	MEP1AP1
ENSG00000228872	0	0.0806178	0.291327	0.181792	ENSG00000228872	AC096664.1
ENSG00000228874	0	0	0	0	ENSG00000228874	AC090954.1
ENSG00000228875	1.18829	1.24558	2.61925	5.26816	ENSG00000228875	CSNK2B
ENSG00000228879	0.926792	0	0.529935	0.322353	ENSG00000228879	AL591848.1
ENSG00000228881	1.82591	0.98202	3.18287	0.727701	ENSG00000228881	TRIM26
ENSG00000228882	0.0446986	0.0608853	0.0302719	0	ENSG00000228882	CICP9
ENSG00000228883	0.0973281	0.0758412	0.0529561	0.0644326	ENSG00000228883	LY6G5C
ENSG00000228884	0.0186406	0.512891	0.683366	0.21592	ENSG00000228884	RPL23AP26
ENSG00000228887	0	0	0	0	ENSG00000228887	EEF1DP1
ENSG00000228891	0	0	0	0	ENSG00000228891	DDX39BP1
ENSG00000228892	7.66957	11.1713	6.87323	0	ENSG00000228892	AGPAT1
ENSG00000228896	8.10942	7.81457	9.08597	7.06332	ENSG00000228896	SKIV2L
ENSG00000228897	0	0	1.12496	1.78599	ENSG00000228897	AC012441.2
ENSG00000228898	0	0	0	0	ENSG00000228898	MTCO1P43
ENSG00000228900	2.13296	1.99934	1.44905	2.25545	ENSG00000228900	BX927182.1
ENSG00000228901	0	0	0	0	ENSG00000228901	HMGN2P36
ENSG00000228902	0	0	0	0	ENSG00000228902	ST6GALNAC2P1
ENSG00000228903	0.542889	0.440599	0.814009	0.524568	ENSG00000228903	RASA4CP
ENSG00000228904	0.0174175	0.000999815	0	0.0522935	ENSG00000228904	USP8P1
ENSG00000228907	1.35259	0.556113	1.36117	0.483865	ENSG00000228907	RNF5
ENSG00000228912	0	0	0.347911	0	ENSG00000228912	IFITM4P
ENSG00000228913	0	0	0	0	ENSG00000228913	UBD
ENSG00000228914	0	0	0	0.649681	ENSG00000228914	OR1H1P
ENSG00000228915	0.360995	1.40704	1.37821	2.23	ENSG00000228915	OR7E128P
ENSG00000228919	0.717096	1.21049	1.35429	3.62909	ENSG00000228919	AC097381.1
ENSG00000228920	0	0	0.147215	0.181405	ENSG00000228920	AL162415.1
ENSG00000228921	0	2.07805	3.22713	4.62504	ENSG00000228921	CR759762.1
ENSG00000228922	0	0	0	0	ENSG00000228922	AC234771.2
ENSG00000228926	0	0	0	0	ENSG00000228926	UQCRHP1
ENSG00000228927	0	0	0.0341145	0	ENSG00000228927	TSPY3

ENSG00000228928	2.03109	5.86135	12.1233	6.16401	ENSG00000228928	KPNA2P2
ENSG00000228929	0.935722	2.26486	1.16948	2.01554	ENSG00000228929	RPS13P2
ENSG00000228930	0	0	0	0	ENSG00000228930	MTCO1P3
ENSG00000228935	0.0275382	0.185788	0.0479881	0.0604429	ENSG00000228935	AL353132.1
ENSG00000228937	0	0	0.0342311	0.0860643	ENSG00000228937	AC005539.1
ENSG00000228938	0	0	0	0	ENSG00000228938	SNRPD2P1
ENSG00000228940	0	0	0	0	ENSG00000228940	AL391730.1
ENSG00000228941	0.0250612	0.0968572	0.0439157	0.0553834	ENSG00000228941	UBE3AP2
ENSG00000228943	0	0	0	0	ENSG00000228943	AL137792.2
ENSG00000228945	0	0	0.0394885	0.0991844	ENSG00000228945	CLUHP2
ENSG00000228948	0.717237	1.94976	0.911949	5.50506	ENSG00000228948	SLC25A6P5
ENSG00000228949	0	0	0	0	ENSG00000228949	UGT1A12P
ENSG00000228953	0	0	0	0	ENSG00000228953	AC006026.2
ENSG00000228954	0	0.0458373	0.0827353	0.200941	ENSG00000228954	BX927178.1
ENSG00000228955	2.50805	2.34543	1.04906	3.78591	ENSG00000228955	AL591623.2
ENSG00000228957	0.156854	0	0.0681175	0.170175	ENSG00000228957	AL512590.1
ENSG00000228958	0	0	0.174084	0	ENSG00000228958	PIGPP3
ENSG00000228960	6.17414	8.9714	10.2612	9.24103	ENSG00000228960	OR2A9P
ENSG00000228963	0	0	0.0603209	0	ENSG00000228963	AF186996.2
ENSG00000228964	26.4129	2.75763	2.92251	2.8066	ENSG00000228964	HLA-B
ENSG00000228965	0.144017	0.0692533	0.062573	0.156471	ENSG00000228965	RPSAP60
ENSG00000228966	0	0	0	0	ENSG00000228966	HOMER2P1
ENSG00000228970	0	0.149054	0	0	ENSG00000228970	UBTFL6
ENSG00000228974	0	0	0	0	ENSG00000228974	AC006483.1
ENSG00000228976	1.16991	4.10965	3.77366	10.8609	ENSG00000228976	SUMO2P8
ENSG00000228977	0	0	0	0	ENSG00000228977	OR2W1
ENSG00000228978	0	0.0972142	0.0314959	0.390965	ENSG00000228978	TNF
ENSG00000228979	0.0260193	0	0	0.167494	ENSG00000228979	AC113554.1
ENSG00000228981	0.587323	1.06096	1.02512	2.22425	ENSG00000228981	AC097658.1
ENSG00000228982	0	0	0	0	ENSG00000228982	AL627095.1
ENSG00000228983	0.151964	0.145667	0.131522	0.127173	ENSG00000228983	SLC47A1P1
ENSG00000228984	0	0	0	0	ENSG00000228984	AC021451.1
ENSG00000228985	0	0	0	0	ENSG00000228985	TRDD3
ENSG00000228986	0	0	0.0286367	0.110864	ENSG00000228986	AC234781.3
ENSG00000228987	0.105419	0	0.189226	0	ENSG00000228987	HLA-DRA
ENSG00000228990	0	0.00880756	0.00776227	0	ENSG00000228990	KRT18P1
ENSG00000228991	9.76542	28.8339	0.0504299	2.86993	ENSG00000228991	RP11-318K12.1
ENSG00000228992	0	0	0	0.235028	ENSG00000228992	RPL5P32
ENSG00000228993	0	0	0	0	ENSG00000228993	GPR53P
ENSG00000228995	0.132299	0.384402	0.68983	1.07947	ENSG00000228995	MTND1P9
ENSG00000228997	0.184682	0.353424	0.159552	0.785086	ENSG00000228997	AL136452.1
ENSG00000228998	2.84622	2.80017	4.82266	4.97551	ENSG00000228998	AC091167.2
ENSG00000229000	0	0.24846	0	0.189527	ENSG00000229000	SEPT7P8
ENSG00000229001	0.0558236	0.0537307	0.0485563	0.304381	ENSG00000229001	ACTBP14
ENSG00000229002	0	0	0	0	ENSG00000229002	AC246785.1
ENSG00000229006	5.77242	1.88458	6.53603	4.03609	ENSG00000229006	TRIM27
ENSG00000229007	0.151964	1.16533	2.13874	1.83477	ENSG00000229007	EXOSC3P1
ENSG00000229009	2.26231	0.286928	0.646713	1.32489	ENSG00000229009	TMPRSS11GP
ENSG00000229010	1.49691	3.63539	3.3529	5.26065	ENSG00000229010	AL161672.1
ENSG00000229013	0	0	0	0	ENSG00000229013	AC083939.1
ENSG00000229014	0	0.256685	0	0.282708	ENSG00000229014	RPL30P13
ENSG00000229016	0.470206	0.993992	0.734639	0.610161	ENSG00000229016	AC096638.2
ENSG00000229018	0.71074	4.8845	5.37206	5.199	ENSG00000229018	PMS2P7
ENSG00000229020	1.16763	3.73073	4.90485	2.22808	ENSG00000229020	AKR7A2P1

ENSG00000229022	0	0.145436	0.131232	0.163949	ENSG00000229022	AL365366.1
ENSG00000229023	0.452181	1.19972	0.788863	3.51486	ENSG00000229023	AC067945.1
ENSG00000229027	0.0424709	0	0.0369719	0	ENSG00000229027	HSFY1P1
ENSG00000229028	0.720023	0	0	0	ENSG00000229028	KRT223P
ENSG00000229029	1.22744	1.18671	0.97322	1.68338	ENSG00000229029	CDCA4P1
ENSG00000229030	0	0	0	0	ENSG00000229030	BX276092.3
ENSG00000229031	0.770763	1.09772	0.968321	2.08906	ENSG00000229031	MTCO1P25
ENSG00000229032	0	0	0	0.583839	ENSG00000229032	AL445685.2
ENSG00000229034	0	0	0.165242	0.129105	ENSG00000229034	MCCD1P2
ENSG00000229035	0	0	0	0	ENSG00000229035	SPRR2C
ENSG00000229037	0	0	0	0	ENSG00000229037	BX323845.3
ENSG00000229038	0.051091	0	0.0451445	0.0287014	ENSG00000229038	RANP1
ENSG00000229040	0	0	0.00828591	0	ENSG00000229040	CR774181.1
ENSG00000229045	0	0	0	0.027414	ENSG00000229045	DDX6P1
ENSG00000229046	1.50788	4.03501	2.26452	3.97618	ENSG00000229046	HMGN1P2
ENSG00000229048	2.08632	1.75907	5.24531	2.67696	ENSG00000229048	DUTP1
ENSG00000229052	2.98628	6.62744	6.71452	11.2708	ENSG00000229052	AL449283.1
ENSG00000229054	0	3.35318	2.76052	1.10229	ENSG00000229054	RPS29P14
ENSG00000229057	0	0.532302	0.313531	0.195424	ENSG00000229057	RPS3AP54
ENSG00000229058	0.588993	1.16103	1.17473	1.07712	ENSG00000229058	AGER
ENSG00000229060	0.126135	0.332323	0.218587	0.707289	ENSG00000229060	AL451124.1
ENSG00000229061	0.449589	0.763133	1.27499	0.973813	ENSG00000229061	ATAT1
ENSG00000229063	0	0	0	0	ENSG00000229063	TRBV23OR9-2
ENSG00000229064	0	0	0	0	ENSG00000229064	AC104073.1
ENSG00000229067	0	0	0	0	ENSG00000229067	AL714022.1
ENSG00000229068	0.0161927	0.00793847	0.00709454	0.0446566	ENSG00000229068	TMPOP1
ENSG00000229069	0	0.0275452	0	0.0234623	ENSG00000229069	BX248093.1
ENSG00000229071	0.0315493	0.0750009	0.205173	0.116243	ENSG00000229071	PRRT1
ENSG00000229072	0	0	0	0	ENSG00000229072	HMGN2P24
ENSG00000229074	0	0.169104	0	0.190528	ENSG00000229074	HLA-DRB1
ENSG00000229077	0.323279	0.093444	0.258819	0.412492	ENSG00000229077	SLC44A4
ENSG00000229079	0	0.840973	0.915578	1.41601	ENSG00000229079	CR848007.2
ENSG00000229080	0	0	0.0881096	0.109681	ENSG00000229080	MTCO3P30
ENSG00000229082	0.0613006	0.294909	0.0541145	0.333842	ENSG00000229082	OR5AW1P
ENSG00000229083	0	0	0.178286	0.329113	ENSG00000229083	PSMA6P2
ENSG00000229086	0.124009	1.17255	0.995435	2.23285	ENSG00000229086	LINC01548
ENSG00000229087	0.808405	0.259103	0.46377	0.849623	ENSG00000229087	AC007738.1
ENSG00000229088	1.17188	2.44968	3.33789	3.89039	ENSG00000229088	MTND1P10
ENSG00000229089	0.570904	1.59105	1.15527	1.38149	ENSG00000229089	ANKRD20A8P
ENSG00000229090	0.3	0.701655	0.224751	0.984313	ENSG00000229090	FO082842.1
ENSG00000229091	0.049328	0.0951124	0	0.053859	ENSG00000229091	HSPA8P8
ENSG00000229092	0	0	0.247259	0.451868	ENSG00000229092	IGHV3-47
ENSG00000229093	0	0.10806	0.097592	0.485039	ENSG00000229093	OR51AB1P
ENSG00000229094	0	0	0.105105	0.0887849	ENSG00000229094	POU5F1
ENSG00000229097	3.27034	7.00052	6.36466	11.7674	ENSG00000229097	CALM2P2
ENSG00000229099	0	0	0.0360102	0	ENSG00000229099	CR933540.2
ENSG00000229100	0	0	0	0	ENSG00000229100	BX248413.1
ENSG00000229101	0	0.520754	0	0.573277	ENSG00000229101	ELOCP20
ENSG00000229103	0.000124398	0.000187449	0.000167498	0.00014757	ENSG00000229103	WASF5P
ENSG00000229104	0	0	0.0576843	0.219205	ENSG00000229104	YY1P2
ENSG00000229106	0	0	0	0	ENSG00000229106	BTBD6P1
ENSG00000229107	0	0	0	0	ENSG00000229107	ABHD17AP4
ENSG00000229110	0.121738	0.117315	0.13967	0.332811	ENSG00000229110	AC006355.1
ENSG00000229112	0	0	0	0	ENSG00000229112	AL356583.2

ENSG00000229115	0	0.48182	0.860638	0.519212	ENSG00000229115	AL390774.1
ENSG00000229117	1180.24	1249.78	873.08	530.251	ENSG00000229117	RPL41
ENSG00000229119	0	0.824494	0	0	ENSG00000229119	AC026403.1
ENSG00000229120	0	1.39689	0.510545	0.615065	ENSG00000229120	CYCSP4
ENSG00000229125	0.0440785	0.10084	0.119165	0.128925	ENSG00000229125	OR2H1
ENSG00000229129	0	0	0	0	ENSG00000229129	ACTG1P2
ENSG00000229132	0.111981	0.161137	0.0479119	0	ENSG00000229132	EIF4A1P10
ENSG00000229133	0.123962	0	0	0	ENSG00000229133	RPS7P4
ENSG00000229136	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000229136	MAS1LP1
ENSG00000229138	0.0468877	0	0	0	ENSG00000229138	CDY6P
ENSG00000229142	0	0.0936022	0	0	ENSG00000229142	HCG4P8
ENSG00000229143	0	0	0	0	ENSG00000229143	AC009480.2
ENSG00000229145	0.0544207	0	0	0	ENSG00000229145	ACTBP1
ENSG00000229146	0	0	0	0	ENSG00000229146	SNX18P4
ENSG00000229147	0.0703605	0.203788	0.154696	0.193048	ENSG00000229147	SMPD4P2
ENSG00000229149	0	0.0149857	0	0	ENSG00000229149	CR759890.1
ENSG00000229150	0	0	0	0	ENSG00000229150	CRYGEP
ENSG00000229156	0.936938	2.68384	1.41437	1.23626	ENSG00000229156	CR769776.2
ENSG00000229159	0	0	0	0	ENSG00000229159	TSPY23P
ENSG00000229161	0	0.0347215	0	0	ENSG00000229161	TCP1P1
ENSG00000229163	0.0559427	0.322355	0.243646	0.243504	ENSG00000229163	NAP1L1P2
ENSG00000229164	0.254844	1.10317	0.28001	1.17894	ENSG00000229164	TRAC
ENSG00000229165	0	0	0	0	ENSG00000229165	GDI2P1
ENSG00000229168	0	0	0	0	ENSG00000229168	RPL19P20
ENSG00000229169	1.09115	1.53806	0	1.65482	ENSG00000229169	AL096701.2
ENSG00000229172	1.44558	2.97855	2.73508	5.59158	ENSG00000229172	AC073065.1
ENSG00000229173	0.183443	0.528809	0.159232	1.09149	ENSG00000229173	AC108059.1
ENSG00000229176	0	0.994558	0.324168	2.00239	ENSG00000229176	SAPCD1
ENSG00000229179	0	0	0	0	ENSG00000229179	CR388407.1
ENSG00000229182	0	0	0	0	ENSG00000229182	MRPS16P1
ENSG00000229183	0.16399	0.502358	0.28688	0.557148	ENSG00000229183	PGA4
ENSG00000229184	0	0.304541	0.137489	0.339319	ENSG00000229184	ATP5HP2
ENSG00000229185	0.0330719	0.060823	0.0385538	0.0189047	ENSG00000229185	OR2H2
ENSG00000229186	1.52154	3.0668	3.52764	2.67276	ENSG00000229186	ADAM1A
ENSG00000229187	0.00724298	0	0	0.00789492	ENSG00000229187	MICC
ENSG00000229189	0	0	0	0	ENSG00000229189	UQCRHP1
ENSG00000229194	1.16587	0.906666	0.309764	0.310221	ENSG00000229194	HLA-V
ENSG00000229197	0	0.21621	0	0	ENSG00000229197	RPS15AP28
ENSG00000229198	0	0	0.8849	1.90096	ENSG00000229198	RP11-12A20.4
ENSG00000229200	0	0.756736	0.195316	1.78328	ENSG00000229200	TRBV7-8
ENSG00000229202	1.24177	1.79606	3.14341	2.86624	ENSG00000229202	PRR3
ENSG00000229204	0	0.162807	0	0.191895	ENSG00000229204	PTGES3P3
ENSG00000229207	0.193412	0.463027	0.168401	0.263998	ENSG00000229207	SERPINH1P1
ENSG00000229208	0	0	0	0.0650983	ENSG00000229208	RBMY2NP
ENSG00000229210	0	0	0	0	ENSG00000229210	SUMO2P1
ENSG00000229211	0	0.0955193	0.118802	0.245823	ENSG00000229211	KCTD9P6
ENSG00000229212	3.75726	3.60218	4.86905	2.34872	ENSG00000229212	AC044860.1
ENSG00000229213	0	1.32115	0	0	ENSG00000229213	AL033527.1
ENSG00000229215	53.9091	7.08621	0.189178	0.132326	ENSG00000229215	HLA-A
ENSG00000229216	0.0579419	0.0677367	0.106788	0.0857336	ENSG00000229216	PPIAP9
ENSG00000229217	0	0	0.275371	0.346885	ENSG00000229217	CYCSP11
ENSG00000229220	0.352013	0.591982	0.305591	0.285819	ENSG00000229220	AC096633.1
ENSG00000229221	0.0670043	0.257891	0.0582253	0.218745	ENSG00000229221	HNRNPA1P66

ENSG00000229222	0.184947	0.596026	1.1725	0.520656	ENSG00000229222	KRT18P4
ENSG00000229226	0	0	0	0	ENSG00000229226	BTF3L4P4
ENSG00000229230	0	0	0	1.04874	ENSG00000229230	MT1P3
ENSG00000229231	0	0	0	0	ENSG00000229231	FEM1AP1
ENSG00000229232	0	0	0	0	ENSG00000229232	KRT18P53
ENSG00000229234	0	0	0	0	ENSG00000229234	RBMY1KP
ENSG00000229235	1.57354	6.40904	9.43453	11.6829	ENSG00000229235	RPL37P18
ENSG00000229237	0	0	0.154525	0	ENSG00000229237	HMGN1P37
ENSG00000229238	0	0	0	0	ENSG00000229238	PPP1R12BP1
ENSG00000229239	0.0505443	0.0973168	0.131936	0.165554	ENSG00000229239	AL451000.1
ENSG00000229241	0.145924	0.211397	0.275787	0.268416	ENSG00000229241	PNPT1P1
ENSG00000229247	0	0	0	0	ENSG00000229247	AL627313.1
ENSG00000229248	0	0	0	0	ENSG00000229248	AC104961.1
ENSG00000229250	0	0	0.119987	0	ENSG00000229250	USP9YP31
ENSG00000229251	0.142225	0	0.188043	0.236854	ENSG00000229251	HNRNPA1P8
ENSG00000229252	16.4661	29.8937	16.2765	16.1278	ENSG00000229252	HLA-E
ENSG00000229253	0.0773985	0.121619	0.973648	1.17022	ENSG00000229253	ZBTB22
ENSG00000229254	0	0	0	0	ENSG00000229254	OR8C1P
ENSG00000229256	0	0	0	0	ENSG00000229256	ST13P13
ENSG00000229259	0.0631994	0.152247	0.193987	0.183923	ENSG00000229259	LRRC37A12P
ENSG00000229265	0	0.0332499	0	0	ENSG00000229265	USP8P1
ENSG00000229266	0	0	0	0	ENSG00000229266	POM121L8P
ENSG00000229268	0.065848	0.0318266	0.114852	0	ENSG00000229268	PES1P2
ENSG00000229273	4.11457	5.10514	7.53395	1.49032	ENSG00000229273	BX664615.1
ENSG00000229280	0	0	0	0	ENSG00000229280	EEF1DP6
ENSG00000229281	0	0	0	0	ENSG00000229281	GPR53P
ENSG00000229284	0.00830609	0.0255328	0.0140436	0.0169609	ENSG00000229284	DPCR1
ENSG00000229286	0	0	0	0	ENSG00000229286	AP000522.1
ENSG00000229287	0	0	0	0	ENSG00000229287	FABP5P4
ENSG00000229288	0.0134337	0.0388434	0.0351159	0.0443134	ENSG00000229288	AL451142.2
ENSG00000229292	0.138654	0	0	0	ENSG00000229292	RFPL4AL1
ENSG00000229293	0	0	0.117234	0	ENSG00000229293	HLA-T
ENSG00000229295	1.10981	1.12457	0.827989	0.209739	ENSG00000229295	HLA-DPB1
ENSG00000229298	1.37097	3.62466	2.24622	3.95534	ENSG00000229298	TUBB8P1
ENSG00000229300	15.4939	23.7762	42.5623	13.313	ENSG00000229300	C6orf48
ENSG00000229302	0	0	0	0	ENSG00000229302	TAF9P2
ENSG00000229303	0	0	0	0	ENSG00000229303	PPIAP25
ENSG00000229305	0	0.0545456	0.148371	0.062032	ENSG00000229305	AL358876.1
ENSG00000229310	0	0	0	0	ENSG00000229310	RPP40P1
ENSG00000229314	0.454877	1.06455	0.277463	1.23858	ENSG00000229314	ORM1
ENSG00000229316	0.105051	0.302675	0.0911169	0.226699	ENSG00000229316	HMGB1P45
ENSG00000229320	2.20404	4.06863	4.28189	3.71344	ENSG00000229320	KRT8P12
ENSG00000229322	0.0667835	0.0952754	0.113969	0.0713369	ENSG00000229322	AC244197.1
ENSG00000229324	0	0	0.204692	0	ENSG00000229324	NUTF2P7
ENSG00000229326	0	0	0	0.145178	ENSG00000229326	AC069154.1
ENSG00000229328	0	0	0	0	ENSG00000229328	OR2W1
ENSG00000229332	0.38618	0.247037	0.115724	0.276422	ENSG00000229332	PGBD4P8
ENSG00000229336	0.800414	1.82831	0.347875	1.23376	ENSG00000229336	AP000568.1
ENSG00000229338	0	0	0.819964	0.658477	ENSG00000229338	AL136084.1
ENSG00000229339	0.876019	1.12014	1.26429	2.03133	ENSG00000229339	AC093414.1
ENSG00000229341	0.23436	0.169341	0.106284	0	ENSG00000229341	TNXB
ENSG00000229342	0	0	0	0	ENSG00000229342	MYL8P
ENSG00000229343	0.0371995	0	0	0	ENSG00000229343	CDY22P

ENSG00000229344	0.428094	0.412406	0.524503	0.258722	ENSG00000229344	MTCO2P12
ENSG00000229346	0	0.0739473	0.0453175	0.16538	ENSG00000229346	TRIM10
ENSG00000229347	0	0	0	0	ENSG00000229347	AL596268.1
ENSG00000229349	1.28077	2.12418	1.58374	2.48347	ENSG00000229349	ACTG1P9
ENSG00000229351	0	0	0	0	ENSG00000229351	KRTAP9-11P
ENSG00000229353	0.413741	0.504397	0.221397	0.191903	ENSG00000229353	TNXB
ENSG00000229357	0	0.299717	0	0.813883	ENSG00000229357	CYCSP51
ENSG00000229358	0.608688	2.06527	1.39807	3.0852	ENSG00000229358	DPY19L1P1
ENSG00000229359	0	0	0	0.135112	ENSG00000229359	PIN1P1
ENSG00000229360	0	0.336501	0	0.125776	ENSG00000229360	PPP1R2P5
ENSG00000229361	0	0.0988547	0	0.056049	ENSG00000229361	UBTFL7
ENSG00000229363	4.30996	3.46615	2.38813	2.98449	ENSG00000229363	NELFE
ENSG00000229364	0	0	0	0	ENSG00000229364	DDX39BP1
ENSG00000229365	0	0	0	0	ENSG00000229365	AC006967.1
ENSG00000229367	0	0	0	0	ENSG00000229367	HMGN2P19
ENSG00000229369	0	0.231602	0.418294	0.259533	ENSG00000229369	AL450263.2
ENSG00000229375	0	0	0	0	ENSG00000229375	USP24P1
ENSG00000229376	0.12115	0.137093	0.672693	0	ENSG00000229376	CICP3
ENSG00000229381	0	0.179114	0.11303	0.436998	ENSG00000229381	TRIM10
ENSG00000229384	0	0.0652987	0.0589391	0.072959	ENSG00000229384	HMGB1P16
ENSG00000229386	0	0	0	0	ENSG00000229386	OR8B9P
ENSG00000229387	1.7628	2.16846	2.52261	0	ENSG00000229387	AC103801.2
ENSG00000229390	0.212651	0	0	0	ENSG00000229390	MICD
ENSG00000229391	1.07059	1.73355	1.53151	1.89055	ENSG00000229391	HLA-DRB6
ENSG00000229394	0	0.0184226	0	0	ENSG00000229394	ZNF70P1
ENSG00000229398	0	0.0881348	0	0.0992262	ENSG00000229398	AL031667.1
ENSG00000229399	0	1.38478	0.313281	0.96158	ENSG00000229399	AL592148.1
ENSG00000229405	0	0	0	0	ENSG00000229405	AC092580.1
ENSG00000229406	0.101783	0	0.0587302	0.0555595	ENSG00000229406	OFD1P4Y
ENSG00000229408	0.0440785	0.10084	0.119165	0.128925	ENSG00000229408	OR2H1
ENSG00000229409	0	0	0	0	ENSG00000229409	AL117328.1
ENSG00000229411	0	0	0	0.321672	ENSG00000229411	MCCD1P1
ENSG00000229412	0	0.00838819	0.0181864	0	ENSG00000229412	OR10C1
ENSG00000229413	0.639452	0	2.49697	12.3249	ENSG00000229413	AC018638.1
ENSG00000229415	0.547229	1.69398	1.15224	1.65124	ENSG00000229415	SFTA3
ENSG00000229416	0	0	0	0	ENSG00000229416	USP9YP8
ENSG00000229417	0.451699	0.676281	1.13728	0.841303	ENSG00000229417	NPM1P25
ENSG00000229419	0.779201	2.47718	1.82944	3.19916	ENSG00000229419	RALGAPA1P1
ENSG00000229420	0.19277	0.30763	0.012302	0	ENSG00000229420	RP11-782C8.7
ENSG00000229421	0	0	0.242239	1.47591	ENSG00000229421	AC133141.1
ENSG00000229422	1.74533	2.14784	1.85549	0.129401	ENSG00000229422	AL512625.2
ENSG00000229423	0	0	0.158998	0	ENSG00000229423	RPL27AP8
ENSG00000229427	0.131294	0.315685	0.174955	0.714259	ENSG00000229427	ANKRD26P4
ENSG00000229428	0	0	0	0	ENSG00000229428	HLA-U
ENSG00000229430	0	7.43E-05	0	0	ENSG00000229430	RPL3P2
ENSG00000229432	0	0	0	0	ENSG00000229432	C6orf15
ENSG00000229435	0.0540198	0	0	0.239801	ENSG00000229435	PIP5K1P2
ENSG00000229436	0	0.449465	0	0	ENSG00000229436	AC073850.1
ENSG00000229439	0	0.0341391	0.030885	0	ENSG00000229439	BX000531.1
ENSG00000229440	0.658476	0.614744	0	0.660364	ENSG00000229440	AL139413.1
ENSG00000229441	0	0	0	0	ENSG00000229441	CR933537.1
ENSG00000229442	0	0.105098	0.0316678	0.0398291	ENSG00000229442	THEMIS3P
ENSG00000229447	1.63411	5.78549	5.2617	6.22624	ENSG00000229447	AC114495.2
ENSG00000229453	0.736253	0	0.158991	0	ENSG00000229453	SPINK8

ENSG00000229455	0.308418	0.591153	0.667308	0.823841	ENSG00000229455	RPS10P18
ENSG00000229456	0.483639	1.61634	2.04371	1.44529	ENSG00000229456	RLIMP1
ENSG00000229461	0	0	0	0	ENSG00000229461	MICG
ENSG00000229462	0	0.030701	0.0275429	0.0346681	ENSG00000229462	AC127383.1
ENSG00000229464	0.294349	2.28622	2.03017	0	ENSG00000229464	RP11-481A12.6
ENSG00000229465	0	0	0	0	ENSG00000229465	ACTG1P11
ENSG00000229467	0	0	0.016343	0	ENSG00000229467	OR2I1P
ENSG00000229468	0	0	2.36545	0	ENSG00000229468	AC097635.1
ENSG00000229469	0	0.0207547	0.0239362	0	ENSG00000229469	CR788300.2
ENSG00000229470	2.29229	6.13227	5.83065	6.34374	ENSG00000229470	GNL1
ENSG00000229471	0	0	0	0	ENSG00000229471	RP11-95K23.7
ENSG00000229473	2.89642	2.72153	2.47084	3.64272	ENSG00000229473	RGS17P1
ENSG00000229474	1.47966	5.09121	4.01687	5.18435	ENSG00000229474	PATL2
ENSG00000229477	0	0	0	0	ENSG00000229477	FAM90A16P
ENSG00000229478	0	0	0	0	ENSG00000229478	ROBO2P1
ENSG00000229485	0	0	0	0	ENSG00000229485	KSR1P1
ENSG00000229486	0.257929	0.493411	0.422394	0.750484	ENSG00000229486	AC104454.1
ENSG00000229488	0.0315493	0.0750009	0.205173	0.116243	ENSG00000229488	PRRT1
ENSG00000229489	0	0	0	0	ENSG00000229489	ATP5A1P5
ENSG00000229492	0	0.0582131	0.0525419	0.130871	ENSG00000229492	FO681548.1
ENSG00000229493	0.0166366	0	0	0.0350395	ENSG00000229493	HLA-DQB2
ENSG00000229496	23.5097	22.6275	19.8233	15.234	ENSG00000229496	DDX39B
ENSG00000229497	0.337137	0	1.13226	0	ENSG00000229497	AC005189.1
ENSG00000229499	0	0	0	0	ENSG00000229499	MICG
ENSG00000229500	0	0	0	0	ENSG00000229500	RPL17P1
ENSG00000229503	0	0.17357	0	0	ENSG00000229503	AC092155.2
ENSG00000229505	0.269939	0.864598	0.869055	1.1164	ENSG00000229505	AC104455.1
ENSG00000229508	0	0	0	0	ENSG00000229508	PHKG1P4
ENSG00000229509	0	0	0	0	ENSG00000229509	AC244023.1
ENSG00000229510	0	0	0	0	ENSG00000229510	AC018692.2
ENSG00000229511	0.0785704	0	0.0745758	0	ENSG00000229511	GAS2L1P1
ENSG00000229513	0	0	0	0	ENSG00000229513	EIF4EBP1P2
ENSG00000229515	0	0.05275	0	0.0510889	ENSG00000229515	FLT1P1
ENSG00000229518	0.401974	0	0.173433	0	ENSG00000229518	UBE2V1P3
ENSG00000229519	3.47395	3.49232	4.90283	5.39581	ENSG00000229519	AL591866.1
ENSG00000229523	0	2.11454	1.91267	0	ENSG00000229523	RP11-7G23.4
ENSG00000229524	6.25331	6.57542	8.09566	8.12722	ENSG00000229524	BAG6
ENSG00000229526	21.6308	95.578	38.9098	75.0933	ENSG00000229526	KRT16P4
ENSG00000229529	1.65343	1.97778	0.692247	1.1727	ENSG00000229529	HLA-V
ENSG00000229530	0	0.132457	0.239369	0.0748746	ENSG00000229530	AL136097.1
ENSG00000229532	0.0938709	0	0	0.30454	ENSG00000229532	AC105443.1
ENSG00000229534	0.0696298	0.254212	0.0603908	0.0751888	ENSG00000229534	HNRNPA1P53
ENSG00000229535	0	0.0169735	0	0	ENSG00000229535	CR753820.1
ENSG00000229541	0	0	0	0	ENSG00000229541	GAPDHP26
ENSG00000229542	0	0	0	0	ENSG00000229542	SSU72P7
ENSG00000229544	0.861203	0.269305	0.946391	0.48651	ENSG00000229544	NKX1-2
ENSG00000229547	0	0	0	0	ENSG00000229547	UBE2DNL
ENSG00000229549	0	0	0.0341145	0.0791301	ENSG00000229549	TSPY8
ENSG00000229551	0	0.0593314	0	0	ENSG00000229551	GAPDHP17
ENSG00000229552	0	0.328295	0.652699	0.77668	ENSG00000229552	HLA-T
ENSG00000229553	0	0	0	0	ENSG00000229553	USP9YP17
ENSG00000229554	0	0	0	0	ENSG00000229554	RPL21P24
ENSG00000229559	0.0901361	0.0866094	0.0782472	0.0975456	ENSG00000229559	AL353597.2

ENSG00000229560	0.448979	1.16581	1.2403	2.13438	ENSG00000229560	LYARP1
ENSG00000229562	0.0333806	0	0	0	ENSG00000229562	ZFYVE9P1
ENSG00000229567	0	2.15319	0.943714	2.82836	ENSG00000229567	AL139421.1
ENSG00000229568	0.140888	0.135143	0.61005	0.905416	ENSG00000229568	SMC4P1
ENSG00000229570	0	0	0	0	ENSG00000229570	GAPDHP58
ENSG00000229571	0	0	0	0	ENSG00000229571	PRAMEF25
ENSG00000229572	0.0320094	0.0925307	0.223059	0.105308	ENSG00000229572	EIF4BP4
ENSG00000229573	0	0	0.0540797	0.179459	ENSG00000229573	BX927250.1
ENSG00000229575	0.0259809	0.0124808	0.033827	0	ENSG00000229575	RPL7P4
ENSG00000229579	0	0	0	0	ENSG00000229579	USP17L26
ENSG00000229585	0.997221	2.14262	1.32987	4.2222	ENSG00000229585	AC110792.1
ENSG00000229586	1.69061	15.2735	5.66258	14.9043	ENSG00000229586	TNPO1P3
ENSG00000229590	0	0	4.257	5.2515	ENSG00000229590	AC005962.1
ENSG00000229593	0	0.125796	0.342667	0.380264	ENSG00000229593	SUCLA2P3
ENSG00000229594	0	0	0	0	ENSG00000229594	AL159987.2
ENSG00000229595	0	0	0	0	ENSG00000229595	AL109810.1
ENSG00000229596	0	0	0	0	ENSG00000229596	MYL8P
ENSG00000229597	0.0140136	0.0646215	0.0389217	0.0176708	ENSG00000229597	BTNL2
ENSG00000229598	1.46708	4.4755	3.40212	2.74696	ENSG00000229598	PRDX3P1
ENSG00000229601	1.8681	3.39397	5.12447	6.67258	ENSG00000229601	AL590762.4
ENSG00000229604	0	0	0.632473	0	ENSG00000229604	MTATP8P2
ENSG00000229605	0.392346	0.188233	0	0	ENSG00000229605	RPL21P93
ENSG00000229608	0.0842133	0.242244	0.295011	0.364162	ENSG00000229608	GOLGA2P4
ENSG00000229612	0.342559	0.324658	0	0.355581	ENSG00000229612	SUMO1P2
ENSG00000229615	0	0	0	0	ENSG00000229615	AC111200.1
ENSG00000229616	1.58082	4.42765	3.25772	3.14934	ENSG00000229616	AL356095.1
ENSG00000229620	0	0.166051	0.0750047	0	ENSG00000229620	AF196972.2
ENSG00000229622	0.105619	0.45119	0.326138	0.694906	ENSG00000229622	MTND5P2
ENSG00000229623	0.109005	1.15148	1.41801	1.88042	ENSG00000229623	METTL21AP1
ENSG00000229626	0	0	0	0	ENSG00000229626	PIGCP2
ENSG00000229627	0	0.857689	0.387328	0	ENSG00000229627	BSNDP4
ENSG00000229629	0	3.9591	0	4.00342	ENSG00000229629	AL500527.2
ENSG00000229631	0.395612	0.391238	0.300564	0	ENSG00000229631	AL603926.1
ENSG00000229635	0	0.422374	0.635634	0.628456	ENSG00000229635	AL137159.1
ENSG00000229636	0	0.0380581	0.101771	0.130191	ENSG00000229636	KRT8P21
ENSG00000229638	0.121358	0.116742	0.473853	0.2709	ENSG00000229638	RPL4P4
ENSG00000229641	0	0	0	0	ENSG00000229641	CYP2C56P
ENSG00000229644	3.05525	1.61094	6.69741	4.11705	ENSG00000229644	NAMPTP1
ENSG00000229648	0.0750229	0	0	0	ENSG00000229648	RPSAP22
ENSG00000229651	0.00724298	0	0	0.00789492	ENSG00000229651	MICC
ENSG00000229652	0	0	0	0	ENSG00000229652	AL359837.1
ENSG00000229657	0.128727	0.370556	0.22302	0.691056	ENSG00000229657	AL391822.1
ENSG00000229658	0.0541528	0.128632	0.101356	0.235967	ENSG00000229658	PABPC1P9
ENSG00000229659	0.557858	2.66755	1.76586	3.92902	ENSG00000229659	RPL26P6
ENSG00000229661	0	0	0	0	ENSG00000229661	BUD31P2
ENSG00000229662	0	0	0	0	ENSG00000229662	AC245047.2
ENSG00000229663	0.0526371	0.0882314	0.0344652	0.151332	ENSG00000229663	AL672296.1
ENSG00000229665	0	0	0	0	ENSG00000229665	PRR20C
ENSG00000229667	0	0	0.212153	0	ENSG00000229667	UBE2V1P9
ENSG00000229668	0.265599	1.26487	0.685879	1.11466	ENSG00000229668	AL133384.1
ENSG00000229670	0.051906	0.0255166	0.206248	0.116834	ENSG00000229670	PKP4P1
ENSG00000229674	0.198125	1.14882	0.510315	1.14217	ENSG00000229674	AL121578.2
ENSG00000229676	1.0997	2.66413	1.49092	3.08001	ENSG00000229676	ZNF492
ENSG00000229677	0	1.39681	1.40132	1.98754	ENSG00000229677	AC018644.1

ENSG00000229680	0.0330719	0.060823	0.0385538	0.0189047	ENSG00000229680	OR2H2
ENSG00000229682	0.316484	0	0	0	ENSG00000229682	AC114755.2
ENSG00000229683	1.43821	1.33883	4.71452	2.82502	ENSG00000229683	ASNSP5
ENSG00000229684	20.0144	27.9814	5.53441	0.46487	ENSG00000229684	TUBB
ENSG00000229685	0.015404	0.0454515	0.0767526	0.0785761	ENSG00000229685	HLA-DPA1
ENSG00000229687	0	0	0	0	ENSG00000229687	AL049745.1
ENSG00000229689	5.08745	3.89497	6.49989	4.59165	ENSG00000229689	AC009237.3
ENSG00000229690	0	0	0.140857	0.173735	ENSG00000229690	MTCO2P1
ENSG00000229693	0	0	0	0	ENSG00000229693	AL606530.1
ENSG00000229695	0.104213	0.100279	0.0453695	0.574537	ENSG00000229695	AC011242.1
ENSG00000229696	0.162862	1.00433	0.539536	0.678412	ENSG00000229696	KARSP1
ENSG00000229698	19.2612	4.36502	4.07808	2.27019	ENSG00000229698	HLA-F
ENSG00000229700	0.293038	0.152056	0.548802	0	ENSG00000229700	AL008627.1
ENSG00000229701	0	0.19858	0	0.111582	ENSG00000229701	MTND2P20
ENSG00000229704	0.555915	0.597004	0.503125	0.929341	ENSG00000229704	EIF2S2P2
ENSG00000229706	0.0579419	0.0677367	0.106788	0.0857336	ENSG00000229706	PPIAP9
ENSG00000229707	0	0	0	0	ENSG00000229707	SKP1P3
ENSG00000229708	0	0	0	0.130954	ENSG00000229708	MARK2P12
ENSG00000229709	0	0	0.139118	0	ENSG00000229709	USP9YP36
ENSG00000229710	0	0	0	0	ENSG00000229710	MTCO3P1
ENSG00000229713	0	0	0.228626	0.278665	ENSG00000229713	AL353779.1
ENSG00000229714	0.00944618	0.0363638	0.0164323	0	ENSG00000229714	ZNF90P2
ENSG00000229715	0.336237	0.824205	1.20507	2.1396	ENSG00000229715	EEF1DP3
ENSG00000229716	1.51087	2.56893	1.75306	1.8049	ENSG00000229716	RPL23AP19
ENSG00000229721	0.111826	0.322095	0.193929	0.361483	ENSG00000229721	AC104115.1
ENSG00000229724	0	0	0	0	ENSG00000229724	OR2AQ1P
ENSG00000229725	0	0	0	0	ENSG00000229725	AC007322.2
ENSG00000229729	7.09447	8.36289	8.90441	11.156	ENSG00000229729	RP11-159G9.5
ENSG00000229730	0	0	0.124259	0.17279	ENSG00000229730	AC013268.2
ENSG00000229731	0	0	0	0	ENSG00000229731	AC107613.1
ENSG00000229733	0	0	0.468273	0	ENSG00000229733	AL030996.1
ENSG00000229735	0	0	0	0	ENSG00000229735	FTLP16
ENSG00000229737	0	0	0	0	ENSG00000229737	TMEM183AP1
ENSG00000229738	0	0.332753	0.149156	0.369661	ENSG00000229738	AC010240.1
ENSG00000229741	0.0140136	0	0	0.0176708	ENSG00000229741	BTNL2
ENSG00000229742	0	0.699049	0.142185	1.06082	ENSG00000229742	AC092809.1
ENSG00000229744	0.164919	0	0.142633	0	ENSG00000229744	AC011998.2
ENSG00000229745	0	0	0	0	ENSG00000229745	BPY2DP
ENSG00000229747	0	0	0.0825208	0	ENSG00000229747	AL445687.2
ENSG00000229749	0	0	0	0	ENSG00000229749	COTL1P1
ENSG00000229752	0	0	0	0	ENSG00000229752	RPL7P10
ENSG00000229753	0	0	0	0	ENSG00000229753	RPS27AP15
ENSG00000229754	1.1803	3.05441	2.87072	3.61858	ENSG00000229754	CXCR2P1
ENSG00000229756	0.508545	0.969294	0	2.40725	ENSG00000229756	RPL31P20
ENSG00000229757	0	0	0	0	ENSG00000229757	AL031736.2
ENSG00000229758	0	0.685551	0.312049	0.37509	ENSG00000229758	DYNLT3P2
ENSG00000229759	2.99372	1.51586	1.30617	0.620211	ENSG00000229759	MRPS18AP1
ENSG00000229760	0	0	0	0	ENSG00000229760	MTCO1P52
ENSG00000229761	0	0	0	0	ENSG00000229761	RPS20P1
ENSG00000229762	0	0	0.0949305	0	ENSG00000229762	AC092647.3
ENSG00000229765	0	0.309879	0	0	ENSG00000229765	AL354868.1
ENSG00000229767	0	1.22163	2.12343	0	ENSG00000229767	DDR1
ENSG00000229769	0.436152	0.521012	1.22317	0.230566	ENSG00000229769	TRBV10-2
ENSG00000229781	0	0	0.0259032	0.0652287	ENSG00000229781	AC013444.1

ENSG00000229785	0	0.0720515	0	0	ENSG00000229785	SLC25A38P1
ENSG00000229786	0.983022	0	0	0	ENSG00000229786	SNRPFP2
ENSG00000229789	3.58495	2.8366	4.58849	5.73933	ENSG00000229789	RP11-391M20.1
ENSG00000229794	0.448999	0.540157	0.489216	0.979224	ENSG00000229794	MTCYBP32
ENSG00000229795	0	2.47835	2.22232	1.79951	ENSG00000229795	RPS21P1
ENSG00000229798	0.0463114	0	0	0.15283	ENSG00000229798	KRT18P26
ENSG00000229800	0.642666	1.49014	1.84254	1.89143	ENSG00000229800	ATP8A2P2
ENSG00000229802	8.10034	7.04224	6.12923	6.51393	ENSG00000229802	SLC39A7
ENSG00000229806	0.189707	0	0.164099	0	ENSG00000229806	RPS15P5
ENSG00000229808	0.689131	1.97155	1.39399	1.35182	ENSG00000229808	AL391825.1
ENSG00000229809	3.96155	6.96249	7.52009	5.63309	ENSG00000229809	ZNF688
ENSG00000229814	0	0	0	0	ENSG00000229814	RPL35AP21
ENSG00000229815	0	0.0734115	0.0872331	0.500749	ENSG00000229815	CCNB1IP1P1
ENSG00000229816	1.27934	1.91016	2.54407	3.08071	ENSG00000229816	DDX50P1
ENSG00000229817	0.166181	0.374731	0.240225	0.1225	ENSG00000229817	AL133412.1
ENSG00000229818	0	5.1994	4.58046	2.74975	ENSG00000229818	RP11-459A10.3
ENSG00000229820	0.44434	1.68693	2.31566	1.43433	ENSG00000229820	CR391992.1
ENSG00000229822	0.225485	0.430855	0.388992	0.952576	ENSG00000229822	AL353691.1
ENSG00000229824	0	0	0	0	ENSG00000229824	RPL12P34
ENSG00000229825	0	0	0	0	ENSG00000229825	RP5-1052M9.4
ENSG00000229826	0	0	0	0	ENSG00000229826	AC244505.5
ENSG00000229827	0.236298	0.451204	0	0.249331	ENSG00000229827	AC093899.1
ENSG00000229828	0.100243	0.165827	0	0.150463	ENSG00000229828	PDE4DIPP1
ENSG00000229829	0	0.157017	0.0708699	0	ENSG00000229829	DUTP4
ENSG00000229830	0	0	0	0	ENSG00000229830	AL589823.1
ENSG00000229831	0	0.487005	0	0.268673	ENSG00000229831	AC108039.2
ENSG00000229833	48.8592	39.1639	25.9168	29.9787	ENSG00000229833	PET100
ENSG00000229834	0	0	0	0	ENSG00000229834	AL354676.1
ENSG00000229835	0.226163	0.0935472	0.169875	0.141681	ENSG00000229835	KHSRPP1
ENSG00000229836	0	0.0458373	0.0827353	0.200941	ENSG00000229836	AL671883.1
ENSG00000229840	0.628865	1.01177	0.178261	1.10811	ENSG00000229840	ISCA1P2
ENSG00000229842	0.102154	0.0981316	0	0.110304	ENSG00000229842	MTATP6P13
ENSG00000229849	0.184094	0.176893	0	0.199143	ENSG00000229849	PYHIN5P
ENSG00000229853	1.1304	2.35729	1.54447	3.94126	ENSG00000229853	AL034418.1
ENSG00000229856	0	0	0	0	ENSG00000229856	CYP21A1P
ENSG00000229857	0.452998	0.71771	0.316281	0.490184	ENSG00000229857	AL353637.1
ENSG00000229858	0.264299	0.755255	0.227546	0.693498	ENSG00000229858	AC016831.2
ENSG00000229859	0.791779	1.28136	1.19534	2.19383	ENSG00000229859	PGA3
ENSG00000229861	3.6819	4.08555	4.50723	3.12515	ENSG00000229861	MRPS18B
ENSG00000229863	0.245298	0.353123	0.850678	0.395576	ENSG00000229863	AC097358.1
ENSG00000229865	0	0	0	0	ENSG00000229865	RPL31P54
ENSG00000229866	0	0	0.00605942	0	ENSG00000229866	OR2J3
ENSG00000229870	0.504178	1.52682	0.581297	2.1729	ENSG00000229870	RPL21P89
ENSG00000229871	0	0	0	0.0771887	ENSG00000229871	RPSAP20
ENSG00000229875	0.27915	0.530947	0.738035	1.16927	ENSG00000229875	EIF1P1
ENSG00000229877	0	0.0951809	0	0	ENSG00000229877	PAICSP5
ENSG00000229878	4.05738	8.40441	0.67243	9.75335	ENSG00000229878	AL365203.2
ENSG00000229880	0	0	0	0	ENSG00000229880	IMMTP1
ENSG00000229885	0	0	0	0	ENSG00000229885	AC244505.6
ENSG00000229886	0	0	0	0	ENSG00000229886	AC068533.2
ENSG00000229887	0.0647052	0.0622191	0	0.0710411	ENSG00000229887	HNRNPA1P6
ENSG00000229889	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000229889	MAS1LP1
ENSG00000229890	0	0	0	0	ENSG00000229890	ACTP1
ENSG00000229892	0	0	0	0	ENSG00000229892	AL035666.1

ENSG00000229894	0.233206	1.07287	0.796439	0.942936	ENSG00000229894	GK3P
ENSG00000229897	0	0.0445132	0.0402726	0.102072	ENSG00000229897	SEPT7P7
ENSG00000229898	0.0558802	0	0.0241408	0.0296507	ENSG00000229898	ZDHHC20P1
ENSG00000229899	0	0	0	0	ENSG00000229899	AC084290.1
ENSG00000229900	0	0	0	0.522658	ENSG00000229900	HSPD1P21
ENSG00000229906	0	1.07616	0.480325	1.18076	ENSG00000229906	SNRPGP11
ENSG00000229907	0	0	0	0	ENSG00000229907	DEFB108A
ENSG00000229909	0	0	0.173759	0	ENSG00000229909	TRIM60P16
ENSG00000229910	0	0	0	0.147057	ENSG00000229910	HNRNPA1P18
ENSG00000229911	0	0	0	0	ENSG00000229911	AL139148.1
ENSG00000229914	0	0	0	0	ENSG00000229914	AL138899.2
ENSG00000229917	1.71076	1.17745	1.36168	2.06872	ENSG00000229917	RPL7P46
ENSG00000229919	0	0	0	0	ENSG00000229919	ELOCP3
ENSG00000229920	8.71646	22.9958	19.6331	38.8848	ENSG00000229920	RPS4XP5
ENSG00000229924	0	0.0220191	0.0243992	0.17079	ENSG00000229924	FAM90A26
ENSG00000229926	0	0	0	0	ENSG00000229926	AL591424.1
ENSG00000229927	0	1.2274	1.3864	0.568922	ENSG00000229927	RHEBP1
ENSG00000229929	1.40869	1.16201	0.860284	0.269129	ENSG00000229929	TRIM39
ENSG00000229930	0	0	0	0	ENSG00000229930	AC138393.2
ENSG00000229932	0.754621	0.363776	0.327267	0.233333	ENSG00000229932	YWHAZP3
ENSG00000229935	0	0	0	0	ENSG00000229935	MTCYBP9
ENSG00000229936	0	0	0	0	ENSG00000229936	RBM22P9
ENSG00000229937	0	0	0.146771	0.183998	ENSG00000229937	PRPS1L1
ENSG00000229939	6.35821	11.6493	0	25.6206	ENSG00000229939	AL589880.1
ENSG00000229940	0	0	0	0	ENSG00000229940	TSPY22P
ENSG00000229942	1.28298	0	0	0	ENSG00000229942	IFITM4P
ENSG00000229944	14.1516	6.62834	3.63363	2.42778	ENSG00000229944	EIF4EP2
ENSG00000229946	0	0	0	0	ENSG00000229946	B3GNT2P1
ENSG00000229947	5.88679	2.2143	0	3.36143	ENSG00000229947	RP13-766D20.1
ENSG00000229948	0.386992	1.29692	1.07072	2.03289	ENSG00000229948	B3GALNT1P1
ENSG00000229949	0	0	0	0	ENSG00000229949	AC005094.1
ENSG00000229954	0.13213	0.469598	0.605648	1.29374	ENSG00000229954	MTND2P2
ENSG00000229959	0	0.182179	0.286103	0	ENSG00000229959	HLA-K
ENSG00000229965	0.0837137	0	0	0	ENSG00000229965	AL359704.1
ENSG00000229968	0.194746	0.467952	0.37258	1.69253	ENSG00000229968	AL022578.1
ENSG00000229972	4.5234	12.058	15.4933	25.4003	ENSG00000229972	IQCF3
ENSG00000229974	0	0	0	0	ENSG00000229974	AC083862.1
ENSG00000229975	0	0.0973168	0.0880077	0.275923	ENSG00000229975	LIPT1P1
ENSG00000229977	0	0	0.173434	0.212873	ENSG00000229977	AC073264.1
ENSG00000229978	0.0200683	0	0.177255	0.0219617	ENSG00000229978	PRAMEF36P
ENSG00000229979	0	0.210343	0	0	ENSG00000229979	AC243428.1
ENSG00000229982	0	0.0604057	0.0549497	0.137566	ENSG00000229982	GTF3AP6
ENSG00000229985	0.351946	0	0	0	ENSG00000229985	AL590640.2
ENSG00000229988	0	0	0	0	ENSG00000229988	HBBP1
ENSG00000229991	0.0654271	0.187988	0.0606231	0.608932	ENSG00000229991	AKR1B1P1
ENSG00000229992	1.71359	2.41297	1.44451	6.81108	ENSG00000229992	HMGB3P9
ENSG00000229994	0.442458	1.51081	1.23029	2.23399	ENSG00000229994	RPL5P4
ENSG00000229995	0	0	0	0	ENSG00000229995	MICG
ENSG00000229998	11.0877	13.2953	9.93908	10.5618	ENSG00000229998	PPP1R18
ENSG00000230000	0.411817	0.906073	0.842373	0.89556	ENSG00000230000	AC006455.5
ENSG00000230003	0	0	0	0	ENSG00000230003	AL445646.1
ENSG00000230006	8.22979	24.4836	17.4369	36.7132	ENSG00000230006	ANKRD36BP2
ENSG00000230009	0	0	0	0.418099	ENSG00000230009	MTCO2P3
ENSG00000230011	0	0	0	0	ENSG00000230011	CTSLP4

ENSG00000230012	0	0.0288995	0.0208992	0	ENSG00000230012	HTATSF1P1
ENSG00000230016	0	0	0	0	ENSG00000230016	DHFRP2
ENSG00000230018	0	0.148556	0.133925	0	ENSG00000230018	AL133482.1
ENSG00000230019	0	0.563166	0.127852	0.314228	ENSG00000230019	YWHAQP9
ENSG00000230022	0.109626	0.748362	0.191792	1.20711	ENSG00000230022	FNTAP2
ENSG00000230025	0	0	0	0	ENSG00000230025	AC007967.3
ENSG00000230026	0.797291	1.22815	1.50472	2.79091	ENSG00000230026	AL357556.1
ENSG00000230029	0	0	0	0	ENSG00000230029	CDY11P
ENSG00000230031	0	0	0	0	ENSG00000230031	POTEB2
ENSG00000230034	0.483123	7.52829	0.850299	2.01631	ENSG00000230034	PSMB8
ENSG00000230036	92.7167	129.323	148.749	211.764	ENSG00000230036	AL596137.1
ENSG00000230037	0.166163	0	0	0	ENSG00000230037	UBBP1
ENSG00000230039	0.0621083	0	0.0593226	0	ENSG00000230039	AL450487.1
ENSG00000230042	0.822088	2.46756	1.3568	2.45496	ENSG00000230042	AK3P3
ENSG00000230043	0	0	0	4.03258	ENSG00000230043	TMSB4XP6
ENSG00000230044	0	0	0	0	ENSG00000230044	AC110754.1
ENSG00000230045	0.0383418	0.0557242	0	0	ENSG00000230045	FAM90A15P
ENSG00000230047	0	0	0.799175	0	ENSG00000230047	AC017104.2
ENSG00000230048	1.02425	1.71745	2.89525	2.54589	ENSG00000230048	VWA7
ENSG00000230052	0	0	0.716094	0.963152	ENSG00000230052	MTND3P2
ENSG00000230053	0	0	0	0	ENSG00000230053	AC093578.1
ENSG00000230055	5.37653	4.15922	5.25204	4.18245	ENSG00000230055	CISD3
ENSG00000230056	0	0	0	0.00316142	ENSG00000230056	DDX6P1
ENSG00000230060	0.181329	0.151186	0.308192	0.303335	ENSG00000230060	MPIG6B
ENSG00000230062	0.109136	0.512356	0.47834	0.487377	ENSG00000230062	ANKRD66
ENSG00000230064	0	0	0	0	ENSG00000230064	AL772161.1
ENSG00000230067	1.74229	2.4008	3.03061	5.30806	ENSG00000230067	HSPD1P6
ENSG00000230069	1.40466	1.60101	1.44778	1.19888	ENSG00000230069	LRRC37A15P
ENSG00000230071	1.5064	2.01499	2.09566	3.32038	ENSG00000230071	RPL4P6
ENSG00000230072	0.177216	0	0	0	ENSG00000230072	SFTA2
ENSG00000230073	0	0	0	0	ENSG00000230073	AC009947.1
ENSG00000230076	0	1.02196	0	1.67815	ENSG00000230076	RPL10P6
ENSG00000230077	0.859235	0.676088	0.619685	2.46832	ENSG00000230077	MTAPP2
ENSG00000230079	0.139161	0.179267	0.040389	0.0508493	ENSG00000230079	STK24P1
ENSG00000230080	0.049539	0.0476847	0.0431701	0.27046	ENSG00000230080	AC139143.1
ENSG00000230081	1.65319	3.25371	4.63703	7.81345	ENSG00000230081	HSPE1P28
ENSG00000230083	0	0	0	0	ENSG00000230083	AC009237.4
ENSG00000230086	0	0.0720455	0.129073	0.161321	ENSG00000230086	VN1R96P
ENSG00000230087	0.0713225	0.137178	0	0.154989	ENSG00000230087	AC104389.2
ENSG00000230088	15.8811	67.9843	27.6916	45.4621	ENSG00000230088	KRT16P5
ENSG00000230092	1.14615	5.8992	3.15164	5.70936	ENSG00000230092	AL669831.4
ENSG00000230097	0	0	0	0.0319388	ENSG00000230097	ME2P1
ENSG00000230099	0	0	0.233348	0.144446	ENSG00000230099	TRBV5-4
ENSG00000230101	0	0	0	1.85289	ENSG00000230101	TUBB3P2
ENSG00000230104	0.0999421	0.188875	0.0853118	0.424886	ENSG00000230104	AC018712.1
ENSG00000230106	0	0	0	0	ENSG00000230106	SNRPCP15
ENSG00000230108	0.222879	0.099013	0.196978	0.0453146	ENSG00000230108	TNF
ENSG00000230110	9.41013	22.8345	24.9895	36.5359	ENSG00000230110	AC005086.1
ENSG00000230111	0	0	0	0	ENSG00000230111	AC115283.1
ENSG00000230112	0.912684	1.72145	1.47397	1.62192	ENSG00000230112	AL157398.1
ENSG00000230116	0	0	0	0	ENSG00000230116	AL445669.1
ENSG00000230118	0	0	0	0	ENSG00000230118	AC092569.1
ENSG00000230119	0	0	0	0	ENSG00000230119	AC123900.1
ENSG00000230122	0	0	0.140499	0.285548	ENSG00000230122	ECEL1P3

ENSG00000230123	0	0.119393	0.215625	0.534825	ENSG00000230123	DLEC1P1
ENSG00000230125	0	0.933793	0.834589	0.503476	ENSG00000230125	EEF1A1P39
ENSG00000230128	4.65E-10	35.1599	5.83678	11.0089	ENSG00000230128	IER3
ENSG00000230130	0	0	0	0	ENSG00000230130	MTND2P39
ENSG00000230132	0.225573	0.527497	0.285692	0.42241	ENSG00000230132	AC006457.1
ENSG00000230136	0	0.0275452	0	0.0234623	ENSG00000230136	BX927132.2
ENSG00000230137	0.160329	0.153673	0.13874	0	ENSG00000230137	AC004832.2
ENSG00000230141	5.72E-05	0.324416	0.10432	1.04653	ENSG00000230141	HLA-DOA
ENSG00000230143	2.26191	3.7453	2.16044	4.50649	ENSG00000230143	FLOT1
ENSG00000230146	0	0	0.0449977	0	ENSG00000230146	SEPHS1P4
ENSG00000230147	0	0.164251	0.296797	0	ENSG00000230147	AL158071.1
ENSG00000230154	0.333998	0.986727	0.579093	1.77732	ENSG00000230154	AC018463.1
ENSG00000230157	0	0	0	0	ENSG00000230157	ATP5G1P1
ENSG00000230158	0	0.126274	0.180206	0.0820827	ENSG00000230158	MTND1P28
ENSG00000230160	0.268129	0.510854	0.230843	0.844042	ENSG00000230160	AC004854.1
ENSG00000230161	0	0	0	0	ENSG00000230161	AL162395.1
ENSG00000230162	0.197109	0.230624	0.183093	0.253604	ENSG00000230162	CT45A11P
ENSG00000230164	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000230164	MAS1LP1
ENSG00000230165	0.290989	0.276518	0.249965	0	ENSG00000230165	AURKAPS2
ENSG00000230166	0	0	0.63768	1.15623	ENSG00000230166	RPL35AP24
ENSG00000230169	0	1.12521	0.70342	2.84447	ENSG00000230169	RPL30P16
ENSG00000230170	0	0	0	0	ENSG00000230170	HNRNPA1P28
ENSG00000230171	0.4705	0	0	0	ENSG00000230171	RPL22P18
ENSG00000230175	0.332948	2.39232	0.848849	1.24228	ENSG00000230175	AL451074.4
ENSG00000230178	0.124217	0.258945	0.132008	0.192383	ENSG00000230178	OR4F3
ENSG00000230180	2.40146	2.25979	2.22275	3.97845	ENSG00000230180	RPL12P49
ENSG00000230181	0.0288811	0.0197876	0.0178653	0	ENSG00000230181	AL662826.2
ENSG00000230182	0	0.697714	0.211329	0.514875	ENSG00000230182	RNF10P1
ENSG00000230183	0.100848	0	1.15378	0.112892	ENSG00000230183	CNOT6LP1
ENSG00000230185	16.4885	40.1381	43.7754	62.8514	ENSG00000230185	C9orf147
ENSG00000230187	0	0	0	0	ENSG00000230187	AL139109.1
ENSG00000230188	1.50966	2.00361	1.32726	1.30436	ENSG00000230188	AL158156.1
ENSG00000230189	5.87382	11.1997	14.8102	11.5694	ENSG00000230189	AC008267.2
ENSG00000230191	0	0	0	0	ENSG00000230191	AC006970.1
ENSG00000230192	0.0943836	0	0.0819222	0.102056	ENSG00000230192	AC073387.1
ENSG00000230193	0	0	0	0	ENSG00000230193	MYL8P
ENSG00000230194	0.357311	0.338527	1.37348	0.741157	ENSG00000230194	AC000081.1
ENSG00000230195	0	0	0	0	ENSG00000230195	AC118138.2
ENSG00000230196	0	0	0	0	ENSG00000230196	DDX43P3
ENSG00000230198	0	0	0	0	ENSG00000230198	RPL37P4
ENSG00000230199	0	0	0	0	ENSG00000230199	AL603825.1
ENSG00000230201	0.452181	1.29571	1.30129	2.55729	ENSG00000230201	ATP6V0CP1
ENSG00000230202	0	0	0	0	ENSG00000230202	AL450405.1
ENSG00000230203	0	0	0	0	ENSG00000230203	Z99714.1
ENSG00000230204	0	0	0.124364	0	ENSG00000230204	FTH1P5
ENSG00000230207	0.0520901	0.0251961	0	0	ENSG00000230207	RPL4P5
ENSG00000230208	0.131655	0.63156	0.344164	0.565122	ENSG00000230208	IFNNP1
ENSG00000230209	0	0	0	0	ENSG00000230209	HNRNPA1P2
ENSG00000230210	0	0	0	0	ENSG00000230210	FAM35EP
ENSG00000230211	0	0.0169735	0.0627602	0.0560227	ENSG00000230211	AL662847.1
ENSG00000230213	0.0732002	0.209792	0.0638264	0.157982	ENSG00000230213	OR8V1P
ENSG00000230214	0.284873	0.273238	0.246681	0.152511	ENSG00000230214	FTLP18
ENSG00000230216	0.134389	0	0	0.0721368	ENSG00000230216	HSPB1P2

ENSG00000230219	0.690069	1.02347	1.34784	1.73483	ENSG00000230219	FAM92A1P2
ENSG00000230221	0.140893	0.405961	0.303515	0.608034	ENSG00000230221	AL157384.1
ENSG00000230224	1.95145	1.58007	2.86788	2.725	ENSG00000230224	PHBP9
ENSG00000230225	0.281131	0.135317	0.274248	0.825351	ENSG00000230225	MTND5P14
ENSG00000230227	0.0679705	0.130727	0	0	ENSG00000230227	SIAH1P1
ENSG00000230228	0	0	0	0	ENSG00000230228	AL590609.2
ENSG00000230230	0	3.46972	0	0	ENSG00000230230	TRIM26
ENSG00000230231	0	0	0	0	ENSG00000230231	FMO7P
ENSG00000230237	0.241914	0.464278	0.314447	0.520246	ENSG00000230237	AC010975.2
ENSG00000230238	0.132445	0.0092538	0.116046	0	ENSG00000230238	HLA-V
ENSG00000230240	0	0.272724	0.238698	0	ENSG00000230240	RPL34P19
ENSG00000230241	0	0.2823	0	0.598348	ENSG00000230241	AC244636.1
ENSG00000230243	0	0	0	0	ENSG00000230243	FKBP1AP3
ENSG00000230244	0.247652	0.143163	0.129642	0.379568	ENSG00000230244	RAD23BP2
ENSG00000230245	0.815249	1.73066	0	2.24327	ENSG00000230245	BX088651.3
ENSG00000230246	0.397734	0.69061	0.370813	0.835325	ENSG00000230246	SPATA31C1
ENSG00000230247	0.244719	0	0.318131	0.263111	ENSG00000230247	HNRNPH3P1
ENSG00000230249	0.226401	0	0	0	ENSG00000230249	AC112653.1
ENSG00000230251	0	0	0	0	ENSG00000230251	PHBP4
ENSG00000230252	0	0	0.0534295	0.0901304	ENSG00000230252	MTND2P4
ENSG00000230254	16.4661	29.8937	16.2765	16.1278	ENSG00000230254	HLA-E
ENSG00000230255	0.284473	0.218889	0	0.141884	ENSG00000230255	RP11-423O2.1
ENSG00000230256	0	0	0	0.324894	ENSG00000230256	FGFR1OP2P1
ENSG00000230259	0	0	0	0	ENSG00000230259	AC008738.1
ENSG00000230261	0	0	0	0.0724196	ENSG00000230261	OR52J2P
ENSG00000230265	0	0.219383	0	0	ENSG00000230265	AC079178.1
ENSG00000230267	4.23781	9.05361	5.49666	8.61978	ENSG00000230267	HERC2P4
ENSG00000230268	0	0	0	0	ENSG00000230268	SSU72P8
ENSG00000230271	0.196109	2.1816	1.25254	3.66346	ENSG00000230271	AC023141.5
ENSG00000230273	0	0.441653	0	0.244114	ENSG00000230273	AC087163.1
ENSG00000230274	0	0	0	0	ENSG00000230274	PGAM1P3
ENSG00000230275	0	0	0	0	ENSG00000230275	SERBP1P4
ENSG00000230276	0	0.251752	0	0.554798	ENSG00000230276	AL162388.1
ENSG00000230279	0.0274983	0.0159269	0.0264951	0.0206416	ENSG00000230279	LTA
ENSG00000230280	0.549882	1.38359	1.84451	1.40651	ENSG00000230280	HNRNPA1P59
ENSG00000230281	0	0.0491177	0.0443564	0.164295	ENSG00000230281	AL590812.3
ENSG00000230282	0.0877201	0.112743	0.477208	0.569913	ENSG00000230282	RPL7P61
ENSG00000230283	0	0	0	0	ENSG00000230283	RPS12P24
ENSG00000230284	0	0	0	0	ENSG00000230284	AL160275.2
ENSG00000230287	1.25402	5.00306	3.47913	1.26197	ENSG00000230287	AL445928.1
ENSG00000230291	0	0	0	0	ENSG00000230291	AC078817.1
ENSG00000230293	1.42309	3.45529	2.24397	3.08904	ENSG00000230293	MSH5
ENSG00000230295	1.18056	2.87208	4.35124	2.6762	ENSG00000230295	GTF2IP23
ENSG00000230299	0	5.15447	0	16.2032	ENSG00000230299	AC093162.1
ENSG00000230301	0	0	0	0.0593613	ENSG00000230301	OR5H6
ENSG00000230302	0	0.653218	0.482111	1.17539	ENSG00000230302	MTND3P4
ENSG00000230304	0	0	0.173632	0	ENSG00000230304	CICP6
ENSG00000230305	5.83568	12.8708	13.217	22.5265	ENSG00000230305	AC004980.3
ENSG00000230306	0	0	0.387068	0	ENSG00000230306	BANF1P2
ENSG00000230307	0	0	0	0	ENSG00000230307	OR6C5P
ENSG00000230308	1.40869	1.16201	0.860284	0.269129	ENSG00000230308	TRIM39
ENSG00000230311	0	0	0.186035	0	ENSG00000230311	TOMM20P4
ENSG00000230312	0.137952	0.182932	0.109954	0.173159	ENSG00000230312	AC234782.1
ENSG00000230318	0.0354933	0.281256	0.188728	0.315138	ENSG00000230318	XRCC6P3

ENSG00000230320	0	0.332559	0	0.184883	ENSG00000230320	BEND7P1
ENSG00000230321	0.576167	0.18376	0.165905	0.40776	ENSG00000230321	MTCO2P27
ENSG00000230326	0.177216	0.339255	0.612722	1.74969	ENSG00000230326	HMGN1P33
ENSG00000230327	0.0915595	0	0.158959	0.198109	ENSG00000230327	MTCO1P42
ENSG00000230328	0	0	0.0640242	0.081108	ENSG00000230328	AL359893.1
ENSG00000230330	0	0	0	0	ENSG00000230330	HMGN2P3
ENSG00000230331	0	0	0.229694	0.28	ENSG00000230331	AL160004.2
ENSG00000230332	1.66172	0.922352	0.663665	1.08063	ENSG00000230332	RNF39
ENSG00000230335	0.503982	0.168585	0.891978	1.09899	ENSG00000230335	DNAJB5P1
ENSG00000230336	0	0.0655396	0	0.0887849	ENSG00000230336	POU5F1
ENSG00000230338	0	0	0.14042	0.173209	ENSG00000230338	MTND4P19
ENSG00000230339	0.519832	0	0	0.5269	ENSG00000230339	AC015818.1
ENSG00000230341	1.17902	0.798709	0.336089	1.23078	ENSG00000230341	PPP1R18
ENSG00000230342	0	0	0	0	ENSG00000230342	FANCD2P2
ENSG00000230343	0	0	0	0	ENSG00000230343	AC018892.1
ENSG00000230347	0	0.0219476	0.0109151	0.0319741	ENSG00000230347	CT47A8
ENSG00000230350	0.378129	0	0	0.577119	ENSG00000230350	RPL35AP3
ENSG00000230353	0	0	0	0	ENSG00000230353	AC114755.3
ENSG00000230354	0	0	0	0	ENSG00000230354	STK19B
ENSG00000230355	0	0.918071	5.10276	0	ENSG00000230355	AC009474.2
ENSG00000230356	0	0	0	0	ENSG00000230356	NCAPD2P1
ENSG00000230357	0	0	0.241007	0	ENSG00000230357	MCCD1P1
ENSG00000230358	1.06216	1.50757	2.29121	2.23066	ENSG00000230358	SPDYE21P
ENSG00000230359	0.365591	0	1.10401	0	ENSG00000230359	TPI1P2
ENSG00000230360	0.021473	0.143626	0.0925085	0.11773	ENSG00000230360	DDX10P2
ENSG00000230361	0	0	0	0	ENSG00000230361	VN1R32P
ENSG00000230362	0	0	0	0	ENSG00000230362	ACTG1P23
ENSG00000230364	0	0	0.0392824	0.0986583	ENSG00000230364	RPL4P3
ENSG00000230370	0.487142	0.311106	0.948442	1.99616	ENSG00000230370	RPL23AP52
ENSG00000230371	0	0	0.0916057	0.0384129	ENSG00000230371	KARSP2
ENSG00000230373	2.39195	2.33624	2.72858	3.46357	ENSG00000230373	GOLGA6L5P
ENSG00000230375	0	0	0	0	ENSG00000230375	GSTA11P
ENSG00000230376	0	0	0	0.239043	ENSG00000230376	MEMO1P4
ENSG00000230377	0	0.139689	0.126289	0.153766	ENSG00000230377	ELOCP7
ENSG00000230383	0.189045	0	0.253596	0.51633	ENSG00000230383	AC009245.1
ENSG00000230384	0	0	0	0	ENSG00000230384	RPSAP25
ENSG00000230386	0	0	0	0	ENSG00000230386	AC104057.1
ENSG00000230391	0	0.068967	0	0	ENSG00000230391	RPSAP23
ENSG00000230395	0	0	0	0	ENSG00000230395	AC092651.1
ENSG00000230397	0.889458	0	0	7.0399	ENSG00000230397	SPTLC1P1
ENSG00000230398	0	0	0	0	ENSG00000230398	HINT2P1
ENSG00000230399	0.0928688	0.240668	0.247701	0.371463	ENSG00000230399	RBBP8P1
ENSG00000230405	0	0	0.305218	1.11174	ENSG00000230405	RPS3AP52
ENSG00000230406	0	0	0	0	ENSG00000230406	AC079834.1
ENSG00000230407	0	0	0	0	ENSG00000230407	AC018717.1
ENSG00000230409	1.5852	3.33579	3.51635	5.94562	ENSG00000230409	TCEA1P2
ENSG00000230411	0	0	0	0	ENSG00000230411	OR3D1P
ENSG00000230412	0	0	0	0	ENSG00000230412	ELOCP12
ENSG00000230413	0.0156997	0	0	4.98E-09	ENSG00000230413	HLA-G
ENSG00000230416	0.0677928	0	0	0	ENSG00000230416	OR5M4P
ENSG00000230418	0	0	0.135432	0.167174	ENSG00000230418	ARL2BPP7
ENSG00000230419	0	0	0	0	ENSG00000230419	AL845454.1
ENSG00000230422	0.0161927	0.00793847	0.00709454	0.0446566	ENSG00000230422	TMPOP1
ENSG00000230425	0.200436	0.559217	0.1711	0	ENSG00000230425	RSU1P1

ENSG00000230428	0.808485	0	0.343908	0.832747	ENSG00000230428	AL049542.1
ENSG00000230430	0	0	0	0	ENSG00000230430	USP17L25
ENSG00000230441	0	0.00827178	0.059801	0.0281478	ENSG00000230441	UBQLN1P1
ENSG00000230444	0.0907641	0.441786	0.244642	0.103886	ENSG00000230444	TFAMP1
ENSG00000230445	0.342777	0.933692	1.22437	0.619775	ENSG00000230445	LRRC37A6P
ENSG00000230446	0	2.39819	1.57425	1.84999	ENSG00000230446	RP11-423O2.3
ENSG00000230447	0	0.223832	0.20216	0.502	ENSG00000230447	CTF2P
ENSG00000230449	0.0259809	0.0124808	0.033827	0	ENSG00000230449	RPL7P4
ENSG00000230450	0	0	0	0	ENSG00000230450	NEK2P4
ENSG00000230451	0	0	0	0	ENSG00000230451	RPS29P6
ENSG00000230453	9.31516	24.3615	13.1342	15.0455	ENSG00000230453	ANKRD18B
ENSG00000230455	0	0	0	0	ENSG00000230455	BMS1P14
ENSG00000230456	1.362	208.063	83.0381	41.4804	ENSG00000230456	DDR1
ENSG00000230457	1.31434	2.91181	2.23827	1.84503	ENSG00000230457	PA2G4P4
ENSG00000230458	0	0	0	0	ENSG00000230458	GPM6BP1
ENSG00000230459	0.335195	0.746498	0.355343	2.16448	ENSG00000230459	AC060773.1
ENSG00000230463	0.0689261	0.211231	0.202186	0.115076	ENSG00000230463	HLA-DRB3
ENSG00000230465	1.62134	3.26219	2.60456	5.20635	ENSG00000230465	VENTXP4
ENSG00000230467	0	0.180216	0	1.08063	ENSG00000230467	RNF39
ENSG00000230468	0.0644177	0.0859282	0	0	ENSG00000230468	CLUHP5
ENSG00000230469	0	0	0	0	ENSG00000230469	RPL5P26
ENSG00000230474	2.16265	1.22432	0.343162	2.73493	ENSG00000230474	ATP6V1G1P7
ENSG00000230475	0.226783	0.78314	0.938609	3.32873	ENSG00000230475	ABHD16A
ENSG00000230476	0	0	0	0	ENSG00000230476	OFD1P9Y
ENSG00000230477	0	0	0	0.167663	ENSG00000230477	AC005034.1
ENSG00000230478	0	0	0	0	ENSG00000230478	Z96811.1
ENSG00000230480	0	0.255427	0	0.844042	ENSG00000230480	AC093142.1
ENSG00000230481	0	0	0	0	ENSG00000230481	IGKV1OR22-5
ENSG00000230482	0	0.185769	0	0.824326	ENSG00000230482	ATP5G2P3
ENSG00000230484	0	0	0	0	ENSG00000230484	OR51A10P
ENSG00000230485	0	0	0	0.071552	ENSG00000230485	AC000077.1
ENSG00000230491	0	0	0	0	ENSG00000230491	AC234781.4
ENSG00000230493	0	0	0	0	ENSG00000230493	AC106017.1
ENSG00000230495	1.40797	2.77283	3.30064	2.8501	ENSG00000230495	AL132765.1
ENSG00000230496	0	0	0	0	ENSG00000230496	MTCO2P7
ENSG00000230497	0.304065	0	0.615569	0.437884	ENSG00000230497	EEF1B2P8
ENSG00000230501	0.113977	0.138751	0.176977	0.096243	ENSG00000230501	ANKRD30BP3
ENSG00000230502	0	0	0	0	ENSG00000230502	AL953862.1
ENSG00000230504	0	0	0	0	ENSG00000230504	HCG4P8
ENSG00000230505	0	0.00838819	0.0075842	0	ENSG00000230505	OR10C1
ENSG00000230507	0	0	0	0.0897561	ENSG00000230507	RPL7AP8
ENSG00000230508	0	0.0576584	0	0	ENSG00000230508	RPL19P21
ENSG00000230509	0	0	0	0	ENSG00000230509	HLA-N
ENSG00000230510	6.42509	15.9642	14.6362	25.5078	ENSG00000230510	PPP5D1
ENSG00000230511	0.164412	0	0.108894	0.250929	ENSG00000230511	NOP56P1
ENSG00000230514	0.588993	0.403047	1.17473	0.256006	ENSG00000230514	AGER
ENSG00000230519	0.506111	0.620468	0.679534	2.06964	ENSG00000230519	HMGB1P49
ENSG00000230520	0	0	0	0	ENSG00000230520	AC092098.1
ENSG00000230521	0.170639	0	0	0	ENSG00000230521	AL645929.1
ENSG00000230522	0.341337	0.645565	0.80495	0.355179	ENSG00000230522	MBD3L2
ENSG00000230524	0.0950649	0.110954	0.129796	0.523256	ENSG00000230524	COL6A4P1
ENSG00000230528	0.36238	0.608284	0.953448	1.41582	ENSG00000230528	NOS2P3
ENSG00000230529	0	0	0.126783	0.186349	ENSG00000230529	CEACAMP9
ENSG00000230531	0	0.100031	0.0827294	0.0939045	ENSG00000230531	MTND5P7

ENSG00000230535	0.102558	0	0	0	ENSG00000230535	BASP1P1
ENSG00000230538	0.15913	0.48082	0.229366	0.115287	ENSG00000230538	Z82209.1
ENSG00000230543	0	0	0	1.04888	ENSG00000230543	SNX3P1X
ENSG00000230546	0	0	0	0	ENSG00000230546	AL445193.1
ENSG00000230547	0.108652	0	0	0	ENSG00000230547	HMGB1P11
ENSG00000230548	0	0	0	0	ENSG00000230548	MTND4P27
ENSG00000230549	0	0	0.0970886	0.106102	ENSG00000230549	USP17L1
ENSG00000230553	0	0	0	0	ENSG00000230553	RP11-481A12.2
ENSG00000230556	0	0	0	0	ENSG00000230556	AC073264.2
ENSG00000230558	0	0	0	0.586803	ENSG00000230558	CEACAMP2
ENSG00000230559	0	0	0	0	ENSG00000230559	RPL17P12
ENSG00000230562	0	0	0.318126	0.839137	ENSG00000230562	FAM133DP
ENSG00000230564	0.179034	0	0	0	ENSG00000230564	CALM1P2
ENSG00000230567	0.103928	0.140122	0	0.288287	ENSG00000230567	FAM203B
ENSG00000230568	0.237931	1.04337	0.804942	1.53081	ENSG00000230568	SF3A3P1
ENSG00000230570	0	0.0478671	0.129792	0.054295	ENSG00000230570	AL139095.3
ENSG00000230571	0	0	0	0	ENSG00000230571	AC113347.1
ENSG00000230572	0.329899	0.912149	0.561578	0.988254	ENSG00000230572	AC027612.2
ENSG00000230574	0.164412	0	0.108894	0.250929	ENSG00000230574	NOP56P1
ENSG00000230576	0	0	0	0	ENSG00000230576	OR6R1P
ENSG00000230578	0.266988	1.0618	2.3328	3.38267	ENSG00000230578	AC234781.5
ENSG00000230580	0	0	0	0	ENSG00000230580	AC021016.1
ENSG00000230581	0.593558	1.76674	1.22087	1.56083	ENSG00000230581	ACTG1P14
ENSG00000230582	0.159753	0.243112	0.118486	0.198619	ENSG00000230582	PPIAL4F
ENSG00000230583	0.950457	0.801666	0.964108	1.09392	ENSG00000230583	GTF2IRD1P1
ENSG00000230584	0.035481	0	0	0	ENSG00000230584	CCT5P2
ENSG00000230585	0.403864	1.84208	1.19288	2.80668	ENSG00000230585	PHBP12
ENSG00000230589	0	0	0	0	ENSG00000230589	IMP3P1
ENSG00000230592	0	0	0	0	ENSG00000230592	RPSAP8
ENSG00000230593	0.159709	2.88839	1.11977	2.70398	ENSG00000230593	AC090804.1
ENSG00000230594	0	0.0219476	0.0109151	0.0319741	ENSG00000230594	CT47A4
ENSG00000230595	0.494501	0.487564	0.221149	1.562	ENSG00000230595	RSL24D1P2
ENSG00000230596	0.638774	1.46358	1.33668	3.64887	ENSG00000230596	GPAA1P2
ENSG00000230598	0	0	0	0	ENSG00000230598	AL645937.5
ENSG00000230603	0	0	0	0	ENSG00000230603	AC011753.1
ENSG00000230604	0.769904	2.22979	2.65506	2.21128	ENSG00000230604	TSEN15P2
ENSG00000230605	0	0	0	0	ENSG00000230605	MTCYBP6
ENSG00000230607	0	0	0	0	ENSG00000230607	AC005722.1
ENSG00000230609	0	3.16235	0	2.52161	ENSG00000230609	AL513185.2
ENSG00000230610	0	0	0	1.24467	ENSG00000230610	AL929472.1
ENSG00000230611	0.116867	0.448668	1.01508	0.251552	ENSG00000230611	HMGB1P27
ENSG00000230614	0	0	0	0	ENSG00000230614	DYNLL1P7
ENSG00000230616	0.0579419	0.135473	0.213576	0.171467	ENSG00000230616	PPIAP9
ENSG00000230617	4.86404	2.17601	5.37784	8.82731	ENSG00000230617	AC079987.1
ENSG00000230618	0	0	0	0	ENSG00000230618	H3F3AP3
ENSG00000230621	0	1.22949	0.548279	3.30182	ENSG00000230621	AC068138.1
ENSG00000230622	0	0	0	0	ENSG00000230622	UQCRHP1
ENSG00000230624	18.2571	16.0073	20.6009	18.3991	ENSG00000230624	DDX39B
ENSG00000230626	0	0	0	0	ENSG00000230626	AC011005.1
ENSG00000230629	0	0	0.537912	0	ENSG00000230629	RPS23P8
ENSG00000230634	0	0.90577	1.6354	0.844324	ENSG00000230634	AL031597.1
ENSG00000230635	0	0	0.279136	0	ENSG00000230635	CYP4F60P
ENSG00000230636	0	0	0	0	ENSG00000230636	RPL36P1
ENSG00000230637	0.234907	0.811495	0.242059	1.38696	ENSG00000230637	AL022324.1

ENSG00000230638	4.60098	3.16166	5.76895	2.20239	ENSG00000230638	AL445933.1
ENSG00000230639	0	0	0	0	ENSG00000230639	VN1R36P
ENSG00000230643	0	0	0	0	ENSG00000230643	AP000533.3
ENSG00000230646	0.337242	0.334261	0.450479	0.621677	ENSG00000230646	KLF2P2
ENSG00000230650	0.66276	2.14658	2.10165	1.20903	ENSG00000230650	AC140479.2
ENSG00000230654	0	0	0	0	ENSG00000230654	MTCO2P25
ENSG00000230655	0	0.0740377	0.0830281	0.235825	ENSG00000230655	AC139453.1
ENSG00000230657	0	0.555988	0.212344	0.149749	ENSG00000230657	PRB4
ENSG00000230659	0	0	0	0	ENSG00000230659	AL451074.5
ENSG00000230661	0.310392	1.21994	0.820689	1.03862	ENSG00000230661	YY1P1
ENSG00000230662	0.189974	1.02024	0.592297	6.89949	ENSG00000230662	TNPO1P2
ENSG00000230665	0.0519922	0.0499406	0.0338362	0.0572159	ENSG00000230665	THAP12P1
ENSG00000230666	1.10066	2.40803	2.05566	3.45241	ENSG00000230666	CEACAM22P
ENSG00000230667	0.0753796	0	0.0676542	0.12992	ENSG00000230667	SETSIP
ENSG00000230669	1.10486	0.54819	1.3866	1.30105	ENSG00000230669	PSMB8
ENSG00000230671	0	0	0	0	ENSG00000230671	NDUFS5P5
ENSG00000230673	1.38478	3.01594	1.05343	1.66204	ENSG00000230673	PABPC1P3
ENSG00000230675	0.0425612	0	0.145953	0.0990776	ENSG00000230675	HLA-DQB2
ENSG00000230678	7.73343	38.2581	6.43806	6.38408	ENSG00000230678	BRD2
ENSG00000230681	0.395793	0.188551	0.340446	0.627149	ENSG00000230681	CEACAMP4
ENSG00000230682	0	0	0	0	ENSG00000230682	GRPEL2P3
ENSG00000230683	0	0.875754	1.38431	1.9364	ENSG00000230683	DDTP1
ENSG00000230685	5.59717	6.88437	1.63599	4.53468	ENSG00000230685	CLIC1
ENSG00000230691	0	0	0	0	ENSG00000230691	MRPL35P4
ENSG00000230697	0.229787	0	0.937005	0	ENSG00000230697	SAP18P3
ENSG00000230700	4.65475	6.41218	9.55679	14.8934	ENSG00000230700	CSNK2B
ENSG00000230701	1.2968	2.44941	1.8646	1.85234	ENSG00000230701	FBXW4P1
ENSG00000230702	0	0.48236	0	0	ENSG00000230702	AC107081.1
ENSG00000230705	3.85017	4.43194	4.80779	2.8079	ENSG00000230705	TAP1
ENSG00000230706	0.0947176	0.0456832	0.0824297	0.206974	ENSG00000230706	AL035246.1
ENSG00000230707	0	0.0756228	0	0.17192	ENSG00000230707	AL589987.1
ENSG00000230708	1.3885	4.48492	3.28012	4.92203	ENSG00000230708	HLA-DPB1
ENSG00000230711	0	0	0	0	ENSG00000230711	CTAGE13P
ENSG00000230712	0	0	0	0.776614	ENSG00000230712	GGTLC4P
ENSG00000230715	14.504	20.6479	28.8762	32.4961	ENSG00000230715	AC018638.2
ENSG00000230716	0	0.120385	0	0.267648	ENSG00000230716	KRT8P7
ENSG00000230718	0	0.733856	0.221255	0.539772	ENSG00000230718	AC114878.1
ENSG00000230721	0	0	0	0	ENSG00000230721	AL049597.1
ENSG00000230722	0	0.470711	0.115654	2.13E-05	ENSG00000230722	IFITM4P
ENSG00000230726	0.132708	0.0207335	0.166196	0.116951	ENSG00000230726	HLA-DRA
ENSG00000230727	0	0	0.0596416	0.0749651	ENSG00000230727	RBMY2WP
ENSG00000230734	0.192346	1.01267	0.814889	2.46751	ENSG00000230734	RPL10P3
ENSG00000230739	0	0	0	0	ENSG00000230739	AL392003.2
ENSG00000230745	0.212651	0	0.190629	0	ENSG00000230745	MICD
ENSG00000230748	0	0.106906	0	0	ENSG00000230748	AL157714.1
ENSG00000230750	0.120377	0.0993047	0.194952	0.198116	ENSG00000230750	SDAD1P2
ENSG00000230752	0.0144218	0	0.05347	0	ENSG00000230752	BX005432.2
ENSG00000230754	0	0.0415668	0.00939099	0.0470305	ENSG00000230754	CR936918.2
ENSG00000230755	0	0.156526	0	0	ENSG00000230755	MTATP6P23
ENSG00000230756	0	0	0	0	ENSG00000230756	RHOQP3
ENSG00000230757	0.084421	0.162281	0.219911	0	ENSG00000230757	NFU1P1
ENSG00000230758	0.511285	0.48182	1.29096	1.03842	ENSG00000230758	SNAP23P1
ENSG00000230763	0	0.223915	0.211819	0.261232	ENSG00000230763	HLA-DPB1

ENSG00000230764	0	0.00567521	0	0	ENSG00000230764	MTND1P4
ENSG00000230769	2.02865	1.94421	2.55112	1.3335	ENSG00000230769	Z98048.1
ENSG00000230772	0.38687	1.04141	0.739277	0.755756	ENSG00000230772	VN1R108P
ENSG00000230777	0	4.88911	5.66529	5.75841	ENSG00000230777	RPS29P5
ENSG00000230778	4.44418	19.6155	8.91022	39.0883	ENSG00000230778	ANKRD63
ENSG00000230779	0	0	0	0.147335	ENSG00000230779	AL161636.2
ENSG00000230780	0.21123	0.457168	0.423707	0.844127	ENSG00000230780	OR11A1
ENSG00000230781	0	0.0373047	0	0	ENSG00000230781	Z83820.1
ENSG00000230783	0.0858208	0	0.148941	0.186338	ENSG00000230783	AC009961.3
ENSG00000230785	0.0826793	0.0794656	0	0.0901227	ENSG00000230785	AC006326.1
ENSG00000230787	0	0.0532124	0	0	ENSG00000230787	PSAT1P3
ENSG00000230788	0.0474455	0	0.0825802	0.103878	ENSG00000230788	AL512661.1
ENSG00000230791	0	0	0.112516	0	ENSG00000230791	LST1
ENSG00000230793	0	0.0598227	0.10012	0.106055	ENSG00000230793	SMARCE1P5
ENSG00000230795	0.505224	0	0	0	ENSG00000230795	HLA-K
ENSG00000230796	0	0	0	0	ENSG00000230796	AC064862.1
ENSG00000230797	1.21314	2.43625	3.87493	4.25989	ENSG00000230797	YY2
ENSG00000230799	1.83805	3.23964	3.19316	2.9923	ENSG00000230799	AC007279.1
ENSG00000230801	0.507014	1.91286	0.426968	2.57549	ENSG00000230801	AL160175.1
ENSG00000230804	0	0	0	0	ENSG00000230804	C2orf27AP3
ENSG00000230807	0.241792	0.691497	0.416878	0	ENSG00000230807	AC099535.1
ENSG00000230809	0.175411	0.168568	0.228422	0.284871	ENSG00000230809	RPS6P15
ENSG00000230813	0	0	0	0	ENSG00000230813	AL356583.3
ENSG00000230814	0	0	0	0	ENSG00000230814	USP9YP24
ENSG00000230816	0	0	0	0	ENSG00000230816	COL11A2P1
ENSG00000230818	0.0839766	0	0	0	ENSG00000230818	MTND2P16
ENSG00000230819	0	0	0	0	ENSG00000230819	ZNF736P5Y
ENSG00000230820	0	0	0	0	ENSG00000230820	AC000362.1
ENSG00000230821	0	0	0	0	ENSG00000230821	AC245291.2
ENSG00000230823	0.0967251	0.0937466	0.0862406	0.205342	ENSG00000230823	CBX1P1
ENSG00000230828	1.46034	3.19043	0.639793	1.35377	ENSG00000230828	AL583843.1
ENSG00000230829	0	0.192139	0	0	ENSG00000230829	AC025181.1
ENSG00000230832	0.0725412	0.255329	0.293455	0.421834	ENSG00000230832	AC241584.1
ENSG00000230833	0.100374	0.0964297	0.585946	0.542172	ENSG00000230833	RPEP3
ENSG00000230835	0	0	0	0	ENSG00000230835	AP001187.1
ENSG00000230837	0.240286	2.31327	0.410617	1.00949	ENSG00000230837	RPL31P2
ENSG00000230840	0	0	0	0	ENSG00000230840	AC097463.2
ENSG00000230841	1.19216	0	0.298313	0.217212	ENSG00000230841	RPL23AP15
ENSG00000230845	0.124415	0.477571	0.323437	0.133706	ENSG00000230845	GSTA10P
ENSG00000230847	0	0	0	0	ENSG00000230847	AC044797.1
ENSG00000230849	0.0997585	0.0929695	0.088648	0.161922	ENSG00000230849	GOT2P2
ENSG00000230851	0	0	0	0	ENSG00000230851	AP006294.1
ENSG00000230853	0	0	0	0	ENSG00000230853	RPL10P11
ENSG00000230854	0	0	0	0	ENSG00000230854	USP9YP20
ENSG00000230855	0	0	0.0308878	0	ENSG00000230855	OR2J3
ENSG00000230856	0	0	0	0	ENSG00000230856	AC138649.1
ENSG00000230859	0	0	0	0	ENSG00000230859	YRDCP3
ENSG00000230860	0	0	0	0.170937	ENSG00000230860	CCNB1IP1P2
ENSG00000230863	0	0	0	0	ENSG00000230863	AL096829.2
ENSG00000230865	0	0	0	0	ENSG00000230865	TSEN15P1
ENSG00000230867	1.20615	3.41307	2.48738	4.12313	ENSG00000230867	AL157884.1
ENSG00000230869	0.0402344	0	0.174886	0	ENSG00000230869	AGAP10P
ENSG00000230870	0.0791796	0.19164	0.277763	0	ENSG00000230870	FBXW11P1
ENSG00000230871	0.0922108	0	0.0800385	0	ENSG00000230871	RPS6P23

ENSG00000230872	0.27747	0.972172	1.06656	2.25764	ENSG00000230872	MFSD13B
ENSG00000230873	2.10723	3.83041	4.30024	8.56112	ENSG00000230873	STMND1
ENSG00000230874	0	0	0	0	ENSG00000230874	BX248084.3
ENSG00000230878	0.00091433	0	0.000798201	0.000801615	ENSG00000230878	HLA-DPA2
ENSG00000230879	0	0	0	0.249331	ENSG00000230879	RBMX2P4
ENSG00000230882	0.101061	0.151841	0.205075	0.422355	ENSG00000230882	AC005077.4
ENSG00000230885	0.786263	1.75777	1.07424	1.69929	ENSG00000230885	MOG
ENSG00000230886	0	0.11117	0.100407	0.12468	ENSG00000230886	HMGB1P25
ENSG00000230887	0.00724298	0	0	0.00789492	ENSG00000230887	MICC
ENSG00000230888	0	0	0	0	ENSG00000230888	SUMO2P1
ENSG00000230889	0	0.126766	0.0285137	0.0721228	ENSG00000230889	SHC1P1
ENSG00000230891	1.39684	2.41713	2.51789	4.89909	ENSG00000230891	LINC00692
ENSG00000230897	0	0	0	0	ENSG00000230897	AC013248.2
ENSG00000230900	0.00314444	0.0186652	0.023055	0.174972	ENSG00000230900	ATP6V1G2
ENSG00000230902	0.64461	1.1365	0.465857	2.21438	ENSG00000230902	FAM204CP
ENSG00000230903	113.628	81.9587	48.5888	2.12808	ENSG00000230903	PRPL9P8
ENSG00000230904	0	0	0.134639	0.249305	ENSG00000230904	XKRYP2
ENSG00000230907	1.03011	1.49737	0.476154	0.430663	ENSG00000230907	FKBPL
ENSG00000230911	1.52337	1.2826	0	1.29243	ENSG00000230911	AP000907.1
ENSG00000230913	0	0	0.12086	0	ENSG00000230913	NPM1P51
ENSG00000230915	0	0	0	0	ENSG00000230915	HLA-W
ENSG00000230916	0.192263	0	0	0.317016	ENSG00000230916	MTCO1P53
ENSG00000230926	0	0	0	0.0513945	ENSG00000230926	AC239367.2
ENSG00000230927	0	0	0	0.0502891	ENSG00000230927	TMBIM7P
ENSG00000230929	0	1.31915	0.971845	0.401363	ENSG00000230929	AC099513.1
ENSG00000230930	0	0.02877	0.0752155	0.0424258	ENSG00000230930	COL11A2
ENSG00000230931	0	0	0	0	ENSG00000230931	GXYLT1P1
ENSG00000230932	0	0	0	0	ENSG00000230932	AL355306.1
ENSG00000230934	0	0	0	0	ENSG00000230934	BX276092.4
ENSG00000230935	0	0	0	3.40259	ENSG00000230935	RPS3P1
ENSG00000230936	0	0	0.0182029	0.0229524	ENSG00000230936	AC073347.1
ENSG00000230942	0.449423	0	1.13822	0	ENSG00000230942	HMGN1P5
ENSG00000230946	0.887026	1.6119	2.26042	2.95149	ENSG00000230946	HNRNPA1P68
ENSG00000230948	0.363931	0.0583626	0	0.0660749	ENSG00000230948	AP001331.1
ENSG00000230949	0	0.0184226	0	0	ENSG00000230949	ZNF70P1
ENSG00000230950	0.0587981	0	0.153933	0	ENSG00000230950	MTND2P21
ENSG00000230951	0.498572	0.137737	0	0.0773974	ENSG00000230951	GPS2P2
ENSG00000230953	9.45034	28.4047	25.332	13.0665	ENSG00000230953	AC099677.1
ENSG00000230956	0	0	0	0	ENSG00000230956	AL024493.1
ENSG00000230957	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000230957	MAS1LP1
ENSG00000230958	0.947481	0.653218	0.885391	0.828093	ENSG00000230958	AC093166.3
ENSG00000230961	1.12442	2.81928	1.10342	1.11841	ENSG00000230961	MSH5
ENSG00000230964	0	0	0	5.39348	ENSG00000230964	AC233266.1
ENSG00000230965	0	0	0	0	ENSG00000230965	SNX18P13
ENSG00000230973	0	0	0	0.122284	ENSG00000230973	AL049734.2
ENSG00000230977	0	0	0.114793	0	ENSG00000230977	AC023274.1
ENSG00000230979	0.177491	0	0	0.202672	ENSG00000230979	AC079250.1
ENSG00000230980	0.949229	0.599784	1.63605	0.333011	ENSG00000230980	RPL36AP39
ENSG00000230981	0.922649	1.81475	2.02802	2.01692	ENSG00000230981	AC006035.1
ENSG00000230982	6.10313	10.5033	13.3068	13.494	ENSG00000230982	DSTNP1
ENSG00000230985	0.991427	14.9914	5.39992	4.87969	ENSG00000230985	VARS2
ENSG00000230986	0	13.8463	8.59295	2.80413	ENSG00000230986	DDX3P2
ENSG00000230987	0.252199	0.400583	0.568492	0.460408	ENSG00000230987	AL359976.1

ENSG00000230988	1.51693	3.89625	4.33277	8.60188	ENSG00000230988	RPL23AP11
ENSG00000230989	46.3294	25.5675	20.6153	27.9919	ENSG00000230989	HSBP1
ENSG00000230992	3.42732	5.53732	5.84757	7.54342	ENSG00000230992	FAM201B
ENSG00000230993	0.612911	1.1588	0.797619	0.491031	ENSG00000230993	RPL12P15
ENSG00000230994	0	0	0	0	ENSG00000230994	FGFR3P1
ENSG00000230995	5.55483	9.33778	7.87132	5.90532	ENSG00000230995	PPP1R10
ENSG00000230997	0	0.106116	0.127685	0.40025	ENSG00000230997	RAB42P1
ENSG00000230999	0.0561857	0.0540741	0.13207	0.391378	ENSG00000230999	MTND5P8
ENSG00000231000	0	0.0341391	0.030885	0	ENSG00000231000	BX247947.2
ENSG00000231001	0	0	0	0	ENSG00000231001	CCNB1IP1P3
ENSG00000231002	0	1.66778	0.79998	5.35513	ENSG00000231002	TRIM26
ENSG00000231003	0.181329	0.151186	0.308192	0.303335	ENSG00000231003	MPIG6B
ENSG00000231005	0	0	1.27E-08	0	ENSG00000231005	RPL39P39
ENSG00000231006	0.255232	0.721472	0.785172	0.436595	ENSG00000231006	RPL7P32
ENSG00000231007	0.0993475	0.7154	0.395543	0.429727	ENSG00000231007	CDC20P1
ENSG00000231009	0.0636259	0.12306	0.0554232	0.349438	ENSG00000231009	CUBNP1
ENSG00000231011	0.427509	0.40843	0	0.904422	ENSG00000231011	AC092832.1
ENSG00000231017	0	0	0	0	ENSG00000231017	AC013404.1
ENSG00000231018	0	0	0	0	ENSG00000231018	EIF4A1P3
ENSG00000231020	0	0.745847	1.85193	0.206805	ENSG00000231020	AL591043.1
ENSG00000231021	0	0	0	0	ENSG00000231021	CR788250.1
ENSG00000231022	0.164051	0.0788397	0	0.0897699	ENSG00000231022	RPS3AP9
ENSG00000231026	0	0.0766014	0	0.0853309	ENSG00000231026	XKRYP4
ENSG00000231027	0	0	0	0	ENSG00000231027	AC079325.6
ENSG00000231029	0	0	0	0	ENSG00000231029	AL031733.1
ENSG00000231030	0	0.0184226	0	0	ENSG00000231030	ZNF70P1
ENSG00000231031	0.986506	3.49271	2.24707	5.046	ENSG00000231031	LINC01804
ENSG00000231032	0	0	0	0	ENSG00000231032	AC114814.2
ENSG00000231034	0	0	0	0	ENSG00000231034	AL118520.1
ENSG00000231035	0	0	0	0	ENSG00000231035	RPL7L1P9
ENSG00000231041	0	0.0269191	0	0	ENSG00000231041	LINC01556
ENSG00000231043	0	0	0	0	ENSG00000231043	AC007238.1
ENSG00000231044	4.30996	3.46615	2.38813	2.98449	ENSG00000231044	NELFE
ENSG00000231047	2.24485	6.71574	3.2421	6.78641	ENSG00000231047	GCNT1P3
ENSG00000231048	0	0	0.112516	0	ENSG00000231048	LST1
ENSG00000231049	0	0	0.341907	0.285347	ENSG00000231049	OR52B5P
ENSG00000231051	0	0	0	0	ENSG00000231051	USP17L28
ENSG00000231053	0	0	0.230843	0.281347	ENSG00000231053	AL357752.1
ENSG00000231058	0	0	0	0	ENSG00000231058	MSANTD2P1
ENSG00000231060	0	0.127542	0.059107	0.142329	ENSG00000231060	FARSBP1
ENSG00000231063	0.152697	1.83529	0.729525	0.994547	ENSG00000231063	AC006994.1
ENSG00000231066	0.152573	0.877511	0.216282	0.857133	ENSG00000231066	NPM1P9
ENSG00000231067	0	2.93348	0	0	ENSG00000231067	BX005091.1
ENSG00000231068	0	0	0	0	ENSG00000231068	KRTAP21-3
ENSG00000231069	0	0	0	0	ENSG00000231069	BX842568.3
ENSG00000231070	0	0	0	0	ENSG00000231070	OR52Y1P
ENSG00000231071	0.098281	0	0	0.212443	ENSG00000231071	AL133396.1
ENSG00000231072	0.1269	0.532817	0.0984406	0.134006	ENSG00000231072	GAPDHP64
ENSG00000231084	0.473209	1.35991	1.01906	1.76505	ENSG00000231084	AL136133.1
ENSG00000231086	0.170508	0.0819379	0	0	ENSG00000231086	TSSK1A
ENSG00000231087	1.52349	4.01219	9.83179	3.06478	ENSG00000231087	FDPSP7
ENSG00000231091	0	0	0	0	ENSG00000231091	AC138783.13
ENSG00000231093	0	0	0	0	ENSG00000231093	AL391256.1
ENSG00000231094	0.107331	0.409906	0.333308	1.25607	ENSG00000231094	PSORS1C1

ENSG00000231095	0.0638281	0.060692	0.0540679	0.138641	ENSG00000231095	GYG1P3
ENSG00000231096	0.452834	0.212664	0.19905	0.941025	ENSG00000231096	NDUFB4P3
ENSG00000231099	0	0	0	0	ENSG00000231099	BMS1P19
ENSG00000231100	0	0	0	0	ENSG00000231100	AL606752.1
ENSG00000231103	0	0	0	0	ENSG00000231103	PRAMEF30P
ENSG00000231108	0	0.310173	0.28	0.357827	ENSG00000231108	PRELID3BP11
ENSG00000231112	0	0	0	0	ENSG00000231112	MTHFD2P3
ENSG00000231115	0	2.37574	2.34196	0.817843	ENSG00000231115	RING1
ENSG00000231116	14.1863	11.6285	12.687	3.36147	ENSG00000231116	VARS
ENSG00000231118	0.0579419	0.0677367	0.106788	0.0857336	ENSG00000231118	PPIAP9
ENSG00000231120	0	0.149677	0.135405	0	ENSG00000231120	BTF3P10
ENSG00000231122	0.184828	0.118284	0.27768	0.26131	ENSG00000231122	FAM25E
ENSG00000231123	1.48274	2.14109	1.13681	2.05797	ENSG00000231123	SPATA20P1
ENSG00000231124	0	0	0	0	ENSG00000231124	UBE2V1P11
ENSG00000231129	2.98036	0.236712	0.475127	1.40968	ENSG00000231129	ABCF1
ENSG00000231130	0	0	0	0	ENSG00000231130	HLA-T
ENSG00000231135	0.0961644	0.686574	0.460787	0.446605	ENSG00000231135	MDC1
ENSG00000231136	0	0.127103	0	0	ENSG00000231136	AP000705.1
ENSG00000231137	0.139736	0.268217	0.121216	0.204914	ENSG00000231137	RBM22P5
ENSG00000231139	0	0	0	0	ENSG00000231139	AC104843.2
ENSG00000231144	0	0.120253	0.325766	0.403949	ENSG00000231144	EEF1A1P40
ENSG00000231145	1.11114	0	2.2726	0	ENSG00000231145	AC013468.1
ENSG00000231147	0	0	0	0	ENSG00000231147	ARHGAP42P2
ENSG00000231148	0.572719	1.54499	0.794443	2.10472	ENSG00000231148	HMGB1P7
ENSG00000231152	0	0.068122	0	0	ENSG00000231152	MTND2P15
ENSG00000231153	0	0	0	0	ENSG00000231153	AC002429.1
ENSG00000231157	0	0	0	0	ENSG00000231157	SUCLA2P1
ENSG00000231158	0	0	0	0	ENSG00000231158	PTP4A1P1
ENSG00000231159	0	0	0	0	ENSG00000231159	OFD1P8Y
ENSG00000231162	0	0	0.070162	0	ENSG00000231162	COX11P1
ENSG00000231164	0	0	0	0	ENSG00000231164	RPL7P56
ENSG00000231165	0	0	2.50234	0	ENSG00000231165	TRBV26OR9-2
ENSG00000231166	0.16183	0	0.14	0.345442	ENSG00000231166	TUBB4BP6
ENSG00000231167	0.0633996	0.123822	0.0555081	0.138869	ENSG00000231167	YBX1P2
ENSG00000231169	0.617929	1.40636	1.44644	2.52783	ENSG00000231169	EEF1B2P1
ENSG00000231171	0.207883	0.62007	0.833491	1.46366	ENSG00000231171	LINC01098
ENSG00000231179	0.238434	0.898692	1.75628	0.927638	ENSG00000231179	MICB
ENSG00000231181	0.259493	1.49396	0.786808	0.976574	ENSG00000231181	AL954705.1
ENSG00000231184	0	0	0	0.0559035	ENSG00000231184	FAM58DP
ENSG00000231190	0	0.0197876	0.0178653	0	ENSG00000231190	CR759766.2
ENSG00000231192	0	0	0.0577539	0	ENSG00000231192	OR5H1
ENSG00000231195	0	0	0	0	ENSG00000231195	IFNA11P
ENSG00000231197	0	0	0.361934	0	ENSG00000231197	BX927141.1
ENSG00000231198	0.148512	0	0.14992	0.228083	ENSG00000231198	AC004987.1
ENSG00000231199	0.0965693	0.0388826	0.139632	0.378109	ENSG00000231199	MTND5P19
ENSG00000231202	1.64727	1.18186	1.64262	0.978065	ENSG00000231202	TRGVB
ENSG00000231203	0	0	0	0	ENSG00000231203	KRT8P10
ENSG00000231205	9.05249	17.0136	14.0438	16.7355	ENSG00000231205	ZNF826P
ENSG00000231206	0.134232	0.645139	0.279205	0.43753	ENSG00000231206	HNRNPA1P25
ENSG00000231207	0	0	0.224367	0	ENSG00000231207	FO393419.1
ENSG00000231209	0	0.501253	0	0	ENSG00000231209	GLUD1P6
ENSG00000231211	0	0	0	0.8685	ENSG00000231211	RPL17P49
ENSG00000231213	0.0574621	0.252726	0.200334	0.15761	ENSG00000231213	PLSCR5
ENSG00000231219	0	0	0	0	ENSG00000231219	PRAMEF32P

ENSG00000231222	0	0.137719	0	0	ENSG00000231222	ARF4P4
ENSG00000231225	16.1841	2.10385	4.22408	10.4175	ENSG00000231225	MICA
ENSG00000231228	0.564089	0	0	0	ENSG00000231228	AC091874.1
ENSG00000231232	4.78122	8.6537	5.52357	8.40343	ENSG00000231232	AC023141.6
ENSG00000231234	1.41994	2.5542	2.5704	1.87852	ENSG00000231234	SKP1P1
ENSG00000231235	0.288986	0.204647	0.0307218	0.43439	ENSG00000231235	AL139811.2
ENSG00000231237	0.275987	0.51878	0.619222	0.926797	ENSG00000231237	OR6K1P
ENSG00000231240	0	0	0	0	ENSG00000231240	KLF2P1
ENSG00000231241	0.528697	1.98766	0	1.06981	ENSG00000231241	RPS3AP3
ENSG00000231244	0.0458065	0	0.0793169	0.0996303	ENSG00000231244	PSMC1P3
ENSG00000231245	0	0.555149	0	0.255206	ENSG00000231245	C1DP1
ENSG00000231247	1.8072	1.2927	0.902681	1.45118	ENSG00000231247	PPP1R18
ENSG00000231251	0	0	0	0	ENSG00000231251	AL021921.1
ENSG00000231254	0.165888	0.398594	0.144041	0.539383	ENSG00000231254	PCED1CP
ENSG00000231256	2.38606	4.53964	3.5487	7.74101	ENSG00000231256	C17orf105
ENSG00000231257	0.449589	0.763133	0.80941	0.547135	ENSG00000231257	ATAT1
ENSG00000231258	0.138366	0.127402	0.108652	0	ENSG00000231258	ZSWIM5P2
ENSG00000231259	4.90944	6.54919	6.78772	4.22517	ENSG00000231259	AC125232.1
ENSG00000231261	0	0	0	0	ENSG00000231261	HMGN2P10
ENSG00000231264	0	0	0	0	ENSG00000231264	ARAFP1
ENSG00000231267	0	0	0	0	ENSG00000231267	PPIAL4E
ENSG00000231268	0.588993	0.403047	1.17473	0.256006	ENSG00000231268	AGER
ENSG00000231270	0	0.133875	0.122954	0	ENSG00000231270	AL772284.1
ENSG00000231271	0	0	0	0.388439	ENSG00000231271	AP000350.3
ENSG00000231274	0.645307	1.06504	1.0241	0.949647	ENSG00000231274	SBK3
ENSG00000231275	0	0	0	0	ENSG00000231275	HNRNPA1P2
ENSG00000231276	0.106596	0.0513023	0.0463671	0.116925	ENSG00000231276	E2F4P1
ENSG00000231278	9.50333	13.6738	6.92543	18.4974	ENSG00000231278	AC013469.1
ENSG00000231279	0.009462	0.0181999	0.0164453	0.0102936	ENSG00000231279	AL662857.3
ENSG00000231280	0	0	0.0301168	0.0371179	ENSG00000231280	SALL4P6
ENSG00000231283	0	0	0	0	ENSG00000231283	RP11-472D17.6
ENSG00000231286	0.0410584	0	0.0717926	0	ENSG00000231286	HLA-DQB1
ENSG00000231287	0	0	0	0	ENSG00000231287	HCG4B
ENSG00000231288	0	0.0858021	0.0808883	0.0707639	ENSG00000231288	CR759795.1
ENSG00000231289	0.145846	0.224788	0.177171	0.362801	ENSG00000231289	RP11-782C8.6
ENSG00000231292	0.262985	1.56599	1.62964	4.77408	ENSG00000231292	IGKV1OR2-108
ENSG00000231293	0.310687	0	0.799175	0	ENSG00000231293	RPL36AP6
ENSG00000231296	4.65998	6.5074	6.08457	4.46809	ENSG00000231296	AL050341.1
ENSG00000231299	1.14566	4.46036	1.98083	0	ENSG00000231299	SEPT14P24
ENSG00000231300	0	0	0	0	ENSG00000231300	EZH2P1
ENSG00000231301	0.0288811	0.0197876	0.0178653	0	ENSG00000231301	AL645936.1
ENSG00000231302	0	0	0	0.669283	ENSG00000231302	RPL36P2
ENSG00000231307	1.81961	2.02454	2.32753	2.89891	ENSG00000231307	RPS3P2
ENSG00000231309	0.000124398	0.000187449	0.000167498	0.00014757	ENSG00000231309	WASF5P
ENSG00000231311	0	0	0	0	ENSG00000231311	PRYP2
ENSG00000231313	0	0	0	0	ENSG00000231313	AC078875.1
ENSG00000231314	0.013508	0	0.0359938	0.0362078	ENSG00000231314	LTB
ENSG00000231315	0.126266	0.0967412	0	0.249624	ENSG00000231315	AC107613.1
ENSG00000231316	0	0	0	0	ENSG00000231316	AL591419.1
ENSG00000231317	0.383011	1.31129	2.66075	0.541055	ENSG00000231317	AC091812.1
ENSG00000231319	0	0.0131907	0.0059608	0	ENSG00000231319	OR2B3
ENSG00000231320	0	0	0	0	ENSG00000231320	BX908738.3
ENSG00000231321	2.00691	0.902282	1.53736	0.954922	ENSG00000231321	RXRB
ENSG00000231322	0.059775	0.510307	0.411927	0.409136	ENSG00000231322	RPL13AP17

ENSG00000231325	0.0973281	0.0758412	0.0529561	0.0644326	ENSG00000231325	LY6G5C
ENSG00000231328	0	0.138866	0	0.309975	ENSG00000231328	TPT1P7
ENSG00000231331	0	0	0	0	ENSG00000231331	AC103563.3
ENSG00000231333	1.6015	3.65043	3.06308	2.87058	ENSG00000231333	RPL34P6
ENSG00000231340	0.450634	1.11471	0.808279	1.01331	ENSG00000231340	ACTG1P10
ENSG00000231341	0	0	0	0	ENSG00000231341	VDAC1P6
ENSG00000231342	0.014225	0	0.0247501	0.0310757	ENSG00000231342	ATF4P2
ENSG00000231344	1.07252	0.76628	0.230843	0.844042	ENSG00000231344	AL020997.1
ENSG00000231345	3.23321	4.22421	5.1984	6.59184	ENSG00000231345	BEND3P1
ENSG00000231349	0	0	0	0	ENSG00000231349	AC119749.1
ENSG00000231350	0.0874301	0.12896	0.145468	0.26788	ENSG00000231350	MUC21
ENSG00000231351	0	0	0	0	ENSG00000231351	AC111200.2
ENSG00000231353	0.459618	0.866588	0	0	ENSG00000231353	AL355994.1
ENSG00000231356	0	0	0.0529915	0.0663813	ENSG00000231356	AL157698.1
ENSG00000231357	0.442221	1.21549	2.25066	2.69254	ENSG00000231357	AC006028.1
ENSG00000231359	0	0	0.289574	0	ENSG00000231359	AC072052.1
ENSG00000231360	1.49853	3.79067	6.20736	1.36146	ENSG00000231360	AL592284.1
ENSG00000231361	0	2.17601	0	0	ENSG00000231361	RPS29P23
ENSG00000231362	0	0	0	0	ENSG00000231362	AC069271.1
ENSG00000231366	0.728334	0	0	0	ENSG00000231366	RPS26P40
ENSG00000231368	0.212818	0.0682149	0.123271	0.385424	ENSG00000231368	RPSAP40
ENSG00000231369	0	0	0.108148	0.134225	ENSG00000231369	Z97353.1
ENSG00000231370	8.321	22.231	28.1841	30.8755	ENSG00000231370	PRRC2A
ENSG00000231371	0	0	0	0	ENSG00000231371	AKR1B1P8
ENSG00000231372	3.73416	5.21517	1.57056	4.49936	ENSG00000231372	MICB
ENSG00000231375	0	0	0	0	ENSG00000231375	CDY17P
ENSG00000231376	0	0	0	0	ENSG00000231376	HMGN2P16
ENSG00000231377	2.76168	2.81073	3.53901	2.65462	ENSG00000231377	DHX16
ENSG00000231378	0.302158	0.592023	1.5693	1.45378	ENSG00000231378	NDUFAF4P4
ENSG00000231379	0.126173	0.283538	0.109839	0	ENSG00000231379	RP11-237M21.1
ENSG00000231381	0.122024	0.46964	0.486256	0.134831	ENSG00000231381	RNF2P1
ENSG00000231382	0.252242	0.563955	0.280207	0.220597	ENSG00000231382	NBPF21P
ENSG00000231384	0.294494	1.87214	0.652104	1.91794	ENSG00000231384	AC007919.2
ENSG00000231385	0.0596122	0.555518	0	0	ENSG00000231385	BX005091.2
ENSG00000231386	0	0.0962443	0.101121	0.162418	ENSG00000231386	AC007395.1
ENSG00000231388	0	0	0	0	ENSG00000231388	AC079178.2
ENSG00000231389	0.015404	0.0454515	0.0767526	0.0785761	ENSG00000231389	HLA-DPA1
ENSG00000231390	0.481572	0.698348	0.471542	0.554804	ENSG00000231390	SNX18P8
ENSG00000231392	0	0	0	0	ENSG00000231392	AC244157.1
ENSG00000231395	0.726988	1.44097	1.58288	3.34118	ENSG00000231395	ARL4AP4
ENSG00000231396	0	0	0	0	ENSG00000231396	USP17L10
ENSG00000231397	0.592544	0	0	0	ENSG00000231397	AC004941.2
ENSG00000231398	0.49682	0.237484	0.428292	1.30748	ENSG00000231398	AL359385.1
ENSG00000231399	0	0	0	0	ENSG00000231399	SNRPEP8
ENSG00000231402	0.000124398	0.000187449	0.000167498	0.00014757	ENSG00000231402	WASF5P
ENSG00000231404	0	0.23703	0	0.132469	ENSG00000231404	RAC1P3
ENSG00000231408	0.0274983	0.0159269	0.0264951	0.0206416	ENSG00000231408	LTA
ENSG00000231409	3.89438	1.93694	4.11869	1.64028	ENSG00000231409	AC018868.1
ENSG00000231411	0	0	0	0	ENSG00000231411	DUX4L31
ENSG00000231414	0	0	0	0	ENSG00000231414	AC016700.2
ENSG00000231416	0.594987	0.304625	1.27761	0.622484	ENSG00000231416	AL358472.1
ENSG00000231417	0	0.119116	0.0807608	0.0338884	ENSG00000231417	IRX1P1
ENSG00000231423	0	0.0568481	0	0.127456	ENSG00000231423	RAB9AP5
ENSG00000231430	0.0807006	0.000660567	0	0.204045	ENSG00000231430	HCG4P8

ENSG00000231431	0	0	0.176803	0.288443	ENSG00000231431	FAR2P4
ENSG00000231433	0.000124398	0.000187449	0.000167498	0.00014757	ENSG00000231433	WASF5P
ENSG00000231434	0	0.0501155	0	0	ENSG00000231434	AL365440.1
ENSG00000231436	0	0	0	0	ENSG00000231436	RBMY3AP
ENSG00000231442	0	0.208259	0.0752973	0.0479836	ENSG00000231442	LARP1BP1
ENSG00000231443	0.594628	0.624901	1.04409	0.94126	ENSG00000231443	AC124944.2
ENSG00000231445	0	0	0.78326	2.25502	ENSG00000231445	TIMM8AP1
ENSG00000231448	0	0	0	0	ENSG00000231448	RP11-763B22.9
ENSG00000231449	0	0.81547	0.441646	0.553456	ENSG00000231449	AC097359.1
ENSG00000231454	0	0	0	0	ENSG00000231454	AL935212.3
ENSG00000231457	0	0	0	0	ENSG00000231457	RBM22P11
ENSG00000231458	0	0	0	0	ENSG00000231458	AC098850.1
ENSG00000231461	0.00091433	0	0.000798201	0.000801615	ENSG00000231461	HLA-DPA2
ENSG00000231464	0	0	0.21333	0.197841	ENSG00000231464	AC024937.2
ENSG00000231466	0.176321	2.56929	2.48307	2.2138	ENSG00000231466	AL022324.2
ENSG00000231468	0.114797	1.258	0.515417	1.11243	ENSG00000231468	PRDX3P2
ENSG00000231470	0.366215	0	0.105796	0.147009	ENSG00000231470	HMGB3P2
ENSG00000231471	0	0.406422	0.366153	0	ENSG00000231471	HMGN2P34
ENSG00000231475	0	0	0	0	ENSG00000231475	IGHV4-31
ENSG00000231478	0	0	0	0	ENSG00000231478	FCF1P9
ENSG00000231479	0.0393897	0.290961	0.258819	0.412492	ENSG00000231479	SLC44A4
ENSG00000231480	0	0	0	1.0195	ENSG00000231480	SNRPGP13
ENSG00000231484	0.207841	0	0.179448	0.220175	ENSG00000231484	AC023141.7
ENSG00000231488	7.14317	7.31203	6.05223	2.21443	ENSG00000231488	ABHD16A
ENSG00000231489	0	0	0	0	ENSG00000231489	AL606490.4
ENSG00000231490	0	0.0860139	0.0778512	0	ENSG00000231490	RPL7L1P2
ENSG00000231491	0.204966	0.0657069	0.178114	0.297167	ENSG00000231491	JKAMPP1
ENSG00000231494	0	0	0	0	ENSG00000231494	AC104634.1
ENSG00000231500	249.329	186.853	166.574	87.6578	ENSG00000231500	RPS18
ENSG00000231501	0	0	0	0	ENSG00000231501	MTND4LP1
ENSG00000231502	2.05115	3.2431	2.47841	1.71742	ENSG00000231502	LSM2
ENSG00000231503	0	0.41377	0	0	ENSG00000231503	PTMAP4
ENSG00000231504	0	0	0	0	ENSG00000231504	NMD3P2
ENSG00000231508	0.542281	0.506296	1.37176	0.835995	ENSG00000231508	RPL34P20
ENSG00000231511	0	0	0	0	ENSG00000231511	RP11-45O22.3
ENSG00000231513	0	0.210026	0.189644	0.156256	ENSG00000231513	E2F6P4
ENSG00000231514	0	0	0	0	ENSG00000231514	FAM58CP
ENSG00000231516	0	0.124428	0.112341	0.278439	ENSG00000231516	CBX1P5
ENSG00000231517	3.15256	9.80204	9.13201	7.13447	ENSG00000231517	RP11-7G23.5
ENSG00000231523	0	0.618199	0.477939	0.458345	ENSG00000231523	SEPT14P1
ENSG00000231525	0.12099	0	0.105469	0.129864	ENSG00000231525	AC002486.2
ENSG00000231526	0	0	0	0	ENSG00000231526	HLA-DQA2
ENSG00000231531	0.469276	0	0	0	ENSG00000231531	HINT1P1
ENSG00000231537	0	0	0	0	ENSG00000231537	MTCO3P10
ENSG00000231540	0	1.01801	0	3.28449	ENSG00000231540	ELOCP9
ENSG00000231541	0	0	0.0825197	0	ENSG00000231541	RPS6P2
ENSG00000231543	0.291039	0.225961	0.149568	0.149681	ENSG00000231543	C2
ENSG00000231544	0	0	0	0.170819	ENSG00000231544	RSL24D1P11
ENSG00000231546	0.14774	0.186323	0.336774	0.106197	ENSG00000231546	RPL3P5
ENSG00000231547	0	0	0.283065	0	ENSG00000231547	AC096632.1
ENSG00000231548	0.0607263	0.292154	0.052806	0.264605	ENSG00000231548	OR55B1P
ENSG00000231549	0	0	0.902085	5.17682	ENSG00000231549	USMG5P1
ENSG00000231550	0.210101	0.0559633	0.140524	0	ENSG00000231550	PTCHD3P2
ENSG00000231552	0.0619938	0.0594018	0.0543187	0	ENSG00000231552	IGBP1P3

ENSG00000231553	0	0	0	0	ENSG00000231553	RNMTL1P1
ENSG00000231555	43.6012	9.07581	15.2527	3.51745	ENSG00000231555	HSPA1B
ENSG00000231556	0.15599	0	0	0	ENSG00000231556	RSL24D1P3
ENSG00000231558	0.352883	0.231516	0.347544	0.0387109	ENSG00000231558	HLA-DOA
ENSG00000231559	0	0	0	0	ENSG00000231559	Z95118.1
ENSG00000231561	0	0	0.112552	0.070459	ENSG00000231561	CEACAMP5
ENSG00000231562	0.334991	3.30002	1.89058	1.36169	ENSG00000231562	AL512593.1
ENSG00000231564	0.629613	0.598738	1.0653	3.83566	ENSG00000231564	EIF4A1P11
ENSG00000231565	0	0.000493451	0.000253444	0.000258527	ENSG00000231565	NEK2P2
ENSG00000231567	0.0609968	0	0.0544086	0.132609	ENSG00000231567	MTND2P19
ENSG00000231568	0	0	0	0	ENSG00000231568	AC245047.3
ENSG00000231569	0	0	0	0	ENSG00000231569	AL355334.1
ENSG00000231570	0	0	0	0	ENSG00000231570	AC008173.1
ENSG00000231576	0	0	0	0	ENSG00000231576	MTCO2P20
ENSG00000231579	0.74722	1.66578	1.539	1.62507	ENSG00000231579	RPL7P21
ENSG00000231580	0	0.0858021	0.0808883	0.0707639	ENSG00000231580	CR759904.1
ENSG00000231582	0	0	0	0	ENSG00000231582	MTND4LP21
ENSG00000231583	0	0	0	0	ENSG00000231583	AC108938.1
ENSG00000231584	4.96215	6.15897	8.4465	2.06204	ENSG00000231584	FAHD2CP
ENSG00000231586	0	0	0	0	ENSG00000231586	RPS23P9
ENSG00000231588	0.733328	0.480261	0.810326	0.123083	ENSG00000231588	SHQ1P1
ENSG00000231590	0	0	0	0	ENSG00000231590	AC235565.1
ENSG00000231592	0	0	0	0	ENSG00000231592	BX248413.2
ENSG00000231593	0	0	0	0	ENSG00000231593	BX510359.4
ENSG00000231596	0	0	0	0	ENSG00000231596	HLA-DQB3
ENSG00000231600	0	0	0	0	ENSG00000231600	AC236972.1
ENSG00000231602	0.898463	0	0	0.335064	ENSG00000231602	RPL35AP4
ENSG00000231603	0	0	0.0750047	0.0935606	ENSG00000231603	AL606490.5
ENSG00000231608	0.896302	0.271015	0.371536	0.640769	ENSG00000231608	TNXB
ENSG00000231610	0.0680597	0.0654491	0	0.0740036	ENSG00000231610	PIK3CDP1
ENSG00000231615	0	0.510121	0.345156	0.867123	ENSG00000231615	AL645568.2
ENSG00000231617	6.75617	6.80298	10.0751	4.67054	ENSG00000231617	DAXX
ENSG00000231618	3.27886	3.33918	2.21686	1.12312	ENSG00000231618	PPT2
ENSG00000231619	0.218076	1.75773	1.21609	2.7668	ENSG00000231619	AC003685.2
ENSG00000231622	1.11762	4.84764	4.60087	3.30686	ENSG00000231622	RPS29P7
ENSG00000231623	0	0.0169735	0.0627602	0.0560227	ENSG00000231623	BX682535.1
ENSG00000231624	0.357191	0.0509367	0.0789204	0.332033	ENSG00000231624	C6orf15
ENSG00000231625	0.780249	0.0504235	0.180601	0.0571683	ENSG00000231625	AC115989.1
ENSG00000231631	1.83924	1.03846	2.49663	1.87157	ENSG00000231631	PSMB8
ENSG00000231635	0.0733465	0.247306	0.063872	0.0803288	ENSG00000231635	ATP5BP1
ENSG00000231637	0	0	0	0	ENSG00000231637	USP17L29
ENSG00000231641	1.63215	0	0.161397	0.10818	ENSG00000231641	TRIM26
ENSG00000231643	0.72513	0	0.310168	0.37509	ENSG00000231643	Z70280.1
ENSG00000231645	0.0573311	0.398553	0.55976	0.109276	ENSG00000231645	KRT17P6
ENSG00000231649	0.0332292	0.0129693	0.035179	0.0296082	ENSG00000231649	SPATA31B1P
ENSG00000231650	0	0	0	0.26542	ENSG00000231650	RFESDP1
ENSG00000231655	2.37869	3.27277	1.87185	1.387	ENSG00000231655	AC011742.2
ENSG00000231656	0	0	0	0	ENSG00000231656	FAM90A18P
ENSG00000231659	0	0.00827178	0.059801	0.0281478	ENSG00000231659	UBQLN1P1
ENSG00000231660	0	0	0	0	ENSG00000231660	RPS8P6
ENSG00000231665	0.183699	0.419401	0.378425	0.854637	ENSG00000231665	OGFOD1P1
ENSG00000231667	0	0	0	0	ENSG00000231667	OR7E111P
ENSG00000231668	0	0	0	0	ENSG00000231668	PPP2R2DP1
ENSG00000231670	0	0	0.00828591	0	ENSG00000231670	BX248093.2

ENSG00000231672	0.471435	0.879452	2.44814	1.61083	ENSG00000231672	DIRC3
ENSG00000231675	0	0	0	0	ENSG00000231675	AC005042.3
ENSG00000231676	0	0	0	0	ENSG00000231676	OR2J2
ENSG00000231679	0	0	0	0	ENSG00000231679	HLA-DRB3
ENSG00000231684	0	0	0	0	ENSG00000231684	EIF1P3
ENSG00000231686	0	0	0.111642	0	ENSG00000231686	Z97180.1
ENSG00000231688	0	0	0	0	ENSG00000231688	RPL21P43
ENSG00000231694	0	0	0	0	ENSG00000231694	AC244098.3
ENSG00000231697	0.781935	2.30365	1.94784	4.10864	ENSG00000231697	NANOGP5
ENSG00000231699	1.24726	0	2.0545	1.24389	ENSG00000231699	AC020550.1
ENSG00000231700	0	0	0	0	ENSG00000231700	AL356276.2
ENSG00000231701	0	0	1.55546	0	ENSG00000231701	BMS1P13
ENSG00000231702	0	0.663318	1.17116	4.22434	ENSG00000231702	AL645608.4
ENSG00000231706	0	0	0	0	ENSG00000231706	CYCSP43
ENSG00000231707	1.84174	2.5592	2.74067	3.39378	ENSG00000231707	PABPC1P1
ENSG00000231710	0	0.0458373	0.0827353	0.200941	ENSG00000231710	CR759814.1
ENSG00000231712	0	1.16193	0	0.843819	ENSG00000231712	AC104698.1
ENSG00000231715	0	0	0	0	ENSG00000231715	COX6CP2
ENSG00000231716	0	0	0.0503937	0.190748	ENSG00000231716	CDY23P
ENSG00000231719	0	0	0.165242	0.129105	ENSG00000231719	MCCD1P2
ENSG00000231722	0.369696	0.473056	0.985397	0.669991	ENSG00000231722	AC012075.1
ENSG00000231723	0	0	0	0	ENSG00000231723	AC018880.2
ENSG00000231725	0	0.0615134	0.0277951	0.0696936	ENSG00000231725	VN1R110P
ENSG00000231726	0.893427	1.70104	2.85239	8.45651	ENSG00000231726	HMGN2P38
ENSG00000231735	0	0.0688792	0.186686	0.0785157	ENSG00000231735	AC092573.1
ENSG00000231737	5.55483	9.66722	7.87132	5.90532	ENSG00000231737	PPP1R10
ENSG00000231738	1.23057	4.5994	4.35671	5.90512	ENSG00000231738	TSPAN19
ENSG00000231739	0	0.824318	0.452271	0.368928	ENSG00000231739	GAPDHP59
ENSG00000231741	0.0396847	0.0382803	0.0692882	0.219146	ENSG00000231741	AL353743.3
ENSG00000231743	0	0.188551	0.170223	0.418099	ENSG00000231743	AC026396.1
ENSG00000231744	0.232115	0.558692	0.620148	1.01809	ENSG00000231744	AL669818.1
ENSG00000231745	0	0	0.165242	0.129105	ENSG00000231745	MCCD1P2
ENSG00000231746	0	0	0	0	ENSG00000231746	BX119924.1
ENSG00000231747	0.529385	0.752067	0	0.836526	ENSG00000231747	AC079922.1
ENSG00000231750	0	0	0	0	ENSG00000231750	NANOGP10
ENSG00000231752	0.309225	0.981027	0.368848	0.514101	ENSG00000231752	EMBP1
ENSG00000231759	0.163861	0.087706	0.0108646	0.392151	ENSG00000231759	CYP21A1P
ENSG00000231762	0.444039	1.24299	0.892654	2.31823	ENSG00000231762	AL590426.1
ENSG00000231763	0	0.183088	0	0	ENSG00000231763	PQLC1P1
ENSG00000231765	0.230238	1.53899	0.794504	0.486156	ENSG00000231765	PPP1R11P2
ENSG00000231766	0	0	0	0	ENSG00000231766	MTCO2P5
ENSG00000231767	0.178179	0	0	0	ENSG00000231767	AL136454.1
ENSG00000231773	0.0642566	0.230628	0	0.272811	ENSG00000231773	ZDHHC20P2
ENSG00000231775	0	0	0	0	ENSG00000231775	RP11-472D17.4
ENSG00000231777	0	0	0	0	ENSG00000231777	MTND4P21
ENSG00000231780	0.338473	0.320861	1.15829	2.10988	ENSG00000231780	AC090960.1
ENSG00000231784	0.600874	0.810444	1.09749	0.95974	ENSG00000231784	DBIL5P
ENSG00000231785	0.00724298	0.0568987	0	0.00789492	ENSG00000231785	MICC
ENSG00000231787	0.0943192	0.180519	0.162983	0.30056	ENSG00000231787	AC234782.3
ENSG00000231788	0	0	0	0	ENSG00000231788	RPL31P50
ENSG00000231793	0.566787	2.1713	1.50951	2.1369	ENSG00000231793	DOC2GP
ENSG00000231799	0.472066	0.643309	0.517183	1.36932	ENSG00000231799	PA2G4P6
ENSG00000231801	0	0	0	0.144082	ENSG00000231801	ANP32BP2
ENSG00000231802	0.598746	0.172771	0.55984	0.744062	ENSG00000231802	AC009502.2

ENSG00000231804	0.723655	0.157512	0.617128	0.175313	ENSG00000231804	AL353748.1
ENSG00000231809	0.0750877	0.342043	0.123103	0.169714	ENSG00000231809	NANOGP9
ENSG00000231810	0	0	0	0.347802	ENSG00000231810	RPL36AP35
ENSG00000231812	1.47774	0.726771	6.32221	3.51582	ENSG00000231812	SNRPCP9
ENSG00000231821	0.299226	0.329161	0.570019	0.494529	ENSG00000231821	NPM1P48
ENSG00000231822	0.669939	1.14327	1.34668	0.860044	ENSG00000231822	AC019097.1
ENSG00000231823	0	0	0	0	ENSG00000231823	HLA-DQA2
ENSG00000231824	0.267151	0.119678	0.10807	0	ENSG00000231824	AKAIN1
ENSG00000231825	1.1185	8.16453	7.68887	15.2385	ENSG00000231825	PRRC2A
ENSG00000231827	0.110549	0.279204	0.385815	0.487801	ENSG00000231827	AL513523.2
ENSG00000231831	0.163456	0.295228	0.591257	0.247448	ENSG00000231831	MTHFD1P1
ENSG00000231834	3.57071	12.4561	6.57676	0.184164	ENSG00000231834	HLA-A
ENSG00000231837	0	0	0.100407	0	ENSG00000231837	RPS7P2
ENSG00000231839	0.0761747	0.0365239	0.256509	0.120674	ENSG00000231839	AC073055.1
ENSG00000231841	0.293843	0.268186	0.246037	0.407295	ENSG00000231841	FAM192BP
ENSG00000231845	2.60145	3.62182	2.96413	6.26429	ENSG00000231845	HMGB3P14
ENSG00000231848	0	0	0	0.375885	ENSG00000231848	AC012354.2
ENSG00000231849	1.85171	1.85083	3.58915	6.5978	ENSG00000231849	UBE2V2P4
ENSG00000231850	0	0	0	0	ENSG00000231850	GAGE2B
ENSG00000231852	0	0.0247487	0.135193	0.0770113	ENSG00000231852	CYP21A2
ENSG00000231855	0	0	0	0	ENSG00000231855	AL161935.2
ENSG00000231857	0	0.0625594	0.0705745	0.144254	ENSG00000231857	MORF4L1P5
ENSG00000231859	1.09487	1.46479	1.70052	2.08349	ENSG00000231859	AC079781.1
ENSG00000231861	0	0.0561366	0.253669	0.19074	ENSG00000231861	OR5K2
ENSG00000231866	1.05524	0	0	0	ENSG00000231866	AC099677.2
ENSG00000231870	0.33207	0.234901	0.514297	0.0535345	ENSG00000231870	KRT17P3
ENSG00000231874	0	0	0	0	ENSG00000231874	TSPY18P
ENSG00000231875	0.20938	0.604053	0.363866	0.606934	ENSG00000231875	AL359885.1
ENSG00000231878	0	0	0	0	ENSG00000231878	SNRPFP1
ENSG00000231879	0	0	0	0	ENSG00000231879	TXNL1P1
ENSG00000231880	1.46185	1.58457	0.18165	0	ENSG00000231880	KF459542.1
ENSG00000231884	0.998889	0.968596	0	0	ENSG00000231884	NDUFB1P1
ENSG00000231887	0	0	0	0	ENSG00000231887	PRH1
ENSG00000231888	1.63373	2.64175	2.84219	4.06502	ENSG00000231888	MTND5P15
ENSG00000231894	0	0	0	0	ENSG00000231894	WDR95P
ENSG00000231895	0	0	0	0	ENSG00000231895	HLA-DPA3
ENSG00000231897	0	0	0.0479684	0.0596198	ENSG00000231897	MARK2P14
ENSG00000231900	0	0	0	0	ENSG00000231900	GOT2P1
ENSG00000231904	0	0	0	0	ENSG00000231904	HLA-H
ENSG00000231905	0.626234	0.888021	1.25435	3.3459	ENSG00000231905	SETP10
ENSG00000231906	1.05739	1.98766	0.902243	14.4424	ENSG00000231906	AC016397.1
ENSG00000231907	0.0641911	0.0622365	0.167419	0.144628	ENSG00000231907	GAPDHP37
ENSG00000231909	1.80691	3.81127	2.07517	3.85589	ENSG00000231909	MAP1LC3BP1
ENSG00000231910	0	0.163094	0.147215	0	ENSG00000231910	GAMTP2
ENSG00000231911	0	0	0.278278	0	ENSG00000231911	TPRKBP1
ENSG00000231913	0	0.157993	0	0.175851	ENSG00000231913	RARRES2P3
ENSG00000231915	0	0	0.0287944	0.142115	ENSG00000231915	SALL4P5
ENSG00000231916	0.19345	0.185101	0.517214	0.205342	ENSG00000231916	AC006033.1
ENSG00000231919	0	0	0	0	ENSG00000231919	BX908738.4
ENSG00000231922	1.53701	5.3708	2.83581	5.72775	ENSG00000231922	AL138479.1
ENSG00000231923	0	0	0	0	ENSG00000231923	AC024082.1
ENSG00000231924	2.44266	3.31599	3.27112	7.8216	ENSG00000231924	PSG1
ENSG00000231925	15.4937	37.5856	27.3583	17.8858	ENSG00000231925	TAPBP
ENSG00000231926	0.0509917	0.147264	0.310568	0	ENSG00000231926	SEPHS1P7

ENSG00000231928	0	0	0	0	ENSG00000231928	TRIM26BP
ENSG00000231929	0	0	0.103143	0.128026	ENSG00000231929	HMGB3P31
ENSG00000231930	0	0	0	0	ENSG00000231930	AF228730.3
ENSG00000231931	0	0	0	0	ENSG00000231931	AC024082.2
ENSG00000231939	0	0	0	0	ENSG00000231939	HLA-DQB1
ENSG00000231940	0.619604	3.09416	1.93511	2.51846	ENSG00000231940	RPS7P3
ENSG00000231941	0	0	0.982321	0.783254	ENSG00000231941	HCG4B
ENSG00000231942	0.0653284	0.315469	0.284082	0.213351	ENSG00000231942	HNRNPA1P36
ENSG00000231945	8.64845	19.9862	15.1149	15.5244	ENSG00000231945	VARS
ENSG00000231947	0	0	0	0	ENSG00000231947	MTND2P24
ENSG00000231952	0.174946	0.26658	0.498423	0.604976	ENSG00000231952	DPY19L1P2
ENSG00000231954	1.36371	1.43923	0.354219	3.05839	ENSG00000231954	MTND2P22
ENSG00000231956	0	0	0	0	ENSG00000231956	HNRNPA1P9
ENSG00000231957	0.0687157	0	0	0.0769651	ENSG00000231957	GNAI2P2
ENSG00000231961	0	1.11176	0.753908	0.917761	ENSG00000231961	AL035461.1
ENSG00000231962	0	0	0.0606443	0	ENSG00000231962	VN1R7P
ENSG00000231965	1.29277	5.50878	4.7251	4.15095	ENSG00000231965	AF131215.1
ENSG00000231967	0.676411	2.53351	0.564374	2.03691	ENSG00000231967	AL135786.1
ENSG00000231968	0	0	0	0	ENSG00000231968	UBD
ENSG00000231973	0	0	0.016343	0	ENSG00000231973	OR2I1P
ENSG00000231974	0.164783	0.252772	0.0998859	0.157885	ENSG00000231974	APOM
ENSG00000231975	0.0916753	0.264657	0.272079	0.660025	ENSG00000231975	MCCD1
ENSG00000231978	0	0.956647	1.72746	1.04925	ENSG00000231978	AL590103.1
ENSG00000231981	0.273231	1.15996	0.553472	1.08424	ENSG00000231981	RPL7L1P12
ENSG00000231982	1.41993	2.7093	2.52183	1.10457	ENSG00000231982	AC112907.2
ENSG00000231984	0	0	0	0	ENSG00000231984	AL596266.1
ENSG00000231988	0.08321	0.567566	0.289001	0.459894	ENSG00000231988	OFD1P3Y
ENSG00000231989	0.129426	0.214754	0.31299	0.475072	ENSG00000231989	PPP1R2P3
ENSG00000231991	3.22876	2.68647	1.21843	4.71481	ENSG00000231991	ANXA2P2
ENSG00000231995	0.99419	0.706159	1.82086	1.36845	ENSG00000231995	AL590399.4
ENSG00000231996	0	0	0	0	ENSG00000231996	AC096949.1
ENSG00000231997	0.572808	4.84854	5.1625	1.43243	ENSG00000231997	FAM27D1
ENSG00000231998	0	0	0	0	ENSG00000231998	MCCD1P1
ENSG00000232000	1.49955	2.43576	1.17049	5.57093	ENSG00000232000	CLCN3P1
ENSG00000232003	0	0	0	0	ENSG00000232003	ZNF736P12Y
ENSG00000232004	0.515559	0.246056	0.134748	0.254006	ENSG00000232004	CAP1P2
ENSG00000232005	2.65289	6.45411	3.41318	7.44577	ENSG00000232005	PBX2
ENSG00000232007	0	0	0	0	ENSG00000232007	POLR2LP1
ENSG00000232009	0	0	0	0	ENSG00000232009	AL591503.2
ENSG00000232011	0	0	0	0.062455	ENSG00000232011	HLA-W
ENSG00000232013	0.370303	0.762164	1.24019	5.21789	ENSG00000232013	AC107021.1
ENSG00000232014	0	0	0	0.130358	ENSG00000232014	MTND1P13
ENSG00000232015	0	0.926064	2.1014	2.77543	ENSG00000232015	HSPE1P25
ENSG00000232017	0.00944618	0	0.0164323	0	ENSG00000232017	ZNF90P2
ENSG00000232022	1.03783	0.859753	0.713694	1.7132	ENSG00000232022	FAAHP1
ENSG00000232024	2.62804	0	5.00E-06	0	ENSG00000232024	LSM12P1
ENSG00000232025	0	2.21801	5.75485	6.27407	ENSG00000232025	RP1-218B13.1
ENSG00000232027	0.458398	1.25714	1.13589	1.34868	ENSG00000232027	AL671986.1
ENSG00000232029	0	0	0	0	ENSG00000232029	ELOCP15
ENSG00000232030	0	0	0	0	ENSG00000232030	MAGEB6P1
ENSG00000232032	2.38157	2.52356	1.88743	0	ENSG00000232032	AC079781.2
ENSG00000232036	0.178051	1.08056	0.736148	1.16796	ENSG00000232036	AL078645.2
ENSG00000232037	1.32816	1.35537	2.89267	2.57276	ENSG00000232037	AL590556.1
ENSG00000232039	0	0	0.175241	0.881229	ENSG00000232039	DEFT1P2

ENSG00000232040	4.42019	7.47097	9.35637	4.10846	ENSG00000232040	ZBED9
ENSG00000232041	0	0.173861	0.313184	0.380795	ENSG00000232041	PSMD10P3
ENSG00000232042	0	0	0	0	ENSG00000232042	AL512286.1
ENSG00000232045	4.06832	4.07993	3.23499	4.27404	ENSG00000232045	EHMT2
ENSG00000232048	0	0	0.193333	0.322188	ENSG00000232048	HNRNPCP9
ENSG00000232049	0	0	0.016343	0	ENSG00000232049	OR2I1P
ENSG00000232050	0	1.52585	1.08021	1.32843	ENSG00000232050	Z98949.2
ENSG00000232054	0.0709429	0.208057	0.0627418	0.308033	ENSG00000232054	NPM1P34
ENSG00000232056	0	0.213529	0	0	ENSG00000232056	AC092687.1
ENSG00000232059	0.751855	4.90812	2.46132	1.55375	ENSG00000232059	AL451007.1
ENSG00000232060	0	0	0	0	ENSG00000232060	SLC4A1APP1
ENSG00000232062	0	0	0	0	ENSG00000232062	HLA-DQA1
ENSG00000232064	0	0	0	0	ENSG00000232064	USP9YP33
ENSG00000232068	0.106992	0	0.0927892	0	ENSG00000232068	AF003529.1
ENSG00000232069	0	0	0	0	ENSG00000232069	RPS29P28
ENSG00000232070	8.84313	4.71238	7.65042	2.50073	ENSG00000232070	TMEM253
ENSG00000232075	0	0.142057	0	0	ENSG00000232075	MRPL35P2
ENSG00000232083	0.648307	0.447306	1.13992	1.48351	ENSG00000232083	AC109327.2
ENSG00000232087	0	0	0	0	ENSG00000232087	HCFC2P1
ENSG00000232089	0	0	0	0	ENSG00000232089	AC011233.1
ENSG00000232090	0	0	0	0	ENSG00000232090	AC016724.1
ENSG00000232091	1.21542	0.968407	1.13855	2.99669	ENSG00000232091	PNLIPP1
ENSG00000232095	0	0.00827178	0.059801	0.0281478	ENSG00000232095	UBQLN1P1
ENSG00000232096	0	0	0	0	ENSG00000232096	YPEL5P1
ENSG00000232097	0	0.891564	1.35654	0.272289	ENSG00000232097	AC079781.3
ENSG00000232099	0.597048	0.883221	0.053838	0.24367	ENSG00000232099	ZFP57
ENSG00000232101	0	0	0	4.91118	ENSG00000232101	AC108059.2
ENSG00000232102	0	1.04294	0	1.10229	ENSG00000232102	MTCO3P2
ENSG00000232105	0	0	0.373294	0	ENSG00000232105	RPL32P28
ENSG00000232106	0	0	0	0	ENSG00000232106	C6orf10
ENSG00000232109	0.179667	0.764527	0.46007	1.25192	ENSG00000232109	VN1R54P
ENSG00000232111	0.00890247	0.0257625	0.00776515	0.0098178	ENSG00000232111	AC073488.1
ENSG00000232112	111.171	81.9838	73.3757	63.1064	ENSG00000232112	TMA7
ENSG00000232114	0	0	0	0	ENSG00000232114	AC018693.2
ENSG00000232115	0	0	0	0	ENSG00000232115	AC026884.1
ENSG00000232119	30.5586	36.2311	38.8944	40.9158	ENSG00000232119	MCTS1
ENSG00000232122	0.0807006	0.000660567	0	0.204045	ENSG00000232122	HCG4P8
ENSG00000232125	0.082606	0.105716	0.143356	0.300944	ENSG00000232125	DYTN
ENSG00000232126	7.29407	33.4002	34.3863	49.617	ENSG00000232126	HLA-B
ENSG00000232127	0	0.539724	0.0232283	0.74788	ENSG00000232127	PSORS1C2
ENSG00000232128	0	0.054854	0.049544	0.125412	ENSG00000232128	MTCO3P45
ENSG00000232129	26.0827	35.4721	44.8412	86.4322	ENSG00000232129	AC011385.2
ENSG00000232133	0.538096	0.501059	0	0.424311	ENSG00000232133	IMPDH1P10
ENSG00000232134	0.226578	2.3951	0.585632	1.15254	ENSG00000232134	RPS15AP12
ENSG00000232135	0	0	0	0	ENSG00000232135	AL031663.1
ENSG00000232136	1.44201	4.8968	5.36306	6.62234	ENSG00000232136	DUXAP7
ENSG00000232138	0	0	0	0	ENSG00000232138	IFNWP5
ENSG00000232141	0.00219419	0.195312	0.0547187	0.0715276	ENSG00000232141	ETF1P1
ENSG00000232142	0.487741	0.459682	0.821615	2.97906	ENSG00000232142	RPS25P9
ENSG00000232143	4.7918	2.11576	2.67785	2.50199	ENSG00000232143	GNL1
ENSG00000232144	0.063868	0.122876	0.111294	0.486625	ENSG00000232144	PSAT1P2
ENSG00000232145	0	0	0	0	ENSG00000232145	AC099548.1
ENSG00000232146	0.009462	0.0181999	0.0164453	0.0102936	ENSG00000232146	BX005432.3

ENSG00000232148	0.0428571	0.0825477	0.223843	0	ENSG00000232148	FMO11P
ENSG00000232149	0.541054	1.34561	1.2134	2.6632	ENSG00000232149	FERP1
ENSG00000232150	0.140762	0.0625102	0	0.368419	ENSG00000232150	ST13P4
ENSG00000232154	0	0	0.0466539	0.126179	ENSG00000232154	MTCYBP15
ENSG00000232155	0	0	0	0	ENSG00000232155	AC244090.1
ENSG00000232156	0	0	0	0	ENSG00000232156	AL662842.1
ENSG00000232158	0	0	0.543493	0.658477	ENSG00000232158	C11orf98P1
ENSG00000232159	0	0	0	0	ENSG00000232159	RAB9BP1
ENSG00000232161	0	0	0	0.448095	ENSG00000232161	AC023141.8
ENSG00000232163	2.38479	5.05676	0.957441	7.10615	ENSG00000232163	RPLP1P13
ENSG00000232165	0	0	0	0	ENSG00000232165	AC006455.6
ENSG00000232166	0.631098	1.09014	0.656256	1.35593	ENSG00000232166	AL122008.2
ENSG00000232167	0	0	0	0	ENSG00000232167	AC137675.1
ENSG00000232168	0.344332	0.463601	0.0598423	0.449248	ENSG00000232168	P2RY10P2
ENSG00000232169	3.61336	5.3999	6.92217	7.77632	ENSG00000232169	ABCF1
ENSG00000232172	0	0	0	0	ENSG00000232172	AL359092.2
ENSG00000232173	0	0.0207547	0.0239362	0	ENSG00000232173	AL645936.2
ENSG00000232174	0	0	0	0	ENSG00000232174	AC113340.1
ENSG00000232175	0	0	0	0	ENSG00000232175	AL122003.1
ENSG00000232176	0	0	0	0	ENSG00000232176	AL161909.1
ENSG00000232177	0	0	0	0	ENSG00000232177	MTND4P24
ENSG00000232178	0	0	0.00605942	0	ENSG00000232178	OR2J3
ENSG00000232179	0	3.1485	6.35347	4.83117	ENSG00000232179	MTATP6P29
ENSG00000232180	0.323279	0.093444	0.258819	0.412492	ENSG00000232180	SLC44A4
ENSG00000232185	0	0	0	0	ENSG00000232185	CNOT7P2
ENSG00000232186	0.289052	0.825228	0.483498	0.728205	ENSG00000232186	AL137013.1
ENSG00000232187	0.34254	0	0.262743	0	ENSG00000232187	FTH1P7
ENSG00000232189	0	0	0	0	ENSG00000232189	TMEM183AP1
ENSG00000232195	0.550262	1.71993	3.6912	0	ENSG00000232195	TOMM22P2
ENSG00000232196	1991.81	1913.56	2598.28	2535.06	ENSG00000232196	MTRNR2L4
ENSG00000232198	0	0	0.100407	0.12468	ENSG00000232198	MTCO2P34
ENSG00000232199	0.100612	0.339008	0.262619	0.164812	ENSG00000232199	RPL3P8
ENSG00000232202	0	0.0619899	0	0.142347	ENSG00000232202	AC098824.1
ENSG00000232203	0	0	0	0	ENSG00000232203	SLC25A6P2
ENSG00000232204	0.07327	0.141123	0.148644	0.493512	ENSG00000232204	TET1P1
ENSG00000232205	0	0	0	0	ENSG00000232205	CDY18P
ENSG00000232208	0.295741	1.06075	0.52802	0	ENSG00000232208	AL139415.1
ENSG00000232210	0	0.509709	0.390715	1.00457	ENSG00000232210	PHBP15
ENSG00000232215	0	0.191586	0	0.24062	ENSG00000232215	OR2L6P
ENSG00000232216	0	0	0	0	ENSG00000232216	IGHV3-43
ENSG00000232217	0.43656	2.06079	2.2166	2.77871	ENSG00000232217	FTLP8
ENSG00000232218	2.3075	2.16335	0.637949	5.39999	ENSG00000232218	AL021937.2
ENSG00000232223	0	0	0	0	ENSG00000232223	CNN2P10
ENSG00000232226	0	0.156038	0	0	ENSG00000232226	ARSFP1
ENSG00000232228	0.316361	1.79953	1.63952	4.29804	ENSG00000232228	AC092431.2
ENSG00000232230	0.712947	2.12697	1.41581	1.02387	ENSG00000232230	TPM4P1
ENSG00000232232	0	0	0	0	ENSG00000232232	HLA-N
ENSG00000232235	0.106699	0.103178	0.0309741	0.194809	ENSG00000232235	CDY3P
ENSG00000232237	0.277891	0.133913	0.338972	0.189673	ENSG00000232237	ASCL5
ENSG00000232238	0	0	0	0	ENSG00000232238	RPS29P8
ENSG00000232239	0	0	0	0	ENSG00000232239	RBPJP5
ENSG00000232240	0	0	0	0	ENSG00000232240	AL356387.2
ENSG00000232241	0	0	0	0	ENSG00000232241	DYNLT3P1
ENSG00000232242	0	0.14724	0.199546	0.166239	ENSG00000232242	ZYG11AP1

ENSG00000232244	0	0	0	0	ENSG00000232244	BX248310.2
ENSG00000232249	0	0	0	0	ENSG00000232249	AC152007.1
ENSG00000232251	0.00830609	0.0255328	0.0140436	0.0169609	ENSG00000232251	DPCR1
ENSG00000232253	0	0	0	0	ENSG00000232253	MICF
ENSG00000232254	0	0.423699	0.765645	0.234294	ENSG00000232254	CSF2RBP1
ENSG00000232258	0	0	0.251453	0.115406	ENSG00000232258	TMEM114
ENSG00000232260	0.684457	0.525357	0.929355	0.558446	ENSG00000232260	BTF3L4P1
ENSG00000232261	0	0	0	0	ENSG00000232261	Z98751.1
ENSG00000232263	0	0	0	0	ENSG00000232263	KRTAP25-1
ENSG00000232264	0	0	0	0	ENSG00000232264	USP17L24
ENSG00000232267	0.0472724	0	0	0.103368	ENSG00000232267	ACTR3P2
ENSG00000232268	0	0.772726	0.165971	0.254887	ENSG00000232268	OR52I1
ENSG00000232270	0	0	0	0	ENSG00000232270	INTS4L2
ENSG00000232273	1.17718	0.668576	0.370641	1.49006	ENSG00000232273	FTH1P1
ENSG00000232276	0	0	0	0	ENSG00000232276	AL845443.2
ENSG00000232277	0.140507	0.269585	0.245576	0.302188	ENSG00000232277	AC104651.2
ENSG00000232280	1.06447	2.0428	0.329265	1.13364	ENSG00000232280	FLOT1
ENSG00000232281	0	0	0	0	ENSG00000232281	IFNWP15
ENSG00000232282	0.333299	0.772167	0.696157	1.89258	ENSG00000232282	MTND1P32
ENSG00000232285	0.728334	0.689776	0.327348	0.380245	ENSG00000232285	ELOBP3
ENSG00000232289	0.21123	0.457168	0.423707	0.844127	ENSG00000232289	OR11A1
ENSG00000232292	0.224621	0.323483	0	0.242007	ENSG00000232292	ALDH7A1P2
ENSG00000232293	0	0.50683	0.338081	0.633351	ENSG00000232293	PAICSP7
ENSG00000232296	0	0	0	0	ENSG00000232296	AL691482.1
ENSG00000232302	0	0.0341391	0.030885	0	ENSG00000232302	AL662869.1
ENSG00000232303	0.0643948	0.920357	0.510925	0.853459	ENSG00000232303	DFFBP1
ENSG00000232305	0	0	0	0	ENSG00000232305	CLCP1
ENSG00000232308	0.00830609	0.0255328	0.0140436	0.0169609	ENSG00000232308	DPCR1
ENSG00000232312	1.92098	2.92839	0.662695	0.448828	ENSG00000232312	GPANK1
ENSG00000232314	0.125723	0.0604787	0	0	ENSG00000232314	PSMC1P13
ENSG00000232320	0.306571	0.287792	0.47382	1.05284	ENSG00000232320	AC009299.2
ENSG00000232326	0.212806	7.87129	1.98347	3.24272	ENSG00000232326	TAP2
ENSG00000232327	0	0.0210132	0.056993	0.289566	ENSG00000232327	AC105917.1
ENSG00000232331	0	0	0	0	ENSG00000232331	HLA-K
ENSG00000232332	0	0	0	0	ENSG00000232332	AC233982.1
ENSG00000232333	0.186412	0.86642	0.491404	0.374448	ENSG00000232333	RPS27AP2
ENSG00000232334	3.82477	3.80455	5.837	6.92454	ENSG00000232334	AL683842.1
ENSG00000232337	0.124879	0.175944	0.15624	0.236008	ENSG00000232337	AC009313.2
ENSG00000232339	0.244895	0.84754	0.458006	0.980532	ENSG00000232339	NOTCH4
ENSG00000232341	0	0	0	0	ENSG00000232341	RPL4P2
ENSG00000232344	0.622217	0.524287	1.0864	0.897058	ENSG00000232344	AC087163.2
ENSG00000232345	0	0	0	0.0861113	ENSG00000232345	MICD
ENSG00000232346	0	0.215851	0.36778	0	ENSG00000232346	Z74021.1
ENSG00000232349	0.552138	4.40742	1.19434	1.92941	ENSG00000232349	YBX1P7
ENSG00000232350	0	1.43205	2.47753	1.4971	ENSG00000232350	AC244250.2
ENSG00000232355	0	0	0	0	ENSG00000232355	AL603650.1
ENSG00000232357	1.5288	1.62628	2.07747	0.55839	ENSG00000232357	HSD17B8
ENSG00000232361	0	0	0	0.308594	ENSG00000232361	AC069304.1
ENSG00000232362	0.330021	0	0	0	ENSG00000232362	ATP5LP2
ENSG00000232366	0	0	0	0	ENSG00000232366	VDAC1P9
ENSG00000232367	3.97772	4.76897	4.26072	3.74213	ENSG00000232367	TAP1
ENSG00000232368	0	0	0	0	ENSG00000232368	FTLP2
ENSG00000232369	0.468559	0.450019	0.135556	0	ENSG00000232369	AL136380.2
ENSG00000232370	0.703833	1.65172	2.32706	1.93867	ENSG00000232370	AF241726.1

ENSG00000232372	8.32573	27.1473	34.2411	23.0934	ENSG00000232372	RP11-504P24.2
ENSG00000232373	0.212346	0.204371	0.138533	0.868802	ENSG00000232373	MTCYBP3
ENSG00000232374	0.585774	1.26748	1.33621	1.11356	ENSG00000232374	GPR79
ENSG00000232375	0	0.279378	0.254374	0.615065	ENSG00000232375	AC092042.2
ENSG00000232376	0	0	0	0	ENSG00000232376	LYPLA2P1
ENSG00000232378	0	0.317129	0.572337	0.176393	ENSG00000232378	RPL29P28
ENSG00000232379	1.41668	2.84329	2.66559	4.06472	ENSG00000232379	AL390879.1
ENSG00000232380	0	0	0	0	ENSG00000232380	ZDHHC20P4
ENSG00000232381	0	0	0.0590612	0	ENSG00000232381	OR52U1P
ENSG00000232382	0	0	0	0	ENSG00000232382	OR5K1
ENSG00000232383	0	0	0.176475	0.432513	ENSG00000232383	AC010677.1
ENSG00000232384	0	0	0	0	ENSG00000232384	RP11-204I15.1
ENSG00000232385	0	0	0.146804	0	ENSG00000232385	RPS3AP25
ENSG00000232387	0	0.241474	0	0.482873	ENSG00000232387	SKA2P1
ENSG00000232389	0	0	0.0977538	0	ENSG00000232389	AL583856.1
ENSG00000232390	0.27915	0.536892	0	0	ENSG00000232390	NDUFA5P1
ENSG00000232391	0	0	0	0	ENSG00000232391	RANP2
ENSG00000232392	0.050348	0	0	0	ENSG00000232392	AC002366.1
ENSG00000232393	0.0714326	0.2061	0.0620852	0.155199	ENSG00000232393	RPL5P6
ENSG00000232397	0	0.00838819	0.0181864	0	ENSG00000232397	OR10C1
ENSG00000232398	0.396127	1.23702	0.476658	0.856125	ENSG00000232398	TMPRSS11CP
ENSG00000232399	0	0	0.0344733	0	ENSG00000232399	USP17L13
ENSG00000232400	0.110211	0.0266001	0.0963073	0.121602	ENSG00000232400	RAD17P1
ENSG00000232403	0	0	0	0	ENSG00000232403	AC009501.2
ENSG00000232407	0.308418	0.376853	0.203159	0.362216	ENSG00000232407	AC104164.2
ENSG00000232409	0	0	0	0	ENSG00000232409	AC019185.3
ENSG00000232414	0	0	0.0409381	0	ENSG00000232414	CYP21A2
ENSG00000232417	0	0	0	0	ENSG00000232417	CT45A3
ENSG00000232418	0	0	0	0	ENSG00000232418	AC074348.1
ENSG00000232420	0	0	0.0589215	0.0984172	ENSG00000232420	IL9RP2
ENSG00000232421	20.0144	27.9814	5.53441	0.46487	ENSG00000232421	TUBB
ENSG00000232422	0.123499	0.163118	0.176634	0.457443	ENSG00000232422	KNOP1P4
ENSG00000232423	5.50E-06	0	0	5.17E-06	ENSG00000232423	PRAMEF6
ENSG00000232424	0	0	0	0	ENSG00000232424	USP9YP29
ENSG00000232429	0.16105	0	0	0	ENSG00000232429	RPL21P131
ENSG00000232430	0	0	0	0	ENSG00000232430	RPL31P15
ENSG00000232431	0	0.0738077	0.0714189	0.0840789	ENSG00000232431	AC055876.1
ENSG00000232433	0.0616875	0.0209455	1.70E-06	0.070422	ENSG00000232433	GXYLT1P3
ENSG00000232434	0.617518	0.938243	1.59867	1.56383	ENSG00000232434	C9orf172
ENSG00000232435	0	0	0	0.00316142	ENSG00000232435	DDX6P1
ENSG00000232437	0	2.09421	1.04171	1.26292	ENSG00000232437	RPS26P42
ENSG00000232438	0	0	0	0	ENSG00000232438	CTSLP7
ENSG00000232439	0.355566	0.545154	0.73803	0.762766	ENSG00000232439	RPL18AP7
ENSG00000232441	0	0	0	0	ENSG00000232441	CR788250.2
ENSG00000232446	0	0	0	0	ENSG00000232446	AC129850.1
ENSG00000232447	0	0.030468	0	0.138673	ENSG00000232447	MTND5P3
ENSG00000232450	0.264458	1.02722	0.99485	1.47444	ENSG00000232450	AL133517.1
ENSG00000232454	1.90249	3.32981	1.87146	3.6467	ENSG00000232454	AL138752.1
ENSG00000232456	0.389077	0.254541	0.18319	0.524215	ENSG00000232456	AL355994.2
ENSG00000232457	0.292994	1.80727	0.322166	0.55405	ENSG00000232457	SLC16A6P1
ENSG00000232459	0	0	0	0.217259	ENSG00000232459	AC107977.1
ENSG00000232460	1.03909	0.136908	0	0	ENSG00000232460	BMPR1APS2
ENSG00000232463	0	0.105583	0.0953305	0	ENSG00000232463	AL359265.2
ENSG00000232466	1.20294	1.60674	2.90423	2.53596	ENSG00000232466	AL356133.1

ENSG00000232467	0.117397	0.5817	0.614436	1.04727	ENSG00000232467	TMA16P2
ENSG00000232469	0.009462	0.0181999	0.0164453	0.0102936	ENSG00000232469	CR753509.2
ENSG00000232471	0.209759	0	0.0169325	0	ENSG00000232471	AC119751.1
ENSG00000232472	0.780539	1.07157	1.14797	2.11691	ENSG00000232472	EEF1B2P3
ENSG00000232473	0	0.00827178	0.059801	0.0281478	ENSG00000232473	UBQLN1P1
ENSG00000232475	0	0	0.2847	0	ENSG00000232475	HSFY5P
ENSG00000232478	9.48E-06	0	0	0	ENSG00000232478	CT45A1
ENSG00000232479	0.349541	0.952692	0.635699	0.587546	ENSG00000232479	AC010900.1
ENSG00000232482	0.19345	0	0	0.410685	ENSG00000232482	AL357134.1
ENSG00000232486	0.0468047	0.205464	0.106435	0.534048	ENSG00000232486	AL592437.2
ENSG00000232489	0.0947176	0.273594	0.208307	0.258717	ENSG00000232489	MFAP1P1
ENSG00000232491	0.375658	1.05756	0.75157	1.1814	ENSG00000232491	SAPCD2P3
ENSG00000232492	0.367666	0.636429	0.511187	0.961028	ENSG00000232492	NPM1P13
ENSG00000232493	0.47694	1.1184	0.597525	2.75571	ENSG00000232493	RPL12P11
ENSG00000232495	0	0	0	0	ENSG00000232495	AC069287.1
ENSG00000232496	0	0.0952786	0	0	ENSG00000232496	RPL3P12
ENSG00000232497	0.0567636	0.327631	0.0989566	0.0627674	ENSG00000232497	ADIPOR1P1
ENSG00000232499	0	0.0661573	0.0610352	0.634655	ENSG00000232499	AL391058.1
ENSG00000232502	0	0.142986	0.118771	0.0673651	ENSG00000232502	AC073464.2
ENSG00000232503	0.65307	1.22453	0.279824	0.400702	ENSG00000232503	CYCSP8
ENSG00000232508	0	0.0661412	0	0	ENSG00000232508	MRPL45P1
ENSG00000232511	0	0	0.0586783	0.0734341	ENSG00000232511	OR2AH1P
ENSG00000232514	0	0	0	0.525939	ENSG00000232514	AL356968.1
ENSG00000232515	0	0	0	0	ENSG00000232515	AC245060.1
ENSG00000232516	0.0524331	0	0	0	ENSG00000232516	ETF1P1
ENSG00000232517	0.00758497	0.00731765	0.066388	0.0335963	ENSG00000232517	AC112198.2
ENSG00000232522	0.276141	0.265339	0.239691	0.398285	ENSG00000232522	ZNF886P
ENSG00000232525	0	0	0	0	ENSG00000232525	SS18L2P1
ENSG00000232526	0	0	0	0	ENSG00000232526	VDAC1P13
ENSG00000232528	1.67043	2.95582	2.97195	3.76373	ENSG00000232528	AL109809.1
ENSG00000232531	0	0	0	0	ENSG00000232531	AC027612.3
ENSG00000232535	0.201795	0.258751	0.584509	0.51212	ENSG00000232535	OR5H8
ENSG00000232540	0	0	0.298175	0.723694	ENSG00000232540	RPL36P19
ENSG00000232541	0.210799	0	0	0.0486394	ENSG00000232541	COL11A2
ENSG00000232543	0	0	0	0	ENSG00000232543	IGHD4-11
ENSG00000232546	0.720062	1.04742	2.30293	2.93323	ENSG00000232546	AC027644.1
ENSG00000232549	0	0	0	0	ENSG00000232549	SRD5A1P1
ENSG00000232551	0	0.071415	0.166116	0.0864996	ENSG00000232551	MTCO1P14
ENSG00000232553	0	0	0	0	ENSG00000232553	CLK2P1
ENSG00000232554	0.531214	0.52463	0.657303	1.96926	ENSG00000232554	RSU1P2
ENSG00000232556	0	0	0	0	ENSG00000232556	AC092570.2
ENSG00000232559	9.22369	9.39843	10.2584	13.3531	ENSG00000232559	GS1-124K5.12
ENSG00000232560	1.17819	2.35068	3.28372	3.15031	ENSG00000232560	LINC01549
ENSG00000232561	11.0426	10.7303	7.2405	7.75891	ENSG00000232561	GTF2IP1
ENSG00000232562	0	0	0	0	ENSG00000232562	TPMTP3
ENSG00000232563	0	0	0	0	ENSG00000232563	CRB3P1
ENSG00000232567	0	0	0	0	ENSG00000232567	GLUD1P8
ENSG00000232568	0.318588	1.91263	1.88917	1.94601	ENSG00000232568	RPL23AP35
ENSG00000232569	3.37473	0.846548	3.84714	1.38176	ENSG00000232569	GABBR1
ENSG00000232571	0	0	0.177171	0	ENSG00000232571	RP11-435B5.2
ENSG00000232572	0	0	0	0	ENSG00000232572	BX001040.1
ENSG00000232573	0	0	0	0	ENSG00000232573	RPL3P4
ENSG00000232575	20.0144	27.9814	5.53441	0.46487	ENSG00000232575	TUBB
ENSG00000232576	0	0	0	0	ENSG00000232576	AL645638.1

ENSG00000232578	0.111455	0.191038	0.390686	0.676995	ENSG00000232578	AC093311.1
ENSG00000232579	0	1.13166	0.506411	3.04698	ENSG00000232579	MTCO1P27
ENSG00000232582	0	0	0	0.0603742	ENSG00000232582	AC234771.3
ENSG00000232583	0.737421	5.53477	2.44932	0.739592	ENSG00000232583	GPR143P
ENSG00000232585	0.0704504	0.0689525	0	0.10818	ENSG00000232585	OFD1P12Y
ENSG00000232587	0.499919	1.99889	1.57208	2.20008	ENSG00000232587	EEF1A1P3
ENSG00000232594	0	0	0	0.258014	ENSG00000232594	AC103563.4
ENSG00000232595	0	0	0	0	ENSG00000232595	CST2P1
ENSG00000232599	0	0.132675	0	0.296338	ENSG00000232599	AL008707.1
ENSG00000232601	0	0	0	0	ENSG00000232601	AC069218.2
ENSG00000232603	0	0	0	0	ENSG00000232603	AC245291.3
ENSG00000232605	0	1.76341	0.43093	0	ENSG00000232605	HMGN2P11
ENSG00000232608	1.89478	4.72005	5.65672	8.32333	ENSG00000232608	TIMM9P2
ENSG00000232610	0	0.105917	0	0.0798849	ENSG00000232610	CCT6P4
ENSG00000232612	0	0	0	0	ENSG00000232612	RPL31P35
ENSG00000232614	0.0958111	0.448521	0.243104	0.307753	ENSG00000232614	USP9YP9
ENSG00000232615	0.228863	0.443736	0.423411	1.05456	ENSG00000232615	AC026412.2
ENSG00000232616	8.10942	7.81457	9.08597	7.06332	ENSG00000232616	SKIV2L
ENSG00000232617	0	0	0.385083	0	ENSG00000232617	AC017019.1
ENSG00000232620	0	0	0	0	ENSG00000232620	TSPY17P
ENSG00000232621	0	0	0	0.346418	ENSG00000232621	C4BPAP2
ENSG00000232622	0.507014	1.43464	2.50141	0.583642	ENSG00000232622	AC114482.1
ENSG00000232625	0	0	0	0	ENSG00000232625	RPL23AP31
ENSG00000232626	0.771348	2.99073	1.8162	2.33626	ENSG00000232626	AC099336.1
ENSG00000232627	1.02169	4.38305	2.20223	2.68673	ENSG00000232627	AC021876.1
ENSG00000232629	0	0.130285	0	0.0988326	ENSG00000232629	HLA-DQB2
ENSG00000232630	2.73791	1.56764	1.56604	2.90915	ENSG00000232630	PRPS1P2
ENSG00000232631	0	0	0	0	ENSG00000232631	MTND2P23
ENSG00000232632	2.04236	5.69475	1.27243	5.75221	ENSG00000232632	GABBR1
ENSG00000232634	0	0.0605519	0.113508	0.150486	ENSG00000232634	NEFLP1
ENSG00000232637	3.66564	4.52153	5.01825	2.99226	ENSG00000232637	WI2-3658N16.1
ENSG00000232639	0	0	0	0	ENSG00000232639	LYPLA2P1
ENSG00000232641	0.777593	0.983953	1.07424	2.44259	ENSG00000232641	MOG
ENSG00000232644	0	0	0	0	ENSG00000232644	AC005297.2
ENSG00000232646	0.676411	2.79018	2.2575	7.46868	ENSG00000232646	AL731563.1
ENSG00000232647	0	0	0	0	ENSG00000232647	POLR3KP1
ENSG00000232649	0	0	0.241007	0	ENSG00000232649	MCCD1P1
ENSG00000232653	4.17715	8.08422	8.52937	8.21138	ENSG00000232653	GOLGA8N
ENSG00000232654	0	0	0	0	ENSG00000232654	FAM136BP
ENSG00000232658	0.638856	0.679631	0.496585	0.767871	ENSG00000232658	AC092638.1
ENSG00000232659	0.0642566	0.230628	0.999093	0.272811	ENSG00000232659	ZDHHC20P2
ENSG00000232662	1.17677	4.24726	4.61469	6.03634	ENSG00000232662	LDHBP1
ENSG00000232663	0	0	0	0	ENSG00000232663	AL139415.2
ENSG00000232664	0	0	0	0	ENSG00000232664	LARP1BP3
ENSG00000232665	0	0	0	0	ENSG00000232665	PHBP10
ENSG00000232668	1.36692	0	0.570064	0.684899	ENSG00000232668	AC010967.3
ENSG00000232671	0.759889	0.956647	1.19895	2.81447	ENSG00000232671	AL391069.2
ENSG00000232672	0.0617434	0.0594255	0	0	ENSG00000232672	ACTG1P21
ENSG00000232676	0	0	0	0	ENSG00000232676	ADH5P2
ENSG00000232678	1.67525	0	0	0	ENSG00000232678	SPTLC1P4
ENSG00000232683	0	0	0	0	ENSG00000232683	UQCRHP1
ENSG00000232687	0	0	0	0	ENSG00000232687	RPL12P9
ENSG00000232690	0	0.329679	0.893464	0.350857	ENSG00000232690	HSPE1P9
ENSG00000232695	0	0	0	0	ENSG00000232695	ELOCP17

ENSG00000232699	0	0	0	0	ENSG00000232699	BDH2P1
ENSG00000232701	0	0	0	0	ENSG00000232701	RPL21P108
ENSG00000232702	13.2955	11.9669	20.7268	9.53498	ENSG00000232702	AL158050.1
ENSG00000232705	0.0394657	0.0375419	0	0	ENSG00000232705	HLA-DRB9
ENSG00000232706	0.0777226	0.0504254	0.208046	0.25169	ENSG00000232706	NUTM2HP
ENSG00000232707	0	0	0	0	ENSG00000232707	AP1B1P2
ENSG00000232708	0	0.061474	3.43264	1.73714	ENSG00000232708	HLA-K
ENSG00000232709	0.0992764	0.0956555	0.209511	0.217628	ENSG00000232709	MARK2P9
ENSG00000232713	2.05141	5.82722	2.72641	4.33232	ENSG00000232713	AC010733.1
ENSG00000232714	0	0	0	0	ENSG00000232714	MTND3P8
ENSG00000232716	0.0331768	0.048211	0.0577945	0.0545453	ENSG00000232716	AC016831.3
ENSG00000232717	0	0	0	0.0556616	ENSG00000232717	TRIM51JP
ENSG00000232718	0	0.0622727	0.112552	0.140918	ENSG00000232718	GAPDHP48
ENSG00000232722	0.0753499	0.0724549	0	0	ENSG00000232722	MROH4P
ENSG00000232723	0	0.656856	0.728501	1.49691	ENSG00000232723	AC013399.1
ENSG00000232724	0.0578716	0.0557993	0.0840808	0.0848374	ENSG00000232724	TRIM80P
ENSG00000232727	0.0867558	0	0.0752841	0.0938118	ENSG00000232727	YWHAEP1
ENSG00000232728	0	0.34154	0.308598	0.231566	ENSG00000232728	PHB2P1
ENSG00000232730	0.198116	0.142241	0.303315	0.161355	ENSG00000232730	FAM8A4P
ENSG00000232733	0	0.313397	0	0.367602	ENSG00000232733	RPL12P1
ENSG00000232734	0.71081	1.02754	1.67137	2.48886	ENSG00000232734	ATP5G1P7
ENSG00000232735	0.410521	0.525131	0.94852	1.46992	ENSG00000232735	ATG4AP1
ENSG00000232736	0	0	0.124687	0.308306	ENSG00000232736	AC007551.1
ENSG00000232742	0	0	0	0	ENSG00000232742	RHOQP2
ENSG00000232743	0.0387274	0.111333	0.0335459	0.0424429	ENSG00000232743	ELF2P3
ENSG00000232744	0	0	0	0	ENSG00000232744	USP9YP16
ENSG00000232745	0.160623	0.484175	0.65102	0.294553	ENSG00000232745	ANKRD20A14P
ENSG00000232747	0	0	0	0	ENSG00000232747	IGKV1D-35
ENSG00000232748	0.718417	0	0	0.669857	ENSG00000232748	AC135050.1
ENSG00000232750	1.3744	1.00224	1.63272	1.4688	ENSG00000232750	AL139132.1
ENSG00000232751	0	0.606654	0	0.998698	ENSG00000232751	AL645568.3
ENSG00000232752	0.196403	1.75104	2.493	3.90554	ENSG00000232752	MTCO3P21
ENSG00000232757	3.98E-06	0	0.109696	2.74E-05	ENSG00000232757	ETF1P1
ENSG00000232760	0.0464809	0	0	0	ENSG00000232760	AC103564.2
ENSG00000232764	0	0	0	0	ENSG00000232764	TRIM60P8Y
ENSG00000232766	0.184063	0	0.158991	0	ENSG00000232766	AC098614.3
ENSG00000232768	16.2144	8.17105	19.2147	9.86659	ENSG00000232768	AL356320.1
ENSG00000232771	0	0	0	0	ENSG00000232771	PPP1R26P5
ENSG00000232772	0	0	0	0.14837	ENSG00000232772	MTND4P22
ENSG00000232773	0	0	0	0	ENSG00000232773	DEFB130D
ENSG00000232774	62.4162	140.758	136.074	246.034	ENSG00000232774	FLJ22447
ENSG00000232775	3.49544	8.71259	7.47196	11.119	ENSG00000232775	BMS1P22
ENSG00000232777	0.472596	0.907361	1.05031	0.498662	ENSG00000232777	MRPL51P2
ENSG00000232778	0.700823	2.17588	3.02298	3.90739	ENSG00000232778	RPL23AP50
ENSG00000232780	0	0	0	0	ENSG00000232780	GAPDHP74
ENSG00000232781	0	0	0	0	ENSG00000232781	BX927167.1
ENSG00000232783	1.67204	1.09116	1.18476	1.83842	ENSG00000232783	FRG2FP
ENSG00000232786	0.830849	0.392519	0.706043	0	ENSG00000232786	TIMM9P3
ENSG00000232787	0	0	0	0	ENSG00000232787	OR7L1P
ENSG00000232789	0	0	3.41318	0	ENSG00000232789	AC053503.3
ENSG00000232791	0	0	0	0.142142	ENSG00000232791	OR11I1P
ENSG00000232792	0.514177	1.27985	0.29337	1.24615	ENSG00000232792	FTH1P25
ENSG00000232793	0	0	0	1.88852	ENSG00000232793	DNAJC19P8
ENSG00000232794	0.0872626	0.084033	0	0	ENSG00000232794	HNRNPDP1

ENSG00000232795	0.0576219	0.332714	0.150347	0.440422	ENSG00000232795	SCAND3P1
ENSG00000232797	0	0	0	0	ENSG00000232797	FAM207CP
ENSG00000232798	0	0.461006	0	0	ENSG00000232798	CR769767.1
ENSG00000232799	0	0	0.236442	0	ENSG00000232799	CRYGFP
ENSG00000232800	0.0431065	0	0.112571	0.329996	ENSG00000232800	SLC7A15P
ENSG00000232801	0	0	0	0	ENSG00000232801	SDCBPP3
ENSG00000232802	3.87616	0	0	0	ENSG00000232802	COL11A2P1
ENSG00000232804	115.275	8.28466	8.74619	2.0516	ENSG00000232804	HSPA1B
ENSG00000232805	0	0	0	0	ENSG00000232805	NIP7P1
ENSG00000232809	0	0	0	0.0779006	ENSG00000232809	VDAC1P10
ENSG00000232810	0.222879	0.099013	0.196978	0.0453146	ENSG00000232810	TNF
ENSG00000232813	0	0	0	0	ENSG00000232813	AC245047.4
ENSG00000232815	9.02348	20.9194	21.9357	7.1217	ENSG00000232815	DUX4L50
ENSG00000232816	0.403816	0.176269	0	0	ENSG00000232816	HLA-K
ENSG00000232818	0.566818	0.820426	0.187301	0.307986	ENSG00000232818	RPS2P32
ENSG00000232823	0.267702	0.373588	0.599482	1.57999	ENSG00000232823	TXNP1
ENSG00000232824	0.414064	0.224602	0	1.42369	ENSG00000232824	PRR13P1
ENSG00000232829	0	0	0	0	ENSG00000232829	GSTO3P
ENSG00000232830	0.228549	1.03927	0.686372	1.19072	ENSG00000232830	AC110994.1
ENSG00000232833	0.978798	4.44659	6.49156	2.10202	ENSG00000232833	FAM27E3
ENSG00000232834	0	0	0	0	ENSG00000232834	AC112492.4
ENSG00000232838	8.70269	7.01681	6.57478	4.60944	ENSG00000232838	PET117
ENSG00000232839	1.40869	1.16201	0.860284	0.269129	ENSG00000232839	TRIM39
ENSG00000232841	0	0	0.768157	0	ENSG00000232841	BRWD1P3
ENSG00000232842	0.131867	0	0	0	ENSG00000232842	AL137845.2
ENSG00000232843	0.194732	0.4064	0.419444	0.302928	ENSG00000232843	SNX18P2
ENSG00000232845	0	0	0	0	ENSG00000232845	TRAPPC2P9
ENSG00000232846	0	0.416096	0.250639	0.470056	ENSG00000232846	SLC25A6P3
ENSG00000232848	0	0	0	0.176123	ENSG00000232848	AL034417.1
ENSG00000232850	1.68533	2.344	2.24792	2.03477	ENSG00000232850	PTGES2-AS1
ENSG00000232851	0	0	0	0	ENSG00000232851	ATP5J2P3
ENSG00000232852	0	0.0737078	0.0269401	0.0389611	ENSG00000232852	CICP4
ENSG00000232853	1.49054	1.23717	0.983415	1.77418	ENSG00000232853	LUZP4P1
ENSG00000232857	0	0.147675	0.200135	0.334105	ENSG00000232857	KATNBL1P2
ENSG00000232858	0	0	0	0	ENSG00000232858	RPL34P27
ENSG00000232859	3.62752	6.69377	6.86943	4.66211	ENSG00000232859	LYRM9
ENSG00000232862	0.524477	0.655975	0.495642	0.747139	ENSG00000232862	AL138787.1
ENSG00000232863	0	0.867741	0.537604	0.199449	ENSG00000232863	RP11-327I22.1
ENSG00000232864	0	0.183375	0	0.103867	ENSG00000232864	NUCKS1P1
ENSG00000232866	0.18806	0	0	0	ENSG00000232866	AL513478.1
ENSG00000232867	0	0	0.29981	0.364036	ENSG00000232867	AL355433.1
ENSG00000232869	0.424055	0.23013	0.274422	0.88173	ENSG00000232869	TRBV29-1
ENSG00000232871	1.28996	4.61443	0.706736	0.658838	ENSG00000232871	SEC1P
ENSG00000232872	0.0932135	0.134359	0.278929	0.369675	ENSG00000232872	CTAGE3P
ENSG00000232873	0.159344	0	0	0	ENSG00000232873	RPL23AP93
ENSG00000232875	0.862099	4.85656	2.19877	6.22029	ENSG00000232875	HMGN2P35
ENSG00000232879	4.74557	6.09109	13.7969	4.42715	ENSG00000232879	AL591806.2
ENSG00000232880	0	0	1.32134	0.80602	ENSG00000232880	NDUFB4P10
ENSG00000232881	0	0	0.14174	0	ENSG00000232881	RPS10P21
ENSG00000232882	0	0.519857	1.49019	1.69686	ENSG00000232882	PHKA1P1
ENSG00000232883	0	0.0645367	0.0583582	0	ENSG00000232883	AL451081.2
ENSG00000232887	0	0	0.320466	0	ENSG00000232887	AC006466.1
ENSG00000232888	3.8839	3.88609	7.57241	9.77221	ENSG00000232888	AC127070.1
ENSG00000232889	0	0	0	1.00697	ENSG00000232889	AC087499.4

ENSG00000232894	0.144406	0.713163	0.255104	0.47442	ENSG00000232894	MRPS31P2
ENSG00000232897	0.268105	0.281708	0.48722	1.54755	ENSG00000232897	AL117329.2
ENSG00000232899	0.0182591	0.0175902	0.0318013	0.120396	ENSG00000232899	CDY9P
ENSG00000232901	2.185	3.79377	0.955822	4.90529	ENSG00000232901	CYCSP10
ENSG00000232905	0.0659811	0	0	0	ENSG00000232905	AL162393.1
ENSG00000232906	0.0478836	0.0461816	0.212529	0.105026	ENSG00000232906	AC092685.1
ENSG00000232908	0.127778	0	0.0544369	0.469419	ENSG00000232908	HSD17B7P1
ENSG00000232910	0	0	0	0	ENSG00000232910	RAB9AP1
ENSG00000232914	0	0	0	0	ENSG00000232914	TRAPPC2P4
ENSG00000232915	0.237749	0.873585	0.916222	1.25229	ENSG00000232915	AC097721.1
ENSG00000232916	0.886168	1.25796	1.11012	3.07677	ENSG00000232916	HMGN2P27
ENSG00000232917	0	0	0.638179	0	ENSG00000232917	HSPE1P6
ENSG00000232918	0	0	0	0	ENSG00000232918	AC118469.1
ENSG00000232922	0	0	0	0	ENSG00000232922	MTND6P24
ENSG00000232924	0	0	0	0	ENSG00000232924	ELOCP4
ENSG00000232925	0	0	0	1.86209	ENSG00000232925	MRPS16P2
ENSG00000232926	1.48832	2.00208	3.96183	2.14801	ENSG00000232926	AC000078.1
ENSG00000232927	0	0	0	0	ENSG00000232927	USP12PY
ENSG00000232928	0.173814	0.98885	1.28119	2.07225	ENSG00000232928	DDX3P1
ENSG00000232938	2.47204	2.701	2.90913	4.00221	ENSG00000232938	RPL23AP87
ENSG00000232941	0	0.813894	4.49386	4.11226	ENSG00000232941	AC090186.1
ENSG00000232943	0	0	0.204316	0	ENSG00000232943	AL050321.1
ENSG00000232944	0.912684	1.72145	0.759086	2.96435	ENSG00000232944	AC092423.1
ENSG00000232945	0	0	0	0	ENSG00000232945	OR2J2
ENSG00000232946	0	0.279378	0	0	ENSG00000232946	AL354707.3
ENSG00000232948	0	0	0	0	ENSG00000232948	DEFB130A
ENSG00000232950	0.0353723	0.0693262	0.154642	0.197784	ENSG00000232950	ZNF519P1
ENSG00000232951	0	0.0541034	0	0.0604979	ENSG00000232951	IPO7P1
ENSG00000232952	0	0	0	0	ENSG00000232952	AL512844.1
ENSG00000232953	0.117325	0.0847955	0.102209	0	ENSG00000232953	HSPA8P18
ENSG00000232957	0	0.0184165	0.329902	0.278882	ENSG00000232957	HLA-DOA
ENSG00000232958	0	0	0	0	ENSG00000232958	AC027119.1
ENSG00000232960	1.18829	1.24558	2.66629	5.26816	ENSG00000232960	CSNK2B
ENSG00000232962	0	0.0184165	0.269711	0.0387109	ENSG00000232962	HLA-DOA
ENSG00000232963	0.421529	0.793112	1.09452	1.74935	ENSG00000232963	HMGN2P20
ENSG00000232965	0	0	0	0	ENSG00000232965	RPS12P18
ENSG00000232968	0.247641	0.83178	0.321903	0.399254	ENSG00000232968	EIF4EP4
ENSG00000232970	0.339073	2.73613	1.05942	1.77469	ENSG00000232970	POLHP1
ENSG00000232974	0	0.0341391	0.030885	0	ENSG00000232974	CR759956.2
ENSG00000232975	0	0	0	0	ENSG00000232975	MTCO1P57
ENSG00000232976	0.175411	0.084284	0.0761406	0.189914	ENSG00000232976	TRIM60P10Y
ENSG00000232979	0	0	0	0	ENSG00000232979	AC092580.3
ENSG00000232981	0	0	0.0501158	0	ENSG00000232981	MTCO1P51
ENSG00000232982	0	0	0	0	ENSG00000232982	MTCO1P45
ENSG00000232983	0	0	0	0	ENSG00000232983	AL160270.2
ENSG00000232984	0.0440785	0.10084	0.119165	0.128925	ENSG00000232984	OR2H1
ENSG00000232988	0	0	0.117234	0	ENSG00000232988	HLA-T
ENSG00000232989	0	3.40513	0	0	ENSG00000232989	AL356010.1
ENSG00000232990	0	0	0	0	ENSG00000232990	MTATP6P7
ENSG00000232992	0	0	0.0390793	0.049082	ENSG00000232992	AHCYP4
ENSG00000232994	0.626748	1.75389	1.038	1.87553	ENSG00000232994	RPL7P14
ENSG00000232997	0.00944618	0	0.0164323	0	ENSG00000232997	ZNF90P2
ENSG00000232999	0	0	0	0	ENSG00000232999	AL133351.3
ENSG00000233003	0	0.40036	0.138699	0.712872	ENSG00000233003	CICP26

ENSG00000233007	0.381652	0.756574	0.363156	1.0398	ENSG00000233007	UBTFL11
ENSG00000233010	1.28844	1.0975	0.812187	1.73572	ENSG00000233010	RPEP4
ENSG00000233011	0	0	0	0.0372629	ENSG00000233011	SLC9A3P1
ENSG00000233012	0.715599	2.44094	3.74179	2.34687	ENSG00000233012	HDAC1P2
ENSG00000233014	0	0	0	0	ENSG00000233014	TBC1D3P7
ENSG00000233015	0	0	0	0	ENSG00000233015	SLC25A6P1
ENSG00000233018	1.20703	0	0	0	ENSG00000233018	AL732292.1
ENSG00000233019	0	0	0	0	ENSG00000233019	CR547123.2
ENSG00000233020	0	0	0.0574945	0	ENSG00000233020	AL354872.1
ENSG00000233023	0	0.470711	0.115654	2.13E-05	ENSG00000233023	IFITM4P
ENSG00000233024	12.5192	28.8764	53.2622	21.3014	ENSG00000233024	AC126755.2
ENSG00000233025	1.00881	2.59845	2.78546	2.82704	ENSG00000233025	CRYZP1
ENSG00000233026	0	0	0	0	ENSG00000233026	MTCO1P5
ENSG00000233028	0	0	0	0	ENSG00000233028	AC006970.2
ENSG00000233031	0	1.88208	0	0	ENSG00000233031	AC125238.1
ENSG00000233036	0	0	0	0	ENSG00000233036	KRTAP8-2P
ENSG00000233037	0.15152	0.145258	0.262308	0	ENSG00000233037	AC009237.5
ENSG00000233039	0	0	0.0575007	0.104158	ENSG00000233039	MTND5P30
ENSG00000233040	0.386234	1.20013	0.516224	1.71571	ENSG00000233040	FAM204BP
ENSG00000233041	0	0	0.322482	0	ENSG00000233041	PHGR1
ENSG00000233045	0	0.107196	0.339289	0.297451	ENSG00000233045	AC097523.1
ENSG00000233046	0	0	0	0.0254603	ENSG00000233046	OR5V1
ENSG00000233049	2.76168	2.81073	3.53901	2.65462	ENSG00000233049	DHX16
ENSG00000233050	0	0	0	0	ENSG00000233050	DEFB130B
ENSG00000233051	16.1841	2.10385	4.22408	10.4175	ENSG00000233051	MICA
ENSG00000233053	1.93885	0.673681	0.561095	0.695858	ENSG00000233053	HLA-Z
ENSG00000233054	0	0.0131907	0.0059608	0	ENSG00000233054	OR2B3
ENSG00000233055	0	0	0	0	ENSG00000233055	AL353621.1
ENSG00000233057	0.0855835	0	0	0.0468863	ENSG00000233057	EEF1A1P14
ENSG00000233063	0	0	0	0	ENSG00000233063	SAR1AP4
ENSG00000233071	0	0	0	0	ENSG00000233071	RPSAP59
ENSG00000233072	0.227416	2.17126	3.37992	3.60067	ENSG00000233072	RPS15AP6
ENSG00000233075	18.0105	33.3731	28.0823	61.0492	ENSG00000233075	AL023583.1
ENSG00000233076	1.24175	1.01416	2.15986	0.700784	ENSG00000233076	DDAH2
ENSG00000233083	0	0	0	0	ENSG00000233083	FTH1P6
ENSG00000233084	0.00070262	0	0	1.43395	ENSG00000233084	RPL23AP25
ENSG00000233087	0.0933395	0.135504	0.192333	0.299603	ENSG00000233087	WTH3DI
ENSG00000233090	0	0	0.773805	0	ENSG00000233090	AC015922.2
ENSG00000233091	0.0259809	0.0124808	0.033827	0	ENSG00000233091	RPL7P4
ENSG00000233094	0.319802	0.352355	0.224248	0.130066	ENSG00000233094	AL592170.1
ENSG00000233095	39.6497	2.57557	0.0363954	1.04662	ENSG00000233095	HLA-G
ENSG00000233105	0	0	0	0	ENSG00000233105	AC103563.5
ENSG00000233106	0	0	0	0	ENSG00000233106	RPL12P3
ENSG00000233107	0.0452403	0.217302	0.0787691	0.049703	ENSG00000233107	SUCLA2P2
ENSG00000233109	10.032	14.9932	17.6594	37.6448	ENSG00000233109	AC013701.1
ENSG00000233111	0.118558	0	0	0	ENSG00000233111	RAB1C
ENSG00000233113	0	0.080909	0	0.0608436	ENSG00000233113	AL844851.2
ENSG00000233114	0.603514	0	1.51923	0.609397	ENSG00000233114	AL358075.3
ENSG00000233115	0.0965427	0.132148	0.300093	0.142872	ENSG00000233115	FAM90A11P
ENSG00000233118	0	0	0.374228	1.05572	ENSG00000233118	UBE2V1P8
ENSG00000233120	0	0	0	0	ENSG00000233120	USP9YP15
ENSG00000233121	0	0.0618938	0	0	ENSG00000233121	VN1R20P
ENSG00000233122	0.293542	0.57512	0.871618	0.322737	ENSG00000233122	CTAGE7P
ENSG00000233125	0.514848	0.562361	0.489965	0.699968	ENSG00000233125	ACTBP12

ENSG00000233126	0	0	0	0.0436224	ENSG00000233126	ZNF736P3Y
ENSG00000233129	0.256605	0	0.525597	0.28015	ENSG00000233129	AL117351.1
ENSG00000233131	0	0	0	0	ENSG00000233131	AC096649.2
ENSG00000233132	0	0	0	0.181691	ENSG00000233132	FAM90A3P
ENSG00000233133	14.917	8.50744	10.679	16.3828	ENSG00000233133	AC104451.1
ENSG00000233134	0	0	0	0.766122	ENSG00000233134	MTND3P17
ENSG00000233135	0	0.478215	1.28091	2.0604	ENSG00000233135	RPS27P18
ENSG00000233136	0.0247832	0.0541723	0.078843	0	ENSG00000233136	USP17L11
ENSG00000233139	0	3.62732	2.33E-06	0	ENSG00000233139	AC244636.2
ENSG00000233141	0	0	0	0	ENSG00000233141	MAS1L
ENSG00000233146	0	0	0	0.0602357	ENSG00000233146	BPIFB5P
ENSG00000233148	0.12236	0.469726	0.848351	1.08778	ENSG00000233148	SYF2P2
ENSG00000233149	2.42888	0.280746	2.20319	1.37523	ENSG00000233149	GTF2H4
ENSG00000233151	0	0.938591	1.12825	3.82517	ENSG00000233151	CYP21A2
ENSG00000233155	1.89716	2.19689	3.19705	2.03179	ENSG00000233155	HMGA1P8
ENSG00000233156	0	0	0	0	ENSG00000233156	HSFY8P
ENSG00000233157	0.0938709	0.0902001	0.162959	0.30454	ENSG00000233157	Z97055.1
ENSG00000233158	0	0	0	0	ENSG00000233158	RPS24P6
ENSG00000233159	0	0	0	0	ENSG00000233159	AC007390.1
ENSG00000233160	0	0	0	0	ENSG00000233160	HNRNPA1P2
ENSG00000233161	0	0	0	0	ENSG00000233161	DHFRP2
ENSG00000233162	0	0	0	0	ENSG00000233162	MORF4L1P6
ENSG00000233163	0.4705	1.34781	1.21763	1.24125	ENSG00000233163	RPS12P17
ENSG00000233164	0.394092	0.258598	0.388434	0.0985426	ENSG00000233164	C6orf136
ENSG00000233167	0.551803	1.82005	1.51959	3.92233	ENSG00000233167	EEF1A1P26
ENSG00000233168	0.0144218	0	0.05347	0	ENSG00000233168	CR753509.3
ENSG00000233170	0.864736	1.28387	2.46503	0.815534	ENSG00000233170	AC138356.2
ENSG00000233171	0	0	0	0	ENSG00000233171	RP11-459O16.3
ENSG00000233172	2.82747	11.7602	17.2207	11.3947	ENSG00000233172	RP11-12A20.6
ENSG00000233173	0.0717171	0	0	0	ENSG00000233173	VN1R34P
ENSG00000233176	0	0	0.069397	0	ENSG00000233176	OR7E157P
ENSG00000233180	0	0.0131907	0.0059608	0	ENSG00000233180	OR2B3
ENSG00000233182	0	0	0	0	ENSG00000233182	CR759834.3
ENSG00000233186	0.101187	0.584469	0.308151	0.441903	ENSG00000233186	KLF4P1
ENSG00000233189	1.29226	2.39474	3.09957	3.034	ENSG00000233189	RPL12P29
ENSG00000233190	0	0	0	0.228747	ENSG00000233190	RPS24P13
ENSG00000233192	0	0.0652533	0.19934	0	ENSG00000233192	HLA-DQA2
ENSG00000233194	0	0.0858021	0.0808883	0.0707639	ENSG00000233194	AL805913.1
ENSG00000233196	0.10018	0.0962443	0	0.657986	ENSG00000233196	AL096803.2
ENSG00000233197	0.280632	0	0	0	ENSG00000233197	TMEM256P1
ENSG00000233198	0.563446	0.377501	0.70798	0.422697	ENSG00000233198	RNF224
ENSG00000233204	0.0815095	0.235038	0.212348	0.618595	ENSG00000233204	MAPRE1P3
ENSG00000233205	0.22024	0	0	0	ENSG00000233205	AC108479.1
ENSG00000233206	0	0.296471	0	0	ENSG00000233206	RPS3AP1
ENSG00000233209	0.0231946	0.18376	0.0258483	0.0457925	ENSG00000233209	HLA-DQB1
ENSG00000233210	0.77868	0.307099	0.210049	2.72786	ENSG00000233210	GPANK1
ENSG00000233211	0	0	0.242239	0	ENSG00000233211	GRPEL2P1
ENSG00000233216	0	0	0	0	ENSG00000233216	AL357373.1
ENSG00000233217	0.189322	0.20299	0.366713	0.254554	ENSG00000233217	MROH3P
ENSG00000233218	1.28921	1.68104	2.37571	1.9422	ENSG00000233218	SNX18P16
ENSG00000233224	13.5367	57.8578	20.2853	18.4043	ENSG00000233224	HIST1H2AM
ENSG00000233225	0.0380884	0.0418716	0	0	ENSG00000233225	AC004987.2
ENSG00000233228	0.037741	0.18178	0.198002	0.123972	ENSG00000233228	LPCAT2BP
ENSG00000233229	0	0.0738963	0	0	ENSG00000233229	CNOT7P1

ENSG00000233231	1.46193	4.83286	3.70463	3.34528	ENSG00000233231	HNRNPA1P49
ENSG00000233232	0.235909	0	0	0	ENSG00000233232	NPIPB7
ENSG00000233235	0	0	0	0	ENSG00000233235	BX119321.1
ENSG00000233238	0	0	0	0	ENSG00000233238	DEFA9P
ENSG00000233239	0	0	2.16616	1.25223	ENSG00000233239	HLA-U
ENSG00000233240	0	0	0	0	ENSG00000233240	CR753309.1
ENSG00000233241	0	0	0	0	ENSG00000233241	DDX39BP1
ENSG00000233243	0	0.16628	0	0.184883	ENSG00000233243	AC112492.5
ENSG00000233247	0	0	0	0	ENSG00000233247	AC002524.1
ENSG00000233248	0	0	0	0	ENSG00000233248	MTND6P9
ENSG00000233252	0	0	0	0	ENSG00000233252	CRIP1P1
ENSG00000233254	0.177621	0	0	0	ENSG00000233254	RPL21P134
ENSG00000233259	0	0	0	0	ENSG00000233259	FABP3P2
ENSG00000233260	0	0	0	0	ENSG00000233260	RPSAP63
ENSG00000233263	0.0907582	0	0	0	ENSG00000233263	AC009518.2
ENSG00000233264	0.118846	0.501006	0.242729	0.833177	ENSG00000233264	AC006042.3
ENSG00000233265	0	0	0	0	ENSG00000233265	MICF
ENSG00000233266	0.586705	1.2938	1.70672	3.28035	ENSG00000233266	HMGB1P31
ENSG00000233268	0	0	0.340446	0.20905	ENSG00000233268	AL691449.1
ENSG00000233270	0.689391	0	0	0	ENSG00000233270	SNRPEP4
ENSG00000233272	0.0823085	0.052886	0.0478106	0.180661	ENSG00000233272	PNPT1P2
ENSG00000233273	0	0	0	0.247919	ENSG00000233273	AMMECR1LP1
ENSG00000233275	0.691415	0.248133	0.224367	0	ENSG00000233275	AC009238.2
ENSG00000233276	36.0648	92.7122	38.2464	42.0978	ENSG00000233276	GPX1
ENSG00000233278	0	0	0	0	ENSG00000233278	RPS26P2
ENSG00000233280	10.7567	14.331	6.59902	10.0658	ENSG00000233280	CRYBG3
ENSG00000233285	0	0	0	0	ENSG00000233285	MTCYBP10
ENSG00000233286	0	0	0	0	ENSG00000233286	MTND3P10
ENSG00000233287	0	0	0	0.442005	ENSG00000233287	AC009362.1
ENSG00000233291	0	0	0.0943368	0	ENSG00000233291	RPL7AP61
ENSG00000233292	0.403085	0.401423	0.711491	1.28187	ENSG00000233292	AL513533.1
ENSG00000233295	0.112967	0	0.344536	0.127889	ENSG00000233295	FAM90A20P
ENSG00000233297	0	0	0	0	ENSG00000233297	RASA4DP
ENSG00000233298	0.655505	0.238136	0	0.419557	ENSG00000233298	IFITM4P
ENSG00000233299	0	0	0	0	ENSG00000233299	HIGD1AP4
ENSG00000233300	0.0670043	0	0	0	ENSG00000233300	EIF4A1P1
ENSG00000233301	0	0	0	0	ENSG00000233301	OR4C14P
ENSG00000233306	0	0	0	0	ENSG00000233306	TRGV2
ENSG00000233307	0	0	0	0	ENSG00000233307	AC011753.3
ENSG00000233309	0.366436	0.0882488	0.399148	0.396218	ENSG00000233309	RPS6P12
ENSG00000233311	0	0	0.0814796	0	ENSG00000233311	MTCO1P54
ENSG00000233312	0.437181	0.465692	0.303908	0.512045	ENSG00000233312	C4B_2
ENSG00000233313	0	0.803129	0	0	ENSG00000233313	HMGA1P5
ENSG00000233314	3.18119	0.998512	1.14687	1.58835	ENSG00000233314	PPP1R11
ENSG00000233317	0	0	0.122685	0	ENSG00000233317	MTCO3P1
ENSG00000233318	0	0	0	0	ENSG00000233318	RPL31P45
ENSG00000233319	0	0.158535	0.286169	0.176393	ENSG00000233319	PPIAP32
ENSG00000233320	0	0.415548	1.26613	1.48666	ENSG00000233320	H2BFXP
ENSG00000233323	0.896302	0.186454	0.384064	0.822335	ENSG00000233323	TNXB
ENSG00000233324	0	0	0.0815403	0	ENSG00000233324	EEF1A1P34
ENSG00000233325	2.80581	1.9479	3.9285	2.74102	ENSG00000233325	MIPEPP3
ENSG00000233327	8.22104	14.0231	14.3631	15.985	ENSG00000233327	USP32P2
ENSG00000233328	0	0	0	0	ENSG00000233328	PFN1P1
ENSG00000233329	0	0	0	0	ENSG00000233329	AC068287.1

ENSG00000233333	0	0	0	0.0940215	ENSG00000233333	RNFT1P2
ENSG00000233335	0	0	0	0	ENSG00000233335	AC016696.1
ENSG00000233337	3.55116	3.95116	6.91873	2.43369	ENSG00000233337	UBE2FP3
ENSG00000233343	1.43982	0.273606	0.741777	1.80747	ENSG00000233343	ATP6V1G1P4
ENSG00000233345	0.684225	2.26394	1.76126	1.30384	ENSG00000233345	MSH5
ENSG00000233347	0.0958913	0	0.257655	0.104337	ENSG00000233347	ERP29P1
ENSG00000233348	6.25331	10.9883	8.09566	8.19787	ENSG00000233348	BAG6
ENSG00000233350	0	0	0	0.0189286	ENSG00000233350	TRIM26BP
ENSG00000233352	0	0	0	0	ENSG00000233352	AL035660.1
ENSG00000233353	0	0.349832	0.31591	0.391965	ENSG00000233353	RPS7P9
ENSG00000233357	0	0.58969	0	0.324046	ENSG00000233357	RPL30P15
ENSG00000233366	0.00944618	0.0363638	0.0164323	0	ENSG00000233366	ZNF90P2
ENSG00000233369	3.27025	2.75588	2.69683	3.74564	ENSG00000233369	GTF2IP4
ENSG00000233370	0.0536842	0.258683	0.186808	0.176083	ENSG00000233370	AC140479.3
ENSG00000233373	0	0	0	0	ENSG00000233373	AC106874.3
ENSG00000233377	0	0	0	0	ENSG00000233377	MTND4P20
ENSG00000233378	0	0	0	0	ENSG00000233378	USP9YP34
ENSG00000233380	0.072224	0.0706515	0	0	ENSG00000233380	AC034268.1
ENSG00000233381	0	0.227817	0	0.547748	ENSG00000233381	AK4P3
ENSG00000233382	2.87506	7.93101	6.98506	11.7639	ENSG00000233382	NKAPP1
ENSG00000233383	0	1.26676	0	1.35794	ENSG00000233383	AC073089.1
ENSG00000233385	0	0.08372	0.153154	0	ENSG00000233385	MTCO3P8
ENSG00000233388	0.333494	0.976784	0.727251	1.16379	ENSG00000233388	AL022334.1
ENSG00000233394	0	0	0	0.0230077	ENSG00000233394	RP11-248D7.2
ENSG00000233401	0.0517551	0.199451	0.0450818	0.282457	ENSG00000233401	PRKAR1AP1
ENSG00000233402	0	0	0.0432639	0	ENSG00000233402	TARDBPP1
ENSG00000233404	2.29454	5.43126	1.63582	6.66187	ENSG00000233404	FLJ20373
ENSG00000233406	1.03503	1.35743	1.97249	1.60056	ENSG00000233406	AL162430.1
ENSG00000233412	0.0685432	0.130245	0.0577539	0.147006	ENSG00000233412	OR5H15
ENSG00000233414	0	0.0854476	0	0.15277	ENSG00000233414	CNN2P5
ENSG00000233416	0.23738	0.907049	1.02346	1.50207	ENSG00000233416	AC012065.2
ENSG00000233418	2.95309	2.81073	2.43432	2.06855	ENSG00000233418	DHX16
ENSG00000233419	0	0	0	0	ENSG00000233419	AL121994.1
ENSG00000233425	0.187891	0.181022	0.0898355	0.051326	ENSG00000233425	KRT18P67
ENSG00000233426	2.5405	4.82977	3.38287	1.67307	ENSG00000233426	EIF3FP3
ENSG00000233428	0.896095	0.893707	0.579359	1.19356	ENSG00000233428	AC019050.1
ENSG00000233432	0.0190617	0.202388	0.0825047	0.04219	ENSG00000233432	AL592494.2
ENSG00000233433	0.8339	1.3684	0.815186	2.32068	ENSG00000233433	AC006144.1
ENSG00000233434	0	0	0	0	ENSG00000233434	BX649567.1
ENSG00000233435	0.131618	0.0950357	0.502275	0	ENSG00000233435	AGGF1P2
ENSG00000233436	0.550179	0.942962	2.02711	2.63201	ENSG00000233436	BTBD18
ENSG00000233437	0.306046	1.07958	0.691332	0.566853	ENSG00000233437	AC118758.1
ENSG00000233438	0.467733	0.203386	0.338549	0.592093	ENSG00000233438	AC109829.1
ENSG00000233439	0.131406	3.16987	1.76297	5.03926	ENSG00000233439	PSORS1C1
ENSG00000233440	0	0	0	0	ENSG00000233440	HMGA1P6
ENSG00000233441	0.286116	2.31745	1.92476	1.78482	ENSG00000233441	CYP2AB1P
ENSG00000233442	0	0	0	0	ENSG00000233442	PPP6R2P1
ENSG00000233444	0	0	0	0	ENSG00000233444	AC013262.1
ENSG00000233445	0.134707	1.16411	0.58381	0	ENSG00000233445	RPL17P11
ENSG00000233446	0	0.0464454	0.125939	0.105392	ENSG00000233446	AL691517.1
ENSG00000233447	0.361889	1.06258	1.38965	0.660426	ENSG00000233447	AC103563.6
ENSG00000233448	0.557377	0	0	0.42242	ENSG00000233448	PMS2P9
ENSG00000233449	0.20192	0.0969904	0.350427	0.109054	ENSG00000233449	MTATP6P14
ENSG00000233450	3.24741	16.7005	2.069	6.32269	ENSG00000233450	KIFC1

ENSG00000233454	0	0	0	0	ENSG00000233454	AC069285.2
ENSG00000233455	0.148754	0.143046	0	0.0807743	ENSG00000233455	AL035414.1
ENSG00000233457	0	0	0	0.112935	ENSG00000233457	AL353705.2
ENSG00000233459	0	0	0	0	ENSG00000233459	AC125238.2
ENSG00000233460	0	0.270729	0	0	ENSG00000233460	RPL35AP31
ENSG00000233462	0	0.080909	0	0.0608436	ENSG00000233462	AL671561.2
ENSG00000233465	0.0488289	0.0266211	0	0	ENSG00000233465	BX927141.2
ENSG00000233466	0.00724298	0	0	0.00789492	ENSG00000233466	MICC
ENSG00000233467	0	0.31894	0.0643639	0.319491	ENSG00000233467	U40455.1
ENSG00000233469	0.609644	0.730459	1.05524	0.814466	ENSG00000233469	ST6GALNAC4P1
ENSG00000233471	0.256922	0.267588	0.777344	0.380334	ENSG00000233471	KRT18P62
ENSG00000233473	0	0.0988976	0.0893272	0	ENSG00000233473	RAD1P2
ENSG00000233476	3.80416	0.893073	1.78683	0.835924	ENSG00000233476	EEF1A1P6
ENSG00000233477	0	0	0	0	ENSG00000233477	AL591363.1
ENSG00000233481	0	0.0114325	0.0103321	0.0258921	ENSG00000233481	OR12D2
ENSG00000233484	0	2.02395	1.68558	3.24951	ENSG00000233484	AL450471.1
ENSG00000233486	0	0.0996855	0	0.0419127	ENSG00000233486	USP8P1
ENSG00000233487	0.804616	1.74994	1.08403	4.91397	ENSG00000233487	RPSAP69
ENSG00000233489	0	0	0	0	ENSG00000233489	PAXBP1P1
ENSG00000233490	0	2.5471	0.38568	1.27526	ENSG00000233490	GPSM3
ENSG00000233493	4.48972	3.33068	1.95861	1.27754	ENSG00000233493	TMEM238
ENSG00000233494	0	2.24602	2.74436	4.83097	ENSG00000233494	AC009963.2
ENSG00000233497	0.0657129	0.0634895	0	0.0717411	ENSG00000233497	HNRNPA1P60
ENSG00000233498	0	0	0	0	ENSG00000233498	PPP1R2P1
ENSG00000233499	0.0675279	0	0	0	ENSG00000233499	AP002345.1
ENSG00000233502	0	0	0	0	ENSG00000233502	AC104794.1
ENSG00000233503	0.117253	0.0762067	0.0342667	0.043326	ENSG00000233503	HNRNPLP1
ENSG00000233504	0	0	0	0	ENSG00000233504	POLR2LP1
ENSG00000233505	0	0.00880756	0.00776227	0	ENSG00000233505	KRT18P1
ENSG00000233506	0	0	0	0	ENSG00000233506	AL929561.3
ENSG00000233511	7.2164	2.55075	4.47567	8.12303	ENSG00000233511	Z98742.2
ENSG00000233514	0	0	0	0	ENSG00000233514	AL356653.1
ENSG00000233518	0	0.0858663	0.0775764	0	ENSG00000233518	RPL7P35
ENSG00000233523	0	0	0	0	ENSG00000233523	PHBP5
ENSG00000233524	0	0.450686	0.577698	0.202878	ENSG00000233524	RANP8
ENSG00000233526	0.145213	0.139666	0.0630965	0	ENSG00000233526	RFC5P1
ENSG00000233531	0	0	0	0	ENSG00000233531	DEFA10P
ENSG00000233533	0	0	0	0	ENSG00000233533	MKNK2P1
ENSG00000233537	0	0	0	0	ENSG00000233537	TEDDM2P
ENSG00000233538	6.32064	11.387	9.06861	18.5941	ENSG00000233538	AC017104.3
ENSG00000233539	3.96052	9.83617	9.63845	16.3058	ENSG00000233539	AC011294.1
ENSG00000233541	0	0	0	0	ENSG00000233541	AP000926.1
ENSG00000233543	0.0382194	0	0.0329383	0.041235	ENSG00000233543	CHTF8P1
ENSG00000233544	0	0	0	0	ENSG00000233544	EIF3KP2
ENSG00000233545	0	0	0	0	ENSG00000233545	CYCSP33
ENSG00000233546	0	0	0	0	ENSG00000233546	PRYP5
ENSG00000233548	0	0	0	0	ENSG00000233548	CYCSP44
ENSG00000233549	0	0.0600684	0.444696	1.8599	ENSG00000233549	CYCSP35
ENSG00000233550	0	0	0	0	ENSG00000233550	MTCYBP8
ENSG00000233551	0	0	0	1.71959	ENSG00000233551	LSM1P1
ENSG00000233555	0	0	0	0	ENSG00000233555	AL591438.1
ENSG00000233557	0.166994	0	0.144426	0.178021	ENSG00000233557	NFU1P2
ENSG00000233558	0.861286	0	1.14584	0.364346	ENSG00000233558	AL050331.1
ENSG00000233560	0.448506	1.22204	0.924456	1.45724	ENSG00000233560	KRT8P39

ENSG00000233561	2.95309	2.81073	2.43432	2.06855	ENSG00000233561	DHX16
ENSG00000233562	0.395372	0.18995	0	0.320448	ENSG00000233562	AL356981.1
ENSG00000233563	0	0	0	0	ENSG00000233563	OR52E7P
ENSG00000233564	0.546796	1.39487	0.984671	1.40641	ENSG00000233564	PRR3
ENSG00000233565	0	0	0.312501	0	ENSG00000233565	AC007690.1
ENSG00000233566	0	0.0269191	0.0728962	0	ENSG00000233566	LINC01556
ENSG00000233573	0.233694	0.0488367	0.325348	0.561387	ENSG00000233573	TRIM31
ENSG00000233575	0	0	0	0	ENSG00000233575	AL358934.1
ENSG00000233576	0	0.0556373	0	0	ENSG00000233576	AC131235.2
ENSG00000233578	0.753099	2.99221	3.36412	3.36032	ENSG00000233578	EIF4EP1
ENSG00000233579	0.0401683	0.116101	0.209831	0.483529	ENSG00000233579	KRT8P15
ENSG00000233583	0.162976	0.754831	0.318897	0.570544	ENSG00000233583	AL356273.1
ENSG00000233584	0.842571	0.334349	1.80616	2.05925	ENSG00000233584	HLA-DPB2
ENSG00000233585	0.0358342	0.0631107	0	0.146523	ENSG00000233585	AC231533.2
ENSG00000233586	0.297136	0.926503	0	0.415873	ENSG00000233586	AC246785.2
ENSG00000233588	0.0885236	0.0852306	0.114543	0.0963919	ENSG00000233588	CYP51A1P2
ENSG00000233592	0	0	0	0	ENSG00000233592	MICG
ENSG00000233594	0.171472	0.163867	0	0.361176	ENSG00000233594	BTF3P5
ENSG00000233595	0.611637	0.38986	0.195878	0.798349	ENSG00000233595	MTND2P29
ENSG00000233597	0.124595	0.358851	0.432935	1.21271	ENSG00000233597	AC133435.1
ENSG00000233599	0.208044	0.749081	0.160154	0.231175	ENSG00000233599	TRIM15
ENSG00000233601	0	0	0	0	ENSG00000233601	NCOR1P3
ENSG00000233603	1.52104	7.17322	8.96634	4.63589	ENSG00000233603	JTBP1
ENSG00000233604	0	0	0	0	ENSG00000233604	DHFRP2
ENSG00000233606	0.0673525	0.0647714	0	0	ENSG00000233606	OR6C66P
ENSG00000233608	1.32709	4.32398	1.78525	17.5008	ENSG00000233608	TWIST2
ENSG00000233609	1.02891	2.27175	1.31402	2.02969	ENSG00000233609	RPL10P19
ENSG00000233614	0	0.254578	0	0.150792	ENSG00000233614	DDX11L10
ENSG00000233615	0.0650703	0	0	0.070838	ENSG00000233615	HNRNPA1P42
ENSG00000233617	0	0	0.0540797	0.179459	ENSG00000233617	CR753818.1
ENSG00000233618	0	0	0.00605942	0	ENSG00000233618	OR2J3
ENSG00000233619	0	0	0	0	ENSG00000233619	AC006328.1
ENSG00000233622	1.33684	2.48796	2.24526	2.27149	ENSG00000233622	CYP2T1P
ENSG00000233623	0.499684	1.24412	0.777996	1.18381	ENSG00000233623	PGAM1P11
ENSG00000233626	0.679202	0.722446	1.36721	0.239043	ENSG00000233626	AC092814.1
ENSG00000233628	0	0	0	0	ENSG00000233628	VN2R5P
ENSG00000233632	0	0	0	0	ENSG00000233632	Z82198.3
ENSG00000233634	0	0.128584	0.116087	0	ENSG00000233634	GOT2P5
ENSG00000233636	0	0	0.00605942	0	ENSG00000233636	OR2J3
ENSG00000233640	0	0	0	0	ENSG00000233640	KRTAP13-5P
ENSG00000233641	0.461121	0.704371	0.620046	0.33653	ENSG00000233641	C6orf136
ENSG00000233646	0.0665741	0.768306	0.694237	0.506937	ENSG00000233646	OR52T1P
ENSG00000233647	0.168606	1.29212	0.583169	0.226497	ENSG00000233647	NENFP1
ENSG00000233648	0	0	0	0	ENSG00000233648	AC010095.1
ENSG00000233650	0	0	0	0	ENSG00000233650	BX248413.3
ENSG00000233652	0	0	0.0551781	0	ENSG00000233652	CICP1
ENSG00000233653	0	0.0844164	0.0048781	0.183655	ENSG00000233653	CICP7
ENSG00000233655	0	0	0	0	ENSG00000233655	IGHD4-4
ENSG00000233659	0.45465	1.08563	0.27317	2.64049	ENSG00000233659	NDUFA5P4
ENSG00000233662	0	0	0.334712	0.821369	ENSG00000233662	CALM2P4
ENSG00000233663	0.297362	0.228912	0.105359	0.259214	ENSG00000233663	AL161722.1
ENSG00000233664	0	0	0	0	ENSG00000233664	NDUFS5P3
ENSG00000233668	1.06969	2.15739	2.31771	4.96403	ENSG00000233668	AL353662.2
ENSG00000233670	0.0284121	0.0685347	0.0743257	0.0469109	ENSG00000233670	PIRT

ENSG00000233671	0.898649	1.89124	1.99218	3.13411	ENSG00000233671	AC083899.2
ENSG00000233673	0.184117	0.0688404	0.158198	0.0409103	ENSG00000233673	ANAPC1P1
ENSG00000233674	0	2.00237	1.80082	3.07159	ENSG00000233674	AL451062.2
ENSG00000233676	0	0	0	0	ENSG00000233676	FDPSP6
ENSG00000233677	0	0	0	0	ENSG00000233677	DDX39BP1
ENSG00000233680	0.261932	0.257892	0.170599	0.362566	ENSG00000233680	HNRNPA1P27
ENSG00000233681	0	0.138309	0.154629	0.258337	ENSG00000233681	CEACAMP1
ENSG00000233683	0	0	0	0	ENSG00000233683	AC004965.1
ENSG00000233685	0.112506	0.404256	0.326478	0.845633	ENSG00000233685	OR6L1P
ENSG00000233686	0	0	0	0	ENSG00000233686	PIEZO1P1
ENSG00000233687	0	0.0131907	0.0059608	0	ENSG00000233687	OR2B3
ENSG00000233688	0	0	0	0	ENSG00000233688	BX842559.2
ENSG00000233690	2.16093	2.72139	3.42429	3.04103	ENSG00000233690	EBAG9P1
ENSG00000233691	0	0.11602	0	0.129473	ENSG00000233691	AL354714.5
ENSG00000233697	0	0	0	0	ENSG00000233697	HLA-DRB8
ENSG00000233700	0.0161927	0.00793847	0.00709454	0.0446566	ENSG00000233700	TMPOP1
ENSG00000233701	0.52775	1.03093	0.946261	2.16455	ENSG00000233701	PRR23C
ENSG00000233702	0.401326	0	0	0.413624	ENSG00000233702	AC107083.1
ENSG00000233703	0	0.801005	0.73885	0	ENSG00000233703	AC027673.1
ENSG00000233707	0	0.472095	0.536427	0	ENSG00000233707	RPL22P11
ENSG00000233708	0.143881	0.0555063	0.100283	0.126285	ENSG00000233708	AL512353.2
ENSG00000233709	0.225485	0.861293	0.777985	0.476288	ENSG00000233709	MTND4P28
ENSG00000233710	0	0	0	0	ENSG00000233710	AL049564.1
ENSG00000233711	0	0	0	0	ENSG00000233711	EIF4EBP2P1
ENSG00000233712	0.13199	0.379895	0.45731	0.283232	ENSG00000233712	AL135929.1
ENSG00000233713	0	0	0	0.588682	ENSG00000233713	AL161447.1
ENSG00000233716	0.10748	0.931077	0.280502	0.767082	ENSG00000233716	AC074367.1
ENSG00000233717	1.11762	1.04294	0.920175	0.551143	ENSG00000233717	RPS29P29
ENSG00000233719	0.0527491	0.367604	0.0455602	0.0557211	ENSG00000233719	GOT2P3
ENSG00000233720	0	0	0	0	ENSG00000233720	AC245517.3
ENSG00000233724	0	0	0	0.186882	ENSG00000233724	AL513321.1
ENSG00000233727	0	0	0.849129	0	ENSG00000233727	AL162389.1
ENSG00000233732	0	0	0	0	ENSG00000233732	IGHV3OR16-10
ENSG00000233733	0.43795	0.837021	0	1.35217	ENSG00000233733	H2AFZP6
ENSG00000233734	6.88E-06	0	6.72E-05	0.556183	ENSG00000233734	PSORS1C1
ENSG00000233737	0	0	0	0	ENSG00000233737	AP003072.1
ENSG00000233740	0	0	0	0	ENSG00000233740	CICP2
ENSG00000233741	0	0.388883	0.17554	0	ENSG00000233741	AC016691.1
ENSG00000233742	0	0	0	0	ENSG00000233742	RP11-472D17.2
ENSG00000233747	0	0.728316	0.276361	0	ENSG00000233747	RPL36AP13
ENSG00000233750	1.2273	2.36374	2.78185	3.75183	ENSG00000233750	CICP27
ENSG00000233751	0	0	0	0	ENSG00000233751	AC104772.2
ENSG00000233752	0.229322	0.43567	0.493198	0.141489	ENSG00000233752	AC009414.1
ENSG00000233762	0.56573	1.65071	0	0	ENSG00000233762	AC007969.1
ENSG00000233764	0	0	0	0	ENSG00000233764	MTCO1P20
ENSG00000233765	0.173126	0.628082	0.774877	0.561049	ENSG00000233765	AL591479.1
ENSG00000233767	0	0	1.01097	0	ENSG00000233767	PSMA6P3
ENSG00000233771	0	0.0298483	0.0431105	0	ENSG00000233771	CICP5
ENSG00000233774	0.107284	0	0.0920344	0	ENSG00000233774	MED14P1
ENSG00000233778	0.552499	0.531682	0	0.293514	ENSG00000233778	AC104339.1
ENSG00000233780	0	0	0	0.141759	ENSG00000233780	HNRNPA1P30
ENSG00000233782	0.724186	0.959303	0.960409	1.71539	ENSG00000233782	ZNF90P3
ENSG00000233786	0	0.148508	0.150306	0.120568	ENSG00000233786	CDC27P1
ENSG00000233787	0	0.049362	0	0.0527675	ENSG00000233787	AC010374.1

ENSG00000233788	0	0	0	0	ENSG00000233788	SPATA31A5
ENSG00000233792	0	0.308903	0	0	ENSG00000233792	PUDPP2
ENSG00000233795	1.68418	2.5917	1.53231	0.855655	ENSG00000233795	ZNRD1
ENSG00000233796	0	0	0	0	ENSG00000233796	AC089999.1
ENSG00000233801	4.30996	3.46615	2.38813	2.98449	ENSG00000233801	NELFE
ENSG00000233802	0	0	0	0	ENSG00000233802	TRIM49D2
ENSG00000233803	0	0	0	0	ENSG00000233803	TSPY4
ENSG00000233805	0	0	0	0	ENSG00000233805	AL365496.1
ENSG00000233807	0	0	0	0	ENSG00000233807	AC097262.1
ENSG00000233810	0	0	0	0	ENSG00000233810	MOB1AP2
ENSG00000233812	0.657643	2.86018	2.27432	1.87583	ENSG00000233812	AC139426.2
ENSG00000233813	3.6819	4.08555	4.50723	3.12515	ENSG00000233813	MRPS18B
ENSG00000233814	0	0	0	0	ENSG00000233814	AL590664.1
ENSG00000233816	0.228274	0.132473	0.168128	0.955555	ENSG00000233816	IFNA13
ENSG00000233819	0.334453	0	0.869675	0	ENSG00000233819	AL353779.2
ENSG00000233820	0	0.283893	0.333834	0.490094	ENSG00000233820	AL589843.2
ENSG00000233822	12.6485	24.4891	9.15388	14.4842	ENSG00000233822	HIST1H2BN
ENSG00000233827	0	0	0.0925994	0.0686366	ENSG00000233827	FAM58BP
ENSG00000233828	18.473	51.8939	47.218	85.6638	ENSG00000233828	LINC01949
ENSG00000233829	0	0.467267	0.633572	0.258014	ENSG00000233829	AC017078.1
ENSG00000233830	0	0	0	0.195209	ENSG00000233830	EIF4HP1
ENSG00000233831	0.404817	0	2.03433	0	ENSG00000233831	ZNF311
ENSG00000233832	0	0	0	0	ENSG00000233832	AL590623.1
ENSG00000233833	0	0.0501115	0.0913797	0.171404	ENSG00000233833	ETF1P3
ENSG00000233836	3.50684	1.39812	1.37985	1.05105	ENSG00000233836	AC139769.1
ENSG00000233837	0.329095	0.0817389	0	0	ENSG00000233837	EIF3LP2
ENSG00000233838	0.703332	1.13155	1.30672	3.17972	ENSG00000233838	DPH3P1
ENSG00000233839	0	0.196381	0	0	ENSG00000233839	AL357055.1
ENSG00000233841	0.726085	2.8839	0.16706	1.20966	ENSG00000233841	HLA-C
ENSG00000233843	0	0	0	0	ENSG00000233843	CYCSP48
ENSG00000233846	0.214745	0.203525	0	0	ENSG00000233846	AL133480.2
ENSG00000233853	0	0	0	0	ENSG00000233853	BX927235.2
ENSG00000233859	0	0.0585563	0.0533334	0	ENSG00000233859	ADH5P4
ENSG00000233861	0	0	0	0	ENSG00000233861	MGAT2P1
ENSG00000233863	0	0	0	0.0218418	ENSG00000233863	AC012215.1
ENSG00000233867	0	0	0	0	ENSG00000233867	SLC9B1P3
ENSG00000233868	0	0.29181	0	0	ENSG00000233868	AC009302.1
ENSG00000233869	0	0	0.0652956	0.0815799	ENSG00000233869	RPSAP27
ENSG00000233870	0	0	0	0	ENSG00000233870	AC007881.1
ENSG00000233872	0	0.0763148	0.137896	0.0861113	ENSG00000233872	AC005033.1
ENSG00000233873	0	0	0	0	ENSG00000233873	RPL7P44
ENSG00000233874	0.0317161	0.0306901	0.0279377	0.0692427	ENSG00000233874	AL118496.1
ENSG00000233876	0	0	0	0	ENSG00000233876	GAPDHP68
ENSG00000233877	0.676454	1.7654	2.66573	2.20751	ENSG00000233877	AL606517.1
ENSG00000233880	0	0	0	0	ENSG00000233880	AL161722.2
ENSG00000233887	0.0325111	0.0939788	0.141593	0.249475	ENSG00000233887	AL354685.1
ENSG00000233888	0	0.192489	0.0924672	0.216459	ENSG00000233888	MTCO2P17
ENSG00000233889	6.38867	11.0716	10.2078	16.1432	ENSG00000233889	AL353698.1
ENSG00000233890	0.0605061	0	0.0332406	8.86E-05	ENSG00000233890	TCF19
ENSG00000233892	0.299832	0	0	0	ENSG00000233892	AL671855.1
ENSG00000233900	0	0	0	0	ENSG00000233900	RPL17P35
ENSG00000233902	0.242295	0.453881	0.613946	0	ENSG00000233902	AL645933.1
ENSG00000233904	16.4661	29.8937	16.2765	16.1278	ENSG00000233904	HLA-E

ENSG00000233905	0.251826	0	0	0	ENSG00000233905	LONRF2P2
ENSG00000233908	0	2.17601	5.37784	6.62048	ENSG00000233908	AL359711.1
ENSG00000233909	0	0	0	0	ENSG00000233909	UBE2V1P4
ENSG00000233910	0.0923821	0.17752	0.0801803	0.0999188	ENSG00000233910	GTF2F2P2
ENSG00000233911	0	0	0.105105	0.0887849	ENSG00000233911	POU5F1
ENSG00000233913	0.258545	0	0.232185	0	ENSG00000233913	RPL10P9
ENSG00000233915	0	0.0673881	0.0702009	0.0769326	ENSG00000233915	UBE2Q2P10
ENSG00000233916	0.0558802	0	0.0241408	0.0296507	ENSG00000233916	ZDHHC20P1
ENSG00000233917	0.0401989	0.154876	0.139995	0.087982	ENSG00000233917	POTEB
ENSG00000233918	0	0	0	0	ENSG00000233918	AC128676.1
ENSG00000233921	0	0	0	0	ENSG00000233921	RPS15AP40
ENSG00000233924	0.14501	0.209242	0.44106	0.407771	ENSG00000233924	RPSAP13
ENSG00000233927	207.083	123.647	61.5663	4.36942	ENSG00000233927	RPS28
ENSG00000233929	0	0	0	0.940213	ENSG00000233929	MT1XP1
ENSG00000233931	0.207097	0.39859	0.54705	0.957843	ENSG00000233931	TRIM40
ENSG00000233932	0	0.0936954	0.0169421	0.106838	ENSG00000233932	CTXN2
ENSG00000233933	0	0	0	0	ENSG00000233933	AL135924.1
ENSG00000233934	0	0	0	0	ENSG00000233934	RPL21P38
ENSG00000233935	0	1.24928	0.0540797	0	ENSG00000233935	AL669813.2
ENSG00000233938	0	0	0	0	ENSG00000233938	PPP1R26P3
ENSG00000233939	0	0	0	0	ENSG00000233939	AC114755.4
ENSG00000233940	0	0	0	0	ENSG00000233940	RPL12P45
ENSG00000233943	0	0	0.19026	0.366643	ENSG00000233943	AC114973.1
ENSG00000233944	0	0	0.266743	0.252982	ENSG00000233944	LINC00265-3P
ENSG00000233946	0	0	0	0	ENSG00000233946	RPS29P4
ENSG00000233947	0	0.0916154	0.0416258	0.104572	ENSG00000233947	AL353705.3
ENSG00000233948	8.05059	7.29991	6.12118	1.22618	ENSG00000233948	TRIM27
ENSG00000233951	0	0	0	0	ENSG00000233951	RCC2P3
ENSG00000233952	0	0	0.240774	0	ENSG00000233952	FTLP15
ENSG00000233954	0	0.186259	0	0.616108	ENSG00000233954	UQCRHL
ENSG00000233955	0	0	0	0.050645	ENSG00000233955	AHCYP3
ENSG00000233956	0.457233	1.6103	1.58448	0.814466	ENSG00000233956	BTF3P6
ENSG00000233961	2.16947	5.46323	7.72845	8.78575	ENSG00000233961	RP11-87H9.2
ENSG00000233962	0	0	0	0.81278	ENSG00000233962	AC064862.2
ENSG00000233963	0.745687	1.9604	1.33025	2.36241	ENSG00000233963	ATP8A2P3
ENSG00000233964	0	0	0	0	ENSG00000233964	HLA-K
ENSG00000233965	0	0.0169735	0.0627602	0.0560227	ENSG00000233965	CT009531.1
ENSG00000233966	0.154502	0.721948	0.748151	0.994777	ENSG00000233966	UBE2SP1
ENSG00000233971	0	0	0	0	ENSG00000233971	RPS20P10
ENSG00000233972	0	0.0858021	0.0808883	0.0707639	ENSG00000233972	CR847849.1
ENSG00000233974	0.864878	3.20639	0.7704	1.36814	ENSG00000233974	AC138951.1
ENSG00000233979	1.1267	1.06723	0.241046	1.79151	ENSG00000233979	AC002553.2
ENSG00000233980	0.451237	0	0	0	ENSG00000233980	FDPSP2
ENSG00000233982	0.0488289	0.0266211	0	0	ENSG00000233982	CR788234.2
ENSG00000233983	0	0	0	0	ENSG00000233983	AL365220.1
ENSG00000233984	1.10296	0.534174	0.957814	0.845636	ENSG00000233984	RPSAP14
ENSG00000233989	0	0	0	0.0488226	ENSG00000233989	UBDP1
ENSG00000233990	0.280728	0.800424	1.688	2.93728	ENSG00000233990	AL353754.1
ENSG00000233991	0.190216	0.301003	0.768313	1.44733	ENSG00000233991	AC116050.1
ENSG00000233994	0.128094	0.122674	0	1.12416	ENSG00000233994	GDI2P2
ENSG00000233995	0	0	0	0.276139	ENSG00000233995	AP000547.1
ENSG00000233996	0.667963	1.04658	1.00395	1.98633	ENSG00000233996	AC013439.1
ENSG00000233998	1.43242	2.47037	3.01295	3.86991	ENSG00000233998	SETP5
ENSG00000233999	0	0	0.459388	0.28	ENSG00000233999	IGKV3OR2-268

ENSG00000234000	1.17902	0.798709	0.336089	1.23078	ENSG00000234000	PPP1R18
ENSG00000234001	0	0	0	0	ENSG00000234001	AC000111.2
ENSG00000234003	0	0	0.194764	0.656048	ENSG00000234003	MTATP6P27
ENSG00000234004	0	0	0	0	ENSG00000234004	AC092017.2
ENSG00000234005	0.406161	0.582784	1.0526	0.430504	ENSG00000234005	GAPDHP22
ENSG00000234008	0	0	0	0	ENSG00000234008	PPP1R2P2
ENSG00000234009	0.146183	0.140916	0	0.0806979	ENSG00000234009	RPL5P34
ENSG00000234012	0.0961644	0.686575	0.460787	0.446605	ENSG00000234012	MDC1
ENSG00000234016	1.5712	0.737941	0.677259	0.787336	ENSG00000234016	GNG10P1
ENSG00000234017	3.7343	3.49921	6.26745	4.85417	ENSG00000234017	AC022018.1
ENSG00000234020	0.053298	0	0	0.0581554	ENSG00000234020	CHIAP3
ENSG00000234025	0.111826	0.715825	0.196221	0.240988	ENSG00000234025	RBPMS2P1
ENSG00000234030	0	0.169628	0.15318	0.25043	ENSG00000234030	TMEM97P1
ENSG00000234031	0.165811	0.878484	0.37113	1.37132	ENSG00000234031	RPS3AP44
ENSG00000234032	3.6052	0.0897054	3.94953	0.947401	ENSG00000234032	VARS2
ENSG00000234033	0	0	0	0.150903	ENSG00000234033	RAC1P8
ENSG00000234036	4.69563	6.96498	7.13577	26.1327	ENSG00000234036	TXNP6
ENSG00000234038	0.330717	1.15121	1.65079	0.881571	ENSG00000234038	AC123768.3
ENSG00000234039	0	0	0	0	ENSG00000234039	NDUFA5P7
ENSG00000234040	2.23027	12.1759	7.95842	14.9673	ENSG00000234040	RPL10P12
ENSG00000234041	6.7057	4.17177	0.920175	8.81828	ENSG00000234041	AL512326.3
ENSG00000234042	3.70654	3.24134	5.44758	9.24699	ENSG00000234042	AL591438.2
ENSG00000234043	0.0886047	0.42568	0	0	ENSG00000234043	NUDT9P1
ENSG00000234044	0	0	0	0	ENSG00000234044	AC108059.3
ENSG00000234046	0	0	0.42406	0.187296	ENSG00000234046	TRIM26
ENSG00000234047	0.34271	7.25857	7.92461	8.46544	ENSG00000234047	AC113612.1
ENSG00000234048	0	0.46102	0.41622	0.342344	ENSG00000234048	FAM96AP1
ENSG00000234058	3.18119	0.998512	1.14687	1.58835	ENSG00000234058	PPP1R11
ENSG00000234059	0	0	0	0.263717	ENSG00000234059	CASKP1
ENSG00000234060	0.86207	0.928847	1.49645	0.774281	ENSG00000234060	EDDM3CP
ENSG00000234061	0.858984	0	0	0	ENSG00000234061	AC007969.2
ENSG00000234064	0	0	0	0	ENSG00000234064	PRAMEF29P
ENSG00000234065	0.0927125	0.089707	0.0752973	0.764623	ENSG00000234065	MTND4P26
ENSG00000234066	0	0.575494	0.288896	0.506297	ENSG00000234066	TAS2R62P
ENSG00000234067	0	0	0.444409	0.230324	ENSG00000234067	RPL5P10
ENSG00000234068	0.686966	0	0	0.185463	ENSG00000234068	PAGE2
ENSG00000234069	0.0678815	0	0	0	ENSG00000234069	GAPDHP53
ENSG00000234071	0	0	0	0	ENSG00000234071	AC010099.3
ENSG00000234073	0	0.548116	0.577918	0.300917	ENSG00000234073	AC011816.1
ENSG00000234074	0.111634	0.322334	0.119037	0.102342	ENSG00000234074	HLA-J
ENSG00000234075	0	0	0	0	ENSG00000234075	AL353777.1
ENSG00000234078	39.6632	10.3894	18.1959	9.14113	ENSG00000234078	DDR1
ENSG00000234080	0	0	0	0	ENSG00000234080	AL596275.1
ENSG00000234081	0	0	0	0.157046	ENSG00000234081	ELOCP10
ENSG00000234085	0.251826	0.363516	0.246988	1.04998	ENSG00000234085	AC064862.3
ENSG00000234086	10.964	12.2201	13.2719	13.8148	ENSG00000234086	AL391994.1
ENSG00000234087	0	0	0	0	ENSG00000234087	AL356299.1
ENSG00000234088	0	0	0	0	ENSG00000234088	RPS15AP7
ENSG00000234092	0	0	0.0584294	0.110658	ENSG00000234092	AL662857.5
ENSG00000234093	2.9091	2.01395	2.7576	1.92551	ENSG00000234093	RPS15AP11
ENSG00000234095	0	0	0	0	ENSG00000234095	HLA-N
ENSG00000234096	1.01276	1.53629	1.07424	1.70412	ENSG00000234096	MOG
ENSG00000234099	0	0.111151	0.100454	0.062951	ENSG00000234099	MTND4P11
ENSG00000234100	0	0	0	0	ENSG00000234100	OR14J1

ENSG00000234101	0	0	0	0	ENSG00000234101	OR2W1
ENSG00000234102	0	0	0.0575591	0	ENSG00000234102	KRT19P4
ENSG00000234106	0	0.537385	0	0.621443	ENSG00000234106	AP004242.1
ENSG00000234107	0	0	0	0	ENSG00000234107	TPT1P1
ENSG00000234108	0	0	0	0	ENSG00000234108	AL596276.2
ENSG00000234109	0	0	0	0	ENSG00000234109	RPL7P36
ENSG00000234110	0.0886047	0.340544	0.230751	0.287735	ENSG00000234110	TSPY25P
ENSG00000234112	0.348685	0.660963	0.596349	0	ENSG00000234112	AC099066.3
ENSG00000234114	1.09785	0	2.48604	2.04872	ENSG00000234114	CCHCR1
ENSG00000234115	0.0960095	0	0.0446036	0.0550204	ENSG00000234115	AL138878.2
ENSG00000234118	1.49309	2.51557	1.69007	1.8538	ENSG00000234118	RPL13AP6
ENSG00000234119	0.0749013	0.110704	0.189516	0.172729	ENSG00000234119	AC079248.1
ENSG00000234120	0	0.890424	0	0	ENSG00000234120	AF228730.4
ENSG00000234121	0	0	0	0	ENSG00000234121	GPM6BP3
ENSG00000234122	0	0	0	0	ENSG00000234122	TRBV22OR9-2
ENSG00000234123	0.058571	0.0563857	0.0254321	0.128539	ENSG00000234123	RHBDF1P1
ENSG00000234124	0	0	0	0	ENSG00000234124	CSN1S2AP
ENSG00000234125	0	0	0	0	ENSG00000234125	EEF1GP8
ENSG00000234127	5.4112	4.49197	8.62028	2.86323	ENSG00000234127	TRIM26
ENSG00000234130	0.099937	0.232393	0.1582	0.0899776	ENSG00000234130	AL359263.1
ENSG00000234131	0	0	0	0	ENSG00000234131	ELOCP8
ENSG00000234135	0.165868	0.663662	0.896152	0.360056	ENSG00000234135	RPL23AP83
ENSG00000234137	0.399977	0.12896	0.145468	0.26788	ENSG00000234137	MUC21
ENSG00000234138	0.590588	1.06889	0.27481	0	ENSG00000234138	RP11-144A16.1
ENSG00000234140	0	0	0	0	ENSG00000234140	DDX39BP2
ENSG00000234143	0.25831	0	0	0.279795	ENSG00000234143	UGT1A13P
ENSG00000234144	0	0	1.01282	6.63749	ENSG00000234144	COX6CP13
ENSG00000234145	0	0	0	0.115018	ENSG00000234145	NAP1L4P3
ENSG00000234146	0	0.0420013	0.075929	0.0953839	ENSG00000234146	AKAP8P1
ENSG00000234152	0	0	0	0	ENSG00000234152	ELOBP1
ENSG00000234154	0	0.00799456	0.00913478	0.00910544	ENSG00000234154	HLA-DMB
ENSG00000234158	0	0	0	0	ENSG00000234158	RPEP2
ENSG00000234159	0.906473	3.01024	2.93461	3.18613	ENSG00000234159	RBPMSLP
ENSG00000234163	1.59464	1.13149	0.409448	4.1087	ENSG00000234163	MTND4LP11
ENSG00000234164	0.0394657	0.0375419	0	0	ENSG00000234164	HLA-DRB9
ENSG00000234167	0.359566	1.70292	1.2284	3.35521	ENSG00000234167	ELOBP4
ENSG00000234175	0.590603	0.538926	0.603013	1.79073	ENSG00000234175	AL355355.2
ENSG00000234176	0.188851	0.0302431	0	0.1716	ENSG00000234176	HSPA8P1
ENSG00000234178	0	0	0	0	ENSG00000234178	DEFA11P
ENSG00000234179	0	0	0	0	ENSG00000234179	MTCYBP1
ENSG00000234187	0.20599	0.130129	0.352279	0.809222	ENSG00000234187	AIMP1P1
ENSG00000234188	0	0	0	0	ENSG00000234188	AL121963.1
ENSG00000234189	0	0	0	0	ENSG00000234189	AC099799.1
ENSG00000234192	0	0	0	0	ENSG00000234192	RPS26P38
ENSG00000234195	0	0	0	0	ENSG00000234195	OR14J1
ENSG00000234196	0.256112	0.212818	0.785449	0	ENSG00000234196	ZBTB12
ENSG00000234200	0	0	0.0289661	0	ENSG00000234200	AC243591.1
ENSG00000234201	0.132807	0.127724	0.0577055	0.0722369	ENSG00000234201	BMI1P1
ENSG00000234202	1.37913	2.56363	0	5.42949	ENSG00000234202	AC104332.2
ENSG00000234204	0	0	0.14965	0	ENSG00000234204	PIGPP2
ENSG00000234213	0	0	0	0.126194	ENSG00000234213	FHP1
ENSG00000234214	0	0.0262294	0	0	ENSG00000234214	SPATA32A4
ENSG00000234216	0	0	0	0	ENSG00000234216	HNRNPA1P2
ENSG00000234217	0	0	0	0	ENSG00000234217	RBPJP7

ENSG00000234218	0.238434	0.898692	1.75628	0.927638	ENSG00000234218	MICB
ENSG00000234219	2.58967	2.39254	1.64244	1.72191	ENSG00000234219	CDCA4P4
ENSG00000234224	0.109043	0.191539	0.155708	0.558141	ENSG00000234224	TMEM229A
ENSG00000234226	0	0	0	0.351646	ENSG00000234226	NDUFS5P2
ENSG00000234227	0.717132	0.256489	0.0856062	0.77069	ENSG00000234227	RPL7L1P1
ENSG00000234228	0	0.0767257	0.034677	0.108973	ENSG00000234228	NCLP2
ENSG00000234231	7.01793	5.78917	4.54385	22.4558	ENSG00000234231	AC093616.1
ENSG00000234234	0	0	0.0258542	0	ENSG00000234234	MTCO2P8
ENSG00000234237	85.9106	122.957	122.542	258.264	ENSG00000234237	AL162431.1
ENSG00000234239	0	0.314035	0	0	ENSG00000234239	CFL1P8
ENSG00000234241	0.0391614	0.0370704	0.0335366	0	ENSG00000234241	AL109618.1
ENSG00000234242	0	0.0627516	0	0	ENSG00000234242	DDX39BP2
ENSG00000234243	0.26308	0.0707527	0.25712	0.0988522	ENSG00000234243	GPSM3
ENSG00000234247	0.0939498	0.0898761	0.243562	2.53708	ENSG00000234247	AC096537.2
ENSG00000234249	0	0	0	0	ENSG00000234249	COL11A2P1
ENSG00000234251	0	0	0	0	ENSG00000234251	HTATSF1P1
ENSG00000234253	0	0	0	0	ENSG00000234253	RPL7P13
ENSG00000234256	0	0	0	0	ENSG00000234256	PTCD2P2
ENSG00000234257	0	0.123519	0.11151	0.276422	ENSG00000234257	SOD2P1
ENSG00000234258	0	0	0.0689541	0	ENSG00000234258	HSPA1L
ENSG00000234259	0	0	0.0629389	0	ENSG00000234259	AC008550.1
ENSG00000234260	0.00091433	0	0.000798201	0.000801615	ENSG00000234260	HLA-DPA2
ENSG00000234262	0.352998	0	0	0	ENSG00000234262	AL356867.1
ENSG00000234267	0	0.0894727	0.0403114	0.276785	ENSG00000234267	TULP3P1
ENSG00000234268	1.01345	3.02982	1.28381	4.74666	ENSG00000234268	AP000936.3
ENSG00000234269	0	0	0	0	ENSG00000234269	AL365396.1
ENSG00000234270	0	0	0.269371	0	ENSG00000234270	RPL36P20
ENSG00000234271	0.979606	0.619509	3.91754	2.38259	ENSG00000234271	Z98752.2
ENSG00000234272	1.21823	4.13138	3.35102	4.16569	ENSG00000234272	RPL30P2
ENSG00000234274	0.566244	1.53233	2.08099	3.94346	ENSG00000234274	COX7BP2
ENSG00000234276	0	0	0	0	ENSG00000234276	SDR42E1P3
ENSG00000234278	0.0713285	0	0.0621184	0	ENSG00000234278	PRR20E
ENSG00000234280	0	0	0	0	ENSG00000234280	C6orf10
ENSG00000234282	0	0	0	0.165722	ENSG00000234282	AL109809.2
ENSG00000234284	3.44779	2.71085	2.89389	2.21338	ENSG00000234284	ZNF879
ENSG00000234285	0.12949	0.249091	0.225104	0.140918	ENSG00000234285	GAPDHP49
ENSG00000234287	0	0	0	0	ENSG00000234287	AC099560.2
ENSG00000234288	0	0	0	0	ENSG00000234288	OR1AA1P
ENSG00000234289	1.93647	0.231134	0.879631	1.26783	ENSG00000234289	H2BFS
ENSG00000234295	0	0	0	0	ENSG00000234295	AC109135.1
ENSG00000234297	0	0.0633555	0.231314	0.0720631	ENSG00000234297	AL592293.2
ENSG00000234298	0.0906025	1.77598	1.85729	2.04818	ENSG00000234298	TCEB3CL
ENSG00000234299	0	0	0	0	ENSG00000234299	CDK2AP2P1
ENSG00000234304	0.109863	0.105391	0.222242	0.202859	ENSG00000234304	SGO1P2
ENSG00000234305	0.0332871	0	0	0.0136277	ENSG00000234305	OR2J1
ENSG00000234309	0	0	0	0	ENSG00000234309	SLC25A18P1
ENSG00000234312	0	0	0	0.190181	ENSG00000234312	SAPCD2P4
ENSG00000234315	0.90414	1.9986	1.30513	0.96604	ENSG00000234315	OSTCP5
ENSG00000234319	0	0	0	0	ENSG00000234319	RPS12P2
ENSG00000234320	0.332272	0.430312	0.971764	3.6762	ENSG00000234320	RP11-381O7.6
ENSG00000234322	0	0	0.0584336	0.0833314	ENSG00000234322	ST13P18
ENSG00000234324	0.263403	0.884552	1.83365	0.917296	ENSG00000234324	AC005517.2
ENSG00000234325	0.231241	0.662479	0.679437	0.488229	ENSG00000234325	MRPS10P2
ENSG00000234328	0	0.0103777	0.17011	0.0956457	ENSG00000234328	TNXA

ENSG00000234329	2.06789	3.74893	4.32428	4.62742	ENSG00000234329	AL604028.2
ENSG00000234332	0	0.205611	0.188192	0.567249	ENSG00000234332	BCAS2P2
ENSG00000234333	2.21352	0.835158	1.49691	3.17545	ENSG00000234333	CYCSP53
ENSG00000234335	0	0	0	0	ENSG00000234335	RPS4XP11
ENSG00000234337	0	0	0	0	ENSG00000234337	AC026462.1
ENSG00000234338	0.341947	1.00222	1.09534	1.02345	ENSG00000234338	AC073349.2
ENSG00000234340	1.03722	2.78169	3.02404	3.78457	ENSG00000234340	AP000705.2
ENSG00000234343	4.65105	3.54583	2.17492	1.03442	ENSG00000234343	NEU1
ENSG00000234344	0	0	0	0	ENSG00000234344	MEP1AP3
ENSG00000234345	0.0584007	0.140499	0.0761862	0.190953	ENSG00000234345	AC234782.4
ENSG00000234347	0.21123	0.457168	0.423707	0.844127	ENSG00000234347	OR11A1
ENSG00000234349	0	0	0	0	ENSG00000234349	GLUD1P9
ENSG00000234351	0	0.0415668	0.00939099	0.0470305	ENSG00000234351	CR753509.4
ENSG00000234353	2.17756	2.82149	6.0554	1.26833	ENSG00000234353	AP000346.2
ENSG00000234354	0	2.07133	1.74209	0.793893	ENSG00000234354	RPS26P47
ENSG00000234355	0	0	0	0	ENSG00000234355	FTH1P27
ENSG00000234356	0	0	0	0	ENSG00000234356	AC009945.1
ENSG00000234358	0.256183	2.32339	0.176423	1.34592	ENSG00000234358	AC003080.1
ENSG00000234359	0	0	0	0	ENSG00000234359	ELK1P1
ENSG00000234360	0	0	0.738867	0	ENSG00000234360	AL135790.2
ENSG00000234363	0	0	0	0	ENSG00000234363	PPIAP27
ENSG00000234364	0	0	0	0	ENSG00000234364	MICF
ENSG00000234367	1.37498	1.26931	0.900864	2.28672	ENSG00000234367	PFN1P3
ENSG00000234369	0.399	1.45234	0.793797	3.14533	ENSG00000234369	TATDN1P1
ENSG00000234370	0.587198	0.9189	1.38855	0.244115	ENSG00000234370	GTF2H4
ENSG00000234371	1.79478	1.52355	1.45946	2.21925	ENSG00000234371	RPSAP31
ENSG00000234372	0	0	0	0	ENSG00000234372	HLA-DPA3
ENSG00000234373	2.47071	2.76468	1.96435	2.44471	ENSG00000234373	SNX18P7
ENSG00000234375	0	0	0	0	ENSG00000234375	VN2R4P
ENSG00000234376	0	0	0	0	ENSG00000234376	UBTFL2
ENSG00000234379	0.118199	0.796364	1.13768	1.06645	ENSG00000234379	HMGB1P48
ENSG00000234381	0.234926	0.52697	0.27206	0.169923	ENSG00000234381	MED15P7
ENSG00000234382	0.221011	0.954003	0.709448	0.475967	ENSG00000234382	AL513174.1
ENSG00000234383	0.320094	1.95714	1.61932	2.79759	ENSG00000234383	CTBP2P8
ENSG00000234385	0.167579	0.488444	0.194538	0.458445	ENSG00000234385	RCC2P1
ENSG00000234386	0.3965	0.39913	0.230402	0.74027	ENSG00000234386	OR7E162P
ENSG00000234388	0	0	0.596349	0.361847	ENSG00000234388	TXNP3
ENSG00000234391	0	0	0	0	ENSG00000234391	AL606490.6
ENSG00000234397	0	0.451569	0	0.167488	ENSG00000234397	AL591122.1
ENSG00000234398	0	0	0	0	ENSG00000234398	AC134915.1
ENSG00000234399	0	0	0.00174067	0.00180714	ENSG00000234399	RBMY2XP
ENSG00000234402	0	0	0.0424124	0	ENSG00000234402	ELK2BP
ENSG00000234404	0	0	0.054688	0.0677963	ENSG00000234404	SPRYD7P1
ENSG00000234406	0	0	0	0	ENSG00000234406	AC004129.2
ENSG00000234409	1.26559	1.78074	2.96658	3.50772	ENSG00000234409	CCDC188
ENSG00000234413	0	0	0	0	ENSG00000234413	AC245102.1
ENSG00000234414	0	0	0	0	ENSG00000234414	RBMY1A1
ENSG00000234415	0	0	0	0.0861113	ENSG00000234415	RPL5P7
ENSG00000234416	0	0	0	0	ENSG00000234416	SNX18P4
ENSG00000234417	0	0.0149857	0	0	ENSG00000234417	AL662831.1
ENSG00000234419	0	0	0.0241881	0.0713278	ENSG00000234419	CICP13
ENSG00000234420	5.84608	11.94	12.7564	20.3837	ENSG00000234420	ZNF37BP
ENSG00000234421	0.0731185	0.0703168	0	0.158859	ENSG00000234421	SLC25A5P4
ENSG00000234422	0	0	0	0	ENSG00000234422	UBE2WP1

ENSG00000234424	0.103955	0	0.051246	0.887225	ENSG00000234424	AL353743.4
ENSG00000234429	0.0931425	0.0450323	0.0812498	0.103249	ENSG00000234429	AC105342.1
ENSG00000234430	0	0	0	0	ENSG00000234430	SNX18P6
ENSG00000234433	1.02425	1.71745	2.89525	2.54589	ENSG00000234433	VWA7
ENSG00000234436	0	0	0	0	ENSG00000234436	AC245884.2
ENSG00000234438	0.0700035	0.134999	0.213598	0.192485	ENSG00000234438	KBTBD13
ENSG00000234439	0	0	0	0	ENSG00000234439	KRT18P2
ENSG00000234441	0	0	0	0	ENSG00000234441	AC105272.1
ENSG00000234442	0	0	0	0	ENSG00000234442	BX276092.5
ENSG00000234443	0.0302896	0.0578806	0	0.032054	ENSG00000234443	LY6G6D
ENSG00000234444	14.7588	31.2076	29.123	28.2935	ENSG00000234444	ZNF736
ENSG00000234448	0	0	0	0	ENSG00000234448	AL606490.7
ENSG00000234450	0	0.722712	0.603595	0.801492	ENSG00000234450	AC005534.2
ENSG00000234451	0	0.109091	0.14789	0.061796	ENSG00000234451	BX005266.3
ENSG00000234454	0.0263015	0.025284	0.0228434	0.0285321	ENSG00000234454	RP1-14D6.2
ENSG00000234457	0	1.33883	1.17863	4.23753	ENSG00000234457	AC006960.1
ENSG00000234458	0	0	0	0	ENSG00000234458	AF186996.3
ENSG00000234463	0	0	0.689168	0	ENSG00000234463	COX6CP12
ENSG00000234465	3.79756	13.9332	4.99628	6.91608	ENSG00000234465	PINLYP
ENSG00000234466	1.18022	1.99537	2.46194	3.02835	ENSG00000234466	AL590240.2
ENSG00000234467	0	0	0	0	ENSG00000234467	SLC25A1P2
ENSG00000234469	0.110115	0.20636	0.279514	0.579365	ENSG00000234469	CLDN34
ENSG00000234470	0	0	0	0	ENSG00000234470	CR753841.1
ENSG00000234473	0.603397	1.63121	2.25852	2.12903	ENSG00000234473	ZNF101P2
ENSG00000234475	0	0.474923	0	0	ENSG00000234475	HSPA1A
ENSG00000234479	1.08321	1.64657	1.60208	1.65367	ENSG00000234479	AP1B1P1
ENSG00000234480	0	0	0	0	ENSG00000234480	MTCO2P18
ENSG00000234485	0	0	0.13545	0.343569	ENSG00000234485	OR7E46P
ENSG00000234487	1.08992	25.4834	6.0677	3.87952	ENSG00000234487	HLA-F
ENSG00000234488	0	0	0	0	ENSG00000234488	AC096664.2
ENSG00000234489	0	0	0	0	ENSG00000234489	ALDH7A1P4
ENSG00000234491	0	0.0721518	0	0.0728075	ENSG00000234491	HNRNPA1P51
ENSG00000234495	4.2109	8.94599	6.32148	5.60851	ENSG00000234495	TRIM27
ENSG00000234496	0	0	0	0	ENSG00000234496	MRPS21P1
ENSG00000234498	1.16628	1.37291	0.221216	0.838314	ENSG00000234498	RPL13AP20
ENSG00000234500	2.17639	0.76896	1.699	1.99683	ENSG00000234500	AC008267.3
ENSG00000234502	0.136828	0.395026	0.118432	0.227002	ENSG00000234502	FYTTD1P1
ENSG00000234507	23.5341	0.845722	2.38479	3.41059	ENSG00000234507	BRD2
ENSG00000234508	0.26308	0.0707527	0.25712	0.0988522	ENSG00000234508	GPSM3
ENSG00000234510	0	0	0	0	ENSG00000234510	HLA-DQB3
ENSG00000234511	0.208657	0.817947	0.759495	1.79974	ENSG00000234511	C5orf58
ENSG00000234512	0.040733	0.0392723	0	0.0448191	ENSG00000234512	TLR12P
ENSG00000234513	0.278896	0.391287	0	0	ENSG00000234513	AC073072.2
ENSG00000234514	0	0	0.112516	0	ENSG00000234514	LST1
ENSG00000234515	0	0	0	0	ENSG00000234515	PPP1R2P1
ENSG00000234518	0	0	0	0.255349	ENSG00000234518	PTGES3P1
ENSG00000234521	0.338473	0	0	0	ENSG00000234521	AC005041.2
ENSG00000234522	0.217233	0.175761	0.692131	0.350074	ENSG00000234522	AC073587.1
ENSG00000234523	0	0	0	0	ENSG00000234523	NDUFB1P2
ENSG00000234524	0	0	0.263811	0.32625	ENSG00000234524	RPL12P43
ENSG00000234528	0	0	0	0	ENSG00000234528	SUMO2P1
ENSG00000234529	0	0	0	0.0672545	ENSG00000234529	GAPDHP19
ENSG00000234530	1.27859	1.68772	2.62759	1.01061	ENSG00000234530	NFKBIL1
ENSG00000234534	0	0.493257	0.250667	0.85364	ENSG00000234534	CSNK1G2P1

ENSG00000234536	7.61626	31.6733	35.0203	24.8085	ENSG00000234536	AC096582.7
ENSG00000234537	0.0304491	0.0895844	0.0817106	0.237342	ENSG00000234537	AL354751.1
ENSG00000234538	0	0	0	0	ENSG00000234538	ZNF114P1
ENSG00000234539	2.91793	7.37074	5.37631	18.2764	ENSG00000234539	ATF6B
ENSG00000234541	0	0	0	0	ENSG00000234541	CHEK2P5
ENSG00000234544	0	0.17987	0.162398	0.199674	ENSG00000234544	PTGES3P5
ENSG00000234545	25.325	35.0535	33.4512	46.7603	ENSG00000234545	FAM133B
ENSG00000234549	0.449589	0.763134	1.27499	0.973813	ENSG00000234549	ATAT1
ENSG00000234557	0	0.206683	0.0933234	0	ENSG00000234557	AL035422.1
ENSG00000234558	0	0.0593743	0	0.0672591	ENSG00000234558	API5P1
ENSG00000234559	0	0	0.627839	0.255811	ENSG00000234559	AC079776.3
ENSG00000234560	0.117197	0.394727	0.0540225	0.385154	ENSG00000234560	OR10G8
ENSG00000234562	1.38906	1.59792	1.46117	2.49953	ENSG00000234562	TPMTP2
ENSG00000234564	0	0	0	0	ENSG00000234564	HSPA8P20
ENSG00000234565	0	0	0	0	ENSG00000234565	COX6B1P1
ENSG00000234566	0	0.043007	0	0.0968853	ENSG00000234566	RPL7AP71
ENSG00000234568	0.273183	0.662118	0.598583	0.498573	ENSG00000234568	BIN2P1
ENSG00000234569	0	0	0	0	ENSG00000234569	RAD1P1
ENSG00000234570	0.0738118	0.142343	0.0965209	0.325212	ENSG00000234570	ZFRP1
ENSG00000234573	0	0	0	0.739592	ENSG00000234573	AL121890.1
ENSG00000234574	0	0.159557	0	0.193505	ENSG00000234574	CR759838.1
ENSG00000234575	0.835503	0.185941	0.182395	0.27977	ENSG00000234575	CTSLP8
ENSG00000234576	0	0	0.21961	0.227754	ENSG00000234576	MTND1P26
ENSG00000234583	0	0	0	0	ENSG00000234583	TSPY19P
ENSG00000234585	3.86132	3.7714	4.97959	6.48402	ENSG00000234585	CCT6P3
ENSG00000234586	0.0499118	0	0.0435611	0	ENSG00000234586	AL161449.1
ENSG00000234587	0	0	0	0	ENSG00000234587	MRPL50P1
ENSG00000234588	0	0	0	0	ENSG00000234588	FABP5P14
ENSG00000234589	0	0	0.100409	0	ENSG00000234589	AC125807.1
ENSG00000234590	0	0	0	0	ENSG00000234590	GNG5P5
ENSG00000234592	0	0.0335753	0	0.0382955	ENSG00000234592	AL359845.1
ENSG00000234594	0	0	0	0	ENSG00000234594	AC008134.1
ENSG00000234602	0.107414	0.158651	0.229769	0.180329	ENSG00000234602	MCIDAS
ENSG00000234603	1.86109	3.11778	2.57701	5.6213	ENSG00000234603	AL356740.1
ENSG00000234604	15.1363	25.0338	19.9906	17.9739	ENSG00000234604	AL021068.2
ENSG00000234605	0	0	0	0.253379	ENSG00000234605	PSORS1C2
ENSG00000234607	0.790473	1.49929	0.889888	2.23958	ENSG00000234607	AL355994.4
ENSG00000234611	0.069606	0	0.120964	0	ENSG00000234611	OR2AT2P
ENSG00000234612	0.230238	0.439712	0.198626	0.243078	ENSG00000234612	H2AFZP5
ENSG00000234618	0.233689	0.105211	0.115707	0.101343	ENSG00000234618	RPSAP9
ENSG00000234619	0.120343	0.949897	1.28845	2.97977	ENSG00000234619	RPL7P11
ENSG00000234620	0	0	0	0	ENSG00000234620	PUDPP1
ENSG00000234623	0.777593	0.983953	1.81207	2.41946	ENSG00000234623	MOG
ENSG00000234624	0.335441	2.09302	0.851082	2.78892	ENSG00000234624	AC016894.1
ENSG00000234627	0	0	0	0	ENSG00000234627	NUS1P3
ENSG00000234629	0.0674958	0	0	0	ENSG00000234629	WDR82P1
ENSG00000234631	0	0.00478888	1.22896	0.459338	ENSG00000234631	AL162407.1
ENSG00000234632	0.0913981	0.263476	0.452605	0.198415	ENSG00000234632	NECAP1P2
ENSG00000234637	0	0	0	0	ENSG00000234637	RPS19P6
ENSG00000234639	0	0	0	0	ENSG00000234639	AC009263.1
ENSG00000234642	0	0	0	0	ENSG00000234642	PPP1R2P1
ENSG00000234643	0	0	0	0	ENSG00000234643	EIF3FP1
ENSG00000234644	0	0	0	0	ENSG00000234644	OTX2P1
ENSG00000234645	0.0859914	0.371567	0.149925	0.837625	ENSG00000234645	YWHAEP5

ENSG00000234648	0	0	0	0	ENSG00000234648	AL162151.2
ENSG00000234651	41.2026	22.7792	21.5078	12.0468	ENSG00000234651	BAG6
ENSG00000234652	0.0603727	0	0.0524996	0.0657713	ENSG00000234652	AGPAT5P1
ENSG00000234654	0	0	0.243493	0.518114	ENSG00000234654	RP11-782C8.8
ENSG00000234655	0	0	0	0	ENSG00000234655	OR7E155P
ENSG00000234658	0	0	0	0	ENSG00000234658	AC013429.1
ENSG00000234664	1.77525	0	2.69904	4.8518	ENSG00000234664	HMGN2P5
ENSG00000234667	0.237537	0.627893	0.480156	0.67599	ENSG00000234667	ACTBP13
ENSG00000234668	0.00314444	0.0186652	0.023055	0.174972	ENSG00000234668	ATP6V1G2
ENSG00000234669	0.597048	3.91864	0.053838	0.24367	ENSG00000234669	ZFP57
ENSG00000234670	0.0779556	0.0749433	0.0677098	0.0845847	ENSG00000234670	OR6C64P
ENSG00000234671	0.0531886	0	0.140933	0.0594442	ENSG00000234671	MTCYBP5
ENSG00000234674	0.402607	0	0.0670335	0	ENSG00000234674	TCF19
ENSG00000234680	0	0.0797839	0	0.0913848	ENSG00000234680	VN2R3P
ENSG00000234681	2.43709	0.131858	0.000279736	0.000166056	ENSG00000234681	HCG4P8
ENSG00000234682	0.258641	0.0903629	0.0816266	0.406774	ENSG00000234682	VDAC2P4
ENSG00000234683	0	0	0	0	ENSG00000234683	AL138799.3
ENSG00000234685	0.589602	0.140953	0.640335	0.244113	ENSG00000234685	NUS1P2
ENSG00000234700	0	0.036649	0.165642	0.0416637	ENSG00000234700	MTCO1P8
ENSG00000234701	0	0	0	0	ENSG00000234701	PRDX3P3
ENSG00000234702	0	0.146332	0	0	ENSG00000234702	VDAC1P3
ENSG00000234704	4.90478	30.0359	69.1337	51.1135	ENSG00000234704	BRD2
ENSG00000234706	0.0951903	0.0913527	0.330079	0.308367	ENSG00000234706	PRUNEP1
ENSG00000234709	0.437382	0.934117	1.37586	2.01098	ENSG00000234709	UPF3AP3
ENSG00000234711	0	0	0	0	ENSG00000234711	TUBB8P11
ENSG00000234713	0	0.125994	0.568763	0.704664	ENSG00000234713	AC022616.1
ENSG00000234716	2.80737	2.50178	3.14573	3.71884	ENSG00000234716	AC092447.6
ENSG00000234719	4.7296	10.2985	7.31557	8.92265	ENSG00000234719	NPIPB2
ENSG00000234720	0	0	0	0	ENSG00000234720	ATP5A1P8
ENSG00000234723	0	0	0	0	ENSG00000234723	AC092421.1
ENSG00000234724	0	0	0.0351347	0.0883213	ENSG00000234724	HDAC1P1
ENSG00000234725	0.0571755	0	0	0.955792	ENSG00000234725	RP11-157L3.1
ENSG00000234726	0	0	0	0	ENSG00000234726	AC245060.3
ENSG00000234728	15.4939	23.7762	42.7954	13.313	ENSG00000234728	C6orf48
ENSG00000234729	0.517402	1.18843	0.934622	1.32964	ENSG00000234729	AGER
ENSG00000234731	0.361889	0	0	0.75018	ENSG00000234731	MTND4LP16
ENSG00000234732	0	0	0	0	ENSG00000234732	RPEP5
ENSG00000234734	2.39183	3.40931	3.26445	6.4608	ENSG00000234734	SPATA31A7
ENSG00000234735	0	0	0	0.270305	ENSG00000234735	AL022237.1
ENSG00000234737	0.138056	0.177197	0.160536	0.200994	ENSG00000234737	KRT18P15
ENSG00000234742	1.00583	3.40573	2.18686	3.37836	ENSG00000234742	AC144530.1
ENSG00000234743	0	0.390198	0.352257	0.217455	ENSG00000234743	EIF5AP4
ENSG00000234744	0	0	0	0	ENSG00000234744	USP9YP26
ENSG00000234745	2.4996	12.3948	5.90804	12.7355	ENSG00000234745	HLA-B
ENSG00000234746	0	0	0	0	ENSG00000234746	OR2J2
ENSG00000234748	0	0.140018	0	0	ENSG00000234748	AL109913.1
ENSG00000234749	1.21E-07	0	0	0	ENSG00000234749	FAM90A21P
ENSG00000234750	1.05374	2.03606	1.4285	2.63589	ENSG00000234750	AC012618.2
ENSG00000234751	0.342043	0.766846	0.494019	0.981134	ENSG00000234751	AP002381.1
ENSG00000234757	0.437807	0.253937	0.365097	0.313371	ENSG00000234757	CA15P2
ENSG00000234761	0.0480612	0	0	0	ENSG00000234761	AC096632.2
ENSG00000234764	0	0	0	0	ENSG00000234764	E2F6P1
ENSG00000234765	0.143844	0.242512	0.24607	0.275735	ENSG00000234765	ELL2P3
ENSG00000234769	23.5783	31.984	24.9678	21.9363	ENSG00000234769	WASH4P

ENSG00000234770	0	0.258727	0.153054	0.381728	ENSG00000234770	GULOP
ENSG00000234776	0.975637	1.16286	1.27311	0.912258	ENSG00000234776	C11orf94
ENSG00000234780	0	0	0	0	ENSG00000234780	AC245047.5
ENSG00000234782	0	0	0	0	ENSG00000234782	TPT1P9
ENSG00000234784	0.533252	4.00626	2.23519	1.0779	ENSG00000234784	AL606517.2
ENSG00000234785	0.0299349	0	0	0.0246767	ENSG00000234785	EEF1GP5
ENSG00000234786	0	0	0	0	ENSG00000234786	HLA-W
ENSG00000234788	0.752513	1.30599	1.23417	1.37686	ENSG00000234788	HSPA8P3
ENSG00000234790	0	0	0	0	ENSG00000234790	NUTF2P4
ENSG00000234792	0	0	0	0	ENSG00000234792	AL450023.2
ENSG00000234794	0.132708	0.0207335	0.166196	0.116951	ENSG00000234794	HLA-DRA
ENSG00000234795	1.48331	1.9915	8.30146	2.15913	ENSG00000234795	RFTN1P1
ENSG00000234797	0	0.260692	0.232838	0	ENSG00000234797	RPS3AP6
ENSG00000234798	1.69617	2.37247	1.46123	0.0777383	ENSG00000234798	DXO
ENSG00000234799	0	0	0	0	ENSG00000234799	HLA-N
ENSG00000234800	0.168797	0.319255	0.430917	0.903425	ENSG00000234800	PCMTD1P3
ENSG00000234801	0	0.222209	0.245544	0.4147	ENSG00000234801	MORF4
ENSG00000234804	0.0332871	0	0	0.0136277	ENSG00000234804	OR2J1
ENSG00000234805	0.0368166	0.0298501	0.0269845	0	ENSG00000234805	AC090505.1
ENSG00000234806	0.185342	0.363248	0.161578	1.57557	ENSG00000234806	RPL26P29
ENSG00000234809	0.463793	1.24111	0.515031	0.408103	ENSG00000234809	NRM
ENSG00000234811	0	0	0	0	ENSG00000234811	AL161932.1
ENSG00000234812	0	0.867741	0.537604	0.199449	ENSG00000234812	BX664727.2
ENSG00000234813	0	0	0	0	ENSG00000234813	AL357520.1
ENSG00000234814	1.21881	0.804603	1.24353	0.984646	ENSG00000234814	SVILP1
ENSG00000234816	0.731728	0.697714	0.21021	0.513815	ENSG00000234816	HIST1H2APS5
ENSG00000234819	0	0	0	0	ENSG00000234819	AL353705.4
ENSG00000234821	0	0	0.272364	0	ENSG00000234821	MRPS33P4
ENSG00000234825	0	0.000856895	0.0382286	0.00118188	ENSG00000234825	XRCC6P2
ENSG00000234829	0	0.160472	0.509436	0.105883	ENSG00000234829	IFNA17
ENSG00000234830	0.378785	1.7731	2.07672	2.3048	ENSG00000234830	FAM197Y9
ENSG00000234831	0.0289227	0	0	0	ENSG00000234831	CR759913.1
ENSG00000234834	0.842571	0.334349	1.80616	2.05925	ENSG00000234834	HLA-DPB2
ENSG00000234835	0.172781	0	0.375024	0.374242	ENSG00000234835	PHBP13
ENSG00000234836	0.128048	0.290488	0.160375	0.21663	ENSG00000234836	AIF1
ENSG00000234837	0.0804205	0.0475118	0.0516648	0.0639076	ENSG00000234837	AC073464.3
ENSG00000234838	5.03E-07	0	0	0	ENSG00000234838	AC092373.1
ENSG00000234839	0	0	0	0	ENSG00000234839	RPS26P30
ENSG00000234841	0.0927828	0.686659	0.886174	0.31937	ENSG00000234841	AC017007.2
ENSG00000234842	0.20036	0	0	0.108229	ENSG00000234842	MTCO2P16
ENSG00000234844	0	0.608582	1.96919	0.833931	ENSG00000234844	CDC42P2
ENSG00000234846	0.660009	0.501914	0.39253	0.47765	ENSG00000234846	NEU1
ENSG00000234849	0	0	0	0.062455	ENSG00000234849	HLA-W
ENSG00000234850	0	0.318976	0.287961	0.177469	ENSG00000234850	MTND2P3
ENSG00000234851	318.888	257.538	124.49	113.888	ENSG00000234851	RPL23AP42
ENSG00000234852	0.256112	0.212818	0	0.639599	ENSG00000234852	ZBTB12
ENSG00000234853	0	0	0.400242	0	ENSG00000234853	NDUFA5P3
ENSG00000234856	0	0	0	0.0488226	ENSG00000234856	UBDP1
ENSG00000234857	9.02135	10.44	10.035	12.9183	ENSG00000234857	HNRNPUL2-BSCL2
ENSG00000234861	0	0	0	0	ENSG00000234861	ATP5A1P1
ENSG00000234863	0	7.01518	3.22464	2.88743	ENSG00000234863	AC096644.2
ENSG00000234865	0.532549	0.553914	0.910184	0.277399	ENSG00000234865	AC026784.1
ENSG00000234872	0	0	0	0	ENSG00000234872	AL358176.5

ENSG00000234876	0.101393	0.329519	0.360664	0.0863238	ENSG00000234876	NOTCH4
ENSG00000234878	0	0	0.541691	0.658477	ENSG00000234878	HSPE1P1
ENSG00000234881	0.73835	1.3169	0.55744	0.569001	ENSG00000234881	PIGFP2
ENSG00000234882	1.57113	2.10381	3.03122	2.32763	ENSG00000234882	EIF3EP1
ENSG00000234886	0.0651448	0.575248	0.40954	1.05179	ENSG00000234886	MTND5P26
ENSG00000234888	0	0	0	0	ENSG00000234888	OFD1P15Y
ENSG00000234889	0.378287	0.877318	0.645942	1.49312	ENSG00000234889	AL391666.1
ENSG00000234890	0	0.337136	0.0761406	0.284871	ENSG00000234890	HNRNPDLP2
ENSG00000234894	0	0	0	0	ENSG00000234894	AL139327.3
ENSG00000234895	0	0	0	0.0747768	ENSG00000234895	OR52X1P
ENSG00000234896	0	0	0.484411	0	ENSG00000234896	OR7E62P
ENSG00000234898	0	0	0	0	ENSG00000234898	CHEK2P3
ENSG00000234901	0	0	0.246681	0.305021	ENSG00000234901	MTND6P13
ENSG00000234903	0	0	0.543625	0	ENSG00000234903	AC133104.1
ENSG00000234904	0	0	0	0	ENSG00000234904	CR936879.1
ENSG00000234906	0.597483	0.758509	0.924882	0.91576	ENSG00000234906	APOC2
ENSG00000234907	0	2.56679	1.11656	0	ENSG00000234907	AL593851.1
ENSG00000234910	0.0465928	0.0897263	0.12165	0.0509152	ENSG00000234910	IL6RP1
ENSG00000234911	0.157618	0.269762	0.137811	0.474423	ENSG00000234911	TEX21P
ENSG00000234920	0.00314444	0.0186652	0.023055	0.174972	ENSG00000234920	ATP6V1G2
ENSG00000234922	0	0	0	0	ENSG00000234922	TSEN15P3
ENSG00000234925	2.24608	6.34271	6.12713	11.388	ENSG00000234925	ATP5HP4
ENSG00000234927	0	0	0	1.27235	ENSG00000234927	HMGN1P18
ENSG00000234931	0.0255943	0.0986802	0	0.0562008	ENSG00000234931	MARK2P15
ENSG00000234932	0	0	0	0	ENSG00000234932	AC009969.1
ENSG00000234933	1.20523	1.80929	1.28011	2.62825	ENSG00000234933	CDC42P1
ENSG00000234934	0	0	0	0	ENSG00000234934	MTND5P29
ENSG00000234937	0.598509	1.79864	1.16989	1.44474	ENSG00000234937	AL139128.1
ENSG00000234939	0	0	0.0592685	0	ENSG00000234939	MTND2P18
ENSG00000234941	0	0	0	0	ENSG00000234941	AL117339.3
ENSG00000234946	1.04547	1.45547	1.16364	1.43755	ENSG00000234946	SDHCP3
ENSG00000234947	0.806788	1.58056	0.607978	0.738067	ENSG00000234947	STK19
ENSG00000234949	0.308648	1.07133	0.624714	1.70181	ENSG00000234949	AC104667.2
ENSG00000234950	0	0	0	0	ENSG00000234950	RBMY2OP
ENSG00000234951	2.89E-08	0.22701	0.346537	0	ENSG00000234951	SAPCD1
ENSG00000234954	0	0	0	0	ENSG00000234954	MAS1L
ENSG00000234958	0	0	0	0	ENSG00000234958	FABP5P13
ENSG00000234964	18.906	7.89729	45.7697	7.52003	ENSG00000234964	FABP5P7
ENSG00000234965	0	0	0	0	ENSG00000234965	SHISA8
ENSG00000234968	0	0	0	0	ENSG00000234968	HLA-DQB3
ENSG00000234969	0.405937	0.635029	2.09343	1.73955	ENSG00000234969	AL627389.1
ENSG00000234970	0	0.284332	0	0	ENSG00000234970	MCCD1P2
ENSG00000234972	7.19851	10.7716	13.9246	9.21124	ENSG00000234972	TBC1D3C
ENSG00000234975	0	0	0	0.327318	ENSG00000234975	FTH1P2
ENSG00000234980	0.0533493	0.0644828	0.0698207	0.0879944	ENSG00000234980	WASF5P
ENSG00000234981	0.041823	0.239945	0.0728865	0.337773	ENSG00000234981	AC244034.1
ENSG00000234982	0.16412	1.23878	0.756558	1.10717	ENSG00000234982	AL441963.1
ENSG00000234983	0	0	0	0	ENSG00000234983	AC010132.2
ENSG00000234984	0	0	0.0338723	0	ENSG00000234984	FMO10P
ENSG00000234985	0	0	0	0.204096	ENSG00000234985	AC074085.2
ENSG00000234992	0	0	0	0	ENSG00000234992	GPR53P
ENSG00000234993	0	0.0254943	0.0230419	0.0578032	ENSG00000234993	CUBNP2
ENSG00000234995	0.167011	0.642267	0.435352	0.311189	ENSG00000234995	AC013429.2
ENSG00000234999	0.859806	2.38454	0.600445	1.86542	ENSG00000234999	SNRPCP19

ENSG00000235001	0	0	0.0923502	0	ENSG00000235001	EIF4A1P2
ENSG00000235002	0	0	0	0	ENSG00000235002	AL513331.1
ENSG00000235003	0	0.867741	0.537604	0.199449	ENSG00000235003	RP11-459O16.7
ENSG00000235004	0	0	0	0.372132	ENSG00000235004	USP9YP30
ENSG00000235008	0.0707696	0.100723	0.0931501	0.376695	ENSG00000235008	AL023775.1
ENSG00000235012	0.0136291	0.0916405	0.0828573	0.0597727	ENSG00000235012	AF121897.1
ENSG00000235013	0	0	0	0	ENSG00000235013	COX20P2
ENSG00000235014	0	0	0	0	ENSG00000235014	REREP2Y
ENSG00000235015	0	0	0	0	ENSG00000235015	GEMIN2P1
ENSG00000235017	0.291039	0.225961	0.301166	0.307951	ENSG00000235017	C2
ENSG00000235018	0.281013	1.70393	0.486728	1.05354	ENSG00000235018	AL137077.1
ENSG00000235022	1.24629	0	0	0	ENSG00000235022	RNF39
ENSG00000235025	0	0	0	0	ENSG00000235025	TRIM10
ENSG00000235028	0	0	0	0	ENSG00000235028	HMGN1P30
ENSG00000235030	4.65E-10	35.1599	5.83678	11.0089	ENSG00000235030	IER3
ENSG00000235034	0.814235	0.156038	0.140857	0.868673	ENSG00000235034	C19orf81
ENSG00000235036	0.288047	1.91812	2.19682	2.0712	ENSG00000235036	AL035456.1
ENSG00000235039	0	0.136993	0	0	ENSG00000235039	MTND6P12
ENSG00000235040	0	0	0	0	ENSG00000235040	MTCO3P1
ENSG00000235043	0	0.180192	0.686474	2.41883	ENSG00000235043	TECRP1
ENSG00000235044	0	0	0.310713	0.160501	ENSG00000235044	PPIAP3
ENSG00000235045	0	0.262379	0.474478	0.591181	ENSG00000235045	RPL7P8
ENSG00000235055	0.0696996	0.201081	0.0605631	0.0761494	ENSG00000235055	AL157407.1
ENSG00000235060	0.153885	0.375856	0.467456	1.16919	ENSG00000235060	VDAC1P4
ENSG00000235061	0	0	0	0.293728	ENSG00000235061	UBE2V1P7
ENSG00000235062	0	0.456089	0	0	ENSG00000235062	BCRP5
ENSG00000235064	0	0	0	0	ENSG00000235064	SLC25A5P2
ENSG00000235065	0.16637	0.318796	0	0	ENSG00000235065	RPL24P2
ENSG00000235067	20.0144	27.9814	5.53441	0.46487	ENSG00000235067	TUBB
ENSG00000235068	0	0.0655396	0	0.0887849	ENSG00000235068	POU5F1
ENSG00000235069	0	0	0	0	ENSG00000235069	AL627082.1
ENSG00000235071	0	0.0622245	0.21519	0.523333	ENSG00000235071	AC073909.1
ENSG00000235073	0	0	0	0	ENSG00000235073	RBM22P10
ENSG00000235074	0	0	0	0	ENSG00000235074	CR788250.3
ENSG00000235076	0.132637	0.0637806	0.115264	0.288583	ENSG00000235076	GAPDHP52
ENSG00000235080	0	0.0334183	0	0	ENSG00000235080	MTND5P23
ENSG00000235081	0.0174955	0	0	0.0380342	ENSG00000235081	AC245052.3
ENSG00000235082	0.519956	1.85553	0.566042	2.8832	ENSG00000235082	SUMO1P3
ENSG00000235083	0	0	0	0	ENSG00000235083	AL929288.2
ENSG00000235084	0	0.206233	0.189416	0.267997	ENSG00000235084	CHCHD2P6
ENSG00000235088	1.8996	3.49907	3.25938	3.39466	ENSG00000235088	AL031667.2
ENSG00000235089	0	0	0	0	ENSG00000235089	AL357632.1
ENSG00000235090	0.146865	0.566458	0.29747	0.106417	ENSG00000235090	RPL7L1P3
ENSG00000235094	0	0	0	0	ENSG00000235094	AC006335.1
ENSG00000235095	0.0293627	0.0947545	0.106788	0	ENSG00000235095	AC099654.2
ENSG00000235098	7.52712	9.14544	4.13429	2.34177	ENSG00000235098	ANKRD65
ENSG00000235101	0	0.439498	0.374507	0.167455	ENSG00000235101	SETP9
ENSG00000235102	0.13684	0	0	0	ENSG00000235102	ADI1P1
ENSG00000235105	0.0929623	1.03091	0.513134	0.991322	ENSG00000235105	AL356968.2
ENSG00000235107	6.73865	3.75922	5.56762	0	ENSG00000235107	RING1
ENSG00000235108	0	0.120834	0	0	ENSG00000235108	IFNA12P
ENSG00000235109	9.5782	5.22704	14.8092	6.6028	ENSG00000235109	ZSCAN31
ENSG00000235110	0	0	0	0	ENSG00000235110	AC107421.1

ENSG00000235112	6.29006	9.04976	11.8909	27.0461	ENSG00000235112	HSPE1P27
ENSG00000235113	3.6377	5.12587	4.79298	4.28325	ENSG00000235113	AL161932.2
ENSG00000235115	0	0	0	0	ENSG00000235115	CHCHD2P8
ENSG00000235116	0	0	0	0	ENSG00000235116	BX649210.1
ENSG00000235124	0	0	0	0	ENSG00000235124	KRT8P17
ENSG00000235125	0	0	0	0	ENSG00000235125	NFKBIL1
ENSG00000235128	0.721476	1.72949	1.72819	4.17543	ENSG00000235128	AC013474.1
ENSG00000235129	1.82046	2.89497	2.38387	7.76284	ENSG00000235129	FABP7P2
ENSG00000235130	0	0	0.000405784	0	ENSG00000235130	MYO5BP1
ENSG00000235132	0.0440785	0.10084	0.119165	0.128925	ENSG00000235132	OR2H1
ENSG00000235133	0	0	0	0	ENSG00000235133	RPL35AP22
ENSG00000235134	1.6306	0.412131	0.484678	0.812423	ENSG00000235134	CYP21A2
ENSG00000235136	0	0	0	0	ENSG00000235136	AL627224.1
ENSG00000235137	0.342347	1.18252	1.16731	2.09115	ENSG00000235137	HSP90AB6P
ENSG00000235141	0	0	0	0	ENSG00000235141	COX6CP17
ENSG00000235144	0	0	0	0.062455	ENSG00000235144	HLA-W
ENSG00000235145	0.627522	0.905394	1.43047	1.89193	ENSG00000235145	RPSAP16
ENSG00000235147	0	0	0.421786	0	ENSG00000235147	AC128677.1
ENSG00000235148	0	0.350649	0.392974	0.417233	ENSG00000235148	HMGB3P23
ENSG00000235150	0.0398284	0.0767257	0.034677	0.0435891	ENSG00000235150	RCBTB2P1
ENSG00000235155	0.310039	0.93125	0	0	ENSG00000235155	B3GALT4
ENSG00000235156	0.232207	0.395463	1.40213	1.35398	ENSG00000235156	TMEM30CP
ENSG00000235162	27.7541	26.972	18.5212	45.21	ENSG00000235162	C12orf75
ENSG00000235163	0	0	0	0	ENSG00000235163	AC096644.3
ENSG00000235165	0	0.278168	0.702293	0.235673	ENSG00000235165	CDK5P1
ENSG00000235169	3.91454	3.53346	1.84271	2.1412	ENSG00000235169	SMIM1
ENSG00000235170	0	0	0	0	ENSG00000235170	MTND1P31
ENSG00000235171	0	0	0	0	ENSG00000235171	HNRNPA1P2
ENSG00000235173	9.58976	7.98272	13.737	5.17421	ENSG00000235173	HGH1
ENSG00000235174	0	0	0	0	ENSG00000235174	AC019205.3
ENSG00000235175	0	0.177544	0.160438	0	ENSG00000235175	RPL26P37
ENSG00000235176	2.4236	1.90335	1.53231	0.855655	ENSG00000235176	ZNRD1
ENSG00000235178	0.281502	0.296324	0.329162	0.107474	ENSG00000235178	ZNF311
ENSG00000235181	0	0	0	0	ENSG00000235181	AC245036.2
ENSG00000235182	3.14782	7.27759	6.67005	19.5088	ENSG00000235182	AC104333.1
ENSG00000235183	1.20227	3.68374	1.29	3.60692	ENSG00000235183	AC015795.1
ENSG00000235184	0.00944618	0	0.0164323	0	ENSG00000235184	ZNF90P2
ENSG00000235186	4.89007	0.3112	0.556236	0	ENSG00000235186	AC103563.8
ENSG00000235190	1.87092	0	0	0	ENSG00000235190	AL008629.1
ENSG00000235193	0.84533	0.540572	1.83015	0	ENSG00000235193	AC006987.2
ENSG00000235194	4.1993	7.66865	6.25732	8.46851	ENSG00000235194	PPP1R3E
ENSG00000235195	0	0	0	0	ENSG00000235195	AL929561.4
ENSG00000235196	0	0	0	0	ENSG00000235196	Z68868.1
ENSG00000235197	0.110919	0.267254	0.314088	0.365163	ENSG00000235197	ZNF33CP
ENSG00000235199	0	0.314981	0	0.174778	ENSG00000235199	CYP2C58P
ENSG00000235203	0	0.0547791	0	0	ENSG00000235203	TBC1D3P3
ENSG00000235205	0	0.0312349	0.107257	0.0652382	ENSG00000235205	TATDN2P3
ENSG00000235207	0.663981	1.29967	2.3301	0.387278	ENSG00000235207	TUBBP6
ENSG00000235208	0	0	0	0	ENSG00000235208	AL135938.1
ENSG00000235211	2.02312	5.6594	0	0	ENSG00000235211	TMSB10P2
ENSG00000235213	0.135941	0	0.0590612	0	ENSG00000235213	OR6E1P
ENSG00000235217	0.905356	1.35862	1.25225	2.12654	ENSG00000235217	TSPY26P
ENSG00000235218	0.371373	0.893455	1.13504	1.41729	ENSG00000235218	AC092638.2
ENSG00000235219	0	0	0	0	ENSG00000235219	AC236972.2

ENSG00000235220	0.730468	6.97939	3.47303	2.35358	ENSG00000235220	HLA-F
ENSG00000235222	1.6958	5.91688	4.66184	4.3906	ENSG00000235222	MSH5
ENSG00000235223	0.0161927	0.00793847	0.00709454	0.0446566	ENSG00000235223	TMPOP1
ENSG00000235224	0.720488	0.664007	0.198186	0.718376	ENSG00000235224	AL591212.2
ENSG00000235225	0	0	0	0	ENSG00000235225	AC016712.1
ENSG00000235226	0	0	0	0	ENSG00000235226	AL445528.1
ENSG00000235227	0	0	0	0	ENSG00000235227	VN1R38P
ENSG00000235228	0	0	0	0	ENSG00000235228	BX120007.2
ENSG00000235231	1.2783	2.90511	2.51398	5.22319	ENSG00000235231	AP000351.10
ENSG00000235232	0	0	0	0	ENSG00000235232	MRPS18BP2
ENSG00000235233	1.40824	28.1595	10.6139	3.35845	ENSG00000235233	MICA
ENSG00000235235	0.917657	0	0	0	ENSG00000235235	IGKV1OR2-1
ENSG00000235238	0	0	0	0	ENSG00000235238	SUMO2P1
ENSG00000235239	0	0	0	0	ENSG00000235239	Z74696.1
ENSG00000235240	0	0	0	0	ENSG00000235240	AC026185.1
ENSG00000235241	1.92034	4.47816	1.01915	0.696559	ENSG00000235241	BX284668.4
ENSG00000235243	0	0	0.270046	0	ENSG00000235243	AC093716.1
ENSG00000235248	0.0645839	0.248472	0.112273	0.35143	ENSG00000235248	OR13C1P
ENSG00000235249	0.124217	0.258945	0.132008	0.192383	ENSG00000235249	OR4F29
ENSG00000235251	0.1346	0.607671	0.294508	0.58259	ENSG00000235251	AC093155.2
ENSG00000235253	1.38012	2.62896	2.70872	2.89855	ENSG00000235253	AC010240.2
ENSG00000235254	0	0	0	0	ENSG00000235254	TMEM185AP1
ENSG00000235256	0	0	0	0	ENSG00000235256	FKBP4P7
ENSG00000235258	0.741751	2.38458	1.27895	2.64141	ENSG00000235258	NDUFB4P6
ENSG00000235259	0.208044	0.749081	0.160154	0.231175	ENSG00000235259	TRIM15
ENSG00000235264	0.0973378	0	0	0	ENSG00000235264	RPL5P28
ENSG00000235265	0	0	0	0.067987	ENSG00000235265	LA16c-4G1.5
ENSG00000235266	0.321672	0.304633	0.275371	0.669283	ENSG00000235266	RPL22P17
ENSG00000235267	0.216322	0.413367	0.373294	0.229324	ENSG00000235267	AC074117.2
ENSG00000235268	0.059501	0.172055	0.176291	0.313666	ENSG00000235268	KDM4E
ENSG00000235272	14.4214	7.68601	6.50939	5.12836	ENSG00000235272	FAM103A2P
ENSG00000235274	0.0514981	0.419795	0.495605	0.846228	ENSG00000235274	Z75741.2
ENSG00000235275	0.0917094	0	0.160445	0	ENSG00000235275	KRT18P16
ENSG00000235278	0.0454662	0.266631	0.0793209	0.28124	ENSG00000235278	ZNF652P1
ENSG00000235282	0	0	0	0	ENSG00000235282	DYNLL1P3
ENSG00000235286	0.281611	0.743413	0.460073	1.61283	ENSG00000235286	AP000925.1
ENSG00000235289	0.361296	0.179383	0.324589	0.412399	ENSG00000235289	BRD7P6
ENSG00000235290	0	0	0	0	ENSG00000235290	HLA-W
ENSG00000235291	5.55483	9.66722	7.87132	5.90532	ENSG00000235291	PPP1R10
ENSG00000235294	0	0	0	0	ENSG00000235294	RPL7AP25
ENSG00000235297	0	0	0.187641	0	ENSG00000235297	AC008021.1
ENSG00000235299	3.141	6.70033	6.55391	5.59921	ENSG00000235299	MRPL53P1
ENSG00000235301	1.93885	0.673681	0.561095	0.695858	ENSG00000235301	HLA-Z
ENSG00000235302	0.0302896	0.0578806	0	0.032054	ENSG00000235302	LY6G6D
ENSG00000235305	0.233474	0.0627516	0.0983601	0.475397	ENSG00000235305	DDX39BP2
ENSG00000235306	0	0	0	0.0848354	ENSG00000235306	GAPDHP34
ENSG00000235307	14.1665	3.28562	4.73205	3.32097	ENSG00000235307	BRD2
ENSG00000235308	1.47489	1.41316	0.992178	0.873889	ENSG00000235308	AL445991.1
ENSG00000235309	0.111634	0.158608	0.105705	0.0712032	ENSG00000235309	HLA-J
ENSG00000235310	0	0.000313329	8.23E-09	0	ENSG00000235310	GXYLT1P6
ENSG00000235312	0	0	0	0	ENSG00000235312	KRTAP19-10P
ENSG00000235315	0	0.169898	0	0	ENSG00000235315	RPL23AP69
ENSG00000235316	1.28052	1.4725	1.65406	1.71718	ENSG00000235316	DUSP8P5
ENSG00000235317	1.86909	1.3845	0.332359	0.329597	ENSG00000235317	HCG4

ENSG00000235318	0	0	0.60666	0	ENSG00000235318	MTND4LP13
ENSG00000235323	0	0	0	0	ENSG00000235323	COTL1P2
ENSG00000235324	0	0	0	0	ENSG00000235324	BX649210.2
ENSG00000235325	0	0	0	0	ENSG00000235325	AC009963.3
ENSG00000235327	0.229804	0	0	0	ENSG00000235327	CYP4F61P
ENSG00000235328	0.622701	2.00983	2.34045	3.7542	ENSG00000235328	AC006946.1
ENSG00000235329	0	0	0	0	ENSG00000235329	AL031183.1
ENSG00000235330	0.201528	0	0.174875	0	ENSG00000235330	RPL12P25
ENSG00000235332	0	0.072194	0.0651358	0	ENSG00000235332	RPSAP76
ENSG00000235333	0.986954	1.49116	0	0	ENSG00000235333	PVRIG2P
ENSG00000235334	0.372784	0.508821	0.323588	0.202067	ENSG00000235334	BTG3P1
ENSG00000235336	0.323279	0.093444	0.258819	0.412492	ENSG00000235336	SLC44A4
ENSG00000235338	0.356426	0.114561	0.154982	0.259503	ENSG00000235338	DUSP5P2
ENSG00000235339	0	0.0907682	0.0842434	0	ENSG00000235339	GEMIN2P2
ENSG00000235340	0	0	0.165242	0.129105	ENSG00000235340	MCCD1P2
ENSG00000235342	0.0259809	0.0124808	0.033827	0	ENSG00000235342	RPL7P4
ENSG00000235346	0	3.50334	0	1.95245	ENSG00000235346	HLA-G
ENSG00000235347	0.644522	1.44833	1.42931	2.29695	ENSG00000235347	Z84478.1
ENSG00000235349	0	0	0	0	ENSG00000235349	AC016769.3
ENSG00000235350	4.40421	9.33662	7.59653	11.5752	ENSG00000235350	AL606490.8
ENSG00000235352	0	0	0	0	ENSG00000235352	AC023128.2
ENSG00000235354	3.93844	7.3367	4.89792	3.75633	ENSG00000235354	RPS29P16
ENSG00000235355	1.06476	2.13062	2.17012	3.76593	ENSG00000235355	RP11-381O7.4
ENSG00000235360	5.76497	3.17014	2.1159	2.93559	ENSG00000235360	C6orf47
ENSG00000235363	0	0	0.653171	2.17363	ENSG00000235363	SNRPGP10
ENSG00000235368	0	0	0	0	ENSG00000235368	SAPCD2P2
ENSG00000235369	1.31911	5.17439	3.71754	9.05093	ENSG00000235369	RPL36AP15
ENSG00000235370	1.6696	3.87738	4.01432	5.27529	ENSG00000235370	DNM1P51
ENSG00000235371	0	0.0466267	0.0313234	0.0266135	ENSG00000235371	AL122018.1
ENSG00000235372	0.00219419	0.195312	0.0547187	0.0715276	ENSG00000235372	ETF1P1
ENSG00000235374	0.706901	1.17453	1.48344	1.01873	ENSG00000235374	SSR4P1
ENSG00000235376	0.181731	0.341699	0.253856	0.519128	ENSG00000235376	RPEL1
ENSG00000235377	0	0	0.0630311	0	ENSG00000235377	AL158047.1
ENSG00000235378	6.64595	11.838	7.32143	18.6036	ENSG00000235378	MRPS10P1
ENSG00000235379	0	0	0	0	ENSG00000235379	RPL7P31
ENSG00000235380	0.212651	0.685299	0.190629	0.0861113	ENSG00000235380	MICD
ENSG00000235382	0	0	0.0381566	0.144046	ENSG00000235382	MTND4P31
ENSG00000235386	0	0	0	0	ENSG00000235386	AC113174.1
ENSG00000235388	0	1.40054	0	8.19597	ENSG00000235388	AC018696.7
ENSG00000235390	0.748701	2.27032	1.90023	4.3197	ENSG00000235390	AC051619.1
ENSG00000235391	0.0127692	0	0.0112498	0.00924291	ENSG00000235391	CR753841.2
ENSG00000235396	0.437903	0.619308	1.06848	0.842227	ENSG00000235396	NOTCH4
ENSG00000235400	0.113208	0.074311	0	0	ENSG00000235400	AC104837.1
ENSG00000235401	0	0	0	0	ENSG00000235401	AL935156.3
ENSG00000235411	0.11115	0.220306	0.0499469	0.210541	ENSG00000235411	AC007041.1
ENSG00000235413	0.316837	1.24615	0.990982	1.7233	ENSG00000235413	KRT18P63
ENSG00000235414	0.290833	0.279723	0.189554	0	ENSG00000235414	RPSAP24
ENSG00000235416	0	0	0.0764747	0.0482504	ENSG00000235416	AC233728.2
ENSG00000235420	0	0.0771037	0	0.0843268	ENSG00000235420	AC009269.1
ENSG00000235421	0	0	0	0	ENSG00000235421	AC114501.2
ENSG00000235422	0.0692343	0.603032	0	0.225805	ENSG00000235422	KATNBL1P3
ENSG00000235424	0.41327	0	0	0.47097	ENSG00000235424	SUMO2P10
ENSG00000235425	0.458535	0.29301	0.661455	0.326716	ENSG00000235425	RPS7P13
ENSG00000235428	0	0	0	0	ENSG00000235428	WI2-2998D17.2

ENSG00000235429	0	2.00251	1.08486	1.33115	ENSG00000235429	AC083875.1
ENSG00000235430	0	0.0361783	0	0.099826	ENSG00000235430	ZSWIM5P1
ENSG00000235432	0	0	0	0.172721	ENSG00000235432	AL663074.2
ENSG00000235433	0	0.0971788	0	0.125017	ENSG00000235433	MTATP6P17
ENSG00000235436	0.342176	1.11745	1.08765	1.46046	ENSG00000235436	DPY19L2P4
ENSG00000235438	2.43674	2.72575	2.72583	2.68623	ENSG00000235438	ESRRAP2
ENSG00000235439	5.60078	3.80072	2.53063	3.16321	ENSG00000235439	DDX39B
ENSG00000235440	1.80656	2.56636	3.35599	4.60526	ENSG00000235440	AC011742.3
ENSG00000235441	0	0.00838819	0.0181864	0	ENSG00000235441	OR10C1
ENSG00000235443	1.68418	2.37659	1.53232	0.855655	ENSG00000235443	ZNRD1
ENSG00000235444	0	0.108529	0	0	ENSG00000235444	PSMB3P2
ENSG00000235447	0	0.0276648	0.0250025	0.0313377	ENSG00000235447	TRAPPC13P1
ENSG00000235449	0	7.87055	7.83854	16.5395	ENSG00000235449	AC098934.3
ENSG00000235451	0	1.29093	1.16491	2.47597	ENSG00000235451	PNPLA4P1
ENSG00000235452	0.329801	0	0.241696	0	ENSG00000235452	LY6G6C
ENSG00000235454	0	0.449122	0.416849	0	ENSG00000235454	HAUS6P3
ENSG00000235458	2.13296	1.99934	1.44905	2.25545	ENSG00000235458	CR753818.2
ENSG00000235459	0.240054	0.285064	0.208623	0	ENSG00000235459	AC006463.2
ENSG00000235462	0.0352815	0.395093	0.355156	0.407376	ENSG00000235462	TAB3P1
ENSG00000235463	0	0.580977	0	0	ENSG00000235463	AC078974.1
ENSG00000235467	1.85699	0.524499	0.0947318	2.11982	ENSG00000235467	RPL10AP5
ENSG00000235469	0	0	0.14174	0.174778	ENSG00000235469	MRPL50P4
ENSG00000235472	0	0	0.0429575	0.054046	ENSG00000235472	EIF4A1P7
ENSG00000235476	0.657209	1.39547	1.84163	3.25208	ENSG00000235476	AF254982.2
ENSG00000235478	0.0510921	0.375842	0.067913	0.339934	ENSG00000235478	LINC01664
ENSG00000235479	0	0	0	0	ENSG00000235479	RAB9AP4
ENSG00000235482	1.54691	4.33429	4.25774	6.11187	ENSG00000235482	RPL21P135
ENSG00000235485	0	0.0246437	0.0592981	0.0852173	ENSG00000235485	AL021877.1
ENSG00000235486	0	0	0	0	ENSG00000235486	AC114755.5
ENSG00000235487	0.0604017	0.294136	6.72E-05	1.25588	ENSG00000235487	PSORS1C1
ENSG00000235489	0.0985624	0.299833	0.579002	0.474361	ENSG00000235489	DBF4P1
ENSG00000235496	0	0	0	0	ENSG00000235496	RP11-101E5.2
ENSG00000235498	0	0	0	0	ENSG00000235498	MICF
ENSG00000235500	0.028215	0.152056	0.116556	0.0824637	ENSG00000235500	SNX19P2
ENSG00000235505	1.2251	1.66147	2.98277	3.55642	ENSG00000235505	AP002004.1
ENSG00000235506	0	0	0	0	ENSG00000235506	SLC20A1P2
ENSG00000235507	0.0558802	0	0.0241408	0.0296507	ENSG00000235507	ZDHHC20P1
ENSG00000235508	0	0	0.0654885	0	ENSG00000235508	RPS2P7
ENSG00000235510	0	0	0	0	ENSG00000235510	BX842568.4
ENSG00000235511	0	0	0.0564162	0	ENSG00000235511	OFD1P18Y
ENSG00000235514	0.439938	0.415081	1.12441	1.65411	ENSG00000235514	LLPHP2
ENSG00000235521	0	0	0	0	ENSG00000235521	USP9YP27
ENSG00000235524	0	0	0.0661119	0	ENSG00000235524	MTCO1P23
ENSG00000235525	0	0	0	0	ENSG00000235525	FTLP1
ENSG00000235528	0.00091433	0	0.000798201	0.000801615	ENSG00000235528	HLA-DPA2
ENSG00000235531	3.78961	6.42493	15.7961	31.3477	ENSG00000235531	MSC-AS1
ENSG00000235534	0	0	0	0	ENSG00000235534	FECHP1
ENSG00000235536	0	0	0	0	ENSG00000235536	MICF
ENSG00000235539	0	0	0	0	ENSG00000235539	MTND1P33
ENSG00000235541	0	0.00880756	0.00776227	0	ENSG00000235541	KRT18P1
ENSG00000235544	0.329838	0.157993	0.570533	0.351703	ENSG00000235544	RPS11P1
ENSG00000235546	0	0.0431549	0.115959	0.145635	ENSG00000235546	AC087499.5
ENSG00000235547	0	0	0	0	ENSG00000235547	NDUFB11P1
ENSG00000235548	1.04782	1.80826	2.6403	3.0923	ENSG00000235548	AC073551.1

ENSG00000235549	0	0	0	0	ENSG00000235549	EIF1P2
ENSG00000235550	0.100365	0.226228	0.0582783	0.256664	ENSG00000235550	ANKRD26P2
ENSG00000235552	0.462715	0.694463	0.416932	0	ENSG00000235552	AP005202.1
ENSG00000235554	0.0683845	0	0.0603493	0.449337	ENSG00000235554	AC005822.1
ENSG00000235555	0	0	0.403436	0	ENSG00000235555	SUMO1P4
ENSG00000235558	0	7.05591	0.93132	0	ENSG00000235558	AC146949.1
ENSG00000235559	0.164412	0	0.108894	0.250929	ENSG00000235559	NOP56P1
ENSG00000235561	0	0.0149857	0	0	ENSG00000235561	CR759281.1
ENSG00000235568	1.24539	1.73489	1.90125	2.46225	ENSG00000235568	NFAM1
ENSG00000235569	2.79541	10.8388	4.77637	12.7262	ENSG00000235569	MSH5
ENSG00000235571	0	0	0	0	ENSG00000235571	SNX18P14
ENSG00000235573	0	0.443566	0	0	ENSG00000235573	AC005005.2
ENSG00000235574	0	0.0546727	0.147259	0.0612015	ENSG00000235574	AC073150.1
ENSG00000235577	0	0	0	0	ENSG00000235577	CR759837.1
ENSG00000235579	7.25853	11.1741	4.90658	10.0045	ENSG00000235579	AC007283.2
ENSG00000235581	0	0	0	0	ENSG00000235581	AC005011.1
ENSG00000235582	0.197438	1.22169	0.891001	1.23623	ENSG00000235582	AL365258.2
ENSG00000235583	0	0.288303	0.137518	1.63732	ENSG00000235583	AC007562.1
ENSG00000235587	0	0.126277	0	0.0787508	ENSG00000235587	GAPDHP65
ENSG00000235588	0.128048	0.290488	0.160375	0.21663	ENSG00000235588	AIF1
ENSG00000235589	0.281502	0.296324	0.329162	0.107474	ENSG00000235589	ZNF311
ENSG00000235592	0	0.172028	0.0777097	0.193771	ENSG00000235592	AC004674.1
ENSG00000235594	0.166393	0.106764	0.0985908	0.370816	ENSG00000235594	AL139824.2
ENSG00000235595	0	0	0	0.0677962	ENSG00000235595	GAPDHP23
ENSG00000235596	0.0579419	0.0677367	0.106788	0.0857336	ENSG00000235596	PPIAP9
ENSG00000235598	0	0	0.0557551	0.138211	ENSG00000235598	RRM2P4
ENSG00000235600	0	0	0	0.0861113	ENSG00000235600	MICD
ENSG00000235602	0.168017	0.247648	0.2122	0.39161	ENSG00000235602	POU5F1P3
ENSG00000235604	0	0	0	0	ENSG00000235604	SPANXB1
ENSG00000235605	0	0.365456	0.337962	0	ENSG00000235605	AL355472.2
ENSG00000235606	0.298611	0.687331	0.128667	0.760123	ENSG00000235606	AK4P6
ENSG00000235608	0	0.0928048	0	0.105295	ENSG00000235608	NKX1-1
ENSG00000235613	0.24706	0.0707393	0.245224	1.02602	ENSG00000235613	NSRP1P1
ENSG00000235616	0	0.0531668	0.0599745	0.273548	ENSG00000235616	ST13P2
ENSG00000235617	0	0	0	0	ENSG00000235617	AC016027.4
ENSG00000235618	0.279761	0.352985	0.522896	0.506146	ENSG00000235618	FAM21EP
ENSG00000235619	2.64479	3.76131	2.54826	7.94253	ENSG00000235619	RPL36AP33
ENSG00000235623	0.656361	0.119965	0.341727	0.246725	ENSG00000235623	OR7E110P
ENSG00000235626	0	0	0	0	ENSG00000235626	KRT18P66
ENSG00000235627	0	0.993829	0	0.534905	ENSG00000235627	SNRPFP4
ENSG00000235630	0	0.0207547	0.0239362	0	ENSG00000235630	BX000688.2
ENSG00000235631	0.305394	0.293646	0.202736	0.580152	ENSG00000235631	RNF148
ENSG00000235632	0.0332871	0	0	0.0136277	ENSG00000235632	OR2J1
ENSG00000235636	0	0.129295	0	0.172604	ENSG00000235636	NUS1P1
ENSG00000235638	0	0	0	0	ENSG00000235638	MTND6P14
ENSG00000235639	0	0.0499703	0.0451639	0.113318	ENSG00000235639	AC002069.1
ENSG00000235640	0	0.103315	0.0467004	0.264727	ENSG00000235640	AC092646.2
ENSG00000235642	0.174826	0	0.151149	0.372132	ENSG00000235642	PTP4A1P5
ENSG00000235644	0	0.231278	0	0.120581	ENSG00000235644	RPL10P5
ENSG00000235645	0.299686	1.41247	1.25599	3.30497	ENSG00000235645	AL450311.1
ENSG00000235646	0	0.0753949	0.367963	0.850875	ENSG00000235646	MTND1P2
ENSG00000235647	0	0	0.0448061	0.112428	ENSG00000235647	AL022319.1
ENSG00000235649	0.027576	0.0469288	0.0428024	0.0681529	ENSG00000235649	MXRA5Y
ENSG00000235650	249.329	186.853	166.574	87.6578	ENSG00000235650	RPS18

ENSG00000235651	0.0838646	1.01539	0.366282	0.833754	ENSG00000235651	AC064850.1
ENSG00000235653	0	0	0.0618038	0.541051	ENSG00000235653	AC007253.1
ENSG00000235655	45.0093	21.6692	18.8789	20.0107	ENSG00000235655	H3F3AP4
ENSG00000235656	0	0	0	0	ENSG00000235656	RPL36P18
ENSG00000235657	29.4825	49.036	203.541	217.517	ENSG00000235657	HLA-A
ENSG00000235658	0.449589	0.763133	0.80941	0.547135	ENSG00000235658	ATAT1
ENSG00000235661	0	0.0676615	0	0	ENSG00000235661	MIR670HG
ENSG00000235666	0	0	0	0	ENSG00000235666	SUMO2P1
ENSG00000235670	0.159835	0	0.13833	0	ENSG00000235670	RPL21P40
ENSG00000235672	0.854227	0.930715	0.633849	1.04286	ENSG00000235672	AC090286.2
ENSG00000235673	0.390205	0.943671	0.653069	0.316317	ENSG00000235673	AL929472.4
ENSG00000235674	0.853784	3.02456	1.07056	2.75975	ENSG00000235674	LDHAP2
ENSG00000235675	0	0.0562105	0.172614	0.114254	ENSG00000235675	AC15196.1
ENSG00000235676	7.14317	7.31203	6.05223	2.21443	ENSG00000235676	ABHD16A
ENSG00000235677	2.27526	6.08644	4.4978	7.21663	ENSG00000235677	NPM1P26
ENSG00000235678	0	0	0	0	ENSG00000235678	OR5AN2P
ENSG00000235679	0	0	0	0.625996	ENSG00000235679	AL161651.1
ENSG00000235680	3.38964	0	0	0	ENSG00000235680	HLA-G
ENSG00000235681	1.50484	2.99661	3.53356	2.83855	ENSG00000235681	AC245884.3
ENSG00000235683	0.0818322	0.341772	0.404891	0.748425	ENSG00000235683	AC018442.1
ENSG00000235684	0.629805	0.569644	0.340183	0.892291	ENSG00000235684	HTATSF1P1
ENSG00000235685	3.29291	14.0133	16.221	18.4051	ENSG00000235685	AC092473.1
ENSG00000235686	0	0.353107	0	1.15	ENSG00000235686	PPIAP20
ENSG00000235689	0.43656	0	0	0	ENSG00000235689	AC253536.4
ENSG00000235690	0	0	0	0	ENSG00000235690	CUBNP3
ENSG00000235691	0	0	0.180163	0	ENSG00000235691	AC006987.3
ENSG00000235692	6.1601	4.34587	5.17631	2.52165	ENSG00000235692	PFDN6
ENSG00000235695	0.670201	1.40009	0.343232	4.17629	ENSG00000235695	AC130472.1
ENSG00000235696	0.446933	0.608648	0.339268	0.149681	ENSG00000235696	C2
ENSG00000235697	0	0	0	0	ENSG00000235697	DDX39BP1
ENSG00000235698	0.101935	0.0982432	0.135327	0.43392	ENSG00000235698	PA2G4P2
ENSG00000235700	1.32992	1.26417	2.83065	3.91562	ENSG00000235700	CYCSP52
ENSG00000235701	0.126954	1.1023	1.22198	0.483689	ENSG00000235701	PCBP2P1
ENSG00000235705	0.0361617	0.0351538	0.062983	0.118826	ENSG00000235705	AL133481.2
ENSG00000235707	0.0549356	0.0528743	0	0	ENSG00000235707	AL158073.1
ENSG00000235708	0	0.02877	0.0752155	0.249432	ENSG00000235708	COL11A2
ENSG00000235711	0.498205	0.918625	1.05939	1.26625	ENSG00000235711	ANKRD34C
ENSG00000235712	0.250304	4.54691	9.62701	5.58063	ENSG00000235712	RXRB
ENSG00000235713	0.209678	0.503443	0	0.565628	ENSG00000235713	AC004522.1
ENSG00000235714	0	0	0	0	ENSG00000235714	MICG
ENSG00000235715	0.130333	8.34994	0.436281	0.476841	ENSG00000235715	PSMB8
ENSG00000235716	0	0	0	0	ENSG00000235716	KRT18P46
ENSG00000235718	0.0244594	2.45E-06	0.0213154	1.72E-06	ENSG00000235718	MFRP
ENSG00000235719	0	0	0	0	ENSG00000235719	FAM197Y10
ENSG00000235720	0	0	0	0	ENSG00000235720	GABPAP
ENSG00000235721	0.225275	0.466738	0.369026	0.46766	ENSG00000235721	AC013268.3
ENSG00000235729	0	0	0.118771	0	ENSG00000235729	AL500522.2
ENSG00000235730	0	0.0684014	0	0	ENSG00000235730	OR2AF1P
ENSG00000235734	0.779536	2.33088	2.96162	3.98547	ENSG00000235734	HMGN1P36
ENSG00000235735	0	0	0	0	ENSG00000235735	RPL7AP72
ENSG00000235737	0.125097	0.3189	0.333178	1.14775	ENSG00000235737	TRIM60P19
ENSG00000235738	0	0.215837	0	0.288441	ENSG00000235738	AC092647.4
ENSG00000235742	0	0	0	0	ENSG00000235742	AC012308.1
ENSG00000235744	0.352883	0.231516	0.347544	0.0387109	ENSG00000235744	HLA-DOA

ENSG00000235746	0	0	0.0386236	0	ENSG00000235746	CTBP2P2
ENSG00000235748	0.144482	2.20668	0.233758	1.61839	ENSG00000235748	SEPT14P12
ENSG00000235750	30.8583	31.7834	11.3876	10.2779	ENSG00000235750	KIAA0040
ENSG00000235754	1.27904	0.000398778	1.35214	0.511397	ENSG00000235754	APOM
ENSG00000235756	0	0.0511973	0.138817	0	ENSG00000235756	AC098657.1
ENSG00000235757	0.087419	4.41E-06	1.45005	0	ENSG00000235757	PTMAP1
ENSG00000235758	4.49328	0	0.758657	3.4111	ENSG00000235758	AGPAT1
ENSG00000235759	0	0	0	0	ENSG00000235759	ARHGAP42P3
ENSG00000235761	0	0	0	0	ENSG00000235761	MTCO3P46
ENSG00000235763	1.96761	4.22959	6.61559	2.11851	ENSG00000235763	SNRPGP5
ENSG00000235764	0.00219419	0.195312	0.0547187	0.0715276	ENSG00000235764	ETF1P1
ENSG00000235768	0	0.0313735	0	0.179415	ENSG00000235768	BRD7P5
ENSG00000235769	0.0327523	0	0	0	ENSG00000235769	LY6G6E
ENSG00000235773	0.463793	1.24111	0.515031	0.408103	ENSG00000235773	NRM
ENSG00000235775	0	0	0	0	ENSG00000235775	AC063976.4
ENSG00000235776	0.390399	0.574159	0.66612	0.992651	ENSG00000235776	AC000089.1
ENSG00000235778	0	0	0.0559347	0	ENSG00000235778	AC130360.1
ENSG00000235780	0	0	0	0	ENSG00000235780	USP17L27
ENSG00000235784	0.144218	0.0803854	0.940877	0.313371	ENSG00000235784	HNRNPA1P29
ENSG00000235787	0	0	0	0	ENSG00000235787	AC092047.1
ENSG00000235794	0	0	0	0	ENSG00000235794	MTND3P21
ENSG00000235797	0.34122	2.39521	0	0.533227	ENSG00000235797	AL160275.3
ENSG00000235803	0	0	0	0	ENSG00000235803	MTCO2P23
ENSG00000235804	0	0	0	0	ENSG00000235804	AL357078.2
ENSG00000235805	0.0369524	0	0.0975746	0	ENSG00000235805	SOCS5P3
ENSG00000235808	0.188033	0	0.324797	0.399348	ENSG00000235808	MYL6P2
ENSG00000235809	0	0.0627516	0	0	ENSG00000235809	DDX39BP2
ENSG00000235810	0	0	0	0	ENSG00000235810	AL731534.1
ENSG00000235811	0	0	0	0	ENSG00000235811	AL691482.2
ENSG00000235812	0	0.110956	0.15804	0.129897	ENSG00000235812	ADAM21P1
ENSG00000235816	0.628022	1.51007	1.3947	2.93649	ENSG00000235816	PRELID1P3
ENSG00000235817	0	0.210569	0.181535	0.222722	ENSG00000235817	AL158214.1
ENSG00000235818	0	0	0	0.0608115	ENSG00000235818	VN1R17P
ENSG00000235821	0.655505	0.238136	0	0.419557	ENSG00000235821	IFITM4P
ENSG00000235825	0	0	0	0	ENSG00000235825	FAM90A9P
ENSG00000235827	0.0464257	0	0	0	ENSG00000235827	TUBB8P9
ENSG00000235828	0.318177	0	0	0	ENSG00000235828	AC005550.2
ENSG00000235829	0	0.57403	0	0.631458	ENSG00000235829	TBCAP2
ENSG00000235832	0	0	0	0	ENSG00000235832	CNN2P3
ENSG00000235833	1.84659	7.43107	2.61664	11.6577	ENSG00000235833	AC017099.1
ENSG00000235836	0	0.110191	0.0995238	0	ENSG00000235836	KIF3AP1
ENSG00000235838	0.733001	1.39358	1.13793	1.69325	ENSG00000235838	HSP90AB7P
ENSG00000235844	0.015404	0.0454515	0.0767526	0.116139	ENSG00000235844	HLA-DPA1
ENSG00000235847	0.34064	0	0.114504	0.512516	ENSG00000235847	LDHAP7
ENSG00000235855	0	0.0636471	0	0	ENSG00000235855	AP003385.2
ENSG00000235857	0	0	0.86678	0	ENSG00000235857	CTBP2P1
ENSG00000235859	1.73338	5.72532	11.1905	6.07285	ENSG00000235859	AC006978.1
ENSG00000235861	0.645454	0	0	0.648746	ENSG00000235861	AC005237.2
ENSG00000235863	3.00312	4.21892	3.25136	3.68408	ENSG00000235863	B3GALT4
ENSG00000235864	0.0372546	0	0	0	ENSG00000235864	HSPA8P6
ENSG00000235868	0.0607325	0	0.172927	0.595361	ENSG00000235868	GAPDHP31
ENSG00000235869	0	0.63845	1.24432	0.302777	ENSG00000235869	Z99127.2
ENSG00000235871	0	0	0	0	ENSG00000235871	AC062016.2
ENSG00000235876	0	0.0285357	0	0.0949183	ENSG00000235876	FEM1AP4

ENSG00000235877	0	0.0149857	0	0	ENSG00000235877	BX294158.1
ENSG00000235878	7.57889	10.014	11.3011	17.5171	ENSG00000235878	AP001468.1
ENSG00000235879	0	0	0	0	ENSG00000235879	FAR1P1
ENSG00000235883	0.980487	0	1.80608	0	ENSG00000235883	AC012379.1
ENSG00000235892	0	0	0.0595516	0	ENSG00000235892	PKMP2
ENSG00000235893	0	0.261565	0.119084	0.901439	ENSG00000235893	BX284632.1
ENSG00000235895	0	0	0	0	ENSG00000235895	AC010154.1
ENSG00000235896	0	0	0	0	ENSG00000235896	IGKV3D-7
ENSG00000235901	0.017607	0.016978	0.0461606	0	ENSG00000235901	AL442644.1
ENSG00000235905	0.208044	0.749081	0.160154	0.231175	ENSG00000235905	TRIM15
ENSG00000235907	0	0.0864598	0.391416	0	ENSG00000235907	AC115285.1
ENSG00000235912	0	0	0	0	ENSG00000235912	AL031729.1
ENSG00000235915	0	0	0.112516	0	ENSG00000235915	LST1
ENSG00000235916	0	0	0	0	ENSG00000235916	AC233279.1
ENSG00000235917	0.0996025	0.326885	0.555371	1.17305	ENSG00000235917	MTCO2P11
ENSG00000235920	0	0	0	0	ENSG00000235920	AC073109.1
ENSG00000235922	0	0	0	0.145178	ENSG00000235922	AL354766.1
ENSG00000235923	0	0	0	0.0189286	ENSG00000235923	TRIM26BP
ENSG00000235924	0	0	0.205622	0.25986	ENSG00000235924	ZNRF2P3
ENSG00000235925	0.151389	0	0	0	ENSG00000235925	LY6G6C
ENSG00000235926	0	0	0	0	ENSG00000235926	RPS29P15
ENSG00000235929	0	0	0	0	ENSG00000235929	TPT1P14
ENSG00000235930	0	1.65556	1.49087	1.68009	ENSG00000235930	HSPE1P12
ENSG00000235931	1.52376	3.75857	3.13814	5.90273	ENSG00000235931	LINC01553
ENSG00000235932	0	0	0.724127	0.755509	ENSG00000235932	AL359955.2
ENSG00000235937	0.203941	1.3661	1.0801	1.89689	ENSG00000235937	AC008280.1
ENSG00000235938	2.36579	2.59115	0.335129	8.68644	ENSG00000235938	RP11-157L3.4
ENSG00000235940	0	0	0	0.397773	ENSG00000235940	MTND1P21
ENSG00000235941	117.949	23.3534	14.1158	0	ENSG00000235941	HSPA1A
ENSG00000235942	0	0.106225	0	0.834677	ENSG00000235942	LCE6A
ENSG00000235944	2.15686	1.23628	1.43915	1.36155	ENSG00000235944	ZNF815P
ENSG00000235945	0.609277	1.68683	1.33436	1.58677	ENSG00000235945	AC002543.1
ENSG00000235946	0.153752	0.774121	1.74495	0.438685	ENSG00000235946	AC234783.1
ENSG00000235950	0	0	0	0	ENSG00000235950	CDUX4L15
ENSG00000235951	0	0	0.0556585	0.139374	ENSG00000235951	AC009965.2
ENSG00000235952	26.7463	33.3819	20.3661	0.228767	ENSG00000235952	AL845454.2
ENSG00000235955	0.0212762	0.0424108	0.0178926	0	ENSG00000235955	CICP20
ENSG00000235956	0.321353	0.543605	0.602107	0.116243	ENSG00000235956	PRRT1
ENSG00000235957	0	0	1.01628	1.4589	ENSG00000235957	COX7CP1
ENSG00000235959	0.577124	0.362746	0.670143	0.606866	ENSG00000235959	AC009237.6
ENSG00000235960	0.208044	0.749081	0.160154	0.231175	ENSG00000235960	TRIM15
ENSG00000235961	0.0867049	0	0.16259	0	ENSG00000235961	PNMA6A
ENSG00000235962	0.253172	1.69452	0.0722152	1.67592	ENSG00000235962	RPL7AP53
ENSG00000235963	0	0	0	0	ENSG00000235963	MCCD1P1
ENSG00000235964	0	0	0.322346	0	ENSG00000235964	FXYD6P2
ENSG00000235966	0	0.0114325	0.0103321	0.0258921	ENSG00000235966	OR12D2
ENSG00000235967	0.246201	3.75529	1.3188	3.91317	ENSG00000235967	COX5BP3
ENSG00000235968	0	0	0	0	ENSG00000235968	AC079112.1
ENSG00000235969	0	0	0	0	ENSG00000235969	CHEK2P4
ENSG00000235974	0.116278	0.228247	0.0506264	0.259768	ENSG00000235974	VN2R19P
ENSG00000235975	0	0	0	0	ENSG00000235975	Z83313.1
ENSG00000235976	0	0.429209	0.601348	1.40003	ENSG00000235976	Z80107.2
ENSG00000235978	2.64091	2.25021	4.5121	5.91261	ENSG00000235978	AC018816.1
ENSG00000235981	0	0	0	0	ENSG00000235981	AC023274.2

ENSG00000235982	2.82875	5.18871	6.37933	9.59894	ENSG00000235982	AC007875.3
ENSG00000235985	0.128048	0.290488	0.160375	0.21663	ENSG00000235985	AIF1
ENSG00000235986	0.253283	2.89752	3.85901	2.69053	ENSG00000235986	GNL1
ENSG00000235988	0	0.139689	0	0	ENSG00000235988	AC245100.5
ENSG00000235990	0	0	0.340446	0.20905	ENSG00000235990	RPL23AP20
ENSG00000235991	0	0	0.113447	0.0471657	ENSG00000235991	BX293995.1
ENSG00000235992	0	0	0	0	ENSG00000235992	GRAMD4P2
ENSG00000235993	0	0	0	0	ENSG00000235993	AC007559.1
ENSG00000235995	0	0	0	0	ENSG00000235995	UBE2V1P6
ENSG00000235998	0	0	0	0	ENSG00000235998	TAAR7P
ENSG00000236002	1.10632	1.34862	1.55465	1.78077	ENSG00000236002	CTB-75G16.1
ENSG00000236004	0.875899	1.46479	1.32263	2.31499	ENSG00000236004	AL139156.3
ENSG00000236005	0	0	0	0.194935	ENSG00000236005	AL389915.2
ENSG00000236007	0	0	0	0	ENSG00000236007	MTCO1P46
ENSG00000236011	0	0	0	0.150993	ENSG00000236011	GPANK1
ENSG00000236012	0	0	0	0	ENSG00000236012	HIGD1AP12
ENSG00000236014	5.41159	12.4717	7.56671	4.24526	ENSG00000236014	VPS52
ENSG00000236015	1.25974	1.58446	1.618	1.1877	ENSG00000236015	AC011290.2
ENSG00000236018	2.35777	4.40756	4.5238	6.43041	ENSG00000236018	AC004898.1
ENSG00000236025	0	0	0	0	ENSG00000236025	AL139135.1
ENSG00000236026	0	0	0	0	ENSG00000236026	AC009237.7
ENSG00000236027	0.0440963	0.169859	0	0.0482141	ENSG00000236027	PATE3
ENSG00000236029	1.80879	4.91969	3.05831	3.46174	ENSG00000236029	AL953854.2
ENSG00000236032	0.056369	0.05425	0	0.0614643	ENSG00000236032	OR5H14
ENSG00000236033	0	0.113461	0	0	ENSG00000236033	HCG4B
ENSG00000236035	1.23297	1.81859	1.26834	2.24284	ENSG00000236035	AL513343.1
ENSG00000236040	0.378321	0	0	0	ENSG00000236040	CHIAP1
ENSG00000236041	0	0	0	0	ENSG00000236041	COX6CP18
ENSG00000236042	0	0.146505	0.132291	0.163358	ENSG00000236042	Z74696.2
ENSG00000236044	0.460128	0.445763	0.986468	0.970793	ENSG00000236044	FABP5P2
ENSG00000236047	1.4481	1.60491	2.52993	2.98463	ENSG00000236047	AC073410.1
ENSG00000236048	0.0597674	0	0.336019	0.444793	ENSG00000236048	AC013470.3
ENSG00000236055	0.239124	0.15282	0.320729	0.643004	ENSG00000236055	RP11-423O2.2
ENSG00000236056	0.0667455	0	0.0580014	0.145207	ENSG00000236056	GAPDHP14
ENSG00000236058	0	0.841989	0.204872	0.577735	ENSG00000236058	RPL17P36
ENSG00000236060	1.15818	1.14261	0	0	ENSG00000236060	HSPB1P1
ENSG00000236062	0.103582	0.103904	0.359437	0.115342	ENSG00000236062	GSTM5P1
ENSG00000236063	7.14317	7.31203	6.05223	2.21443	ENSG00000236063	ABHD16A
ENSG00000236068	0	0.319546	0.241435	0.481379	ENSG00000236068	AC091862.1
ENSG00000236070	0	0	0	0	ENSG00000236070	CR759957.1
ENSG00000236072	0	0	0	0	ENSG00000236072	AL592043.2
ENSG00000236073	5.40934	12.8406	6.23244	12.725	ENSG00000236073	AL627311.1
ENSG00000236077	0.0325351	0.0645822	0	0	ENSG00000236077	BX119904.3
ENSG00000236079	0	0	0	0	ENSG00000236079	Z85994.2
ENSG00000236080	0	0	0	0	ENSG00000236080	YAP1P2
ENSG00000236083	0	0.78539	0.118277	0.81404	ENSG00000236083	OR13E1P
ENSG00000236085	0	0	0	0	ENSG00000236085	ACTG1P4
ENSG00000236086	0	1.33211	1.16719	6.65262	ENSG00000236086	HMGN2P28
ENSG00000236090	0	0	0.108846	0	ENSG00000236090	LDHAP3
ENSG00000236093	0	0	0	0	ENSG00000236093	PPP1R2P1
ENSG00000236097	0	0	0	0	ENSG00000236097	BNIP3P2
ENSG00000236099	0	0	0	0	ENSG00000236099	AC013403.1
ENSG00000236100	0.0259809	0.0124808	0.033827	0	ENSG00000236100	RPL7P4
ENSG00000236101	0.4705	5.39755	2.23232	3.972	ENSG00000236101	RAC1P7

ENSG00000236104	1.63379	2.92338	3.46186	1.3374	ENSG00000236104	ZBTB22
ENSG00000236105	0	0	0	0	ENSG00000236105	PRELID3BP10
ENSG00000236108	1.02114	0.645463	0.873683	2.47597	ENSG00000236108	AC093422.3
ENSG00000236110	0	0	0	0	ENSG00000236110	OR2AM1P
ENSG00000236111	0	0	0	0	ENSG00000236111	AL603882.1
ENSG00000236113	0	0	0.165242	0.129105	ENSG00000236113	MCCD1P2
ENSG00000236114	0.02989	0	0.076513	0.0631425	ENSG00000236114	AL450326.2
ENSG00000236118	0	0	0	0	ENSG00000236118	AC245517.4
ENSG00000236121	0	0	0.0402781	0	ENSG00000236121	HAUS6P2
ENSG00000236122	0	0	0	0	ENSG00000236122	UBQLN1P1
ENSG00000236123	0.658463	0.58126	0.600245	0.797907	ENSG00000236123	CEACAMP11
ENSG00000236124	0.441908	0	0	0.449227	ENSG00000236124	HMGN2P23
ENSG00000236125	0	0	0.131943	0.106102	ENSG00000236125	USP17L4
ENSG00000236126	0	0.0219476	0.0109151	0.0319741	ENSG00000236126	CT47A3
ENSG00000236131	0	0	0	0	ENSG00000236131	MED13P1
ENSG00000236132	0.341108	0.780191	0	0.700441	ENSG00000236132	AL022331.1
ENSG00000236136	1.82431	0.220146	0.0660433	0.990247	ENSG00000236136	ADORA2BP1
ENSG00000236138	0.684899	1.51014	1.02845	0.586992	ENSG00000236138	DUX4L26
ENSG00000236146	0	0	0	0	ENSG00000236146	AL353803.3
ENSG00000236148	0.595247	0.12809	0.63818	0.435858	ENSG00000236148	RPL23AP37
ENSG00000236149	3.61336	5.3999	6.92217	7.77632	ENSG00000236149	ABCF1
ENSG00000236152	0	0	0	0	ENSG00000236152	MRPS36P1
ENSG00000236155	2.79851	6.31862	8.06227	12.6378	ENSG00000236155	AL355877.1
ENSG00000236156	0	0.316665	0	0.985555	ENSG00000236156	CHCHD4P3
ENSG00000236157	0.415501	0.233766	0	0.163986	ENSG00000236157	RP11-187C18.4
ENSG00000236158	0	0	0	0	ENSG00000236158	RFC3P1
ENSG00000236159	0	0	0	0	ENSG00000236159	AL031659.1
ENSG00000236160	0	0	0	0	ENSG00000236160	AC005345.1
ENSG00000236165	0	0.42906	0.522005	0.304705	ENSG00000236165	PRADC1P1
ENSG00000236167	0	0.116883	0	0	ENSG00000236167	GAPDHP57
ENSG00000236168	0	0	0	0	ENSG00000236168	AL133466.1
ENSG00000236170	0	0	0	0	ENSG00000236170	IGHD1-1
ENSG00000236171	0	0	0	0	ENSG00000236171	RPL12P26
ENSG00000236175	0	0	0	0	ENSG00000236175	SSU72P6
ENSG00000236177	0.337328	0.571486	0.48725	0.796529	ENSG00000236177	HLA-DPA1
ENSG00000236178	0.782513	1.13555	0.0322879	2.10691	ENSG00000236178	VARS2
ENSG00000236179	0	0	0	0.0770848	ENSG00000236179	PRAMEF35P
ENSG00000236180	0.197028	0.754203	0.51067	1.04525	ENSG00000236180	AL445669.2
ENSG00000236182	0	0	0.0761624	0.094487	ENSG00000236182	AC009319.1
ENSG00000236183	0.329801	0	0.241696	0	ENSG00000236183	LY6G6C
ENSG00000236184	1.32824	1.93011	2.64572	3.62557	ENSG00000236184	TCEA1P4
ENSG00000236185	0	0	0	0	ENSG00000236185	HNRNPDLP3
ENSG00000236187	0.118822	0.62239	0.409081	0.128157	ENSG00000236187	GJA6P
ENSG00000236189	0	0.138959	1.13048	1.39592	ENSG00000236189	RPL18AP15
ENSG00000236190	0	0	0	0	ENSG00000236190	Z82210.1
ENSG00000236191	0	0.212767	0.384079	0.471099	ENSG00000236191	AC090096.1
ENSG00000236195	0	0	0.114552	0.0739426	ENSG00000236195	RNMTL1P2
ENSG00000236196	1.27859	1.68772	2.62759	1.01061	ENSG00000236196	NFKBIL1
ENSG00000236198	0.0707445	0.223083	0.277249	0.310007	ENSG00000236198	AC104395.2
ENSG00000236203	0	0	0.165242	0.129105	ENSG00000236203	MCCD1P2
ENSG00000236205	0	0.0590526	0	0.267385	ENSG00000236205	AL023773.2
ENSG00000236210	0.0327523	0	0	0	ENSG00000236210	LY6G6E
ENSG00000236211	0	0.0361463	0.0326742	0.0410867	ENSG00000236211	MTCO1P7
ENSG00000236216	0	0	0	0	ENSG00000236216	PPP1R11P1

ENSG00000236217	0	0.190296	0	0	ENSG00000236217	C1DP2
ENSG00000236221	0.088546	0.205629	0.563653	0.4093	ENSG00000236221	TNXB
ENSG00000236222	9.84991	18.5192	19.8375	7.01351	ENSG00000236222	WDR46
ENSG00000236225	0	0	0	0	ENSG00000236225	HCG4
ENSG00000236227	17.3283	30.8664	19.044	15.1809	ENSG00000236227	BRD2
ENSG00000236229	0	0.0754547	0	0.0435042	ENSG00000236229	VEZF1P1
ENSG00000236232	0.0818356	0	0	0	ENSG00000236232	MTCYBP24
ENSG00000236233	3.45825	8.74383	15.5352	12.3468	ENSG00000236233	RP11-12A20.7
ENSG00000236235	0.642251	2.08164	0.0801329	0.532618	ENSG00000236235	AP000542.1
ENSG00000236236	0.987202	0.0312502	0.0599386	0.0198334	ENSG00000236236	TNXB
ENSG00000236237	0.013508	0	0.0359938	0.0362078	ENSG00000236237	LTB
ENSG00000236238	0	0	0	0	ENSG00000236238	AC093106.1
ENSG00000236241	0.100838	0.128997	0.148774	0.509767	ENSG00000236241	AC119744.1
ENSG00000236243	0	0.0707273	0.0638984	0.0798728	ENSG00000236243	RPL6P29
ENSG00000236246	0.0813724	0.389058	0.141262	0.534493	ENSG00000236246	AC073135.1
ENSG00000236247	0.392915	1.53281	0.764473	0.765507	ENSG00000236247	RP11-292B8.2
ENSG00000236248	0	0	0	0	ENSG00000236248	AC104389.3
ENSG00000236249	0	0	0.0657764	0	ENSG00000236249	GAGE2C
ENSG00000236250	2.07367	2.232	2.56416	2.01413	ENSG00000236250	STK19
ENSG00000236251	0.232265	0.119065	0.0689541	0.135567	ENSG00000236251	HSPA1L
ENSG00000236252	0.778162	2.37337	3.57841	6.0477	ENSG00000236252	AL512605.1
ENSG00000236253	0.110394	0.194063	0.478173	0.219482	ENSG00000236253	SLC25A3P1
ENSG00000236254	0.186258	0.270332	0.113418	0.343722	ENSG00000236254	MTND4P14
ENSG00000236257	0.116233	0.055548	0.153059	0.062699	ENSG00000236257	EI24P2
ENSG00000236258	0	0	0	0	ENSG00000236258	TIMM8BP1
ENSG00000236259	0.159901	0.306802	0.486511	0.396416	ENSG00000236259	AC017083.1
ENSG00000236261	0.767064	0.419858	0	3.48919	ENSG00000236261	AC064862.4
ENSG00000236264	0	0.156659	0	0.555446	ENSG00000236264	RPL26P30
ENSG00000236265	0	0	0	0	ENSG00000236265	DDX39BP1
ENSG00000236271	4.5607	7.73356	9.63033	14.4416	ENSG00000236271	FLOT1
ENSG00000236273	0	0.0169735	0.0627602	0.0560227	ENSG00000236273	BX927320.1
ENSG00000236274	0.808045	0.945658	1.19214	1.8526	ENSG00000236274	AC004865.1
ENSG00000236277	0	0	0	0.180832	ENSG00000236277	NIPA2P5
ENSG00000236278	0	0	0	0	ENSG00000236278	PEBP1P3
ENSG00000236279	0.138741	0.473729	0.348943	1.20731	ENSG00000236279	CLEC2L
ENSG00000236280	0.534343	1.13471	3.90038	2.34514	ENSG00000236280	AC114737.2
ENSG00000236281	0	0	0	0	ENSG00000236281	NDUFB9P2
ENSG00000236284	0.0909173	0.262096	0.631437	0.295121	ENSG00000236284	VN1R31P
ENSG00000236285	0	0	0	0.299618	ENSG00000236285	NPM1P8
ENSG00000236287	38.2684	61.9354	61.7201	39.8039	ENSG00000236287	ZBED5
ENSG00000236290	0	0	0	0	ENSG00000236290	EEF1GP7
ENSG00000236294	0	0.558757	0	1.23413	ENSG00000236294	TSRM
ENSG00000236296	2.18322	7.38442	8.62831	14.3475	ENSG00000236296	GUSBP5
ENSG00000236297	0.12029	0.433133	0.340902	0.565063	ENSG00000236297	AC048351.1
ENSG00000236300	0	0	0	0	ENSG00000236300	MTND4LP12
ENSG00000236307	0	0.366907	0.32946	0.222755	ENSG00000236307	EEF1E1P1
ENSG00000236309	0	0	0	0	ENSG00000236309	RP11-508N22.10
ENSG00000236311	0.061057	0.0294587	0.132707	0.100758	ENSG00000236311	TLX1NB
ENSG00000236312	0	0	0	0.275533	ENSG00000236312	RPL34P34
ENSG00000236313	0.333291	0.507555	0.523663	0.878383	ENSG00000236313	VN1R53P
ENSG00000236315	0	0	0	0	ENSG00000236315	NCR3
ENSG00000236316	0	0.0722179	0	0.0855836	ENSG00000236316	OR7E109P
ENSG00000236317	0	0.800284	0	0.850648	ENSG00000236317	AC104333.2
ENSG00000236319	0	0	0	0	ENSG00000236319	AC105021.1

ENSG00000236320	0	0.0549617	0.0165638	0	ENSG00000236320	SLFN14
ENSG00000236323	0	0.0958755	0	0.215644	ENSG00000236323	BMP6P1
ENSG00000236325	0	0.228556	0.20654	0	ENSG00000236325	AC005300.1
ENSG00000236327	1.27245	0.800949	6.13157	6.53508	ENSG00000236327	AL831737.1
ENSG00000236330	0	0	0	0	ENSG00000236330	RPL5P9
ENSG00000236334	0.249671	0.151829	0.272663	0.172474	ENSG00000236334	PPIAL4G
ENSG00000236338	3.7474	3.00054	2.91977	4.06061	ENSG00000236338	AC015987.2
ENSG00000236339	0	0	0	0	ENSG00000236339	POM121L13P
ENSG00000236342	2.98036	0.236712	0.475127	1.40968	ENSG00000236342	ABCF1
ENSG00000236343	0.0564918	0.163104	0.0982725	0.307983	ENSG00000236343	EI24P4
ENSG00000236346	1.27859	1.68772	2.62759	1.01061	ENSG00000236346	NFKBIL1
ENSG00000236348	0.134686	0.782224	0.907638	0.343147	ENSG00000236348	PSMC1P10
ENSG00000236349	0.108363	0.364289	0.0955389	0.120025	ENSG00000236349	SUCLG2P2
ENSG00000236353	3.71521	1.35327	2.09931	1.12017	ENSG00000236353	PBX2
ENSG00000236357	0	0	0	0	ENSG00000236357	EI24P1
ENSG00000236359	0	0	0	0.0922136	ENSG00000236359	OR51B8P
ENSG00000236360	0.524245	0.575941	1.0564	0.744714	ENSG00000236360	AL445183.3
ENSG00000236362	0	0	0	0	ENSG00000236362	GAGE12F
ENSG00000236365	0	0	0	0	ENSG00000236365	AL008987.1
ENSG00000236369	0.0161927	0.00793847	0.00709454	0.0446566	ENSG00000236369	TMPOP1
ENSG00000236371	0	0.0219476	0.0109151	0.0319741	ENSG00000236371	CT47A1
ENSG00000236374	7.95E-09	0	0	0	ENSG00000236374	USP8P1
ENSG00000236375	1.35197	1.69805	1.82169	3.83784	ENSG00000236375	POU5F1P5
ENSG00000236379	0	0	0	0.209582	ENSG00000236379	ZNF736P4Y
ENSG00000236380	0	0	0.0615957	0.0788826	ENSG00000236380	VENTXP7
ENSG00000236382	0	0.120834	0	0	ENSG00000236382	KRTAP10-13P
ENSG00000236386	0	0	0.408176	0	ENSG00000236386	AC009518.3
ENSG00000236391	0	1.22125	0	0.599519	ENSG00000236391	AC092573.2
ENSG00000236395	0	0	0	0	ENSG00000236395	AC093106.2
ENSG00000236396	0	0.118739	0.0541405	0.129327	ENSG00000236396	SLC35G4
ENSG00000236397	1.16928	1.21165	2.24284	1.82345	ENSG00000236397	DDX11L2
ENSG00000236398	0	0	0.0526217	0.131845	ENSG00000236398	TAS2R39
ENSG00000236399	0.207097	0.39859	0.54705	0.957843	ENSG00000236399	TRIM40
ENSG00000236400	0	0.0759672	0	0	ENSG00000236400	KRTAP21-4P
ENSG00000236401	0	0	0	0	ENSG00000236401	SLC4A1APP2
ENSG00000236405	0	0.00827178	0.059801	0.0281478	ENSG00000236405	UBQLN1P1
ENSG00000236407	0.338398	0.324883	0.097803	0.486069	ENSG00000236407	HMGB1P18
ENSG00000236409	4.97511	4.03079	1.52427	1.47615	ENSG00000236409	NRADDP
ENSG00000236411	0.141658	0.465248	0.289226	0.201553	ENSG00000236411	NDUFAF4P3
ENSG00000236413	0	0	0	0	ENSG00000236413	AL662874.1
ENSG00000236415	0.0579419	0.0677367	0.106788	0.02249	ENSG00000236415	PPIAP9
ENSG00000236417	0	0	0	0.0349224	ENSG00000236417	CTSLP1
ENSG00000236418	3.91371	13.1631	9.19258	25.3583	ENSG00000236418	HLA-DQA1
ENSG00000236420	0	0	0	0	ENSG00000236420	CHCHD3P1
ENSG00000236422	0	0.0149857	0	0	ENSG00000236422	BX927214.1
ENSG00000236424	0	0	0.0341145	0	ENSG00000236424	TSPY10
ENSG00000236425	0	0	0	0	ENSG00000236425	AC069213.2
ENSG00000236428	3.1414	2.68498	0	0	ENSG00000236428	PPP1R18
ENSG00000236429	0	0	0	0	ENSG00000236429	GPM6BP2
ENSG00000236430	0.085644	0.206201	0.436477	0.0521792	ENSG00000236430	KRT8P29
ENSG00000236431	1.47123	1.11385	3.62114	2.70835	ENSG00000236431	AC009237.8
ENSG00000236433	0	0	0.355822	0.843537	ENSG00000236433	RPL37P21
ENSG00000236435	0	0.0704158	0.430076	0	ENSG00000236435	TSPY12P
ENSG00000236439	0	0.515851	0.556108	2.09824	ENSG00000236439	AC099336.2

ENSG00000236440	0	0	0	0	ENSG00000236440	AC117947.1
ENSG00000236441	0	0	0	0	ENSG00000236441	DDX39BP1
ENSG00000236442	0	0	0	0.176938	ENSG00000236442	ANKRD54P1
ENSG00000236443	1.10486	0.54819	1.3866	1.30105	ENSG00000236443	PSMB8
ENSG00000236444	0	0	0	0.201663	ENSG00000236444	UBE2L5P
ENSG00000236446	0.044551	0.152141	0	0.340944	ENSG00000236446	CT47B1
ENSG00000236450	0	0.530278	0	0	ENSG00000236450	AL590399.6
ENSG00000236456	0	0	0.114987	0	ENSG00000236456	AL035458.1
ENSG00000236459	0	0	0.0633394	0	ENSG00000236459	HNRNPA1P22
ENSG00000236460	0	0.874768	0	0.961839	ENSG00000236460	SNX2P2
ENSG00000236468	0.0441399	0	0	0.0482615	ENSG00000236468	AC099335.1
ENSG00000236473	0.207426	0.0788051	0.0600806	0.0751695	ENSG00000236473	KRT43P
ENSG00000236474	0.0456895	0.351963	0.238597	0.449444	ENSG00000236474	GCNT1P1
ENSG00000236475	0	0	0	0.0189286	ENSG00000236475	TRIM26BP
ENSG00000236476	0	0	0	0	ENSG00000236476	AL593856.1
ENSG00000236477	0	0	0.208358	0	ENSG00000236477	RPS24P1
ENSG00000236478	0.636957	1.58866	1.75256	2.3962	ENSG00000236478	AC012513.2
ENSG00000236480	0.114253	0	0	0	ENSG00000236480	PKMP1
ENSG00000236483	0.228373	0.21959	0.462933	0.414402	ENSG00000236483	MTND2P40
ENSG00000236484	0	0.101095	0.0913007	0.115924	ENSG00000236484	RRM2P2
ENSG00000236487	0	0.384069	0.520301	0.638618	ENSG00000236487	AC079168.2
ENSG00000236488	0	0	0	0	ENSG00000236488	PPP1R2P1
ENSG00000236489	1.71143	2.67729	3.34516	2.93002	ENSG00000236489	AC133473.1
ENSG00000236490	3.00406	0.67659	7.30993	13.8232	ENSG00000236490	TAPBP
ENSG00000236491	0	0.0436827	0	0.0491869	ENSG00000236491	AC234771.4
ENSG00000236493	0.216286	0.216055	0.197365	0.62113	ENSG00000236493	EIF2S2P3
ENSG00000236496	0.0661039	0.0604057	0.0587445	0.236794	ENSG00000236496	GPS2P1
ENSG00000236500	0	0	0	0	ENSG00000236500	CD24P1
ENSG00000236503	0	0	0	0	ENSG00000236503	AC009784.1
ENSG00000236504	0.0768009	0	0.0667116	0.164887	ENSG00000236504	AC087499.6
ENSG00000236505	0	0	1.71669	0	ENSG00000236505	AL356379.1
ENSG00000236509	0	0	0	0	ENSG00000236509	RPL21P133
ENSG00000236512	0	0.665118	0	0.184883	ENSG00000236512	AL390026.1
ENSG00000236515	3.87478	3.97894	4.95943	2.86778	ENSG00000236515	ZBTB9
ENSG00000236516	0.891813	1.0992	1.12221	2.48356	ENSG00000236516	KLF2P4
ENSG00000236518	0	0	0	0	ENSG00000236518	RP13-77O11.7
ENSG00000236521	0.0330852	0.0317573	0.0287042	0.01811	ENSG00000236521	NPAP1P4
ENSG00000236523	1.9156	3.5982	3.84019	6.04314	ENSG00000236523	NPM1P40
ENSG00000236527	0	0	0	0.302603	ENSG00000236527	ARF4P2
ENSG00000236529	0.501882	1.1578	1.18293	0.27025	ENSG00000236529	AC093582.1
ENSG00000236530	0.290441	0.421537	0.126491	0.652844	ENSG00000236530	KPNA2P1
ENSG00000236533	0.214792	0	0.365674	0	ENSG00000236533	AC009413.1
ENSG00000236534	0	0	0	0	ENSG00000236534	H3F3BP1
ENSG00000236538	2.43744	2.7034	5.58194	2.90424	ENSG00000236538	ZNF863P
ENSG00000236539	6.20137	14.4125	13.821	24.3602	ENSG00000236539	HNRNPA1P54
ENSG00000236541	0.261594	0	0.0568414	0.0711595	ENSG00000236541	VN2R9P
ENSG00000236542	0	1.07267	0.484124	0.452932	ENSG00000236542	MED28P7
ENSG00000236547	0	0.0169735	0.0627602	0.0560227	ENSG00000236547	CR753864.1
ENSG00000236549	1.20414	3.49559	1.96578	4.00282	ENSG00000236549	RPS27AP7
ENSG00000236550	0	0	0	0	ENSG00000236550	AL109809.3
ENSG00000236552	0.257747	0.401739	0	0.462988	ENSG00000236552	RPL13AP5
ENSG00000236554	0.181003	0.21787	0.356291	0.519963	ENSG00000236554	ASNSP3
ENSG00000236555	0	1.17379	0.443209	0.511547	ENSG00000236555	AC115115.1
ENSG00000236560	5.57927	0.587398	9.20817	3.91993	ENSG00000236560	PPP1R11

ENSG00000236561	0.777715	0.983953	1.07424	1.69929	ENSG00000236561	MOG
ENSG00000236562	0	0	0	0	ENSG00000236562	AC116049.1
ENSG00000236564	2.72816	4.98167	5.25939	9.84004	ENSG00000236564	YWHAQP5
ENSG00000236565	0	0	0	0	ENSG00000236565	HNRNPA3P5
ENSG00000236567	0.0292121	0.196855	0.177961	0.449043	ENSG00000236567	TCF3P1
ENSG00000236569	0.135056	0	0	0.153826	ENSG00000236569	HNRNPA1P73
ENSG00000236570	0	0	0	0	ENSG00000236570	RAD23BP1
ENSG00000236571	0	0	0	0	ENSG00000236571	AC245102.2
ENSG00000236574	0.848403	0	0	0.864603	ENSG00000236574	AC092634.6
ENSG00000236575	1.44905	0.989148	0	0	ENSG00000236575	ZNF26
ENSG00000236576	0.0828423	0.451818	0.552469	1.23483	ENSG00000236576	AC241520.1
ENSG00000236577	0.645454	6.35144	0.538806	2.23834	ENSG00000236577	SNRPGP14
ENSG00000236580	0	0	0.273873	0	ENSG00000236580	AC073626.2
ENSG00000236582	0	0.0385649	0	0	ENSG00000236582	PRPF38AP2
ENSG00000236583	0.556407	1.63557	1.08367	3.89202	ENSG00000236583	AP004290.1
ENSG00000236584	0	0	0	0	ENSG00000236584	BX664726.3
ENSG00000236590	3.92E-06	0	0	2.80E-06	ENSG00000236590	MTATP6P4
ENSG00000236592	0	0	0	0	ENSG00000236592	S100A11P2
ENSG00000236594	0	0	0	0	ENSG00000236594	RPS27AP14
ENSG00000236595	0	0	0	0	ENSG00000236595	MED15P5
ENSG00000236596	0	0	0.0807832	0.100844	ENSG00000236596	AC092568.1
ENSG00000236597	0	0	0	0	ENSG00000236597	IGHD7-27
ENSG00000236599	0	0	0	0	ENSG00000236599	ELOCP26
ENSG00000236603	0.051091	0	0.0451445	0.0287014	ENSG00000236603	RANP1
ENSG00000236604	0	0	0	0	ENSG00000236604	LYPLA2P3
ENSG00000236606	0	0.197935	0	0	ENSG00000236606	AC022028.1
ENSG00000236607	0	0	0	0	ENSG00000236607	EEF1DP8
ENSG00000236608	0	0	0	0	ENSG00000236608	EIF4A1P6
ENSG00000236609	0.322978	0.366371	0.342716	1.40607	ENSG00000236609	ZNF853
ENSG00000236610	0	0.126433	0	0.14303	ENSG00000236610	SOCS5P1
ENSG00000236612	0	0	0	0	ENSG00000236612	KRTAP19-11P
ENSG00000236614	0.00944618	0.0363638	0.0164323	0	ENSG00000236614	ZNF90P2
ENSG00000236615	0.603514	1.13166	0.506411	3.06692	ENSG00000236615	AC010086.2
ENSG00000236616	0	0	0	0.120793	ENSG00000236616	BAK1P2
ENSG00000236619	2.13296	1.99934	1.44905	2.25545	ENSG00000236619	AL844851.3
ENSG00000236620	0	0	0	0	ENSG00000236620	XKRYP3
ENSG00000236621	0.142449	0.13699	0	0.0773974	ENSG00000236621	OR52E1
ENSG00000236624	1.61599	3.73621	4.60071	4.34072	ENSG00000236624	CCDC163P
ENSG00000236625	0.437181	0.183949	0.55803	0.564029	ENSG00000236625	C4B
ENSG00000236626	0	0.191616	0.18815	0.0402337	ENSG00000236626	MTND5P17
ENSG00000236629	0	0	0	0	ENSG00000236629	MTCO3P1
ENSG00000236632	19.219	6.72749	2.56494	0.358481	ENSG00000236632	HLA-E
ENSG00000236636	0	1.62394	1.14478	1.31086	ENSG00000236636	AL627308.2
ENSG00000236637	0.239347	0.353364	0.505292	0.712394	ENSG00000236637	IFNA4
ENSG00000236638	0	0.527497	0.285692	1.25993	ENSG00000236638	AC006455.7
ENSG00000236642	0	0	0	0	ENSG00000236642	MICF
ENSG00000236646	0.867263	0.413156	1.10848	2.23981	ENSG00000236646	LAMTOR5P1
ENSG00000236647	0	0	0	0	ENSG00000236647	AC009947.2
ENSG00000236649	3.12559	3.60811	4.85307	3.2767	ENSG00000236649	PPT2
ENSG00000236654	0	0	0.601712	1.79112	ENSG00000236654	AC079780.1
ENSG00000236655	0.512484	0.490882	0.590783	1.45571	ENSG00000236655	AC023347.2
ENSG00000236660	0	0	0	0	ENSG00000236660	FAM90A7P
ENSG00000236667	0	0.479945	0.433277	0.534062	ENSG00000236667	AC104076.2
ENSG00000236669	0.0758406	0.680203	0.499942	0.782898	ENSG00000236669	AC006372.1

ENSG00000236670	0.412873	0.574653	0.736285	2.10287	ENSG00000236670	KRT18P5
ENSG00000236672	0	0	0.0379426	0	ENSG00000236672	C6orf10
ENSG00000236674	0.0433226	0.292534	0.113427	0.237247	ENSG00000236674	AL049636.1
ENSG00000236675	0.0566686	0.0141613	0.0404738	0.0282926	ENSG00000236675	MTX1P1
ENSG00000236679	0	0	0	0.376075	ENSG00000236679	RPL23AP24
ENSG00000236680	0	0.0927478	0.126391	0.0526507	ENSG00000236680	AL356000.1
ENSG00000236681	0	1.23371	1.19643	1.53811	ENSG00000236681	DSTNP5
ENSG00000236683	0.469761	0.120024	0.659887	0.280429	ENSG00000236683	HMGA1P1
ENSG00000236684	34.3472	94.5075	79.6773	159.983	ENSG00000236684	AL645728.3
ENSG00000236686	0.0480989	0.0465133	0.0418858	0.477107	ENSG00000236686	BZW1P1
ENSG00000236688	0	0	0	0	ENSG00000236688	HLA-N
ENSG00000236689	0	0	0	0.108229	ENSG00000236689	MTCO2P21
ENSG00000236690	0	0	0.626527	0	ENSG00000236690	AC007274.2
ENSG00000236691	0	0	0	0	ENSG00000236691	NDUFA4P2
ENSG00000236692	0.024824	0.0730334	0.166529	0.170461	ENSG00000236692	AC099654.3
ENSG00000236693	0	0.223915	0.211819	0.261232	ENSG00000236693	HLA-DPB1
ENSG00000236695	0	0	0	0	ENSG00000236695	HNRNPA1P47
ENSG00000236697	0.26308	0.0707527	0.25712	0.0988522	ENSG00000236697	GPSM3
ENSG00000236698	0.732233	2.69622	0.132272	1.50337	ENSG00000236698	EIF1AXP1
ENSG00000236699	3.04118	2.92452	5.58864	7.63956	ENSG00000236699	ARHGEF38
ENSG00000236701	0.128887	0.245232	0.553262	0.572207	ENSG00000236701	AL512594.1
ENSG00000236704	0	0	0.04343	0.0545018	ENSG00000236704	CNOT4P1
ENSG00000236706	0	0	0	0	ENSG00000236706	HLA-U
ENSG00000236710	0.0909173	0.436827	0.0789296	0.397861	ENSG00000236710	AC108448.2
ENSG00000236712	0.239476	0	0	0	ENSG00000236712	AC079448.1
ENSG00000236713	0.239476	0.457111	0.41308	0.518283	ENSG00000236713	AL356292.1
ENSG00000236718	0	0	0	0	ENSG00000236718	RBMY2QP
ENSG00000236722	0	0	0	0.259182	ENSG00000236722	AC116036.1
ENSG00000236727	0.00724298	0	0	0.00789492	ENSG00000236727	MICC
ENSG00000236731	0	0	0	0	ENSG00000236731	AL135929.2
ENSG00000236732	0.335704	0.633974	0.143084	0.176393	ENSG00000236732	AC094019.1
ENSG00000236735	0	0	0	0	ENSG00000236735	RPL31P63
ENSG00000236736	0	0	0	0	ENSG00000236736	UQCRC2P1
ENSG00000236737	0	0	0	0	ENSG00000236737	GAGE12B
ENSG00000236739	0	0	0.148989	0.179854	ENSG00000236739	CLIC4P1
ENSG00000236741	0	0	0	0	ENSG00000236741	Z98751.2
ENSG00000236742	0	0	0	0	ENSG00000236742	CTD-2340F8.3
ENSG00000236745	1.61152	3.50811	3.19931	5.33016	ENSG00000236745	YRDCP2
ENSG00000236746	0.314537	0	0	0	ENSG00000236746	HLA-W
ENSG00000236748	0	0	0	0	ENSG00000236748	AC009500.1
ENSG00000236750	0.364225	0.257851	0	0.851989	ENSG00000236750	AC009237.9
ENSG00000236759	0.78392	2.16977	1.84773	2.39349	ENSG00000236759	EHMT2
ENSG00000236761	0	0.150668	0.235999	0.0609689	ENSG00000236761	CTAGE9
ENSG00000236762	0	0	0	0	ENSG00000236762	RPL19P16
ENSG00000236763	0	0	0	0	ENSG00000236763	TRMT112P4
ENSG00000236764	0	0	0	0	ENSG00000236764	COX7A2P2
ENSG00000236765	0	0	0.358605	4.82993	ENSG00000236765	DXO
ENSG00000236768	0	0.269408	0	0.150882	ENSG00000236768	AC124916.1
ENSG00000236770	0.0743771	0	0	0	ENSG00000236770	AC079325.1
ENSG00000236771	0	0	0.00828591	0	ENSG00000236771	CR388415.3
ENSG00000236773	0	0	0	0	ENSG00000236773	AC092809.3
ENSG00000236775	0	0.136672	0.0823547	0.206787	ENSG00000236775	AL512637.2
ENSG00000236776	0	0.32931	0	2.19884	ENSG00000236776	RPL21P23
ENSG00000236777	0	0.789965	0.285267	0.539621	ENSG00000236777	AL157831.1

ENSG00000236779	0.453853	1.62411	1.45132	1.8119	ENSG00000236779	AL512306.1
ENSG00000236783	0	0.262949	0	0.289479	ENSG00000236783	RPS15AP27
ENSG00000236785	0	0	0	0	ENSG00000236785	SDR42E1P5
ENSG00000236786	0	0	0	0	ENSG00000236786	TSPY15P
ENSG00000236787	0	0	0	1.6129	ENSG00000236787	RP11-592B15.6
ENSG00000236791	0	0	0	0	ENSG00000236791	OR2AI1P
ENSG00000236792	0	0	0	0	ENSG00000236792	AL513175.2
ENSG00000236794	1.82059	1.09661	0.97389	0.485812	ENSG00000236794	BCRP8
ENSG00000236796	0.151929	0.0975064	0.220322	0.221165	ENSG00000236796	AL157884.3
ENSG00000236797	0	0.169055	0.305327	0.187898	ENSG00000236797	SPA17P1
ENSG00000236798	0.0999439	0.239336	0.563214	0.38701	ENSG00000236798	CR788282.1
ENSG00000236801	0.52385	2.82133	0.307399	3.56325	ENSG00000236801	RPL24P8
ENSG00000236802	0.310039	0.93125	0	0	ENSG00000236802	B3GALT4
ENSG00000236803	0.0698397	0.201858	0.091259	0.155636	ENSG00000236803	SDAD1P4
ENSG00000236804	0.104291	0.264228	0.455814	0.48339	ENSG00000236804	RPS3AP12
ENSG00000236806	0.0408189	0	0.141784	0.486791	ENSG00000236806	AC242426.2
ENSG00000236807	0.317633	0	0	0	ENSG00000236807	AC092066.1
ENSG00000236808	1.68418	1.90335	2.99782	1.76915	ENSG00000236808	ZNRD1
ENSG00000236809	0	0.489944	0.638083	0.511197	ENSG00000236809	SNX25P1
ENSG00000236811	0.309509	0.714734	0.538154	1.1462	ENSG00000236811	GAPDHP2
ENSG00000236813	0	0.0804462	0	0.163662	ENSG00000236813	BTF3P8
ENSG00000236814	0	0	0.358911	0	ENSG00000236814	AC046176.1
ENSG00000236816	0	0	0	0	ENSG00000236816	ANKRD20A7P
ENSG00000236818	0	0	0	0	ENSG00000236818	ARL5AP2
ENSG00000236825	0	0	0	0	ENSG00000236825	RAB28P2
ENSG00000236826	1.68931	2.39654	1.67597	1.42651	ENSG00000236826	LSM2
ENSG00000236829	4.59168	6.46196	7.15991	10.9511	ENSG00000236829	Z97634.1
ENSG00000236831	0	0	0	0	ENSG00000236831	YME1L1P1
ENSG00000236832	0.419	3.40427	2.23076	2.44045	ENSG00000236832	AC073465.3
ENSG00000236843	0.463793	1.24111	0.515031	0.408103	ENSG00000236843	NRM
ENSG00000236844	0	0	0	0	ENSG00000236844	AC069213.3
ENSG00000236847	0.416941	0.345954	1.44216	1.21478	ENSG00000236847	AC018892.2
ENSG00000236848	0	0.95176	1.16108	0.453635	ENSG00000236848	RPL23AP95
ENSG00000236851	0	0	0	0	ENSG00000236851	DHFRP2
ENSG00000236852	0.0570364	0	0.0991656	0.187263	ENSG00000236852	BX322784.1
ENSG00000236853	0.206325	0.33122	0.478106	0.373884	ENSG00000236853	OR2R1P
ENSG00000236857	0	0	0	0.569658	ENSG00000236857	RAP1BP1
ENSG00000236860	0	0	0.307219	0	ENSG00000236860	RPL39P29
ENSG00000236862	0.506814	0	0	0	ENSG00000236862	RPS20P24
ENSG00000236863	0.663899	1.74879	1.14936	2.83101	ENSG00000236863	RPL23AP23
ENSG00000236867	1.5224	3.50927	6.47714	6.84998	ENSG00000236867	Z98885.1
ENSG00000236870	0	0	0	0	ENSG00000236870	AL121882.1
ENSG00000236872	0	0.31143	0.289057	0.961509	ENSG00000236872	AL451136.1
ENSG00000236873	7.66957	11.1713	6.87323	0	ENSG00000236873	AGPAT1
ENSG00000236875	0.848917	0.675773	1.8701	1.86534	ENSG00000236875	DDX11L5
ENSG00000236876	0	0	0	0	ENSG00000236876	TMSB4XP1
ENSG00000236877	0	0	0	0	ENSG00000236877	SETD6P1
ENSG00000236878	0	0	0.0895038	0.111365	ENSG00000236878	MTATP6P26
ENSG00000236880	0	0	0	0	ENSG00000236880	Z85995.1
ENSG00000236881	0.639125	0	0	0	ENSG00000236881	BX005428.3
ENSG00000236882	4.11144	6.38512	6.33005	6.91271	ENSG00000236882	LINC01554
ENSG00000236884	0	3.40E-05	0	1.86E-05	ENSG00000236884	HLA-DRB1
ENSG00000236887	0.382947	0.183959	0.162575	0.399905	ENSG00000236887	AL357055.2
ENSG00000236888	0	0	0	0	ENSG00000236888	RPS20P5

ENSG00000236890	3.10952	3.6619	5.13567	5.6324	ENSG00000236890	AC016027.5
ENSG00000236893	0.0978959	0.141148	0	0.0531361	ENSG00000236893	ASS1P7
ENSG00000236895	2.11447	0	1.93356	1.13112	ENSG00000236895	GTF2H4
ENSG00000236898	0	0	0	0	ENSG00000236898	HLA-DPA2
ENSG00000236900	3.79335	6.49941	4.18886	10.7299	ENSG00000236900	TIMM9P1
ENSG00000236902	0.0302896	0.0578806	0	0.032054	ENSG00000236902	LY6G6D
ENSG00000236905	0.485491	0.894962	0.280297	0.51883	ENSG00000236905	AC104333.3
ENSG00000236907	0.914453	1.05206	1.19901	2.20444	ENSG00000236907	AC023141.9
ENSG00000236909	0	0	0	0	ENSG00000236909	AL662791.3
ENSG00000236910	0	0.0184226	0	0	ENSG00000236910	ZNF70P1
ENSG00000236913	0	0	0	0	ENSG00000236913	AC025750.2
ENSG00000236917	0	0	0.0435135	0	ENSG00000236917	DNAJA1P2
ENSG00000236918	0.0144218	0	0.05347	0	ENSG00000236918	BX908738.5
ENSG00000236919	0	0	0	0	ENSG00000236919	AC109635.1
ENSG00000236925	0.013508	0	0.0359938	0.0362078	ENSG00000236925	LTB
ENSG00000236926	0.0558802	0	0.0241408	0.0296507	ENSG00000236926	ZDHHC20P1
ENSG00000236927	0	0	0	0	ENSG00000236927	OR14J1
ENSG00000236928	0.980967	1.9804	1.46057	2.573	ENSG00000236928	AC008267.4
ENSG00000236929	0	0.27794	0.502605	0.316598	ENSG00000236929	AC112498.1
ENSG00000236930	0	0.157512	0	0	ENSG00000236930	AC099782.1
ENSG00000236931	0.163876	0.157017	0	0.174778	ENSG00000236931	BX664608.1
ENSG00000236932	0.331594	0	0	0	ENSG00000236932	CEACAMP8
ENSG00000236937	0	0	0.224642	0	ENSG00000236937	PTGES3P4
ENSG00000236939	0	1.50841	0	0.985772	ENSG00000236939	BAALC-AS2
ENSG00000236940	0.170828	0	0.147696	0.363927	ENSG00000236940	AL589765.3
ENSG00000236941	0.706504	1.75348	1.83216	4.14728	ENSG00000236941	AC106872.1
ENSG00000236942	1.12829	2.63432	2.55041	3.10224	ENSG00000236942	AC096533.1
ENSG00000236944	0	0.23574	0	0.260334	ENSG00000236944	CCDC58P2
ENSG00000236946	0	0	0	0	ENSG00000236946	HNRNPA1P70
ENSG00000236949	1.68418	2.37659	1.53232	0.855655	ENSG00000236949	ZNRD1
ENSG00000236956	0	0	0.0347613	0	ENSG00000236956	NF1P8
ENSG00000236957	1.59214	2.87831	2.92124	3.35817	ENSG00000236957	AL139010.1
ENSG00000236959	0	0	0	0.211699	ENSG00000236959	SULT1D1P
ENSG00000236960	0	0	0	0	ENSG00000236960	AL354695.1
ENSG00000236965	0.0670043	0	0	0.145761	ENSG00000236965	OR52N3P
ENSG00000236966	0	0	0	0	ENSG00000236966	AL773545.2
ENSG00000236967	1.24629	0	0	0	ENSG00000236967	RNF39
ENSG00000236969	0.434723	0	0.129069	0	ENSG00000236969	GGT8P
ENSG00000236971	0	0	0	0	ENSG00000236971	SUMO2P1
ENSG00000236972	0	0	0	0	ENSG00000236972	FABP5P1
ENSG00000236973	0.185216	0.475215	0.053683	0.757204	ENSG00000236973	GAPDHP51
ENSG00000236976	0	0	0	0	ENSG00000236976	AC091685.2
ENSG00000236978	0	0	0	0	ENSG00000236978	AC073873.1
ENSG00000236979	0	0	0	0	ENSG00000236979	NCR3
ENSG00000236980	0.210957	0.289127	0.843608	0.24343	ENSG00000236980	C3orf84
ENSG00000236981	0	0	0.0580758	0	ENSG00000236981	OR10G9
ENSG00000236982	0	0	0	0	ENSG00000236982	BLOC1S2P1
ENSG00000236984	0	0	0	0	ENSG00000236984	Xxbac-B33L19.10
ENSG00000236987	0	0	0.716799	0	ENSG00000236987	NDUFA5P8
ENSG00000236988	0.937853	2.27391	2.32917	5.68595	ENSG00000236988	AL359641.1
ENSG00000236992	0.341548	0	0.434972	0.889648	ENSG00000236992	RPL12P12
ENSG00000236993	0	0	0	0	ENSG00000236993	GAPDHP21
ENSG00000236994	0	0	0	0	ENSG00000236994	YBX1P9
ENSG00000236998	0.0953271	0.229459	0.0832848	0.36451	ENSG00000236998	AL354794.2

ENSG00000237000	0	0.285436	0	0	ENSG00000237000	PTMAP6
ENSG00000237003	0	0.884536	1.33196	1.29619	ENSG00000237003	AC126124.2
ENSG00000237004	1.87747	1.45576	1.13653	1.32841	ENSG00000237004	ZNRF2P1
ENSG00000237005	0	0	0	0	ENSG00000237005	HIGD1AP15
ENSG00000237007	0.183795	0.360844	0.792356	0.410263	ENSG00000237007	KRT18P52
ENSG00000237008	0	0	0	0	ENSG00000237008	LAPTM4BP1
ENSG00000237012	0.461121	0.704371	0.620046	0.33653	ENSG00000237012	C6orf136
ENSG00000237014	0	0	0	0	ENSG00000237014	AC004074.1
ENSG00000237016	0.628876	0.745202	0	0.495356	ENSG00000237016	AC013410.1
ENSG00000237020	0	0	0	0	ENSG00000237020	IGHD1-20
ENSG00000237022	3.0538	64.9803	3.92587	0.357868	ENSG00000237022	HLA-C
ENSG00000237023	0.780819	1.53003	1.04504	1.5234	ENSG00000237023	USP9YP3
ENSG00000237024	0	0	0	0	ENSG00000237024	RPL21P33
ENSG00000237025	1.14659	1.82281	1.61066	3.27748	ENSG00000237025	AL121601.2
ENSG00000237026	0	0.619509	0	0	ENSG00000237026	AC104073.2
ENSG00000237032	0.143067	0	0	0.15541	ENSG00000237032	RPSAP7
ENSG00000237033	0	0	0	0	ENSG00000237033	CASP3P1
ENSG00000237034	0.00724298	0	0	0.00789492	ENSG00000237034	MICC
ENSG00000237038	0	0	0	0	ENSG00000237038	USP17L8
ENSG00000237039	0	0	0	0	ENSG00000237039	AC018738.1
ENSG00000237040	0	0	0	0	ENSG00000237040	DPH3P2
ENSG00000237041	0	2.322	1.04854	0.858939	ENSG00000237041	AC007679.3
ENSG00000237042	0	0	0	0	ENSG00000237042	MICG
ENSG00000237043	0	0	0	0	ENSG00000237043	AL929561.5
ENSG00000237046	0.00462984	0.00875722	0.0165025	0	ENSG00000237046	TRIM40
ENSG00000237049	0	0	0	0	ENSG00000237049	RPL34P1
ENSG00000237051	5.55225	0.656342	18.2259	0.829038	ENSG00000237051	GABBR1
ENSG00000237052	0.26308	0.0707527	0.25712	0.0988522	ENSG00000237052	GPSM3
ENSG00000237053	0	0.0419653	0.0758018	0.190451	ENSG00000237053	FUCA1P1
ENSG00000237055	0	0	0	0	ENSG00000237055	MTCO1P48
ENSG00000237056	1.63379	2.92338	3.46186	1.3374	ENSG00000237056	ZBTB22
ENSG00000237064	0.0649144	0	0.279641	0.140129	ENSG00000237064	EIF3IP1
ENSG00000237065	0	0	0	0	ENSG00000237065	NANOGP4
ENSG00000237068	0	0	0.0649066	0.243353	ENSG00000237068	RPL5P2
ENSG00000237071	1.0354	1.51916	1.45742	0.989143	ENSG00000237071	TRIM27
ENSG00000237072	0	0	0	0	ENSG00000237072	AL161727.1
ENSG00000237075	0	0	0.260716	0	ENSG00000237075	RP11-497H16.2
ENSG00000237077	0	0	1.22466	0	ENSG00000237077	AC105399.1
ENSG00000237078	3.18119	38.4044	43.4104	34.0233	ENSG00000237078	AC007272.1
ENSG00000237082	2.53582	5.90397	4.80235	2.83912	ENSG00000237082	COX5BP6
ENSG00000237083	0.348685	1.98289	2.08722	1.08554	ENSG00000237083	AL162725.1
ENSG00000237085	0	0	0	0	ENSG00000237085	AC127391.1
ENSG00000237086	0	0	0	0	ENSG00000237086	RBPJP2
ENSG00000237088	0	1.53097	1.35519	2.10989	ENSG00000237088	AL163193.1
ENSG00000237089	0	0	0	0.155917	ENSG00000237089	PCNPP4
ENSG00000237090	0.223741	0.0429972	0.0799227	0.303979	ENSG00000237090	AL512353.3
ENSG00000237095	0.600581	2.71671	1.21032	1.35815	ENSG00000237095	MDC1
ENSG00000237098	0	0	0.117234	0	ENSG00000237098	HLA-T
ENSG00000237099	0	0	0	0	ENSG00000237099	GYG1P2
ENSG00000237100	0.461121	0.704371	0.620046	0.33653	ENSG00000237100	C6orf136
ENSG00000237102	0.137342	0.00229023	0	0	ENSG00000237102	AC040160.1
ENSG00000237103	0	0	0	0	ENSG00000237103	NCR3
ENSG00000237106	0.338206	0	1.14671	0.678971	ENSG00000237106	FABP5P15
ENSG00000237107	0	0	0	0	ENSG00000237107	AL591473.1

ENSG00000237109	0	0	0	0	ENSG00000237109	RPL21P111
ENSG00000237110	0	0.169743	0.41054	1.28255	ENSG00000237110	TAAR9
ENSG00000237111	0	0	0	0	ENSG00000237111	IGHJ3P
ENSG00000237112	2.04236	3.60359	1.27243	6.09971	ENSG00000237112	GABBR1
ENSG00000237114	0	0	0	6.74485	ENSG00000237114	CDSN
ENSG00000237115	0.0228128	0.0664702	0	0.328187	ENSG00000237115	AL139805.2
ENSG00000237118	0	0.167098	0.234522	0.350789	ENSG00000237118	CYP2F2P
ENSG00000237120	0	0	0	0	ENSG00000237120	CR933540.3
ENSG00000237121	0	0	0	0	ENSG00000237121	PIEZO1P2
ENSG00000237122	0	0	0	0	ENSG00000237122	FAM90A19P
ENSG00000237123	0	2.10801	1.16133	18.9708	ENSG00000237123	CDSN
ENSG00000237124	0.424463	0.20543	1.10441	0.80138	ENSG00000237124	MTND2P11
ENSG00000237127	0	0	0	0	ENSG00000237127	AC245028.2
ENSG00000237129	0.101553	0.0975577	0.0881096	0.219361	ENSG00000237129	MTCYBP34
ENSG00000237130	0.48832	1.62063	1.07054	1.27906	ENSG00000237130	MRPS6P2
ENSG00000237131	0	0	0	0	ENSG00000237131	AL021397.1
ENSG00000237132	0	0	0	0	ENSG00000237132	VN2R6P
ENSG00000237135	0.0292469	0.338227	0.203905	0.385012	ENSG00000237135	DDX10P1
ENSG00000237136	0.694639	0	1.18775	0.743183	ENSG00000237136	C4orf51
ENSG00000237137	0	0	0	0	ENSG00000237137	AL159169.1
ENSG00000237139	0	0.734372	1.32199	2.00112	ENSG00000237139	RPS26P41
ENSG00000237140	0	0.269524	0.46377	0.292084	ENSG00000237140	HSPE1P16
ENSG00000237141	0	0	0	0.327456	ENSG00000237141	DNAJC19P1
ENSG00000237145	0	0	0	0	ENSG00000237145	MTCO3P1
ENSG00000237148	0	0	0	0	ENSG00000237148	HIGD1AP2
ENSG00000237154	0.846965	0.506403	1.19924	1.09211	ENSG00000237154	MCFD2P1
ENSG00000237155	4.65E-10	35.1599	5.83678	11.0089	ENSG00000237155	IER3
ENSG00000237156	0.087419	0.412726	0	0.298453	ENSG00000237156	PTMAP1
ENSG00000237158	0	1.84739	0.877647	1.65915	ENSG00000237158	AL353718.1
ENSG00000237160	0	0.790588	0	0	ENSG00000237160	AC004022.2
ENSG00000237161	0.153258	0.366418	0.363074	0.34104	ENSG00000237161	AC068446.1
ENSG00000237162	1.97074	2.15547	2.97053	4.40609	ENSG00000237162	AC007098.1
ENSG00000237163	0	0	0	0	ENSG00000237163	AC099794.2
ENSG00000237164	0	0	0	0	ENSG00000237164	SLC25A15P2
ENSG00000237165	0	0.262778	1.07516	4.26745	ENSG00000237165	CDSN
ENSG00000237168	2.2733	10.9241	9.0484	7.10769	ENSG00000237168	RP11-353N4.3
ENSG00000237169	0	0	0	0	ENSG00000237169	RPL12P27
ENSG00000237170	0.61051	0.937252	0.634775	1.96881	ENSG00000237170	RPS7P15
ENSG00000237171	0	0	0	0	ENSG00000237171	AC005297.3
ENSG00000237172	6.18995	6.44918	6.26827	6.67524	ENSG00000237172	B3GNT9
ENSG00000237173	0	0	0	0	ENSG00000237173	AC099796.2
ENSG00000237175	0	0.439712	0	0	ENSG00000237175	NME1P1
ENSG00000237176	0	0	0	0	ENSG00000237176	AC079905.1
ENSG00000237178	1.09487	1.5517	0.566841	0.694496	ENSG00000237178	AC019080.2
ENSG00000237180	0	0	0	0	ENSG00000237180	CYP46A4P
ENSG00000237182	0	0	0	0	ENSG00000237182	BX276092.6
ENSG00000237183	0	0	0	0	ENSG00000237183	KRTAP9-10P
ENSG00000237185	0	0	0	0	ENSG00000237185	VN1R66P
ENSG00000237186	0	0	0	0.120494	ENSG00000237186	AC092418.1
ENSG00000237190	6.96255	10.2016	9.54347	8.46132	ENSG00000237190	CDKN2AIPNL
ENSG00000237191	0	0	0	0	ENSG00000237191	RP11-120E5.2
ENSG00000237192	0	0	0	0	ENSG00000237192	TRIM10
ENSG00000237193	0	0	0	0	ENSG00000237193	AL451054.2
ENSG00000237194	0	0	0	0	ENSG00000237194	SNAI1P1

ENSG00000237195	0	0	0.440214	0	ENSG00000237195	DLGAP5P1
ENSG00000237197	0	0	0	0	ENSG00000237197	IGHD1-7
ENSG00000237198	0	0.156762	0.374626	0	ENSG00000237198	FAM27E1
ENSG00000237202	0	0	0	0	ENSG00000237202	AJ239321.1
ENSG00000237205	0	0.0902001	0	0	ENSG00000237205	RPL7P34
ENSG00000237206	0.150964	0.109068	0.164582	0.0829669	ENSG00000237206	IMPDH1P4
ENSG00000237207	0	0.0799098	0	0.253335	ENSG00000237207	RBM17P3
ENSG00000237210	0	0	0.0354097	0.0445039	ENSG00000237210	AC073324.1
ENSG00000237211	0.146773	0.353238	0.127918	1.12303	ENSG00000237211	SETP4
ENSG00000237213	0	0	0.460861	0.187283	ENSG00000237213	RPL23AP22
ENSG00000237214	0	0	0	0.140843	ENSG00000237214	AL080243.2
ENSG00000237215	0	0	0	0	ENSG00000237215	DEFB131D
ENSG00000237216	0	3.50334	0	1.95245	ENSG00000237216	HLA-G
ENSG00000237217	0.382732	1.09853	2.47973	0.203177	ENSG00000237217	AC008074.2
ENSG00000237218	0	0	0	0	ENSG00000237218	HLA-H
ENSG00000237223	2.55073	5.83572	4.41834	7.30223	ENSG00000237223	SULT1C2P1
ENSG00000237225	0	0	0	0	ENSG00000237225	OR13K1P
ENSG00000237226	0	0	0	0	ENSG00000237226	AC127526.2
ENSG00000237227	0.336416	0.318882	3.45492	0.349749	ENSG00000237227	AL162739.1
ENSG00000237230	0	0	0	0	ENSG00000237230	KRTAP2-5P
ENSG00000237235	0	0	0	0	ENSG00000237235	TRDD2
ENSG00000237236	0	0	0	0	ENSG00000237236	AC023141.10
ENSG00000237238	1.85255	0.675507	2.90826	5.04251	ENSG00000237238	BMS1P10
ENSG00000237242	0	1.0888	0.491881	0.299759	ENSG00000237242	BTF3P15
ENSG00000237247	1.65E-07	0	0	0	ENSG00000237247	MBD3L5
ENSG00000237249	0.218076	1.26266	0.940902	1.61396	ENSG00000237249	Z99127.3
ENSG00000237251	0	0	0.156733	0.195796	ENSG00000237251	AC004987.3
ENSG00000237252	0	0.0820738	0.148179	0.182544	ENSG00000237252	AC233981.1
ENSG00000237254	0	0	0.0776102	0	ENSG00000237254	TRBV30
ENSG00000237256	0.771079	0.745968	0.832577	1.22765	ENSG00000237256	PGAM3P
ENSG00000237257	0	0.194939	0.200374	0.210594	ENSG00000237257	MTND2P8
ENSG00000237258	0.21123	0.457168	0.423707	0.844127	ENSG00000237258	OR11A1
ENSG00000237260	0.550236	2.73274	1.1098	0.195165	ENSG00000237260	AC073069.1
ENSG00000237261	7.61206	19.5062	18.9896	28.4743	ENSG00000237261	Metazoa_SRP
ENSG00000237263	1.38252	4.02701	3.21121	3.31051	ENSG00000237263	MAPK6PS3
ENSG00000237264	0.295778	0	0	0	ENSG00000237264	FTH1P11
ENSG00000237268	0	0.292957	0.817129	1.70933	ENSG00000237268	AC092447.7
ENSG00000237269	0	0	0	0	ENSG00000237269	RBMY2TP
ENSG00000237272	0.0696996	0	0.181689	0.0757663	ENSG00000237272	OR51R1P
ENSG00000237273	0.161764	0.748818	0	1.32962	ENSG00000237273	RSL24D1P8
ENSG00000237274	0.310148	0.236484	0.267147	0.0669245	ENSG00000237274	GTF3AP1
ENSG00000237275	0	0	0	0	ENSG00000237275	AL450023.3
ENSG00000237276	5.63771	5.12357	4.5306	3.85425	ENSG00000237276	ANO7L1
ENSG00000237278	0	0	0	0	ENSG00000237278	RLIMP2
ENSG00000237279	0	0	0	0	ENSG00000237279	AC099677.3
ENSG00000237284	0	0	0	0	ENSG00000237284	MAS1L
ENSG00000237285	0	0	0	0	ENSG00000237285	HNRNPA1P2
ENSG00000237289	32.9004	66.8894	59.2952	17.1067	ENSG00000237289	CKMT1B
ENSG00000237294	0	0.0738887	0.133583	0.0927799	ENSG00000237294	EIF4BP9
ENSG00000237295	0	0	0	0	ENSG00000237295	HNRNPA1P2
ENSG00000237296	57.3726	120.479	83.574	105.105	ENSG00000237296	SMG1P1
ENSG00000237297	0.0883029	0	0	0	ENSG00000237297	AL713922.1
ENSG00000237299	0	0	0	0	ENSG00000237299	AP000534.2
ENSG00000237300	0.303929	0.583224	0.793674	0.981983	ENSG00000237300	MTCO1P19

ENSG00000237302	0	0	0	0	ENSG00000237302	OFD1P11Y
ENSG00000237303	0	0	0.706043	0	ENSG00000237303	HIGD1AP8
ENSG00000237306	0.300568	0.570873	0.257999	0.314092	ENSG00000237306	HSPE1P22
ENSG00000237307	0.150493	0.371095	0.424307	0.711345	ENSG00000237307	SRRM1P3
ENSG00000237308	0	0.141588	0	0	ENSG00000237308	AC009237.10
ENSG00000237309	0.0622099	0.172077	0.264487	0.292314	ENSG00000237309	MTND2P6
ENSG00000237313	0	0.0269191	0.0728962	0	ENSG00000237313	LINC01556
ENSG00000237314	0	0	0	0	ENSG00000237314	RPL12P39
ENSG00000237317	0.133836	0.514839	0.348903	1.01903	ENSG00000237317	AL022400.1
ENSG00000237319	0.582264	1.15081	0.977534	3.66603	ENSG00000237319	AL118496.2
ENSG00000237322	4.03367	10.821	12.0061	18.6592	ENSG00000237322	RPL7L1P10
ENSG00000237323	0	0	0	0	ENSG00000237323	AC245036.3
ENSG00000237325	0.0866791	0.0833019	0.225763	0.281602	ENSG00000237325	AP000563.1
ENSG00000237329	1.48939	2.99821	4.79714	2.86711	ENSG00000237329	AL356320.2
ENSG00000237330	4.09638	1.03069	1.8514	3.11506	ENSG00000237330	RNF223
ENSG00000237332	0	0.0518337	0	0.0587522	ENSG00000237332	RP5-878I13.1
ENSG00000237333	0.684225	2.75176	2.62643	1.30384	ENSG00000237333	MSH5
ENSG00000237334	1.93885	0.673681	0.561095	0.695858	ENSG00000237334	HLA-Z
ENSG00000237335	5.71416	2.89829	3.53188	3.21515	ENSG00000237335	PFDN6
ENSG00000237344	2.08115	2.61489	2.74121	2.27258	ENSG00000237344	PBX2
ENSG00000237345	0	0	0	0	ENSG00000237345	AC245047.6
ENSG00000237347	1.53117	4.23768	2.36923	2.66999	ENSG00000237347	AC004461.1
ENSG00000237349	0.781289	0.739411	0.998473	2.01416	ENSG00000237349	BX679664.2
ENSG00000237350	0	0.169601	0	0	ENSG00000237350	CDC42P6
ENSG00000237351	0.382714	0.689972	0.500865	0.444952	ENSG00000237351	AL513366.1
ENSG00000237353	3.67103	10.2334	8.78736	14.0348	ENSG00000237353	PATE4
ENSG00000237354	0	0	0	0	ENSG00000237354	OR52S1P
ENSG00000237358	0	0	0	0	ENSG00000237358	AC007064.1
ENSG00000237360	0	0.189264	0	0	ENSG00000237360	CHCHD4P2
ENSG00000237363	0	0	0	0	ENSG00000237363	AP006288.1
ENSG00000237366	0.0144218	0	0.05347	0	ENSG00000237366	AL662857.6
ENSG00000237369	0	0	0	0.0488226	ENSG00000237369	UBDP1
ENSG00000237375	0	0	0	0	ENSG00000237375	CBX072566.1
ENSG00000237379	0	0	0	0	ENSG00000237379	CBX1P3
ENSG00000237381	0.210425	0.336541	0.226482	0.479968	ENSG00000237381	AL023280.1
ENSG00000237382	0.676624	1.00017	0.950474	0.800885	ENSG00000237382	AC127537.2
ENSG00000237383	0	0.640782	0.404342	0.2315	ENSG00000237383	CNN2P11
ENSG00000237388	0	0	0	0	ENSG00000237388	OR4A47
ENSG00000237393	0.0369345	0.142322	0	0.0808963	ENSG00000237393	SLC9A3P4
ENSG00000237395	0	0.0431034	0	0	ENSG00000237395	MICD
ENSG00000237398	0	0	0	0	ENSG00000237398	HLA-DPA3
ENSG00000237403	3.18119	0.998512	1.14687	1.58835	ENSG00000237403	PPP1R11
ENSG00000237405	0.588993	1.16103	1.17473	1.07712	ENSG00000237405	AGER
ENSG00000237406	0.48556	2.11021	1.86468	4.25854	ENSG00000237406	NDUFA9P1
ENSG00000237408	0.152411	0.146092	0	0.325786	ENSG00000237408	ART2BP
ENSG00000237409	0.192056	0.36752	0.33181	0	ENSG00000237409	AL513302.1
ENSG00000237412	0.109697	0.36608	0.0226263	0.265015	ENSG00000237412	PRSS56
ENSG00000237415	0.0851483	0	0	0	ENSG00000237415	NRBF2P3
ENSG00000237417	0	0.0612801	0.111274	0	ENSG00000237417	XRCC6P1
ENSG00000237418	1.39721	9.9395	8.0158	1.37487	ENSG00000237418	AC069257.2
ENSG00000237421	0	0	0	0.0488226	ENSG00000237421	UBDP1
ENSG00000237425	0	0	0.0206295	0.0258112	ENSG00000237425	RPSAP2
ENSG00000237426	0.902938	1.29238	2.23711	2.00364	ENSG00000237426	ZIK1P1
ENSG00000237427	0	0	0	0	ENSG00000237427	TOMM22P1

ENSG00000237428	0.222082	0.42788	0.521376	0.65194	ENSG00000237428	ASH2LP2
ENSG00000237432	0	0.117708	0.106293	0	ENSG00000237432	RPS7P12
ENSG00000237433	0	0.0693374	0	0	ENSG00000237433	RPSAP11
ENSG00000237434	0	0	0	0.169977	ENSG00000237434	AL512635.1
ENSG00000237435	1.22768	1.69917	1.51501	2.11526	ENSG00000237435	AC099566.1
ENSG00000237437	1.02064	0.752241	1.82647	0.955562	ENSG00000237437	ASS1P12
ENSG00000237439	0	0	0	0	ENSG00000237439	Z83839.1
ENSG00000237440	8.36814	11.8239	7.28214	8.6939	ENSG00000237440	ZNF737
ENSG00000237441	7.25125	9.35149	5.98272	5.07131	ENSG00000237441	RGL2
ENSG00000237442	0.45279	0.378581	0.941547	1.25187	ENSG00000237442	HNRNPA1P57
ENSG00000237443	0	0.0667588	0	0	ENSG00000237443	OR13D2P
ENSG00000237444	0.283316	0.135877	0.368015	0.455107	ENSG00000237444	AP001342.1
ENSG00000237446	1.0624	2.7827	2.12255	4.89463	ENSG00000237446	RHEBP3
ENSG00000237447	0	0.158309	0.0878955	0	ENSG00000237447	CDC27P2
ENSG00000237448	0	0.0160402	0	0	ENSG00000237448	RPL3P2
ENSG00000237449	0	0	0	0	ENSG00000237449	TAAR4P
ENSG00000237450	0	0	0	0	ENSG00000237450	RPL23AP71
ENSG00000237451	0	0.245224	0.437986	0	ENSG00000237451	CDK2AP2P2
ENSG00000237452	0.0400601	0.0193103	0.0174585	0.0221608	ENSG00000237452	BHMG1
ENSG00000237456	0	0.200251	0.386093	0.760189	ENSG00000237456	AC104849.1
ENSG00000237458	0	0	0	0	ENSG00000237458	TUBB4BP3
ENSG00000237459	0.181329	0.151186	0.308192	0.303335	ENSG00000237459	MPIG6B
ENSG00000237462	3.55819	9.04703	0.638249	1.50002	ENSG00000237462	TRIM27
ENSG00000237466	0.896688	0	1.02667	0.974387	ENSG00000237466	MTCO3P41
ENSG00000237467	0.203879	1.16958	0.176098	1.08032	ENSG00000237467	USP9YP35
ENSG00000237469	4.17E-05	0	0	0	ENSG00000237469	TUBB8P10
ENSG00000237470	0.885526	1.94692	2.08851	3.02214	ENSG00000237470	DCLRE1CP1
ENSG00000237472	0	0	0	0	ENSG00000237472	AC245054.2
ENSG00000237474	0.34271	7.25857	7.92461	8.46544	ENSG00000237474	AC233263.2
ENSG00000237475	0	0.172028	0.715507	0	ENSG00000237475	RPL7P53
ENSG00000237478	0	0	0	0	ENSG00000237478	AL390023.1
ENSG00000237482	0.0327523	0	0	0	ENSG00000237482	LY6G6E
ENSG00000237483	1.08534	2.42336	2.2792	4.16281	ENSG00000237483	RPS27AP8
ENSG00000237487	0.0592009	0	0.0514842	0	ENSG00000237487	VN1R48P
ENSG00000237490	0	0.167375	0.302298	0	ENSG00000237490	RPS27AP17
ENSG00000237492	0	0	0	0	ENSG00000237492	OR2L9P
ENSG00000237493	1.2633	1.95797	2.06467	2.9108	ENSG00000237493	AC034102.1
ENSG00000237495	0.0973281	0.0758412	0.0529561	0.0644326	ENSG00000237495	LY6G5C
ENSG00000237501	0	0	0	0	ENSG00000237501	AC108667.1
ENSG00000237503	0	0	0	0	ENSG00000237503	AC239798.3
ENSG00000237506	5.53293	0	0.640297	0.696478	ENSG00000237506	RPSAP15
ENSG00000237508	0.73055	6.07825	3.47303	2.35358	ENSG00000237508	HLA-F
ENSG00000237510	0.353492	0.453205	0.112192	0.705	ENSG00000237510	GPAT2P1
ENSG00000237514	0.592429	1.4419	1.40417	2.43904	ENSG00000237514	PTP4A1P7
ENSG00000237515	6.06606	12.6102	11.8835	35.0709	ENSG00000237515	SHISA9
ENSG00000237521	0.196619	0.237683	0.134976	0.280301	ENSG00000237521	OR7E24
ENSG00000237522	1.11367	2.67585	2.75061	1.16359	ENSG00000237522	NONOP2
ENSG00000237524	0.323661	1.05056	0.419999	0.929566	ENSG00000237524	TEX51
ENSG00000237528	0	0	0	0	ENSG00000237528	AL929410.2
ENSG00000237533	0	0	1.00116	0	ENSG00000237533	PFN1P6
ENSG00000237536	0	0.0288995	0.0208992	0	ENSG00000237536	HTATSF1P1
ENSG00000237539	0.394855	1.10191	1.15437	0.94639	ENSG00000237539	AC003669.1
ENSG00000237540	0	0	0	0.361847	ENSG00000237540	RPL36AP36
ENSG00000237541	0.114237	0.0784046	0.141054	0	ENSG00000237541	HLA-DQA2

ENSG00000237542	0	0.301418	0.38035	0	ENSG00000237542	MTCO3P17
ENSG00000237544	0.00730832	0.00703285	0.0254239	0.0637217	ENSG00000237544	MAS1LP1
ENSG00000237545	0	0	0	0	ENSG00000237545	POLR2LP1
ENSG00000237546	0	0	0	0	ENSG00000237546	XKRYP6
ENSG00000237547	0	6.67216	2.87171	4.46442	ENSG00000237547	IGHJ2P
ENSG00000237549	0.0971854	0.392865	0.253098	0.108212	ENSG00000237549	AC092570.3
ENSG00000237550	113.628	81.9587	48.5888	2.12808	ENSG00000237550	RPL9P9
ENSG00000237551	0.358067	1.24101	0.861827	0.190516	ENSG00000237551	AC096775.1
ENSG00000237553	0	0	0	0.642634	ENSG00000237553	AL133547.1
ENSG00000237554	0	0.080909	0	0.0608436	ENSG00000237554	CR925767.1
ENSG00000237555	0	0	0	0	ENSG00000237555	AL031681.1
ENSG00000237557	0	0.0878255	0	0	ENSG00000237557	YWHABP1
ENSG00000237558	0.473845	0.417932	0.381437	0.529374	ENSG00000237558	CDY7P
ENSG00000237559	0	0	0	0	ENSG00000237559	HLA-S
ENSG00000237565	0	0	0	0	ENSG00000237565	SSU72P5
ENSG00000237566	0	0	0	0	ENSG00000237566	AC090955.1
ENSG00000237569	0	0	0	0	ENSG00000237569	TUBAP
ENSG00000237572	0	0	0	0	ENSG00000237572	AC092001.1
ENSG00000237575	0.786309	1.48888	0.959317	0.123459	ENSG00000237575	PYY2
ENSG00000237578	4.17571	5.58769	8.54254	12.7681	ENSG00000237578	RP11-174M13.1
ENSG00000237580	0	0	0	0	ENSG00000237580	GCSHP3
ENSG00000237582	0.0792565	0.253763	0	0.291808	ENSG00000237582	POU5F1
ENSG00000237583	0	0	0.270845	0.658477	ENSG00000237583	AC093166.4
ENSG00000237584	0.124127	0	0	0	ENSG00000237584	RAC1P4
ENSG00000237586	2.31866	1.12972	0.676197	1.72964	ENSG00000237586	AC090192.1
ENSG00000237589	0.948338	1.84058	0.79827	1.80015	ENSG00000237589	HMGN1P32
ENSG00000237591	0	0	0	0	ENSG00000237591	HLA-DRB9
ENSG00000237592	0.248992	0	0	0	ENSG00000237592	IGKV1OR10-1
ENSG00000237593	0.135056	0.249077	0.246826	0.417985	ENSG00000237593	AL445220.1
ENSG00000237597	0	0	0	0	ENSG00000237597	GAGE13
ENSG00000237599	27.1048	0	25.4225	19.8002	ENSG00000237599	TAP2
ENSG00000237601	0	0	0	0	ENSG00000237601	AP000358.1
ENSG00000237603	0	0.250725	0.226367	0.704015	ENSG00000237603	HMGB3P12
ENSG00000237606	0	0	0	0	ENSG00000237606	AC091286.1
ENSG00000237608	0	0	0	0	ENSG00000237608	CR388407.2
ENSG00000237610	0	0	0	0	ENSG00000237610	OR4C50P
ENSG00000237611	25.4593	38.9356	29.1521	50.8176	ENSG00000237611	Metazoa_SRP
ENSG00000237616	0	0	0	0	ENSG00000237616	USP9YP32
ENSG00000237617	0.769166	0.721116	0	0.771427	ENSG00000237617	AC013410.2
ENSG00000237618	0	0.10806	0.097592	0	ENSG00000237618	BTBD7P2
ENSG00000237619	0.0353729	0	0.030734	0	ENSG00000237619	OR3B1P
ENSG00000237620	0.0999289	0	0.0861149	0.214432	ENSG00000237620	GCNT1P5
ENSG00000237621	0.0330326	0	0.086119	0.132953	ENSG00000237621	OR9A1P
ENSG00000237622	0	0	0	0.596456	ENSG00000237622	ELOCP18
ENSG00000237623	0	0	0	0	ENSG00000237623	AL591503.3
ENSG00000237624	0	0.219951	0.22448	0.0848181	ENSG00000237624	OXCT2P1
ENSG00000237625	0	0	0	0	ENSG00000237625	RP11-144A16.2
ENSG00000237628	0.354598	0.794069	0.102443	0.27809	ENSG00000237628	MTCO2P19
ENSG00000237629	0	0	0	0	ENSG00000237629	UQCRHP2
ENSG00000237630	1.26655	1.82244	2.77827	0.657218	ENSG00000237630	NIFKP9
ENSG00000237631	0.380506	0.978969	1.21468	0.989603	ENSG00000237631	AL161454.1
ENSG00000237632	0	0	0	0	ENSG00000237632	S100A11P1
ENSG00000237634	0	0.0269191	0	0	ENSG00000237634	LINC01556

ENSG00000237635	0	0	0	0	ENSG00000237635	DUX4L29
ENSG00000237636	0.020036	0.289767	0.228102	0.220253	ENSG00000237636	ANKRD26P3
ENSG00000237639	0	1.34241	0	0.711302	ENSG00000237639	AC064862.5
ENSG00000237641	1.2604	6.44944	5.43645	5.83901	ENSG00000237641	AC073476.1
ENSG00000237642	0.764059	0.484712	1.38827	1.57542	ENSG00000237642	HMGB3P5
ENSG00000237645	0	0	0	0	ENSG00000237645	AC092967.1
ENSG00000237649	3.24741	16.7005	2.069	6.32269	ENSG00000237649	KIFC1
ENSG00000237650	0	0	0	0	ENSG00000237650	OR11Q1P
ENSG00000237651	4.87812	5.70753	6.52912	4.72344	ENSG00000237651	C2orf74
ENSG00000237653	0	0	0	0.173209	ENSG00000237653	AC026320.2
ENSG00000237659	2.61667	3.69659	6.29869	0	ENSG00000237659	RNASEH2CP1
ENSG00000237661	0	0.0890761	0	0	ENSG00000237661	AC092474.2
ENSG00000237662	0	0.125049	0	0	ENSG00000237662	SOCS2P1
ENSG00000237663	0.231269	0.387848	1.41824	2.08803	ENSG00000237663	DNAJC19P7
ENSG00000237666	0	0.166255	0.00620756	0	ENSG00000237666	AC097527.1
ENSG00000237668	0.24398	0	0	0.257773	ENSG00000237668	RPS15AP38
ENSG00000237669	0	0	0	0	ENSG00000237669	AL671277.2
ENSG00000237671	0	0	0	0	ENSG00000237671	GAGE12C
ENSG00000237672	2.68105	4.55249	3.99209	5.63821	ENSG00000237672	KRR1P1
ENSG00000237674	0.179034	0	0	0	ENSG00000237674	GSTA7P
ENSG00000237676	0	0	0	0	ENSG00000237676	RPL30P4
ENSG00000237677	0.775955	0	4.18303	0	ENSG00000237677	AC113612.2
ENSG00000237679	0	0.306949	0.578025	0.571912	ENSG00000237679	VDAC1P11
ENSG00000237682	0.000282307	0	1.69E-06	0.0773425	ENSG00000237682	AC234775.2
ENSG00000237683	4.32914	8.73624	14.7313	19.5521	ENSG00000237683	AL627309.1
ENSG00000237684	0	0	0.136853	0.0854686	ENSG00000237684	RPSAP35
ENSG00000237690	0.009462	0.0181999	0.0164453	0.0102936	ENSG00000237690	CR936918.3
ENSG00000237691	0	0	0.533973	0	ENSG00000237691	IFNWP2
ENSG00000237693	1.25696	2.10167	2.01655	3.65632	ENSG00000237693	IRGM
ENSG00000237698	0	0	0	0	ENSG00000237698	GPR53P
ENSG00000237700	0	0	0	0	ENSG00000237700	PRAMEF33
ENSG00000237701	0	0	0	0	ENSG00000237701	ATP5JP1
ENSG00000237702	0	0	0	0	ENSG00000237702	TRBV3-1
ENSG00000237703	0	0	0	0	ENSG00000237703	TRIM10
ENSG00000237704	0.119946	0.693188	0.835449	2.14403	ENSG00000237704	AP004289.2
ENSG00000237706	0	0	0.0998971	0	ENSG00000237706	TRIM51EP
ENSG00000237708	0	0	0	0	ENSG00000237708	AL139397.2
ENSG00000237709	0	0	0	0	ENSG00000237709	EEF1A1P28
ENSG00000237710	0	0.223915	0.211819	2.4135	ENSG00000237710	HLA-DPB1
ENSG00000237711	0.953313	2.5341	0.794041	3.71501	ENSG00000237711	MTCO3P11
ENSG00000237717	0	0	0	0	ENSG00000237717	BX276092.8
ENSG00000237719	1.56625	2.7326	2.8831	4.57328	ENSG00000237719	Z95152.1
ENSG00000237722	0	0	0	0	ENSG00000237722	MTND1P29
ENSG00000237723	0	0.0184226	0	0	ENSG00000237723	ZNF70P1
ENSG00000237724	0	0	0	0	ENSG00000237724	HSPA1A
ENSG00000237725	0	0	0.016343	0	ENSG00000237725	OR2I1P
ENSG00000237727	0.128048	0.290488	0.160375	0.21663	ENSG00000237727	AIF1
ENSG00000237729	0	0	0	0	ENSG00000237729	AC002075.2
ENSG00000237730	0	0	0	0	ENSG00000237730	AC078991.1
ENSG00000237731	0	0	0.158396	0.592278	ENSG00000237731	RNGTTP1
ENSG00000237732	9.3807	19.9094	22.4838	38.4928	ENSG00000237732	AC010980.1
ENSG00000237733	0	0	1.32733	0	ENSG00000237733	RNF39
ENSG00000237740	0.351537	0.493913	0.248555	0.567271	ENSG00000237740	NPAP1P3
ENSG00000237743	0	0	0.468273	0	ENSG00000237743	FBP2P1

ENSG00000237745	0	0	0	0	ENSG00000237745	AC009963.4
ENSG00000237746	0.0664813	0.128112	0.173716	0.0728659	ENSG00000237746	ZNF101P1
ENSG00000237747	0	0	0.0801803	0.0999188	ENSG00000237747	AL160279.1
ENSG00000237748	0.866195	4.7094	3.88193	2.17819	ENSG00000237748	UQCRBP1
ENSG00000237749	0	0	0	0	ENSG00000237749	AL034379.1
ENSG00000237752	0	0	0	0	ENSG00000237752	AL354685.2
ENSG00000237754	0	1.21313	0.973432	2.61856	ENSG00000237754	AC093655.2
ENSG00000237757	0.0707543	0.236489	0.153672	0.217205	ENSG00000237757	EEF1A1P30
ENSG00000237758	7.58509	17.7804	5.34733	20.9312	ENSG00000237758	BANF1P3
ENSG00000237763	0.0388844	0.472031	0.0489813	0.182038	ENSG00000237763	AMY1A
ENSG00000237765	16.9053	22.8332	21.2753	12.1086	ENSG00000237765	FAM200B
ENSG00000237766	0.12196	0.243454	0.256659	0.250386	ENSG00000237766	GGTA2P
ENSG00000237770	0	0.0325427	0.0147114	0.0371858	ENSG00000237770	SPATA31D2P
ENSG00000237774	1.54343	3.17497	2.19843	3.71441	ENSG00000237774	AC126615.1
ENSG00000237777	0	0	0	0	ENSG00000237777	OR14J1
ENSG00000237782	0	0	0	0	ENSG00000237782	AL020989.1
ENSG00000237783	0	0	0	0	ENSG00000237783	AL356441.2
ENSG00000237784	0	0	0	0	ENSG00000237784	AC097713.2
ENSG00000237787	0.369696	0	0.106795	0.132469	ENSG00000237787	C3orf79
ENSG00000237788	0.140164	0.67919	0.516135	0.71111	ENSG00000237788	AL162615.1
ENSG00000237792	0.0545784	0.16822	0.0457725	0.171732	ENSG00000237792	RP11-203I2.1
ENSG00000237793	0.139608	0	0.120746	0.0748266	ENSG00000237793	RPL18AP16
ENSG00000237799	0	0	0.0419127	0	ENSG00000237799	CICP11
ENSG00000237801	0	0.0606185	0.0545585	0.137944	ENSG00000237801	AMD1P2
ENSG00000237804	0	0	0	0	ENSG00000237804	HNRNPA1P39
ENSG00000237806	0.212898	0.203385	0.183672	0.450522	ENSG00000237806	FAUP2
ENSG00000237808	0	0	0	0	ENSG00000237808	NCR3
ENSG00000237810	0	0	0	0	ENSG00000237810	AC104852.1
ENSG00000237811	0	0	0	0	ENSG00000237811	GPR53P
ENSG00000237814	0	0	0	0	ENSG00000237814	SFTA2
ENSG00000237815	10.9229	16.4167	15.7166	17.5991	ENSG00000237815	AC007000.11
ENSG00000237816	0	0	0	0	ENSG00000237816	RPL21P109
ENSG00000237818	0	0.261868	0.294013	0.205688	ENSG00000237818	RPS3AP29
ENSG00000237821	0.0660842	0	0.112426	0	ENSG00000237821	AC083873.1
ENSG00000237823	0.0356931	0	0.12443	0.0422853	ENSG00000237823	CDY19P
ENSG00000237824	0	0	0	0.375796	ENSG00000237824	RPL23AP33
ENSG00000237825	5.86561	7.28875	5.7293	4.35313	ENSG00000237825	RGL2
ENSG00000237827	0.641263	1.68631	1.42541	3.09562	ENSG00000237827	RPS15AP29
ENSG00000237828	0	0.151736	0.371266	0.169103	ENSG00000237828	PA2G4P1
ENSG00000237829	0	9.54811	0	0	ENSG00000237829	PPP1R11
ENSG00000237831	0	0	0.870044	1.06268	ENSG00000237831	RP11-499O7.4
ENSG00000237833	0.061278	0.137914	0.0533573	0.0895414	ENSG00000237833	AL391380.1
ENSG00000237834	0.777749	2.51665	1.07424	1.9156	ENSG00000237834	MOG
ENSG00000237835	0	0	0	0	ENSG00000237835	AC007064.3
ENSG00000237840	0.87943	0.756801	2.08874	0.559786	ENSG00000237840	FAM21FP
ENSG00000237841	0	0	0	0	ENSG00000237841	KRTAP19-9P
ENSG00000237842	0	0.0416649	0.0740587	0.0461069	ENSG00000237842	AL157713.1
ENSG00000237846	1887.05	590.5	456.322	740.007	ENSG00000237846	AL773545.3
ENSG00000237847	0	0	0	0	ENSG00000237847	FAM231A
ENSG00000237848	0	1.05834	2.35966	1.13786	ENSG00000237848	AL606489.2
ENSG00000237849	0.196944	0.431578	0.284639	0.212711	ENSG00000237849	NFYAP1
ENSG00000237850	0	0	0	0	ENSG00000237850	AC091304.1
ENSG00000237854	16.8949	7.90849	4.79055	12.08	ENSG00000237854	LINC00674
ENSG00000237859	0.133248	0.0256517	0	0	ENSG00000237859	EEF1A1P31

ENSG00000237860	0.179783	0.495723	0.745437	0.180923	ENSG00000237860	BX119904.4
ENSG00000237861	0.0593803	0.457582	0.258415	0.518065	ENSG00000237861	AL513325.1
ENSG00000237865	0	0	0	0	ENSG00000237865	SUCLA2P1
ENSG00000237868	0	0	0	0	ENSG00000237868	AC097533.1
ENSG00000237869	0.207934	0.114639	0.10359	0.378992	ENSG00000237869	RP11-459O16.1
ENSG00000237871	1.93885	0.673681	0.561095	0.695858	ENSG00000237871	HLA-Z
ENSG00000237872	0.42739	0.401331	0.680804	0.804407	ENSG00000237872	POU5F1P4
ENSG00000237873	0	0	0	0	ENSG00000237873	AL158053.1
ENSG00000237875	0	0	0	0	ENSG00000237875	AL353691.2
ENSG00000237876	0.0680597	0	0	0.0742113	ENSG00000237876	AKR1B1P4
ENSG00000237881	0	0	0.0379426	0	ENSG00000237881	C6orf10
ENSG00000237882	0	0	0	0	ENSG00000237882	PPIAP13
ENSG00000237884	0	0	0	0	ENSG00000237884	AL845454.3
ENSG00000237885	0	0	0	0	ENSG00000237885	AL359672.1
ENSG00000237887	0.17475	0.503226	0.322223	5.16996	ENSG00000237887	RPL23AP32
ENSG00000237888	0.16786	0	0	0.206504	ENSG00000237888	AC087650.1
ENSG00000237889	6.16981	9.25035	6.9961	6.31738	ENSG00000237889	DDX39B
ENSG00000237891	0	0	0	0	ENSG00000237891	AL441985.1
ENSG00000237896	0	0.271979	0.162854	0.302928	ENSG00000237896	AC005008.2
ENSG00000237897	0.242016	0	0.207718	0.265196	ENSG00000237897	AL512844.2
ENSG00000237900	0.256112	0.212818	0	0.639599	ENSG00000237900	ZBTB12
ENSG00000237901	0.708894	1.35132	1.09133	0.575303	ENSG00000237901	AC009161.1
ENSG00000237902	0	0	0	0	ENSG00000237902	TSPY21P
ENSG00000237904	0	0	0	0	ENSG00000237904	BX284632.2
ENSG00000237905	0	0	0.6145	0.621573	ENSG00000237905	HCG4
ENSG00000237906	1.27461	1.83466	0.110444	4.51735	ENSG00000237906	MUPP
ENSG00000237910	0	0.0793418	0	0.135193	ENSG00000237910	MTCO1P18
ENSG00000237911	0	2.07737	2.97041	2.81611	ENSG00000237911	SRP68P3
ENSG00000237913	0	0	0	0	ENSG00000237913	FTLP19
ENSG00000237916	1.64386	6.54266	4.78513	8.21438	ENSG00000237916	AC011753.4
ENSG00000237917	0.193424	0.0230653	0	0.0381418	ENSG00000237917	PARP4P1
ENSG00000237918	1.16778	4.05256	1.95973	2.95491	ENSG00000237918	SAPCD1
ENSG00000237920	0	0	0	0	ENSG00000237920	AL162591.2
ENSG00000237922	0.106788	0.608905	0.555093	0.338041	ENSG00000237922	AL450309.1
ENSG00000237924	0	0	0	0	ENSG00000237924	RPL21P112
ENSG00000237926	0	0	0	0	ENSG00000237926	AC239367.3
ENSG00000237929	0	0	0	0	ENSG00000237929	RPL31P3
ENSG00000237930	0	0	0	0	ENSG00000237930	AC007563.3
ENSG00000237931	0.0890398	0	0	0	ENSG00000237931	CLIC4P3
ENSG00000237936	0	0	0	0	ENSG00000237936	AL353093.1
ENSG00000237939	0	0.707667	0.185291	0.228582	ENSG00000237939	AC097523.2
ENSG00000237948	0	0	0	0	ENSG00000237948	MTATP6P20
ENSG00000237951	0	0	0	0	ENSG00000237951	PPIL1P1
ENSG00000237952	0.308759	0	0	0	ENSG00000237952	RPL7AP73
ENSG00000237953	1.30968	1.64864	1.1083	0	ENSG00000237953	AC013267.1
ENSG00000237955	0	0	0	0	ENSG00000237955	AC245884.4
ENSG00000237956	0	0	0	0	ENSG00000237956	TRIAP1P1
ENSG00000237957	0	0.0219476	0.0109151	0.0319741	ENSG00000237957	CT47A5
ENSG00000237959	0.308931	0.293178	0	1.7281	ENSG00000237959	RPL36AP10
ENSG00000237961	0.684597	1.11264	0.519187	0.316694	ENSG00000237961	AC118282.1
ENSG00000237962	0.0874301	0.12896	0.145468	0.26788	ENSG00000237962	MUC21
ENSG00000237963	0	0	0	0.112239	ENSG00000237963	AL441964.1
ENSG00000237964	0.904877	0.720222	0.730643	0.515544	ENSG00000237964	AC068042.1
ENSG00000237968	0	0	0	0	ENSG00000237968	AC007322.3

ENSG00000237970	0	0	0	0	ENSG00000237970	TMEM161BP1
ENSG00000237971	0	0.208484	0.12189	0.382598	ENSG00000237971	AL445523.1
ENSG00000237972	0.0870756	0.714766	0.4213	0.47527	ENSG00000237972	TUBG1P
ENSG00000237973	1.95602	1.62142	3.47415	3.17072	ENSG00000237973	MTCO1P12
ENSG00000237974	0	0	0	0	ENSG00000237974	AC000111.3
ENSG00000237977	0.775473	0.62135	0	0.421191	ENSG00000237977	EIF4HP2
ENSG00000237979	0.082218	0.551009	0.649332	0.443909	ENSG00000237979	AC007389.4
ENSG00000237982	0.794357	1.06753	0.549957	2.37511	ENSG00000237982	AP006193.1
ENSG00000237984	0.878661	1.8248	1.68539	1.76993	ENSG00000237984	PTENP1
ENSG00000237988	0	0	0.016343	0	ENSG00000237988	OR2I1P
ENSG00000237991	0	0	0	0	ENSG00000237991	RPL35P1
ENSG00000237997	0	0	0	0	ENSG00000237997	RCC2P2
ENSG00000237999	0	0	0	0	ENSG00000237999	ACTG1P19
ENSG00000238000	0	0.0903049	0	0	ENSG00000238000	AC116347.1
ENSG00000238001	0.173109	0	0	0	ENSG00000238001	SNRPCP1
ENSG00000238002	0	0	0	0.0171724	ENSG00000238002	NPAP1P6
ENSG00000238003	0	0	0	0	ENSG00000238003	RPL10P4
ENSG00000238008	0	1.74777	0	3.14231	ENSG00000238008	COX6CP10
ENSG00000238013	0.867024	0.818364	0.733899	0.888968	ENSG00000238013	AC109583.1
ENSG00000238015	0.199928	0.559385	1.01014	1.44783	ENSG00000238015	AC104837.2
ENSG00000238021	0.029892	0.0866965	0.148272	0.0748208	ENSG00000238021	ARMC4P1
ENSG00000238024	0.233474	0.0627516	0.0983601	0.475397	ENSG00000238024	DDX39BP2
ENSG00000238025	0	0.0570323	0.413743	1.55996	ENSG00000238025	ZDHHC4P1
ENSG00000238026	0.153375	0	0	0.0832404	ENSG00000238026	AC117434.1
ENSG00000238029	0	0.0840649	0.225014	0.188138	ENSG00000238029	AC012493.1
ENSG00000238032	0	0	0	0	ENSG00000238032	AC245047.7
ENSG00000238037	0	0.785039	0	0	ENSG00000238037	OOSP1P1
ENSG00000238038	0	1.02909	0	0.519212	ENSG00000238038	ATP6V0E1P3
ENSG00000238040	0	0.090904	0.0498814	0.0621995	ENSG00000238040	SALL4P2
ENSG00000238041	0	0	0	0	ENSG00000238041	AP004245.1
ENSG00000238046	0	0.772435	0	0	ENSG00000238046	MTND5P22
ENSG00000238047	0	0	0.121614	0	ENSG00000238047	MTND1P30
ENSG00000238048	0.156618	0.150563	0.408091	0.594729	ENSG00000238048	ART2P
ENSG00000238049	0	0	0	0.444484	ENSG00000238049	Z92846.1
ENSG00000238051	0	0	0.154705	0	ENSG00000238051	ISCUP1
ENSG00000238053	0.0558802	0	0.0241408	0.0296507	ENSG00000238053	ZDHHC20P1
ENSG00000238055	0.906496	0.879503	0	1.23985	ENSG00000238055	Z98742.3
ENSG00000238056	0.321353	0.543605	0.602107	0.116243	ENSG00000238056	PRRT1
ENSG00000238059	0.396877	0.634378	0	0	ENSG00000238059	HSPE1P21
ENSG00000238061	0.0637894	0.73635	0.499135	0.486035	ENSG00000238061	AL356273.2
ENSG00000238065	0	0	0	0	ENSG00000238065	AC010740.1
ENSG00000238066	0	0.406422	0.374365	1.32484	ENSG00000238066	AC005002.2
ENSG00000238067	0	0	0.134639	0.249305	ENSG00000238067	XKRYP1
ENSG00000238069	0	0.196263	0	0	ENSG00000238069	RPLP0P7
ENSG00000238070	0	0	0	0	ENSG00000238070	CR933783.2
ENSG00000238072	0	6.46697	0.534914	1.09989	ENSG00000238072	AC009244.1
ENSG00000238073	0.09254	0.0889179	0.401613	0.600561	ENSG00000238073	RBMY2HP
ENSG00000238074	0	0	0	0	ENSG00000238074	TSPY9P
ENSG00000238075	0.141272	0.271018	0.24468	0.151435	ENSG00000238075	RPSAP32
ENSG00000238076	0.217553	0.104472	0.188674	0.118001	ENSG00000238076	MRPL48P1
ENSG00000238077	0.0723431	0	0.185665	0.232192	ENSG00000238077	NMNAT1P3
ENSG00000238079	2.28273	1.28182	0	0	ENSG00000238079	AL356121.1
ENSG00000238081	0	0	0	0	ENSG00000238081	AC099063.2
ENSG00000238082	0	0.183789	0.339996	0.210734	ENSG00000238082	AC009948.2

ENSG00000238083	5.34123	6.24355	14.4025	8.10829	ENSG00000238083	LRRC37A2
ENSG00000238084	0	0	0.538835	0.188622	ENSG00000238084	AL031284.1
ENSG00000238085	0	0	0	0	ENSG00000238085	AL590682.1
ENSG00000238086	0.195215	0.572256	0.725556	1.02111	ENSG00000238086	PPP1R26P1
ENSG00000238087	0	0.0346926	0.0627211	0	ENSG00000238087	FMO8P
ENSG00000238088	0	0	0.121237	0.285563	ENSG00000238088	OFD1P7Y
ENSG00000238090	0	0.392182	0	0.616679	ENSG00000238090	AC006195.1
ENSG00000238091	6.69777	14.0557	12.0261	21.2531	ENSG00000238091	AC016745.1
ENSG00000238092	0	0.175642	0	0	ENSG00000238092	CEACAMP6
ENSG00000238094	0.078525	0	0	0.163728	ENSG00000238094	AC245036.4
ENSG00000238098	1.03376	1.77838	1.6266	2.9204	ENSG00000238098	ABCA17P
ENSG00000238101	0.0127692	0	0.0112498	0.00924291	ENSG00000238101	FAM8A5P
ENSG00000238103	1.34618	0.588212	0	0	ENSG00000238103	RPL9P7
ENSG00000238104	5.55483	9.33778	7.87132	5.90532	ENSG00000238104	PPP1R10
ENSG00000238105	6.02278	14.9046	13.9696	13.8094	ENSG00000238105	GOLGA2P5
ENSG00000238108	0	0	0	0	ENSG00000238108	AL139135.2
ENSG00000238109	0.378518	0.972131	0.624192	1.66805	ENSG00000238109	AC004893.1
ENSG00000238110	0.299548	0.117095	0.266416	0.112436	ENSG00000238110	AL353572.2
ENSG00000238111	0	0	0.343552	1.1093	ENSG00000238111	AC066692.1
ENSG00000238114	0.013508	0	0.0359938	0.0362078	ENSG00000238114	LTB
ENSG00000238116	0.06078	0.146218	0	0.100043	ENSG00000238116	Z95327.2
ENSG00000238118	0	0	0	0.290119	ENSG00000238118	SLC25A24P2
ENSG00000238125	0.0560558	0.0359792	0.0373761	0.0933923	ENSG00000238125	SLC9A3P2
ENSG00000238126	0	0	0	0	ENSG00000238126	UQCRHP1
ENSG00000238127	0	0	0	0	ENSG00000238127	RP11-552J9.15
ENSG00000238130	0.0274983	0.0159269	0.0264951	0.0188624	ENSG00000238130	LTA
ENSG00000238132	0.0904613	0	0.119783	0	ENSG00000238132	CASC4P1
ENSG00000238134	4.06832	4.07993	3.23499	4.27404	ENSG00000238134	EHMT2
ENSG00000238135	0.401937	0.118136	0	0	ENSG00000238135	USP9YP10
ENSG00000238137	0.161618	0.401337	0.482662	0.747526	ENSG00000238137	ARPC3P2
ENSG00000238138	0	0	0	0	ENSG00000238138	AC027124.2
ENSG00000238139	0	0	0	0	ENSG00000238139	AL590559.1
ENSG00000238143	0.316772	0.455425	0.274146	0.0297045	ENSG00000238143	AL161631.1
ENSG00000238145	0.150762	0.193551	0.132479	0.109735	ENSG00000238145	AL731892.1
ENSG00000238149	0	1.43971	0.956139	1.72175	ENSG00000238149	AC104978.1
ENSG00000238150	0	0	0.332541	0	ENSG00000238150	AC008753.1
ENSG00000238151	5.02698	7.6894	4.08506	10.2008	ENSG00000238151	MLLT10P1
ENSG00000238152	0	0	0	0	ENSG00000238152	AC092865.3
ENSG00000238153	0	0.668426	0.400608	1.2258	ENSG00000238153	Z99755.1
ENSG00000238154	0.222196	0.209391	0.328949	1.00082	ENSG00000238154	USP9YP4
ENSG00000238161	0.137019	0.236144	0.627654	0.447041	ENSG00000238161	OR7E117P
ENSG00000238162	0	0	0	0	ENSG00000238162	AC009237.11
ENSG00000238165	0	0	0.550323	0	ENSG00000238165	AC007560.1
ENSG00000238166	0	0	0	0	ENSG00000238166	AC022748.1
ENSG00000238168	2.18076	3.38512	3.71087	5.82556	ENSG00000238168	AC137055.1
ENSG00000238172	0.435475	0.389996	0.82537	1.01284	ENSG00000238172	RPS2P35
ENSG00000238173	2.71184	1.39118	1.21435	0	ENSG00000238173	RPL39P6
ENSG00000238180	0	0	0	0.169744	ENSG00000238180	AC017079.2
ENSG00000238181	0.0454891	0.0438431	0.162888	0	ENSG00000238181	AHCYP2
ENSG00000238183	0	0	0	2.6345	ENSG00000238183	RPS27P5
ENSG00000238188	0.701204	1.45817	1.02444	0.641507	ENSG00000238188	AL049733.1
ENSG00000238190	0	0.179226	0	0.0994901	ENSG00000238190	HMGB1P15
ENSG00000238191	0	0.0484699	0	0	ENSG00000238191	CLUHP1

ENSG00000238193	0	0	0	0	ENSG00000238193	AC112656.1
ENSG00000238196	0.0415768	0.235639	0.339843	0.331051	ENSG00000238196	NOTCH4
ENSG00000238199	0.19901	0.177969	1.29356	0.592879	ENSG00000238199	UBE2V2P3
ENSG00000238200	0	0	0	0	ENSG00000238200	MGAT2P2
ENSG00000238203	1.02425	1.71745	2.89525	2.54589	ENSG00000238203	VWA7
ENSG00000238205	0	0	0	0.419162	ENSG00000238205	MPC1L
ENSG00000238208	19.9521	46.3396	44.9851	98.2818	ENSG00000238208	RP11-112N13.1
ENSG00000238211	0	0	0	0	ENSG00000238211	POLR2LP1
ENSG00000238213	0	0.046795	0	0.102557	ENSG00000238213	TARDBPP2
ENSG00000238215	0	0.0876057	0	0.149164	ENSG00000238215	AL513185.3
ENSG00000238220	0.222669	0.463191	1.63286	1.64679	ENSG00000238220	AP000275.1
ENSG00000238222	0.198121	0.151257	0.568684	1.78121	ENSG00000238222	MKRN4P
ENSG00000238223	0.0381208	0.071319	0.0660104	0.0402735	ENSG00000238223	AL121878.1
ENSG00000238225	0	0	0	0	ENSG00000238225	CRIP1P2
ENSG00000238227	24.3048	19.4125	26.2536	13.7936	ENSG00000238227	TMEM250
ENSG00000238228	0.23797	0.579098	1.1773	0.423032	ENSG00000238228	OR7E7P
ENSG00000238231	0	1.31077	1.69745	3.88772	ENSG00000238231	AL512288.2
ENSG00000238235	0	0	0	0	ENSG00000238235	TSPY11P
ENSG00000238236	0.997367	2.57982	2.26635	4.92237	ENSG00000238236	MTCYBP14
ENSG00000238238	0.0916753	0.264657	0.272079	0.660025	ENSG00000238238	MCCD1
ENSG00000238240	0	0	2.2575	0.678971	ENSG00000238240	RP4-740C4.5
ENSG00000238241	0	0	0.0541898	0	ENSG00000238241	CCR12P
ENSG00000238243	0.202827	0.469277	0.156626	0.304306	ENSG00000238243	OR2W3
ENSG00000238244	0	0.0591298	0.0268719	0.101303	ENSG00000238244	GABARAPL3
ENSG00000238245	0	0	0.0425021	0	ENSG00000238245	MYO5BP2
ENSG00000238247	0.0383437	0	0	0.0430236	ENSG00000238247	AC006210.2
ENSG00000238248	0	0	0	0	ENSG00000238248	CR933540.4
ENSG00000238249	0.835871	1.9758	0.710686	1.2897	ENSG00000238249	HMGN2P17
ENSG00000238251	0	0.304458	0	0	ENSG00000238251	AL133477.1
ENSG00000238254	0	0	0	0	ENSG00000238254	AC008496.1
ENSG00000238255	0.0259809	0.0124808	0.033827	0	ENSG00000238255	RPL7P4
ENSG00000238256	2.3607	1.55086	2.96619	0	ENSG00000238256	MTND5P20
ENSG00000238257	0	0	0	0	ENSG00000238257	AP000244.1
ENSG00000238259	1.40346	2.1937	1.19924	4.46602	ENSG00000238259	AC067940.1
ENSG00000238263	0	0.178586	0.322482	0.396622	ENSG00000238263	RPL21P88
ENSG00000238267	0	0	0.141297	0	ENSG00000238267	AC104850.1
ENSG00000238269	0.363952	0.445999	0.150646	0.185463	ENSG00000238269	PAGE2B
ENSG00000238271	9.17717	13.9399	29.6553	21.0619	ENSG00000238271	IFNWP19
ENSG00000238275	0	0	0	0	ENSG00000238275	HOMER2P2
ENSG00000238278	0.441908	0.469377	2.36438	0.902717	ENSG00000238278	ALG1L6P
ENSG00000238283	0	0	0	0	ENSG00000238283	TBC1D3P1
ENSG00000238285	0.165178	0.153673	0.27748	0.513516	ENSG00000238285	MRPL50P2
ENSG00000238286	0.515464	0.637329	0.895842	1.52628	ENSG00000238286	SLC35E1P1
ENSG00000238288	0.270794	1.94647	0.749383	1.13598	ENSG00000238288	MTND3P23
ENSG00000238289	0.238434	0.898692	2.23005	0.927638	ENSG00000238289	MICB
ENSG00000239198	0	0.0689401	0	0	ENSG00000239198	RPL5P22
ENSG00000239199	0	0.17364	0	0.153277	ENSG00000239199	RPL21P6
ENSG00000239200	0	1.12317	0.271061	0.4965	ENSG00000239200	CR383656.1
ENSG00000239201	0.162337	0.155598	0	0.173323	ENSG00000239201	AC025164.1
ENSG00000239207	0.633321	0.975431	0.613371	1.30971	ENSG00000239207	GAPDHP39
ENSG00000239210	0	0	0	0	ENSG00000239210	RPS26P55
ENSG00000239212	0	0	0	0	ENSG00000239212	RPL6P7
ENSG00000239215	0.218975	0.842464	0.764373	0.248215	ENSG00000239215	AC117503.1
ENSG00000239218	1.25886	2.36614	2.03737	4.72268	ENSG00000239218	RPS20P22

ENSG00000239223	0	0	0	0	ENSG00000239223	AC026254.2
ENSG00000239226	0	0	0	0	ENSG00000239226	MRPS17P3
ENSG00000239227	0	0	0	0	ENSG00000239227	AC069439.1
ENSG00000239238	0	0	0	0	ENSG00000239238	MEMO1P3
ENSG00000239246	0.248253	0.647324	0	0.634968	ENSG00000239246	AC008026.1
ENSG00000239253	0	0	0	0	ENSG00000239253	RPS4XP23
ENSG00000239254	0.304655	1.06949	1.41342	1.58019	ENSG00000239254	AC009220.2
ENSG00000239255	0	0	0	0	ENSG00000239255	AC007620.1
ENSG00000239256	0	0	0	0	ENSG00000239256	AC005412.2
ENSG00000239257	0.504956	0.43427	0.423746	0.412063	ENSG00000239257	RPL23AP1
ENSG00000239261	0	0	0	0	ENSG00000239261	RPL31P41
ENSG00000239263	1.46193	7.22066	2.31729	5.56542	ENSG00000239263	RBM43P1
ENSG00000239264	79.0094	114.841	41.1707	64.7456	ENSG00000239264	TXNDC5
ENSG00000239269	0	0	0	0	ENSG00000239269	RPSAP4
ENSG00000239272	0.156521	0.301577	0.718956	1.00304	ENSG00000239272	RPL21P10
ENSG00000239275	0	0	0	0.325725	ENSG00000239275	RP4-675G8.2
ENSG00000239280	1.51462	6.7027	5.31059	5.83064	ENSG00000239280	AC108693.1
ENSG00000239281	0	3.46659	0	0	ENSG00000239281	RPS29P2
ENSG00000239282	9.30742	6.38723	5.84872	7.36884	ENSG00000239282	CASTOR1
ENSG00000239285	0	0	0.721208	1.78051	ENSG00000239285	LY6G5B
ENSG00000239288	0.0406547	0.114299	0.230423	0.197363	ENSG00000239288	AC063923.1
ENSG00000239291	0.886845	1.73261	0.994052	3.64848	ENSG00000239291	AC002558.1
ENSG00000239293	0	0	0	0	ENSG00000239293	OR9P1P
ENSG00000239304	0	0	0	0	ENSG00000239304	DNM1P48
ENSG00000239305	25.0964	18.3767	16.1766	16.9887	ENSG00000239305	RNF103
ENSG00000239306	25.5939	50.7404	39.5288	40.1135	ENSG00000239306	RBM14
ENSG00000239315	0	0	0	0	ENSG00000239315	RPL19P13
ENSG00000239317	0.546367	4.63209	2.71499	2.36459	ENSG00000239317	AC091959.1
ENSG00000239320	1.11762	3.12882	2.76052	2.20457	ENSG00000239320	RPS29P26
ENSG00000239323	0	0	0	0.133856	ENSG00000239323	AL163973.1
ENSG00000239327	0	0	0	0	ENSG00000239327	AL163195.1
ENSG00000239329	0	0	0.00913478	0.00910544	ENSG00000239329	HLA-DMB
ENSG00000239332	0.722374	2.31905	0.711289	4.25656	ENSG00000239332	LINC01119
ENSG00000239334	0.860773	1.9956	1.39852	2.77829	ENSG00000239334	GSTTP2
ENSG00000239344	0.198785	0.999354	0.306124	0	ENSG00000239344	AC090686.1
ENSG00000239345	0.0562136	0	0.0495979	0.123983	ENSG00000239345	HNRNPA1P26
ENSG00000239350	0	0	0	0	ENSG00000239350	AC105265.1
ENSG00000239351	0.323798	1.23974	1.02541	2.89691	ENSG00000239351	NPM1P29
ENSG00000239354	0.268129	0	0	0	ENSG00000239354	RPS17P15
ENSG00000239365	0	0.275026	0.248592	0	ENSG00000239365	AL590326.1
ENSG00000239374	0.332932	0	0.314074	0	ENSG00000239374	AC090013.1
ENSG00000239382	12.9117	13.3634	14.11	8.26775	ENSG00000239382	ALKBH6
ENSG00000239383	0	0	0	0	ENSG00000239383	AC108724.1
ENSG00000239388	0.809888	1.3982	1.6207	1.16718	ENSG00000239388	ASB14
ENSG00000239389	0.0865499	0.0682183	0.0623268	0.109141	ENSG00000239389	PCDHA13
ENSG00000239392	0.0381123	0.0734633	0	0.0418821	ENSG00000239392	AL354989.2
ENSG00000239393	0.262009	0.50039	1.57807	1.10235	ENSG00000239393	AC146507.1
ENSG00000239397	0.106116	0	0	0	ENSG00000239397	AC084878.1
ENSG00000239402	0.389831	1.15974	0.451925	1.88435	ENSG00000239402	CYP4F62P
ENSG00000239405	0	0	0	0	ENSG00000239405	TMED10P2
ENSG00000239408	0	0	0	0	ENSG00000239408	AC108751.1
ENSG00000239412	0	0	0	0	ENSG00000239412	RPL21P71
ENSG00000239413	0.491964	0.463823	0.413933	0	ENSG00000239413	RPS27P23
ENSG00000239426	0	0.0770195	0.208752	0	ENSG00000239426	OR8F1P

ENSG00000239428	0	0	0	0	ENSG00000239428	GM2AP2
ENSG00000239429	0.218647	0.327687	0.394624	1.09168	ENSG00000239429	AF274854.1
ENSG00000239432	0	0.265443	0	0	ENSG00000239432	AF186996.4
ENSG00000239435	0.169199	0.743035	0.117137	0.942689	ENSG00000239435	KCNMB3P1
ENSG00000239438	0	0	0	0	ENSG00000239438	RPS26P48
ENSG00000239439	0	0	0	0.173735	ENSG00000239439	RFKP2
ENSG00000239443	0	0	0	0	ENSG00000239443	PABPC1P10
ENSG00000239455	0.0322389	0.0310788	0.0562936	0.389366	ENSG00000239455	AC074043.1
ENSG00000239457	0	0.113748	0.874059	0	ENSG00000239457	HLA-DOB
ENSG00000239463	0.438161	0.200969	0.356435	0.33828	ENSG00000239463	HLA-DMA
ENSG00000239465	0.324797	2.17371	1.01553	2.61704	ENSG00000239465	AC090543.1
ENSG00000239470	0	0.265417	0	0.303907	ENSG00000239470	AC011979.1
ENSG00000239473	0	0	0	0	ENSG00000239473	RPL7P38
ENSG00000239474	0.225059	0.3984	0.746895	0.600288	ENSG00000239474	KLHL41
ENSG00000239475	0.0700634	0.201666	0.113753	0.145522	ENSG00000239475	HYDIN2
ENSG00000239481	0	0	0	0	ENSG00000239481	RPS3AP41
ENSG00000239483	2.81316	4.8236	4.60775	5.81391	ENSG00000239483	AC023598.1
ENSG00000239486	0.392685	1.44698	1.01005	1.87658	ENSG00000239486	AC091390.3
ENSG00000239490	0	0.165229	0	0	ENSG00000239490	RPS4XP18
ENSG00000239492	33.2252	31.92	51.6477	10.3114	ENSG00000239492	GFAM25HP
ENSG00000239497	0	0	0.721208	1.78051	ENSG00000239497	LY6G5B
ENSG00000239500	0	0.684979	0.145749	0.252647	ENSG00000239500	RP1-169K13.3
ENSG00000239503	1.6791	3.21188	4.7438	6.26983	ENSG00000239503	MARK2P8
ENSG00000239510	0	0	0	0.530815	ENSG00000239510	AL135752.1
ENSG00000239511	0.28191	0.493256	0.474159	0.875819	ENSG00000239511	POM121L7P
ENSG00000239516	0	0.0291544	0.0527579	0.0663627	ENSG00000239516	FLYWCH1P1
ENSG00000239517	1.84277	0	0	0	ENSG00000239517	AC116337.2
ENSG00000239520	0.065495	0.495595	0.45387	0.23425	ENSG00000239520	RPL17P42
ENSG00000239521	7.84598	10.0715	19.4613	15.0317	ENSG00000239521	GATS
ENSG00000239524	0.21391	0.240371	0.392917	0.331457	ENSG00000239524	RPL32P34
ENSG00000239525	0	0	0	0	ENSG00000239525	RPL30P5
ENSG00000239527	0	0.17368	0	0	ENSG00000239527	RPS23P7
ENSG00000239528	0.732116	0	1.26772	0.513815	ENSG00000239528	RPS14P8
ENSG00000239532	0.16334	0	0	0	ENSG00000239532	AC108022.1
ENSG00000239539	0.351773	0.665081	0.300684	1.09211	ENSG00000239539	HMGN1P20
ENSG00000239544	0.249555	0.952292	2.05246	0.752441	ENSG00000239544	AL442663.1
ENSG00000239556	5.15025	3.14444	6.0926	3.13471	ENSG00000239556	AC004951.2
ENSG00000239557	0.202557	0.0990004	0.270134	0.279419	ENSG00000239557	AC092045.1
ENSG00000239559	0.384178	0	0	0	ENSG00000239559	AP003385.3
ENSG00000239568	0	0	0	0	ENSG00000239568	AC104435.1
ENSG00000239570	0	0	0	0	ENSG00000239570	SETP11
ENSG00000239571	0	0	0	0	ENSG00000239571	IGKV2D-30
ENSG00000239576	2.15486	4.00514	1.82274	5.76835	ENSG00000239576	COX6CP14
ENSG00000239581	0.318525	2.28986	1.17301	2.19702	ENSG00000239581	RP11-19G24.1
ENSG00000239586	0	0	0.122107	0.305491	ENSG00000239586	MTND1P16
ENSG00000239590	0	0	0	0	ENSG00000239590	OR1J4
ENSG00000239600	0	0	0	0	ENSG00000239600	AP000797.1
ENSG00000239602	0.932755	1.80084	5.4613	1.94911	ENSG00000239602	AC091959.2
ENSG00000239605	3.44248	7.98322	9.09928	12.1124	ENSG00000239605	STPG4
ENSG00000239614	1.68124	3.23492	5.36954	5.60618	ENSG00000239614	HMGN1P7
ENSG00000239615	0	0.178586	0	0	ENSG00000239615	AC104109.1
ENSG00000239617	0.514835	0.20754	0.646234	0	ENSG00000239617	AC073610.1
ENSG00000239618	0.281646	0.863301	1.48808	0	ENSG00000239618	HLA-L
ENSG00000239620	0	0.112672	0	0	ENSG00000239620	AC133681.1

ENSG00000239622	0	0.221988	0.200384	0.245651	ENSG00000239622	AC005165.2
ENSG00000239626	1.99958	3.56087	3.60375	1.86871	ENSG00000239626	RPSAP41
ENSG00000239627	0	0	0	0.173596	ENSG00000239627	RPL12P20
ENSG00000239632	0	0	0	0.843537	ENSG00000239632	MTND4LP3
ENSG00000239642	1.15092	2.62964	1.27373	5.3672	ENSG00000239642	MEIKIN
ENSG00000239648	0.196476	0.18708	0.455303	0.0712481	ENSG00000239648	MTND1P3
ENSG00000239649	0.212448	0.412519	0.278981	0.459169	ENSG00000239649	MYADML
ENSG00000239650	3.89954	4.27591	3.68062	4.52799	ENSG00000239650	GUSBP4
ENSG00000239659	0	0	0	0	ENSG00000239659	AC104971.1
ENSG00000239665	23.1067	43.8504	47.3791	54.6045	ENSG00000239665	AL157392.3
ENSG00000239670	0.516197	0.567318	1.60366	0.881059	ENSG00000239670	AL355864.2
ENSG00000239671	0.318863	1.56226	0.705577	0.878424	ENSG00000239671	AC100793.1
ENSG00000239672	59.2934	51.2123	41.2688	32.1585	ENSG00000239672	NME1
ENSG00000239683	0	0	0	0	ENSG00000239683	AC007998.1
ENSG00000239684	0	0.229841	0	0	ENSG00000239684	PTGER4P3
ENSG00000239686	1.91487	3.27475	4.40581	3.41087	ENSG00000239686	AL158801.1
ENSG00000239689	0	0	0	0	ENSG00000239689	AC015864.1
ENSG00000239694	0.143818	0	0.0624866	0.234387	ENSG00000239694	RPSAP38
ENSG00000239696	0.207204	0.435124	0.466499	0.683737	ENSG00000239696	AC092104.1
ENSG00000239697	1.41049	1.0617	0.573571	1.93461	ENSG00000239697	TNFSF12
ENSG00000239699	0	0	0.111421	0.277398	ENSG00000239699	HNRNPA3P8
ENSG00000239701	0	0.351246	0.158257	0	ENSG00000239701	AC006512.1
ENSG00000239704	3.13883	10.0516	17.9004	11.8691	ENSG00000239704	CDRT4
ENSG00000239706	0.474963	0	0	0	ENSG00000239706	AC117392.1
ENSG00000239713	3.9658	17.6325	5.18443	7.71029	ENSG00000239713	APOBEC3G
ENSG00000239719	1.11687	2.04285	0	0	ENSG00000239719	AC004890.1
ENSG00000239722	0	0.157017	0.14174	0	ENSG00000239722	IMP3P2
ENSG00000239732	0.0669127	0.0966603	0.255936	0.105784	ENSG00000239732	TLR9
ENSG00000239736	0.021805	0.27787	0.407957	0.25065	ENSG00000239736	CEACAMP3
ENSG00000239741	0.0272928	0.112493	0.0254114	0.0148391	ENSG00000239741	LY6G6F
ENSG00000239754	0.0860657	0.424376	1.71916	0.355053	ENSG00000239754	CFB
ENSG00000239763	1.99458	1.58964	2.45212	5.52407	ENSG00000239763	AC009120.1
ENSG00000239779	24.3191	29.5644	33.9325	22.0471	ENSG00000239779	WBP1
ENSG00000239780	0	0	0	0	ENSG00000239780	AC090638.1
ENSG00000239783	0.240588	0.459069	0	0.760789	ENSG00000239783	AL121776.1
ENSG00000239784	0.504956	0.43427	0.423746	0.412063	ENSG00000239784	RPL23AP1
ENSG00000239789	7.17529	10.9048	14.2461	11.0756	ENSG00000239789	MRPS17
ENSG00000239792	0	0	0	0	ENSG00000239792	C2orf27AP2
ENSG00000239793	0	0	0	0	ENSG00000239793	AC098818.1
ENSG00000239797	0.185303	0	0	0	ENSG00000239797	RPL21P39
ENSG00000239804	0.462929	0	0	0	ENSG00000239804	AC092902.1
ENSG00000239805	0	0	0	0	ENSG00000239805	AC007547.2
ENSG00000239809	0	0.256685	0.46377	0	ENSG00000239809	AC008026.2
ENSG00000239810	0	0	0	0	ENSG00000239810	PRAMEF11
ENSG00000239819	0	0	0	0	ENSG00000239819	IGKV1D-8
ENSG00000239827	2.27516	3.89813	5.38475	5.65614	ENSG00000239827	SUGT1P3
ENSG00000239829	0.0400147	0.0392927	0.0348595	0	ENSG00000239829	KRT8P25
ENSG00000239830	0.343804	0.249541	0.147195	0.745983	ENSG00000239830	RPS4XP22
ENSG00000239831	0	0	0	0	ENSG00000239831	RNF7P1
ENSG00000239835	1.4985	4.63412	3.25188	4.86004	ENSG00000239835	AC092910.1
ENSG00000239836	0.400964	1.56665	0.740797	1.8861	ENSG00000239836	PSMB9
ENSG00000239839	0	0	0	0	ENSG00000239839	DEFA3
ENSG00000239840	0.187276	0.537677	0.485453	0.795921	ENSG00000239840	RPL23AP72
ENSG00000239855	0	0	0.200304	0	ENSG00000239855	IGKV1-6

ENSG00000239857	16.6876	16.6756	17.8086	10.9703	ENSG00000239857	GET4
ENSG00000239861	0.16336	0	0.282594	0.348492	ENSG00000239861	AP001486.1
ENSG00000239862	0	0	0	0	ENSG00000239862	IGKV1-37
ENSG00000239865	1.37862	7.435	4.52186	0.664077	ENSG00000239865	RPP21
ENSG00000239870	0	0	0.140857	0.347469	ENSG00000239870	AC112206.1
ENSG00000239872	0	0	0	0.321803	ENSG00000239872	RPL35AP19
ENSG00000239873	0	0	0.0524388	0.328479	ENSG00000239873	GAPDHP27
ENSG00000239880	1.94019	4.8527	0.461515	11.9546	ENSG00000239880	AC068760.1
ENSG00000239881	0	0.611401	0.708785	0.173194	ENSG00000239881	AC003982.1
ENSG00000239882	0	0.352718	0.916186	0.387972	ENSG00000239882	CYP21A1P
ENSG00000239883	2.89494	4.97372	5.09086	6.13934	ENSG00000239883	PARGP1
ENSG00000239886	0	0	0	0	ENSG00000239886	KRTAP9-2
ENSG00000239887	0.657446	0.258761	0.378048	0.652134	ENSG00000239887	C1orf226
ENSG00000239893	2.06448	2.05425	0.673873	0.776712	ENSG00000239893	ZNF736P9Y
ENSG00000239900	24.5941	37.6631	30.3537	33.1028	ENSG00000239900	ADSL
ENSG00000239903	0.122563	0.190745	0.191272	0	ENSG00000239903	RP11-353N4.2
ENSG00000239912	4.69806	10.4913	5.90501	6.73833	ENSG00000239912	RPL39P36
ENSG00000239917	0.3121	1.77087	1.11374	0.492925	ENSG00000239917	RPS10P16
ENSG00000239919	1.20991	0.593101	1.11504	2.17461	ENSG00000239919	SNRPGP3
ENSG00000239924	0	0	0	0	ENSG00000239924	RPL29P22
ENSG00000239926	0.529817	0.763625	2.45301	4.79393	ENSG00000239926	PRDX3P4
ENSG00000239927	0	0	0	0	ENSG00000239927	RPP21
ENSG00000239939	0	0	0	0	ENSG00000239939	RPSAP34
ENSG00000239944	0.427147	0	0	0	ENSG00000239944	TRBV8-2
ENSG00000239951	0	0	0	0	ENSG00000239951	IGKV3-20
ENSG00000239959	0	0.132912	0.0599499	0.375388	ENSG00000239959	ENPP7P2
ENSG00000239961	0.0332516	0.0790378	0.102802	0	ENSG00000239961	LILRA4
ENSG00000239967	0	0	2.58697	0	ENSG00000239967	OR2A41P
ENSG00000239969	2.96246	3.28193	3.39168	2.80129	ENSG00000239969	AC091390.4
ENSG00000239974	0.036129	2.09376	1.22181	1.7452	ENSG00000239974	EGFL8
ENSG00000239975	0	0.353614	0.240317	0	ENSG00000239975	IGKV1D-33
ENSG00000239978	0.111165	0	0.302282	0.232594	ENSG00000239978	AF186996.5
ENSG00000239981	0	0.183094	0.121778	0	ENSG00000239981	OR2A15P
ENSG00000239983	0	0	0	0	ENSG00000239983	AC016687.1
ENSG00000239985	0	0	0	0	ENSG00000239985	AC073210.2
ENSG00000239986	0	0	0	0	ENSG00000239986	AL445584.1
ENSG00000239988	0.492402	1.64917	0.636543	1.03673	ENSG00000239988	RPL31P60
ENSG00000239989	0	0	0	0	ENSG00000239989	AC008132.2
ENSG00000239992	0.159659	0	0	0	ENSG00000239992	TRBVA
ENSG00000239995	0	0	0	0.163358	ENSG00000239995	TPT1P11
ENSG00000239997	0	0	0.105362	0.517893	ENSG00000239997	FCF1P3
ENSG00000239998	0.541289	0.571145	0.330792	1.93053	ENSG00000239998	LILRA2
ENSG00000240002	0.415406	0.865555	0.300803	0.827952	ENSG00000240002	YBX1P3
ENSG00000240003	0.17575	0.0843565	0	0.190202	ENSG00000240003	RPL7P24
ENSG00000240007	0.829687	3.41261	2.20849	0.959835	ENSG00000240007	RP6-206I17.4
ENSG00000240008	0.0272928	0.112493	0.0254114	0.0148391	ENSG00000240008	LY6G6F
ENSG00000240021	11.5723	28.4157	28.5762	46.2451	ENSG00000240021	TEX35
ENSG00000240023	0	0	0	0	ENSG00000240023	AL133163.1
ENSG00000240024	2.2706	3.0444	4.33197	3.42797	ENSG00000240024	LINC00888
ENSG00000240027	0	0	0.402115	0	ENSG00000240027	AC084357.1
ENSG00000240031	0.0361047	0.173614	0.0313733	0.247134	ENSG00000240031	OR9A3P
ENSG00000240034	0.898847	1.27153	1.85396	1.22874	ENSG00000240034	MTND6P6
ENSG00000240036	0.567914	0.563264	0.25904	0.299473	ENSG00000240036	AC104563.1
ENSG00000240038	10.2002	20.8152	23.263	23.0453	ENSG00000240038	AMY2B

ENSG00000240041	0	0	0	0	ENSG00000240041	IGHJ4
ENSG00000240042	0	0	0	0	ENSG00000240042	AC098789.1
ENSG00000240043	0	0	0.454094	0	ENSG00000240043	RPS27P26
ENSG00000240047	0	0.164414	0	0.403046	ENSG00000240047	AC087672.1
ENSG00000240048	0.025752	0.0495991	0.0674906	0.311588	ENSG00000240048	DDX50P2
ENSG00000240051	0	0	0.145792	0	ENSG00000240051	RPL23AP10
ENSG00000240052	0.495688	0	0.193229	0.570305	ENSG00000240052	AC108114.1
ENSG00000240053	2.57102	1.31578	4.39079	2.34871	ENSG00000240053	LY6G5B
ENSG00000240058	0.557765	0.671148	0.762339	1.42202	ENSG00000240058	AC093267.1
ENSG00000240065	0	0.67211	0	0.492761	ENSG00000240065	PSMB9
ENSG00000240068	0	0	0	0.181241	ENSG00000240068	RPL21P42
ENSG00000240069	0	0	0	0.383859	ENSG00000240069	GPAA1P1
ENSG00000240074	0.125015	1.56689	0.433314	2.68667	ENSG00000240074	AC104982.1
ENSG00000240083	0.170256	0.245467	0.221755	0.737709	ENSG00000240083	RPS3AP22
ENSG00000240084	0	0	0	0	ENSG00000240084	MTND4LP10
ENSG00000240087	0.10783	0.100901	0	0	ENSG00000240087	RPSAP12
ENSG00000240089	1.52686	0.543432	0.250824	1.34927	ENSG00000240089	BMS1P3
ENSG00000240096	0	0.260042	0.117452	0.145178	ENSG00000240096	AL132838.1
ENSG00000240097	0.0947697	0.227373	0.267167	0.310296	ENSG00000240097	AC104164.3
ENSG00000240100	0	0	0	0	ENSG00000240100	AC083806.1
ENSG00000240103	1.0455	1.32671	2.12131	5.19645	ENSG00000240103	AC132825.1
ENSG00000240107	0.202321	0.236833	0.203569	0.322528	ENSG00000240107	AC046144.1
ENSG00000240108	0.741673	0.718772	0.640259	0	ENSG00000240108	NCOR1P1
ENSG00000240118	0	0.67211	0	0.963161	ENSG00000240118	PSMB9
ENSG00000240121	0	0	0	0	ENSG00000240121	RPS27P20
ENSG00000240122	0	0	0	0	ENSG00000240122	FABP5P11
ENSG00000240125	0.177481	0.242177	0.306712	0	ENSG00000240125	RPL23AP75
ENSG00000240128	0	0	0	0.12504	ENSG00000240128	KRT18P43
ENSG00000240131	0	0	1.13112	0	ENSG00000240131	AL049829.1
ENSG00000240132	1.78382	5.05731	4.30568	5.37199	ENSG00000240132	AC005996.1
ENSG00000240135	0	0.166127	0.150974	0.0947303	ENSG00000240135	AC114876.1
ENSG00000240138	0.0904311	0.0435461	0.275519	0.049421	ENSG00000240138	EEF1GP4
ENSG00000240156	0	0	0	0	ENSG00000240156	COX6CP6
ENSG00000240159	0.0783088	0	0.0683676	0	ENSG00000240159	AC079080.1
ENSG00000240163	67.3811	66.3686	30.5506	103.912	ENSG00000240163	AC087385.1
ENSG00000240167	0	0	0	0	ENSG00000240167	RPS7P7
ENSG00000240174	0	0	0.108589	0	ENSG00000240174	AP000852.1
ENSG00000240179	0.780761	0.511001	0.953455	2.62935	ENSG00000240179	AL133162.1
ENSG00000240180	0	0	0	0	ENSG00000240180	RPL12P28
ENSG00000240184	31.149	28.3866	14.0336	28.6208	ENSG00000240184	PCDHGC3
ENSG00000240194	0	0	0	0	ENSG00000240194	CYMP
ENSG00000240197	0.428706	0	0	0	ENSG00000240197	AC245884.5
ENSG00000240201	0.177209	0.17471	0.0770099	0.29766	ENSG00000240201	AL133372.1
ENSG00000240204	0.237076	0.578848	0.505071	0.660547	ENSG00000240204	SMKR1
ENSG00000240210	0.242757	0.840458	0.281548	1.24281	ENSG00000240210	AL122013.1
ENSG00000240215	0	0	0	0	ENSG00000240215	TRBV25OR9-2
ENSG00000240216	0.310687	1.33264	0.288709	1.14781	ENSG00000240216	CPHL1P
ENSG00000240224	0	0.0922408	0.548429	0.0884481	ENSG00000240224	UGT1A5
ENSG00000240225	20.5837	13.5117	14.0249	13.7334	ENSG00000240225	ZNF542P
ENSG00000240230	7.03887	11.4219	18.2194	8.09568	ENSG00000240230	COX19
ENSG00000240231	0	0	0	0	ENSG00000240231	RPS27P29
ENSG00000240236	0	0.0513462	0.0928592	0.0582502	ENSG00000240236	HNRNPA1P23
ENSG00000240237	0	0	0	0	ENSG00000240237	AF305872.1
ENSG00000240238	0.162633	0	0	0	ENSG00000240238	AC092754.1

ENSG00000240240	0.598822	0.164069	0	0.308669	ENSG00000240240	BX664727.3
ENSG00000240244	0	0.175505	0.158603	1.12587	ENSG00000240244	GAPDHP33
ENSG00000240246	1.89257	6.36775	2.78657	8.61856	ENSG00000240246	AC108751.2
ENSG00000240247	0	0	0	0	ENSG00000240247	DEFA1B
ENSG00000240253	2.22174	3.60117	5.83149	9.42288	ENSG00000240253	FAR2P3
ENSG00000240255	0	0	0	0	ENSG00000240255	PSMC1P6
ENSG00000240257	0	0	0.0657764	0	ENSG00000240257	GAGE2D
ENSG00000240265	2.62281	8.32686	3.99153	9.99993	ENSG00000240265	AC099328.1
ENSG00000240268	0	0	0	0	ENSG00000240268	MOXD2P
ENSG00000240270	0.308418	0.390688	0	0	ENSG00000240270	RPL12P37
ENSG00000240271	0	0.654509	0.443309	0.54589	ENSG00000240271	AC090142.1
ENSG00000240279	0	0	0	0	ENSG00000240279	AL353997.4
ENSG00000240280	0.498682	0.999485	0.688137	0.866276	ENSG00000240280	TCAM1P
ENSG00000240281	0	0	0	0	ENSG00000240281	AC034222.1
ENSG00000240286	0.901703	0.856309	1.548	0.647447	ENSG00000240286	MEAF6P1
ENSG00000240296	0	0	0	0	ENSG00000240296	AC245052.5
ENSG00000240298	0.624705	0.697714	0.21021	0.513815	ENSG00000240298	AC015820.1
ENSG00000240303	12.5622	24.3342	23.9315	18.5609	ENSG00000240303	ACAD11
ENSG00000240305	0.0764611	0.749183	0.265671	0.664277	ENSG00000240305	AC091152.1
ENSG00000240309	0.0847336	0.0816061	0.0737631	0.185364	ENSG00000240309	MTCO1P6
ENSG00000240311	0.126837	0.243432	0	0.408714	ENSG00000240311	AC004224.1
ENSG00000240320	0	0	0	0	ENSG00000240320	RPS29P27
ENSG00000240328	0.277683	1.8487	1.43504	2.03624	ENSG00000240328	AC091805.1
ENSG00000240338	1.69507	3.20457	2.40461	5.9263	ENSG00000240338	AC009078.2
ENSG00000240342	8.23643	0.602558	13.5604	13.0934	ENSG00000240342	AC026366.1
ENSG00000240344	21.1006	47.3164	39.1954	46.8694	ENSG00000240344	PPIL3
ENSG00000240356	3.54318	6.69696	6.31332	4.88647	ENSG00000240356	RPL23AP7
ENSG00000240359	0	0	0	0	ENSG00000240359	UBL5P3
ENSG00000240361	0.0664888	0	0	0	ENSG00000240361	OR4G11P
ENSG00000240364	0	0.27794	0	0.30592	ENSG00000240364	AP001025.1
ENSG00000240366	0	0	0	0	ENSG00000240366	AC113208.1
ENSG00000240370	2.31131	3.21756	3.52154	7.00564	ENSG00000240370	RPL13P5
ENSG00000240371	0	0	0	0	ENSG00000240371	RPS4XP13
ENSG00000240375	0.189966	0.12241	0.0554329	0.691701	ENSG00000240375	VPS26AP1
ENSG00000240376	0.229557	0.112262	0.201013	0.248901	ENSG00000240376	AC010343.1
ENSG00000240382	0	0	0	0	ENSG00000240382	IGKV1-17
ENSG00000240385	0	3.12882	0.920175	0.551143	ENSG00000240385	RPS29P20
ENSG00000240386	1.35834	0.567192	0.411629	5.21408	ENSG00000240386	LCE1F
ENSG00000240388	0	0	0	0.1852	ENSG00000240388	AC008799.1
ENSG00000240389	0.036129	2.09376	1.22181	1.7452	ENSG00000240389	EGFL8
ENSG00000240392	0	0.479846	0	0.538271	ENSG00000240392	AL121594.1
ENSG00000240393	0.0806223	0.0774966	0.0700146	0	ENSG00000240393	AC092691.2
ENSG00000240395	0.716833	0.638756	1.02926	0.964104	ENSG00000240395	RPL5P23
ENSG00000240399	1.02058	1.20108	1.19292	2.39815	ENSG00000240399	AC004801.2
ENSG00000240403	0.0131325	0.00949554	0.0125962	0.044165	ENSG00000240403	KIR3DL2
ENSG00000240404	0	1.45812	1.40588	3.12935	ENSG00000240404	AC017015.1
ENSG00000240409	0	0	0	0	ENSG00000240409	MTATP8P1
ENSG00000240411	0.248398	0.0790889	0.0714518	0.178596	ENSG00000240411	RPL5P16
ENSG00000240412	0	0	0.0611358	0	ENSG00000240412	RPL5P15
ENSG00000240416	0	0	0	0.334641	ENSG00000240416	CYCSP20
ENSG00000240418	5.45227	5.77898	14.3811	8.04451	ENSG00000240418	AC020917.1
ENSG00000240419	0	0	0	0	ENSG00000240419	AC022206.1
ENSG00000240424	0	0	0	0	ENSG00000240424	AC092824.1
ENSG00000240426	0	0	0	0	ENSG00000240426	AC096743.1

ENSG00000240427	0	0	0	0	ENSG00000240427	AC090255.1
ENSG00000240429	0.584305	0.783543	0.610737	0.879959	ENSG00000240429	LRRFIP1P1
ENSG00000240432	0.0952505	0	0	0	ENSG00000240432	KRTAP13-3
ENSG00000240433	0	0	0	0	ENSG00000240433	LY6G5B
ENSG00000240435	0.570061	1.08291	0	0.650935	ENSG00000240435	AC020978.1
ENSG00000240436	0.310687	1.29225	1.33196	2.21246	ENSG00000240436	AC114982.1
ENSG00000240438	0	0	0	0	ENSG00000240438	OFD1P5Y
ENSG00000240441	0	0.452506	0.597169	0.44336	ENSG00000240441	AC007622.1
ENSG00000240443	0	0	0	0	ENSG00000240443	RPS10P20
ENSG00000240445	1.17509	1.99906	2.79667	1.5195	ENSG00000240445	FOXO3B
ENSG00000240452	0	1.7889	0	1.17243	ENSG00000240452	MTCO1P29
ENSG00000240454	8.9892	21.0624	12.1524	11.8707	ENSG00000240454	AC013828.1
ENSG00000240458	0	0	0	0	ENSG00000240458	AC072046.1
ENSG00000240459	0	0	0	0	ENSG00000240459	AC093663.1
ENSG00000240463	0.553281	1.56018	1.1227	4.42431	ENSG00000240463	RPS19P3
ENSG00000240471	0	0.0882996	0	0	ENSG00000240471	PHBP8
ENSG00000240477	0	0.44394	0.095565	0.306652	ENSG00000240477	AC022494.1
ENSG00000240480	0	0.763761	0.468111	0.785581	ENSG00000240480	RPL29P2
ENSG00000240484	0	0	0.231885	0	ENSG00000240484	AC091544.1
ENSG00000240486	0	0	0.171514	0	ENSG00000240486	RPL23AP54
ENSG00000240487	0.106262	0.0682495	0.0925424	0.0388034	ENSG00000240487	AC093010.1
ENSG00000240489	0	0.0860284	0.0783367	0.0986046	ENSG00000240489	SETP14
ENSG00000240494	0	0	0	0	ENSG00000240494	AC005726.1
ENSG00000240505	1.50957	2.55298	2.92364	4.47124	ENSG00000240505	TNFRSF13B
ENSG00000240508	0.169023	0.0380732	1.16434	0.0741571	ENSG00000240508	PSMB9
ENSG00000240509	0	0	0.457618	0	ENSG00000240509	RPL34P18
ENSG00000240510	0.875123	1.37777	1.41358	0	ENSG00000240510	AL589765.1
ENSG00000240511	0	0	0	0	ENSG00000240511	MED28P2
ENSG00000240513	0	0	0	0	ENSG00000240513	AL049830.2
ENSG00000240518	0	0.303038	0.547746	0.332899	ENSG00000240518	AC116353.1
ENSG00000240519	0	1.0198	0.472829	1.16072	ENSG00000240519	AC091675.1
ENSG00000240520	0.140343	0	0.121942	0.228813	ENSG00000240520	UOX
ENSG00000240522	7.80693	3.38087	2.78223	3.38421	ENSG00000240522	RPL7AP10
ENSG00000240524	0	0.650256	0.604654	0.739259	ENSG00000240524	RP5-1061H20.3
ENSG00000240531	0.79009	1.59516	0.683685	1.52406	ENSG00000240531	AC104564.1
ENSG00000240534	0	0	0	0	ENSG00000240534	RPL34P17
ENSG00000240540	0	0	0.0441851	0.0571051	ENSG00000240540	RPL3P9
ENSG00000240542	0.689175	0.979827	1.179	2.86155	ENSG00000240542	KRTAP9-1
ENSG00000240554	0	0	0	0	ENSG00000240554	AL135933.1
ENSG00000240563	1.43807	2.03121	4.74626	5.0038	ENSG00000240563	L1TD1
ENSG00000240566	0	0	0	0	ENSG00000240566	AC010153.1
ENSG00000240568	0	0	0	0.948027	ENSG00000240568	AC107626.1
ENSG00000240572	2.08395	0	0	2.06806	ENSG00000240572	AC107297.1
ENSG00000240578	0.28503	0	0.244685	0	ENSG00000240578	TRBV22-1
ENSG00000240579	0.651292	2.26094	1.89718	3.90867	ENSG00000240579	AC006529.1
ENSG00000240583	0.772658	0.34266	0.203005	0.801399	ENSG00000240583	AQP1
ENSG00000240590	0.294803	0.35413	0.260185	1.0614	ENSG00000240590	RPSAP48
ENSG00000240592	0.949115	1.66713	2.35958	2.46363	ENSG00000240592	EGFL8
ENSG00000240601	0	0	0	0	ENSG00000240601	RPL9P15
ENSG00000240602	0.140824	0.452495	0.240712	0.45673	ENSG00000240602	AADACP1
ENSG00000240611	0.230062	0.0737287	0.0666134	0.166481	ENSG00000240611	AC010307.1
ENSG00000240616	1.13159	1.01954	1.23659	0.959123	ENSG00000240616	RPS6P25
ENSG00000240621	0.844741	1.21083	2.00473	1.56514	ENSG00000240621	OR2AO1P
ENSG00000240622	0	0	0	0	ENSG00000240622	RPL7P15

ENSG00000240624	0	0	0.119119	0	ENSG00000240624	AL138976.1
ENSG00000240627	0	0	0	0	ENSG00000240627	AC026798.1
ENSG00000240631	0	0	0	0	ENSG00000240631	RPL30P12
ENSG00000240632	0.0448785	0.0432971	0.0391662	0.0412303	ENSG00000240632	SPATA31D5P
ENSG00000240634	1.798	3.17028	3.74786	5.70959	ENSG00000240634	AC145285.1
ENSG00000240651	0.17592	0	0	0	ENSG00000240651	SEPT7P4
ENSG00000240652	0	0	0	0	ENSG00000240652	AP001024.1
ENSG00000240654	0.838495	1.52795	1.01478	1.79184	ENSG00000240654	C1QTNF9
ENSG00000240665	0	0	0	0	ENSG00000240665	LSP1P2
ENSG00000240667	3.96175	1.00254	0.811489	1.10228	ENSG00000240667	AL450992.3
ENSG00000240668	0.115496	0.153556	0.0726804	0.270912	ENSG00000240668	KRT8P36
ENSG00000240669	1.5528	1.35007	1.12814	1.286	ENSG00000240669	AC023424.1
ENSG00000240671	0	0	0	0	ENSG00000240671	IGKV1-8
ENSG00000240673	0.160248	0.45814	0.664267	0.664535	ENSG00000240673	AC006539.1
ENSG00000240674	0.521699	0	0	0	ENSG00000240674	AC106872.2
ENSG00000240677	0	0.842427	0.912902	0.56185	ENSG00000240677	MYL6P4
ENSG00000240680	0	0	0	0.174874	ENSG00000240680	AC016831.4
ENSG00000240682	14.4737	13.6291	15.6147	15.0134	ENSG00000240682	ISY1
ENSG00000240694	2.0821	2.59116	2.5453	5.27553	ENSG00000240694	PNMA2
ENSG00000240695	0.276037	1.7193	2.65669	5.38087	ENSG00000240695	AC117382.1
ENSG00000240698	0.101953	0.391758	0.796087	0.330275	ENSG00000240698	AP002453.1
ENSG00000240704	0.359714	2.07177	1.67427	4.80395	ENSG00000240704	KLF7P1
ENSG00000240720	0.621378	1.36719	1.81063	3.15736	ENSG00000240720	LRRD1
ENSG00000240721	0.0817774	0.549562	0.214664	0.265756	ENSG00000240721	RPS4XP15
ENSG00000240724	0	0	0	0	ENSG00000240724	AP002852.1
ENSG00000240729	0.0202094	3.73441	2.91042	4.97061	ENSG00000240729	AC146507.2
ENSG00000240738	0	0	0	0	ENSG00000240738	AF279873.2
ENSG00000240739	0	0	0	0.334641	ENSG00000240739	AC006511.1
ENSG00000240747	6.3011	7.64763	7.09744	2.31844	ENSG00000240747	KRBOX1
ENSG00000240751	0.174399	0.783485	1.47022	1.33531	ENSG00000240751	AC026348.1
ENSG00000240752	0	0.81354	0.551017	0.901045	ENSG00000240752	AC055731.1
ENSG00000240755	0	0.237651	0.214602	0.266169	ENSG00000240755	ERLEC1P1
ENSG00000240759	0	0	0	0	ENSG00000240759	RPS27P21
ENSG00000240760	0	0	0	0	ENSG00000240760	AC109462.1
ENSG00000240761	0	1.02343	1.1071	0.306621	ENSG00000240761	AC098831.1
ENSG00000240764	1.69876	3.25128	2.67471	6.7763	ENSG00000240764	PCDHGC5
ENSG00000240771	1.20956	1.50941	1.443	6.49316	ENSG00000240771	ARHGEF25
ENSG00000240774	0	0	0	0.271027	ENSG00000240774	AC126182.1
ENSG00000240775	0.269468	0.770055	2.08696	9.12567	ENSG00000240775	AC021205.1
ENSG00000240776	0	0.299046	0	0.498489	ENSG00000240776	AC079944.1
ENSG00000240785	0	0	0	0	ENSG00000240785	RPL36AP21
ENSG00000240787	0.426603	0.228078	0.185453	0.469832	ENSG00000240787	AC092916.2
ENSG00000240791	0	1.66201	1.33078	1.34246	ENSG00000240791	MTND4LP7
ENSG00000240793	0.459888	1.98251	3.31655	5.11798	ENSG00000240793	AC023818.1
ENSG00000240796	0	0	0	0.835997	ENSG00000240796	MTND2P14
ENSG00000240800	0	0	0	0.145918	ENSG00000240800	ATP8A2P1
ENSG00000240804	0.381979	0.479672	0.3447	0.259764	ENSG00000240804	NPM1P28
ENSG00000240808	0.746391	2.82599	0.95563	3.86138	ENSG00000240808	AC126389.1
ENSG00000240809	0.813302	0.625534	0.348281	0.402228	ENSG00000240809	AC026877.1
ENSG00000240813	0	0.156526	0	0.348492	ENSG00000240813	AC015908.1
ENSG00000240821	0	0	0.0256979	1.27E-08	ENSG00000240821	AC055855.1
ENSG00000240824	0	0.525586	0	0.957994	ENSG00000240824	MTND3P7
ENSG00000240827	0	0.377982	0.227505	0.281866	ENSG00000240827	AC021660.1

ENSG00000240828	0.173592	0.759015	0	0.366561	ENSG00000240828	AC135721.1
ENSG00000240834	0	0.133369	0.188921	0	ENSG00000240834	IGKV1D-12
ENSG00000240845	0.504956	0.43427	0.423746	0.412063	ENSG00000240845	RPL23AP1
ENSG00000240846	0	0	0	0	ENSG00000240846	RPS15P9
ENSG00000240849	71.8448	39.9566	35.0296	28.9616	ENSG00000240849	TMEM189
ENSG00000240854	0.141797	0.0923643	0.083666	0.214613	ENSG00000240854	AC117409.1
ENSG00000240857	13.106	16.1306	12.4182	8.43676	ENSG00000240857	RDH14
ENSG00000240861	0.615006	1.01116	0.399371	1.91253	ENSG00000240861	AC009153.1
ENSG00000240864	0	0	0	0	ENSG00000240864	IGKV1-16
ENSG00000240870	0.375112	0.842423	0.541643	0.403001	ENSG00000240870	AP003551.1
ENSG00000240871	0	0	0	0.435068	ENSG00000240871	KRTAP4-7
ENSG00000240873	1.16089	8.70362	6.72114	18.4479	ENSG00000240873	RPS29P22
ENSG00000240874	0	0	0	0	ENSG00000240874	AC025271.1
ENSG00000240881	0	0	0	0	ENSG00000240881	AC068472.1
ENSG00000240882	0.0486018	0	0.0845869	0.212347	ENSG00000240882	AC063952.2
ENSG00000240890	0.100056	0.120798	0.196236	0.330735	ENSG00000240890	AC020633.1
ENSG00000240891	19.8514	24.8262	21.858	27.3586	ENSG00000240891	PLCXD2
ENSG00000240898	2.92799	5.10695	5.98945	3.699	ENSG00000240898	AC132942.1
ENSG00000240902	0.27296	0	0.354558	0.585163	ENSG00000240902	APOOP2
ENSG00000240906	1.75296	5.59931	1.01276	1.91963	ENSG00000240906	AP000356.1
ENSG00000240912	0	0	0	0	ENSG00000240912	AC092896.1
ENSG00000240914	0	0	0	0	ENSG00000240914	AL121612.1
ENSG00000240919	0	0	0	0	ENSG00000240919	AC022034.3
ENSG00000240925	8.70974	16.3768	9.49581	23.7741	ENSG00000240925	AC004263.1
ENSG00000240929	0.804794	0.350305	2.37237	1.32152	ENSG00000240929	HIST2H2BB
ENSG00000240934	0	0.194232	0	0.861008	ENSG00000240934	AC066616.1
ENSG00000240935	1.33138	2.79395	2.8676	3.67584	ENSG00000240935	PLGLA
ENSG00000240950	0	0	0.0950264	0	ENSG00000240950	AC021074.1
ENSG00000240951	0.098655	0.0947952	0.111215	0	ENSG00000240951	MTCO2P6
ENSG00000240954	0	0.0446752	0	0.152069	ENSG00000240954	RPL4P1
ENSG00000240957	0.0272928	0.112493	0.0254114	0.0148391	ENSG00000240957	LY6G6F
ENSG00000240959	0.0902931	0	0	0	ENSG00000240959	ST13P14
ENSG00000240960	0	0	0	0	ENSG00000240960	AC082651.2
ENSG00000240970	6.51878	5.35984	5.1432	5.49502	ENSG00000240970	RPL23AP64
ENSG00000240972	230.532	265.072	111.106	108.29	ENSG00000240972	MIF
ENSG00000240974	5.73408	13.3713	6.46715	15.6649	ENSG00000240974	RPS27AP10
ENSG00000240975	0	0	1.90758	0	ENSG00000240975	AC021723.1
ENSG00000240979	0.628259	0.99958	3.30245	3.60384	ENSG00000240979	AL353813.1
ENSG00000240983	0	0	0	0	ENSG00000240983	AC090311.1
ENSG00000240991	0.82198	0.472535	0.524619	1.77717	ENSG00000240991	RPL23AP67
ENSG00000240992	0	0	0	0	ENSG00000240992	RPS23P4
ENSG00000240995	0	0	0.144859	0.178576	ENSG00000240995	AC069454.1
ENSG00000241002	2.7061	5.01001	6.34545	8.10602	ENSG00000241002	AC017007.3
ENSG00000241003	3.43899	9.41436	8.40683	3.63075	ENSG00000241003	AC108860.1
ENSG00000241007	0.214171	1.1858	0.849029	1.59098	ENSG00000241007	SEPT7P6
ENSG00000241008	0.759714	0.271474	0.572337	0.509159	ENSG00000241008	AC044810.1
ENSG00000241011	0	0	1.33392	1.63038	ENSG00000241011	AC108073.2
ENSG00000241015	6.32557	10.5744	7.55635	10.6629	ENSG00000241015	TPM3P9
ENSG00000241018	0.0781559	0.0753904	0	0.0856471	ENSG00000241018	RCC2P5
ENSG00000241020	0	0	0	0	ENSG00000241020	AP000873.1
ENSG00000241022	0.118874	0.0540741	0.195484	0.183801	ENSG00000241022	NIPA2P2
ENSG00000241026	0.31967	0.942444	0.829979	2.38926	ENSG00000241026	AC105910.1
ENSG00000241030	0.7049	1.33287	1.37233	0.374567	ENSG00000241030	AC063943.1
ENSG00000241035	1.28317	1.22309	0.221255	3.50852	ENSG00000241035	AL161747.1

ENSG00000241043	3.35035	7.52005	6.77936	12.8975	ENSG00000241043	GVQW1
ENSG00000241045	0	0.168002	0.0759053	0.189286	ENSG00000241045	RPL7P43
ENSG00000241052	0.515883	1.64655	0.72097	1.11617	ENSG00000241052	RPL23AP70
ENSG00000241057	2.38431	2.44936	3.08241	2.77517	ENSG00000241057	AC004951.3
ENSG00000241058	3.89737	8.73528	7.55429	5.81819	ENSG00000241058	NSUN6
ENSG00000241061	0	0	0.0619297	0	ENSG00000241061	RPL5P1
ENSG00000241067	1.82772	1.35962	1.75433	3.44403	ENSG00000241067	AC136624.1
ENSG00000241069	4.50836	0	0	0	ENSG00000241069	AC125388.1
ENSG00000241081	0	0	0.669117	1.58944	ENSG00000241081	AF111169.1
ENSG00000241088	0	0	0	0	ENSG00000241088	AC100843.1
ENSG00000241095	0.0411226	0.0398838	0	0	ENSG00000241095	CYP51A1P1
ENSG00000241097	0	0	0.269371	0	ENSG00000241097	AP001324.2
ENSG00000241102	0.848843	2.01843	0.895766	1.80154	ENSG00000241102	AC011005.2
ENSG00000241103	1.17657	1.39689	1.51546	1.53766	ENSG00000241103	AC109925.1
ENSG00000241104	0.721906	1.31443	1.90966	3.10151	ENSG00000241104	CEACAMP10
ENSG00000241105	0	0	0	0	ENSG00000241105	AC022730.1
ENSG00000241106	0.00120316	0	4.20655	1.43395	ENSG00000241106	HLA-DOB
ENSG00000241112	3.85036	9.46108	11.3877	6.67215	ENSG00000241112	RPL29P14
ENSG00000241114	0	0	0.426459	0	ENSG00000241114	AC008280.2
ENSG00000241119	0	0	0	0	ENSG00000241119	UGT1A9
ENSG00000241120	3.79214	7.6228	7.90106	10.6	ENSG00000241120	HMGN1P8
ENSG00000241123	0.0523826	0.0756352	0.138032	0.178617	ENSG00000241123	KRTAP10-5
ENSG00000241127	12.5102	9.7574	12.1553	7.78527	ENSG00000241127	YAE1D1
ENSG00000241128	0	0	0	0	ENSG00000241128	OR14A2
ENSG00000241129	0.245069	0.22897	0.41308	0.75751	ENSG00000241129	AC093719.1
ENSG00000241130	0.393154	0	0	0.842634	ENSG00000241130	AC012100.1
ENSG00000241132	1.60728	2.24266	4.92688	0	ENSG00000241132	LY6G5B
ENSG00000241134	0	0.132265	0.291739	1.0149	ENSG00000241134	BET1P1
ENSG00000241136	0	0	0.161189	0.556706	ENSG00000241136	PAICSP6
ENSG00000241143	0	0	0	0	ENSG00000241143	RPL32P9
ENSG00000241146	1.22331	1.91516	1.91106	3.68603	ENSG00000241146	RPL7P41
ENSG00000241149	0.255549	0.377378	0.197559	0.210327	ENSG00000241149	AC115220.1
ENSG00000241150	0.161891	0.528467	0.375555	1.00084	ENSG00000241150	RP11-308D16.2
ENSG00000241157	0.254375	1.6971	1.61106	1.60483	ENSG00000241157	AC104763.1
ENSG00000241166	0	0	0	0	ENSG00000241166	HLA-L
ENSG00000241170	6.06909	6.65209	7.52928	9.73891	ENSG00000241170	AP001992.1
ENSG00000241179	0.520845	1.24067	0.6731	1.3674	ENSG00000241179	AC010301.1
ENSG00000241183	0	0.168527	0.133124	0	ENSG00000241183	AC009022.1
ENSG00000241185	1.82799	4.12882	2.09727	4.15224	ENSG00000241185	AC005410.1
ENSG00000241186	0.94159	1.61017	2.34234	3.07689	ENSG00000241186	TDGF1
ENSG00000241187	0	0.325128	0.160554	0.718165	ENSG00000241187	AC008379.1
ENSG00000241200	0.157092	0.612546	0.0684905	0.340857	ENSG00000241200	ZNF736P7Y
ENSG00000241203	0.28207	0.268156	0	0.30508	ENSG00000241203	HMGN2P26
ENSG00000241204	0	0	0	0	ENSG00000241204	AC022730.2
ENSG00000241207	0	0	0	0	ENSG00000241207	AC245047.8
ENSG00000241216	0	0.660963	1.1927	2.04861	ENSG00000241216	SNAPC5P1
ENSG00000241218	0.0429281	0	0.149475	0.748485	ENSG00000241218	AC063944.2
ENSG00000241221	0.366437	0	0	0.408353	ENSG00000241221	MTND4LP17
ENSG00000241225	0	0	0	0	ENSG00000241225	NMTRS-TGA3-1
ENSG00000241228	0.889028	0.851023	1.38366	1.232	ENSG00000241228	RPL12P31
ENSG00000241233	0.20277	0.341605	0.0882147	0.110689	ENSG00000241233	KRTAP5-8
ENSG00000241241	0.0947525	0.27943	0.523282	0.788594	ENSG00000241241	KRTAP4-16
ENSG00000241244	0	0	0	0	ENSG00000241244	IGKV1D-16
ENSG00000241250	0	0	0	0.164904	ENSG00000241250	AC022483.2

ENSG00000241251	0	0	0	0	ENSG00000241251	AC090525.1
ENSG00000241253	0.406167	0.769389	1.44896	0.880637	ENSG00000241253	CFB
ENSG00000241255	0	0.202963	0.183207	0.22451	ENSG00000241255	AL136126.1
ENSG00000241257	0	0	0	0	ENSG00000241257	AC124945.1
ENSG00000241258	17.8739	16.238	19.4062	15.7111	ENSG00000241258	CRCP
ENSG00000241261	0.13199	0.379895	0	0.70808	ENSG00000241261	RPL17P19
ENSG00000241278	2.20641	5.15425	3.80298	6.31471	ENSG00000241278	ENPP7P4
ENSG00000241281	0	0	0.237826	0	ENSG00000241281	AC010683.1
ENSG00000241282	0.29058	0	0	0	ENSG00000241282	RPL34P33
ENSG00000241286	1.70455	4.19903	4.46141	8.12923	ENSG00000241286	RPL29P25
ENSG00000241293	0	0	0	0	ENSG00000241293	PPATP1
ENSG00000241294	0	0	0	0	ENSG00000241294	IGKV2-24
ENSG00000241296	0	0.00799456	0.00913478	0.00910544	ENSG00000241296	HLA-DMB
ENSG00000241305	0.0587315	0.960789	0.102155	0.324177	ENSG00000241305	ACTG1P13
ENSG00000241307	0.234793	0	0.101752	0.631654	ENSG00000241307	AC104472.2
ENSG00000241318	0	0.130264	0	0.148143	ENSG00000241318	WDR82P2
ENSG00000241319	0.509459	0.556661	0.583905	2.1279	ENSG00000241319	SETP6
ENSG00000241322	7.45832	2.61093	2.80753	1.82944	ENSG00000241322	CDRT1
ENSG00000241334	0	0	0	0	ENSG00000241334	AC099521.1
ENSG00000241341	0	0	0	0	ENSG00000241341	RP11-395E19.2
ENSG00000241343	212.546	195.307	162.08	113.35	ENSG00000241343	RPL36A
ENSG00000241344	0	0	0	0	ENSG00000241344	RPL21P47
ENSG00000241346	0.737421	0.691847	0	0	ENSG00000241346	SNRPCP11
ENSG00000241350	0	0	0.676795	0	ENSG00000241350	PMS2P11
ENSG00000241351	0	0.421998	0.571384	0.933355	ENSG00000241351	IGKV3-11
ENSG00000241352	0.566079	0.528692	0.439912	1.59475	ENSG00000241352	AC007688.1
ENSG00000241353	0	0.114215	0	0.128026	ENSG00000241353	PPP1R2P4
ENSG00000241354	0	0	0	0	ENSG00000241354	AL049874.1
ENSG00000241356	0	0	0.0508766	0.03667	ENSG00000241356	OR5G3
ENSG00000241358	0	0.104255	0	0	ENSG00000241358	AC069528.1
ENSG00000241360	1.36293	1.02661	0.739099	2.41954	ENSG00000241360	PDXP
ENSG00000241361	0.0376783	0	0.128197	0.232392	ENSG00000241361	SLC25A24P1
ENSG00000241362	2.02225	1.29586	1.2133	0	ENSG00000241362	AC013787.1
ENSG00000241367	0	0	0	0	ENSG00000241367	RPL7AP23
ENSG00000241370	7.19836	6.17259	4.19729	0	ENSG00000241370	RPP21
ENSG00000241385	0	0	0	0.61995	ENSG00000241385	AC023245.1
ENSG00000241386	0.98526	2.69547	0	0.500217	ENSG00000241386	HLA-DOB
ENSG00000241394	0.0119765	0.64033	0.14315	0.0810543	ENSG00000241394	HLA-DMA
ENSG00000241399	2.08599	4.06179	3.38014	5.17239	ENSG00000241399	CD302
ENSG00000241400	0	0	0.21712	0	ENSG00000241400	AC022215.1
ENSG00000241404	1.32792	0.493213	0.396675	0.139891	ENSG00000241404	EGFL8
ENSG00000241411	0	0	0.0953706	0	ENSG00000241411	AC104619.1
ENSG00000241416	0	0	0	0.531811	ENSG00000241416	KRT8P13
ENSG00000241418	0	0	0	0.157546	ENSG00000241418	MCRIP2P1
ENSG00000241423	0	0	0	0	ENSG00000241423	RPL21P103
ENSG00000241429	0.798148	1.76375	0.899298	1.18054	ENSG00000241429	EEF1A1P25
ENSG00000241431	0.771483	1.3257	2.10434	1.61233	ENSG00000241431	RPL37P6
ENSG00000241434	0	0	0	0	ENSG00000241434	AC022137.1
ENSG00000241438	0.181296	1.56572	0.519606	2.03205	ENSG00000241438	TDGF1P6
ENSG00000241439	0	0	0	0	ENSG00000241439	AC092903.1
ENSG00000241451	0	0	0.447037	0	ENSG00000241451	RPS27P22
ENSG00000241458	0	0	0	0.124416	ENSG00000241458	RPL7P19
ENSG00000241462	0	0	0	0.802917	ENSG00000241462	AC100832.1
ENSG00000241464	0	1.3475	0	0	ENSG00000241464	RPL39P38

ENSG00000241465	0	0	0	0	ENSG00000241465	GAGE12I
ENSG00000241468	165.628	133.651	106.454	65.7152	ENSG00000241468	ATP5J2
ENSG00000241473	0.228216	0.17157	0.0543812	0.202084	ENSG00000241473	AC108734.2
ENSG00000241476	0	0	0	0	ENSG00000241476	SSX2
ENSG00000241478	0	0	0.0246679	0	ENSG00000241478	HSPA8P9
ENSG00000241484	25.1959	28.2886	35.9373	22.2307	ENSG00000241484	ARHGAP8
ENSG00000241489	2.02481	0.432533	0.910996	2.83725	ENSG00000241489	AC244197.3
ENSG00000241493	1.98798	14.7876	9.37529	3.7899	ENSG00000241493	AC018638.3
ENSG00000241494	0	0	0.323201	0	ENSG00000241494	AL355032.1
ENSG00000241499	2.26054	3.67723	1.38415	1.3463	ENSG00000241499	AL132838.2
ENSG00000241506	0	0	0	0	ENSG00000241506	PSMC1P1
ENSG00000241511	0.436007	0.418239	1.35979	0.276688	ENSG00000241511	AC026979.1
ENSG00000241526	0	0	0	0	ENSG00000241526	AC112771.1
ENSG00000241527	0.830298	0.357332	1.46388	0.453997	ENSG00000241527	CA15P1
ENSG00000241532	0.620251	1.13614	1.61098	0.876219	ENSG00000241532	AGGF1P3
ENSG00000241534	0.406167	1.02153	2.6685	0.880637	ENSG00000241534	CFB
ENSG00000241535	1.29047	3.34325	3.71076	5.57223	ENSG00000241535	CBX5P1
ENSG00000241536	0	0	0	0	ENSG00000241536	RP11-381G8.1
ENSG00000241537	0.604841	0.583089	0.584612	1.61193	ENSG00000241537	AC134050.1
ENSG00000241539	0	0.296636	0.255124	0.604218	ENSG00000241539	AC079804.1
ENSG00000241546	4.3115	11.5508	6.72466	7.63312	ENSG00000241546	AC092910.2
ENSG00000241547	3.45079	2.41184	2.99535	3.72503	ENSG00000241547	ACTG1P20
ENSG00000241549	2.99868	7.22824	6.72252	12.6538	ENSG00000241549	GUSBP2
ENSG00000241553	82.3835	56.5619	59.2109	51.0666	ENSG00000241553	ARPC4
ENSG00000241556	0.971681	0	0	0.221731	ENSG00000241556	AC018475.1
ENSG00000241562	0	0	0	0	ENSG00000241562	RPL7P5
ENSG00000241563	0.570155	0.155071	0.860479	1.08329	ENSG00000241563	CORT
ENSG00000241566	0	0	0	0	ENSG00000241566	IGKV2D-24
ENSG00000241571	0.092713	0	0	0	ENSG00000241571	ATP5A1P7
ENSG00000241573	0	0	0	0	ENSG00000241573	AC011005.3
ENSG00000241582	0	0	0	0	ENSG00000241582	RPL23AP8
ENSG00000241590	0	0	0	0	ENSG00000241590	RPL17P37
ENSG00000241592	0	0	0	0	ENSG00000241592	AC021074.2
ENSG00000241595	0	0	0	0	ENSG00000241595	KRTAP9-4
ENSG00000241597	0.370577	1.65962	1.49866	1.06221	ENSG00000241597	AC022121.1
ENSG00000241598	0	0.320085	0.189116	0.420963	ENSG00000241598	KRTAP5-4
ENSG00000241607	0	0	0	0	ENSG00000241607	AC245096.1
ENSG00000241612	0	0	0.152168	0	ENSG00000241612	AC114728.1
ENSG00000241621	0	0.03195	0	0	ENSG00000241621	GOLGA2P6
ENSG00000241622	0.321653	1.48688	0.656852	0.750177	ENSG00000241622	RARRES2P1
ENSG00000241627	0.779563	0.0469609	0.54851	0.280198	ENSG00000241627	UBQLN4P1
ENSG00000241634	0.761828	2.6643	1.15375	3.96006	ENSG00000241634	AC069499.1
ENSG00000241635	2.08129	3.65708	4.36351	4.83895	ENSG00000241635	UGT1A1
ENSG00000241640	0.504178	0.483034	0.728424	0.895674	ENSG00000241640	AC092757.1
ENSG00000241641	0.833402	2.54537	1.50937	1.21268	ENSG00000241641	RPS23P6
ENSG00000241644	1.89305	3.26272	3.70231	6.52026	ENSG00000241644	INMT
ENSG00000241651	0.236331	0.906712	0.451121	0.770367	ENSG00000241651	AC099340.1
ENSG00000241654	0	0	0	0.132163	ENSG00000241654	AC087501.2
ENSG00000241656	0	0	0	0	ENSG00000241656	UBA52P7
ENSG00000241661	0	0	0.107435	0	ENSG00000241661	PPP1R2P6
ENSG00000241668	0	0	0	0	ENSG00000241668	RPL19P11
ENSG00000241670	0.891002	0	0	0	ENSG00000241670	AP006222.1
ENSG00000241671	0	0	0	0	ENSG00000241671	AC117394.1
ENSG00000241673	0	0	0	0.475397	ENSG00000241673	RPS27P12

ENSG00000241674	0	0.00799456	0.00913478	0.00910544	ENSG00000241674	HLA-DMB
ENSG00000241678	1.25006	0.877863	1.04838	1.6223	ENSG00000241678	AC091564.1
ENSG00000241680	0.23867	0.469772	0.820326	0	ENSG00000241680	AC002350.1
ENSG00000241685	108.518	53.855	39.935	44.5631	ENSG00000241685	ARPC1A
ENSG00000241690	0	0	0	0	ENSG00000241690	AL035460.1
ENSG00000241695	0	0	0	0	ENSG00000241695	GM2AP1
ENSG00000241697	1.82367	2.01052	1.02565	1.67309	ENSG00000241697	TMEFF1
ENSG00000241713	0	0.619036	0	2.10257	ENSG00000241713	LY6G5B
ENSG00000241717	0.136307	0.0364013	0.0493661	0.0669159	ENSG00000241717	VWFP1
ENSG00000241721	0	0	0.289574	0.351646	ENSG00000241721	SUMO1P1
ENSG00000241722	0	0	0	0	ENSG00000241722	AC083795.1
ENSG00000241723	0.114325	0.658469	0.49544	0.863106	ENSG00000241723	AC074276.1
ENSG00000241735	0.141421	0.655494	0.566819	0.308004	ENSG00000241735	FABP5P3
ENSG00000241737	0	0	0	0	ENSG00000241737	FAM90A23P
ENSG00000241738	0.636399	1.51441	1.35426	2.69477	ENSG00000241738	ZNF90P1
ENSG00000241739	0.486321	0.155454	0	0	ENSG00000241739	AC010469.2
ENSG00000241741	0	0	0	0	ENSG00000241741	RPL7AP30
ENSG00000241744	0.0482857	0.233135	0.142609	0.324907	ENSG00000241744	AC079953.1
ENSG00000241746	0.332002	0.637843	1.34442	0.655681	ENSG00000241746	AC104212.2
ENSG00000241749	10.2609	11.2988	2.0981	14.7423	ENSG00000241749	RPSAP52
ENSG00000241755	0.20625	0.197155	0	0	ENSG00000241755	IGKV1-9
ENSG00000241765	0	0.800424	0.243195	0	ENSG00000241765	RPS26P45
ENSG00000241776	0.288188	0.349983	0.066068	0.161269	ENSG00000241776	AC117482.1
ENSG00000241777	0	0	0	0	ENSG00000241777	AC092185.1
ENSG00000241778	0	0	0.858347	0	ENSG00000241778	AC005077.9
ENSG00000241779	0	0	0.74619	3.29875	ENSG00000241779	RPP21
ENSG00000241782	0.657584	0.965934	0.853111	1.07113	ENSG00000241782	AP002812.1
ENSG00000241787	0	0.165505	0.0373997	0.281925	ENSG00000241787	MTND4P16
ENSG00000241788	1.16453	2.18904	2.44384	1.17736	ENSG00000241788	COX6B1P2
ENSG00000241790	0.315909	1.67619	2.25172	0	ENSG00000241790	ENO1P4
ENSG00000241794	11.2672	1.94308	4.18002	4.67672	ENSG00000241794	SPRR2A
ENSG00000241804	0	0	0	0.282561	ENSG00000241804	AC126121.1
ENSG00000241808	0	0.430647	0.583488	0.238144	ENSG00000241808	RPS15AP34
ENSG00000241809	0	0	0	0	ENSG00000241809	AC022133.1
ENSG00000241810	0	0	0.356669	0	ENSG00000241810	HMGN2P13
ENSG00000241815	0	0	0	0.191797	ENSG00000241815	AC107015.1
ENSG00000241822	0	0.112493	0.0254114	0	ENSG00000241822	LY6G6F
ENSG00000241825	0.199588	0.191751	0.182959	0	ENSG00000241825	RPL7P42
ENSG00000241828	0	0	0	0	ENSG00000241828	AC006517.1
ENSG00000241829	0	0	0.440214	0.183166	ENSG00000241829	AC026801.1
ENSG00000241837	46.2964	44.5636	37.6382	32.0454	ENSG00000241837	ATP5O
ENSG00000241838	0	0	0	0	ENSG00000241838	AP000529.1
ENSG00000241839	6.54678	8.42823	5.18193	7.25898	ENSG00000241839	PLEKHO2
ENSG00000241846	0	0	0	0	ENSG00000241846	AC092451.1
ENSG00000241847	0.824745	1.37083	2.28132	0.736943	ENSG00000241847	VDAC1P8
ENSG00000241850	0	0	0	0	ENSG00000241850	GSTTP1
ENSG00000241852	17.3244	13.0768	17.0609	14.2557	ENSG00000241852	C8orf58
ENSG00000241853	0	0	0	0	ENSG00000241853	AC097484.1
ENSG00000241859	0.44221	1.31778	1.35714	2.13779	ENSG00000241859	ANOS2P
ENSG00000241861	0	0	0	0	ENSG00000241861	GAPDHP50
ENSG00000241863	7.19836	6.17259	4.19729	0	ENSG00000241863	RPP21
ENSG00000241870	0	0	0	0	ENSG00000241870	AC008620.1
ENSG00000241874	0	0	0	4.58884	ENSG00000241874	TOMM22P6
ENSG00000241877	0	0	0	0	ENSG00000241877	AC095041.1

ENSG00000241878	28.6674	31.8905	31.3819	23.4385	ENSG00000241878	PISD
ENSG00000241879	0	0	0	0	ENSG00000241879	KLF3P2
ENSG00000241880	0.504956	0.43427	0.423746	0.412063	ENSG00000241880	RPL23AP1
ENSG00000241888	0.0784272	0	0	0.0850875	ENSG00000241888	RPSAP37
ENSG00000241889	0.564355	0.45873	0.243636	1.2159	ENSG00000241889	AC079944.2
ENSG00000241890	0.257453	2.96444	2.78775	2.07317	ENSG00000241890	AC105137.1
ENSG00000241891	0	0	0	0	ENSG00000241891	RPL9P6
ENSG00000241899	0	0	0	0	ENSG00000241899	TPT1P3
ENSG00000241905	0	0	0	0	ENSG00000241905	NDUFS6P1
ENSG00000241907	1.09757	4.48712	5.65702	6.68367	ENSG00000241907	RPS20P4
ENSG00000241910	1.96138	0	0	0	ENSG00000241910	HLA-DOB
ENSG00000241911	0.207032	0.39587	0.446982	0.767737	ENSG00000241911	TRBVB
ENSG00000241913	0	4.22773	2.79453	2.23135	ENSG00000241913	RPS29P21
ENSG00000241917	0.358684	0	0.344394	0.183715	ENSG00000241917	AC084398.1
ENSG00000241923	0	0.324116	0.097839	0	ENSG00000241923	RPL14P3
ENSG00000241926	0.0886047	0.255408	0.615337	0.479558	ENSG00000241926	MTCO1P55
ENSG00000241929	0	0	0.105467	0.0656958	ENSG00000241929	AC108751.3
ENSG00000241932	0	0	0	0	ENSG00000241932	AC092324.1
ENSG00000241935	2.25398	2.19402	1.68686	2.93503	ENSG00000241935	HOGA1
ENSG00000241941	0	0	0	0	ENSG00000241941	AC048341.1
ENSG00000241942	0	0	1.44628	4.99338	ENSG00000241942	RPS20P20
ENSG00000241945	26.4624	33.4471	30.2141	23.6063	ENSG00000241945	PWP2
ENSG00000241946	0	0	1.0577	0	ENSG00000241946	AC068298.1
ENSG00000241947	0	0	0	0.127585	ENSG00000241947	HNRNPA1P24
ENSG00000241950	0.182766	0	0	0.583396	ENSG00000241950	RPL29P23
ENSG00000241961	0.130018	0.124738	0	0.139559	ENSG00000241961	AC011037.1
ENSG00000241962	14.7286	14.8581	14.9627	12.5744	ENSG00000241962	AC079447.1
ENSG00000241965	0	0	0	0	ENSG00000241965	RPS2P25
ENSG00000241973	14.7768	28.0375	26.8805	40.3899	ENSG00000241973	PI4KA
ENSG00000241975	7.1953	10.3074	15.3363	10.3465	ENSG00000241975	ELOCP19
ENSG00000241978	23.3458	23.0431	29.597	41.3182	ENSG00000241978	AKAP2
ENSG00000241981	0.340534	0.81547	1.17772	1.11867	ENSG00000241981	AF213884.1
ENSG00000241984	0.804315	0.343465	1.16365	0.774279	ENSG00000241984	RPL7AP2
ENSG00000241991	0.256635	2.20157	0.885021	2.69886	ENSG00000241991	AC114982.2
ENSG00000241993	1.38928	0.650743	1.15926	3.48511	ENSG00000241993	RPL38P1
ENSG00000242001	0	0	0	0	ENSG00000242001	AF186996.6
ENSG00000242013	1.38013	1.17717	1.80446	1.6481	ENSG00000242013	USP27X
ENSG00000242017	0.262147	0	0.413708	0	ENSG00000242017	ALG1L15P
ENSG00000242019	0	0	0	0	ENSG00000242019	KIR3DL3
ENSG00000242022	0.0151711	0.0536059	0.0442655	0.0942871	ENSG00000242022	OR12D3
ENSG00000242028	4.25581	9.85997	11.3196	15.5379	ENSG00000242028	HYPK
ENSG00000242034	0	0	0	0.324204	ENSG00000242034	AC097493.1
ENSG00000242036	0.338473	0	0	0	ENSG00000242036	AC128713.1
ENSG00000242038	1.19969	2.56371	2.89687	3.05625	ENSG00000242038	EGFL8
ENSG00000242039	0.504956	0.43427	0.423746	0.412063	ENSG00000242039	RPL23AP1
ENSG00000242041	0	0	0	0	ENSG00000242041	RPL35AP28
ENSG00000242052	0	0.213937	0.0965509	0	ENSG00000242052	RPL10P7
ENSG00000242058	0	0.0864598	0.240668	0.0973796	ENSG00000242058	RPS4XP19
ENSG00000242060	0	0	0	0	ENSG00000242060	RPS3AP49
ENSG00000242061	0	0	0	0	ENSG00000242061	AL160314.1
ENSG00000242062	0.211085	0.202984	0.183408	0.305899	ENSG00000242062	MARK2P6
ENSG00000242067	0	0	0	0	ENSG00000242067	AC091179.1
ENSG00000242068	0.414125	1.03303	1.24072	1.77451	ENSG00000242068	AC108734.3
ENSG00000242070	0	0.355826	0.234758	0.317919	ENSG00000242070	NPM1P17

ENSG00000242071	1.05566	0.787713	0.202946	1.20141	ENSG00000242071	RPL7AP6
ENSG00000242073	0	0.903329	0.19355	1.80078	ENSG00000242073	AC211429.1
ENSG00000242076	0	0	0	0	ENSG00000242076	IGKV1-33
ENSG00000242080	0	0	0	0	ENSG00000242080	AC008571.1
ENSG00000242083	0.166433	0.159704	1.01056	0.363698	ENSG00000242083	AC068620.1
ENSG00000242085	0.854407	1.37126	1.32965	1.58212	ENSG00000242085	AL928654.1
ENSG00000242087	1.04939	10.5286	5.72744	15.5553	ENSG00000242087	RPL36AP41
ENSG00000242088	0	0	0.832714	0	ENSG00000242088	AC090602.1
ENSG00000242092	0	0	0.00913478	0.00910544	ENSG00000242092	HLA-DMB
ENSG00000242097	1.34135	2.90109	2.81249	4.45155	ENSG00000242097	AC068647.1
ENSG00000242100	2.17995	3.51788	2.99976	4.78941	ENSG00000242100	RPL9P32
ENSG00000242103	0	0	0	0	ENSG00000242103	AC079841.1
ENSG00000242107	0	0	0.166515	0.411884	ENSG00000242107	LINC01100
ENSG00000242109	0	0.217406	0.130855	0.338638	ENSG00000242109	NPM1P23
ENSG00000242110	4.09474	4.13771	5.8472	3.33686	ENSG00000242110	AMACR
ENSG00000242111	0.256419	1.35799	0.859172	1.09959	ENSG00000242111	TOPORSLP1
ENSG00000242114	3.49867	8.69031	3.39906	3.30449	ENSG00000242114	MTFP1
ENSG00000242115	0.0485927	0.140084	0.168732	0.26263	ENSG00000242115	PRSS3P3
ENSG00000242119	0	0	0	1.14855	ENSG00000242119	AC117454.1
ENSG00000242123	0	0.320861	0.579147	1.75823	ENSG00000242123	AC053481.1
ENSG00000242134	3.58658	1.9045	0.983066	4.79786	ENSG00000242134	RPL5P13
ENSG00000242135	0.531776	4.9267	0.613269	4.90662	ENSG00000242135	RPL17P2
ENSG00000242137	0	0	0	0.148169	ENSG00000242137	AC063943.2
ENSG00000242140	0	0	0	0	ENSG00000242140	AC083904.1
ENSG00000242142	0.0816247	0.231762	0	1.03959	ENSG00000242142	SERBP1P3
ENSG00000242150	0.31273	0.183122	0.543892	0.208773	ENSG00000242150	RP11-134G8.6
ENSG00000242151	0	0	0	0	ENSG00000242151	DYNLL1P5
ENSG00000242152	0.197692	0.760522	0.175094	0.573553	ENSG00000242152	AC108729.1
ENSG00000242153	0.802069	0.878275	1.24161	1.4744	ENSG00000242153	OFD1P6Y
ENSG00000242156	0	8.23263	9.0879	12.0246	ENSG00000242156	AC000041.1
ENSG00000242159	0	0.0296053	0.0268302	0.0336547	ENSG00000242159	ABCF2P1
ENSG00000242162	0	0	0	0	ENSG00000242162	AC018639.1
ENSG00000242163	0.851808	2.64646	1.83736	2.03452	ENSG00000242163	AL121769.1
ENSG00000242169	0	0	0	0.11443	ENSG00000242169	AC093789.1
ENSG00000242173	7.79672	16.6094	18.5754	30.6786	ENSG00000242173	ARHGDIG
ENSG00000242176	0	0	0	0	ENSG00000242176	AC009127.1
ENSG00000242178	0	0.254207	0	0.217769	ENSG00000242178	MTND4P17
ENSG00000242180	0	0	0.0745768	0.124804	ENSG00000242180	OR51B5
ENSG00000242185	0	0	0	0	ENSG00000242185	CT45A2
ENSG00000242186	0	0	0	0	ENSG00000242186	AC231760.1
ENSG00000242193	12.5438	20.0878	13.042	25.0193	ENSG00000242193	AL359075.1
ENSG00000242195	0.215938	0.439794	0.721815	0.290724	ENSG00000242195	SRRM1P2
ENSG00000242197	0.737475	1.82966	0.629349	1.14569	ENSG00000242197	AC098869.1
ENSG00000242198	1.62636	3.097	2.61907	4.9676	ENSG00000242198	AC008897.1
ENSG00000242199	1.14131	1.35364	1.33665	1.63231	ENSG00000242199	AC022336.1
ENSG00000242206	0	0	0	0	ENSG00000242206	AP004217.1
ENSG00000242208	0.0355219	0.0341541	0	0.0385293	ENSG00000242208	RPL5P29
ENSG00000242209	0	0	0	0	ENSG00000242209	AC006445.1
ENSG00000242214	0	0	0.415429	0.395722	ENSG00000242214	MTND3P6
ENSG00000242220	0.781434	0.151783	0.310183	0.137039	ENSG00000242220	TCP10L
ENSG00000242221	2.0761	3.69191	3.7269	8.3344	ENSG00000242221	PSG2
ENSG00000242222	0	0	0.346175	0	ENSG00000242222	AC092989.1
ENSG00000242227	0	0	0	0	ENSG00000242227	HLA-L
ENSG00000242229	0.274095	0.35509	1.02049	0.619777	ENSG00000242229	RPS3AP14

ENSG00000242244	0	0	0	0	ENSG00000242244	ATP5G1P3
ENSG00000242246	0	0.721116	0.637949	0.771427	ENSG00000242246	AL603908.1
ENSG00000242247	22.1374	21.8753	23.1261	27.7564	ENSG00000242247	ARFGAP3
ENSG00000242248	0	0.079846	0.0723854	0	ENSG00000242248	RPL7AP57
ENSG00000242252	1.12071	1.8941	2.06598	1.14045	ENSG00000242252	BGLAP
ENSG00000242255	1.34231	6.22985	0	0	ENSG00000242255	RPL39P34
ENSG00000242259	3.38984	4.43895	3.95221	5.39902	ENSG00000242259	C22orf39
ENSG00000242261	0	0	0	0	ENSG00000242261	AC018635.1
ENSG00000242262	0	0.123939	0	0	ENSG00000242262	AC092597.1
ENSG00000242265	0.765052	5.72225	4.82638	7.34281	ENSG00000242265	PEG10
ENSG00000242267	9.84165	21.0778	19.4468	43.2069	ENSG00000242267	SKINT1L
ENSG00000242272	0	0.402166	0.737955	0.45223	ENSG00000242272	AK2P2
ENSG00000242276	0.0713196	0.205681	0.495942	0.464327	ENSG00000242276	RPL5P3
ENSG00000242278	0	0.0803192	0.150349	0.110151	ENSG00000242278	AC074051.1
ENSG00000242279	0	0	0	0	ENSG00000242279	AP000893.1
ENSG00000242280	0	0.0740025	0	0	ENSG00000242280	SLC16A1P1
ENSG00000242284	0	0	0	0	ENSG00000242284	CT45A5
ENSG00000242285	0.0759015	0.0729832	0.131894	0.164804	ENSG00000242285	RPL6P8
ENSG00000242291	0	0	0	0	ENSG00000242291	RPL36AP51
ENSG00000242292	0	0	0	0	ENSG00000242292	AC010631.1
ENSG00000242293	0	0	0	0	ENSG00000242293	RPS29P1
ENSG00000242294	49.3959	68.5254	64.7008	58.6555	ENSG00000242294	STAG3L5P
ENSG00000242295	0	0	0	0.293728	ENSG00000242295	AC087477.1
ENSG00000242296	0	1.56212	1.30374	1.98303	ENSG00000242296	DEFB109A
ENSG00000242299	3.7191	6.97232	6.7743	8.54161	ENSG00000242299	AC073861.1
ENSG00000242301	0	0	0	0	ENSG00000242301	RP11-93P10.3
ENSG00000242307	0.539469	1.28343	2.08907	1.13083	ENSG00000242307	AC010401.1
ENSG00000242308	0	0	0	0	ENSG00000242308	AC048334.1
ENSG00000242314	0	0	0	0	ENSG00000242314	RPL12P32
ENSG00000242318	0.657584	1.57512	1.84841	1.92844	ENSG00000242318	AC058823.1
ENSG00000242320	0	0	0.14042	0	ENSG00000242320	RPL21P126
ENSG00000242321	0.222669	1.91398	0.192039	0.705769	ENSG00000242321	RPL23AP40
ENSG00000242324	0.0332406	0	0	0	ENSG00000242324	AL049634.1
ENSG00000242325	1.29267	0.617561	1.54621	0.911438	ENSG00000242325	RPS12P31
ENSG00000242326	0.297025	0.71197	0.89991	0.635367	ENSG00000242326	AC104629.1
ENSG00000242327	0	0	0.153712	0	ENSG00000242327	AC023906.1
ENSG00000242329	0.409731	0.387309	2.78838	0.843537	ENSG00000242329	AC007215.1
ENSG00000242335	0.673506	1.02153	1.99239	0.654293	ENSG00000242335	CFB
ENSG00000242337	0.134011	0.305356	0.636041	0.653743	ENSG00000242337	TFP1
ENSG00000242338	5.74894	10.4066	10.2916	8.76291	ENSG00000242338	BMS1P4
ENSG00000242352	0.256503	0.187324	0.655451	0.373483	ENSG00000242352	FAM91A3P
ENSG00000242353	0	0	0	0	ENSG00000242353	RPL12P30
ENSG00000242358	1.00574	3.31943	5.13085	3.06928	ENSG00000242358	RPS21P4
ENSG00000242361	0.14792	0.0277777	0.144251	0.0815791	ENSG00000242361	HLA-DMA
ENSG00000242362	0	0.0219476	0.0109151	0.0319741	ENSG00000242362	CT47A2
ENSG00000242364	0	0	0	0	ENSG00000242364	AC108725.1
ENSG00000242365	0	0	0	0	ENSG00000242365	NDUFA5P5
ENSG00000242366	0	0	0	0	ENSG00000242366	UGT1A8
ENSG00000242371	0	0	0	0	ENSG00000242371	IGKV1-39
ENSG00000242372	145.717	86.9096	76.5097	43.5015	ENSG00000242372	EIF6
ENSG00000242384	8.86783	10.4515	11.179	6.39946	ENSG00000242384	TBC1D3H
ENSG00000242386	0	0.00799456	0.00913478	0.00910544	ENSG00000242386	HLA-DMB
ENSG00000242387	0	0	0	0	ENSG00000242387	HIST1H2APS2
ENSG00000242389	0	0	0	0	ENSG00000242389	RBMY1E

ENSG00000242390	0	0	0	0	ENSG00000242390	RPL6P9
ENSG00000242393	0	0	0	0	ENSG00000242393	AC010141.3
ENSG00000242399	0	0	0	0	ENSG00000242399	RPS20P23
ENSG00000242405	0.736866	1.36192	0.514153	1.65961	ENSG00000242405	AC007537.2
ENSG00000242411	0	0.221081	0	0	ENSG00000242411	AC011506.1
ENSG00000242412	0.112657	0.512784	0.330838	0.809886	ENSG00000242412	DBIL5P2
ENSG00000242417	0	0.253263	0	0.141616	ENSG00000242417	RPL18P1
ENSG00000242419	0.558722	0.910862	1.14382	1.80262	ENSG00000242419	PCDHGC4
ENSG00000242423	0.162337	0.155553	0.14042	0.870475	ENSG00000242423	RPL12P36
ENSG00000242429	0.426139	1.96856	1.37909	1.54342	ENSG00000242429	RP11-19G24.2
ENSG00000242431	1.04344	0.754301	1.0276	1.00854	ENSG00000242431	AC107398.1
ENSG00000242435	0.545674	1.76644	0.805174	0.967653	ENSG00000242435	UPK3BP1
ENSG00000242439	0.199286	0.95356	0.185197	0.63403	ENSG00000242439	AC127024.1
ENSG00000242441	0.0562467	0.133369	0.203962	0.197325	ENSG00000242441	GTF2A1L
ENSG00000242444	0.764225	0.87903	1.71978	1.79694	ENSG00000242444	AC007207.1
ENSG00000242445	0	0.246674	0	0.468365	ENSG00000242445	RPL7AP11
ENSG00000242456	0	0	0	0	ENSG00000242456	MTCO3P38
ENSG00000242457	0.145312	1.17862	0.878988	1.02235	ENSG00000242457	RBBP4P2
ENSG00000242461	0	0	0	0	ENSG00000242461	AC089999.1
ENSG00000242472	0	0	0	0	ENSG00000242472	IGHJ5
ENSG00000242473	0	0	0	0	ENSG00000242473	KIR2DP1
ENSG00000242477	0	0	0	0	ENSG00000242477	AC091429.1
ENSG00000242479	0.371911	0.654049	0.521432	0.673376	ENSG00000242479	AC109992.1
ENSG00000242485	477.365	355.325	275.279	170.428	ENSG00000242485	MRPL20
ENSG00000242488	2.02304	5.1418	4.99679	8.92424	ENSG00000242488	AF107885.1
ENSG00000242498	5.91974	7.14004	7.95316	9.5983	ENSG00000242498	ARPIN
ENSG00000242507	0.215316	0.310179	0.317946	0.232215	ENSG00000242507	FO393401.2
ENSG00000242510	0.547544	3.13431	2.593	6.01243	ENSG00000242510	NDUFB4P1
ENSG00000242511	4.88614	0	0	0	ENSG00000242511	RPL23AP1
ENSG00000242515	0	0	0	0	ENSG00000242515	UGT1A10
ENSG00000242520	0.37233	0.186436	0.176885	0.436679	ENSG00000242520	MAGEA5
ENSG00000242524	0	0.0415668	0.00939099	0.0470305	ENSG00000242524	AL672167.3
ENSG00000242525	0.424587	0.408538	0.327087	1.10735	ENSG00000242525	OR7E100P
ENSG00000242527	0	0	0.341744	0.413624	ENSG00000242527	AC100771.1
ENSG00000242529	0	0	0	0	ENSG00000242529	AHCYP8
ENSG00000242531	13.1719	9.21005	13.7502	5.77982	ENSG00000242531	AC083798.1
ENSG00000242534	0	0	0.289574	0	ENSG00000242534	IGKV2D-28
ENSG00000242537	0.0295355	0.0259883	0.0230869	0.117148	ENSG00000242537	MRE11P1
ENSG00000242550	2.64768	0.944432	1.15434	2.07943	ENSG00000242550	SERPINB10
ENSG00000242551	0	0.0609926	0.271638	0.340189	ENSG00000242551	POU5F1P6
ENSG00000242552	0	0	0.157364	0	ENSG00000242552	MRPL42P4
ENSG00000242561	0	0	0	0	ENSG00000242561	ATP5LP5
ENSG00000242562	0	0.0887771	0	0	ENSG00000242562	DCAF13P1
ENSG00000242571	0	0	0.312376	0	ENSG00000242571	RPL21P11
ENSG00000242573	0.073576	0.0714337	0	0.0768778	ENSG00000242573	ACTR3P3
ENSG00000242574	0.236301	0.933108	0.629886	2.02443	ENSG00000242574	HLA-DMB
ENSG00000242575	0	0.0445437	0.0402614	0.0505556	ENSG00000242575	AC012501.2
ENSG00000242580	0	0.266738	0	0.14894	ENSG00000242580	IGKV1D-43
ENSG00000242583	0	0	0	0	ENSG00000242583	AC008040.2
ENSG00000242586	0.279678	0.218026	0	0	ENSG00000242586	AC108740.1
ENSG00000242588	19.0806	45.9578	47.1428	45.5674	ENSG00000242588	AC108010.1
ENSG00000242595	0	1.7987	1.29919	2.79544	ENSG00000242595	RPL26P26
ENSG00000242598	0	0	0	0	ENSG00000242598	MED28P8
ENSG00000242599	0.180101	0.319413	0.312253	0.203153	ENSG00000242599	CSAG4

ENSG00000242600	2.93511	4.48063	6.16014	8.91521	ENSG00000242600	MBL1P
ENSG00000242602	3.80072	9.04366	7.02298	12.2759	ENSG00000242602	AC008953.1
ENSG00000242607	0.139676	0.708664	0.385661	0.610158	ENSG00000242607	AC068587.1
ENSG00000242608	0	0	0	0	ENSG00000242608	RPS23P5
ENSG00000242609	0.0774277	0.367597	0.134929	0.248997	ENSG00000242609	AC105265.2
ENSG00000242610	0	0	0.0593712	0.148583	ENSG00000242610	OR5BH1P
ENSG00000242612	17.0185	19.2519	12.6025	14.2119	ENSG00000242612	DECR2
ENSG00000242613	0	0	0	0	ENSG00000242613	AC063952.3
ENSG00000242615	4.54575	2.7456	3.27417	2.47261	ENSG00000242615	AC022415.1
ENSG00000242616	16.696	12.8125	9.81177	8.24461	ENSG00000242616	GNG10
ENSG00000242631	7.0337	13.3135	8.5861	6.87301	ENSG00000242631	
ENSG00000242634	0.883181	1.89899	2.28636	3.0334	ENSG00000242634	RPS24P16
ENSG00000242635	0	0	0	0	ENSG00000242635	RPS14P7
ENSG00000242636	0	0	0	0	ENSG00000242636	RPL21P129
ENSG00000242640	0	0	0	0	ENSG00000242640	RPS29P11
ENSG00000242654	0	0	0	0	ENSG00000242654	RPL32P14
ENSG00000242660	4.16654	0	0	1.57858	ENSG00000242660	AC015911.1
ENSG00000242661	0.083821	0	0.151348	0.273969	ENSG00000242661	RPS3AP43
ENSG00000242667	0	0.147392	0.133125	0.329209	ENSG00000242667	AC087385.2
ENSG00000242670	0	0	0.232914	0.567992	ENSG00000242670	RPL22P13
ENSG00000242675	0	0	0	0	ENSG00000242675	RPS16P9
ENSG00000242676	0.232505	0.482257	0.623935	0.762302	ENSG00000242676	
ENSG00000242683	0.144406	0.713218	0.646163	0.618277	ENSG00000242683	RPL12P21
ENSG00000242685	0.438161	0.200969	0.356435	0.33828	ENSG00000242685	HLA-DMA
ENSG00000242689	1.36596	2.14552	2.13369	2.08756	ENSG00000242689	CNTF
ENSG00000242692	0	0	0	0	ENSG00000242692	RPS27AP1
ENSG00000242697	0.0753197	0	0.0654725	0	ENSG00000242697	RPL5P12
ENSG00000242703	0.037093	0.142995	0	0.0814638	ENSG00000242703	CCT4P1
ENSG00000242705	0	0	0.0519591	0	ENSG00000242705	ICE2P2
ENSG00000242706	0.205736	0	0.288525	0.818682	ENSG00000242706	RPS27AP9
ENSG00000242709	0	0	0	0	ENSG00000242709	RPL30P9
ENSG00000242711	0.169023	0.0380732	1.16434	0.0741571	ENSG00000242711	PSMB9
ENSG00000242715	0.444851	1.75946	1.69854	1.59249	ENSG00000242715	CCDC169
ENSG00000242726	0	0	1.02588	3.09962	ENSG00000242726	RPP21
ENSG00000242727	0.203879	0	0	0	ENSG00000242727	AC104687.1
ENSG00000242728	0.954973	0.842676	0.357736	3.46121	ENSG00000242728	UQCRHP4
ENSG00000242729	0	0	0	0.706403	ENSG00000242729	AC021006.1
ENSG00000242731	0	0.749819	0.728766	0.370578	ENSG00000242731	FAM86LP
ENSG00000242732	0.273163	0.466705	0.931379	1.30719	ENSG00000242732	RTL5
ENSG00000242735	0	0.720955	0.179456	0.965572	ENSG00000242735	RPSAP26
ENSG00000242736	0	0	0	0	ENSG00000242736	TRBV1
ENSG00000242737	1.53345	1.21751	1.76318	2.90228	ENSG00000242737	AC012170.1
ENSG00000242747	0	0.157488	0.149576	0.175459	ENSG00000242747	AC090515.1
ENSG00000242748	0.991165	2.57323	0.944428	2.65651	ENSG00000242748	RPL23AP81
ENSG00000242752	0	0	0	5.85406	ENSG00000242752	NMTRQ-TTG12-1
ENSG00000242756	0	0.787338	0.314457	0.408309	ENSG00000242756	RHOT1P3
ENSG00000242757	0	0	0	0	ENSG00000242757	AL606462.1
ENSG00000242766	0	0	0	0	ENSG00000242766	IGKV1D-17
ENSG00000242768	0	0	0	0.268673	ENSG00000242768	AC096576.1
ENSG00000242771	0	0	0	0	ENSG00000242771	TRBV5-2
ENSG00000242779	16.9021	22.8055	14.5472	14.964	ENSG00000242779	ZNF702P
ENSG00000242793	0.16183	0.155087	0	0.172721	ENSG00000242793	AC135999.1
ENSG00000242802	29.5312	16.0221	26.2621	14.6232	ENSG00000242802	AP5Z1
ENSG00000242807	0	0	0	0.200373	ENSG00000242807	AP002371.1

ENSG00000242810	0	0	0	0	ENSG00000242810	MRPL42P6
ENSG00000242814	0	0	0	0	ENSG00000242814	AC113398.1
ENSG00000242829	1.07787	0.256685	0	1.97896	ENSG00000242829	RPS26P21
ENSG00000242834	0	0	0.0713391	0.0890581	ENSG00000242834	RPL7AP56
ENSG00000242836	0	0.0802301	0.165624	0.452326	ENSG00000242836	MTCO3P35
ENSG00000242837	0	0	0	0.34337	ENSG00000242837	RPL21P13
ENSG00000242841	0	0	0	0.0482227	ENSG00000242841	KRT8P35
ENSG00000242849	0	0	0	0	ENSG00000242849	ALDOAP1
ENSG00000242850	0	0	0.393372	0.195212	ENSG00000242850	RPL23AP68
ENSG00000242852	2.48044	2.94921	2.13528	5.25671	ENSG00000242852	ZNF709
ENSG00000242854	0.156521	0.150146	0.138384	0	ENSG00000242854	DNM1P24
ENSG00000242856	0	0	0	0	ENSG00000242856	VN1R105P
ENSG00000242858	0.117322	0	0	0	ENSG00000242858	AC020899.1
ENSG00000242866	3.09125	4.63855	6.89526	4.55808	ENSG00000242866	STRC
ENSG00000242875	0	0	0	0	ENSG00000242875	RBMY1B
ENSG00000242879	0	1.27301	1.99473	2.84676	ENSG00000242879	AC006335.2
ENSG00000242882	0	0.068124	0.0615601	0.153881	ENSG00000242882	RPL5P11
ENSG00000242887	0	0	0	0	ENSG00000242887	IGHJ3
ENSG00000242888	0.554967	0.45729	0.757272	1.90369	ENSG00000242888	AL133368.1
ENSG00000242899	0.0896991	0	0	0.0970951	ENSG00000242899	RPL7P16
ENSG00000242911	0.253108	0.48236	0.218122	0	ENSG00000242911	AC140059.1
ENSG00000242915	0	0	0	0	ENSG00000242915	SNRPGP7
ENSG00000242922	0	0	0.421261	0.173209	ENSG00000242922	RPL21P104
ENSG00000242931	0.472778	1.00094	1.23106	1.65005	ENSG00000242931	RPL7P49
ENSG00000242936	0.555366	0	0	0.290891	ENSG00000242936	RPL30P6
ENSG00000242941	0	0	0.133856	0.165244	ENSG00000242941	RPL12P7
ENSG00000242943	0	0	0	0	ENSG00000242943	NKAIN1P1
ENSG00000242945	0.496335	0.792467	0.858506	1.05836	ENSG00000242945	AC015524.1
ENSG00000242948	1.0025	2.14693	1.79238	3.42115	ENSG00000242948	EPS15P1
ENSG00000242950	18.1438	45.918	50.2135	60.7361	ENSG00000242950	ERVW-1
ENSG00000242951	0	0	0	0.226666	ENSG00000242951	AC007182.2
ENSG00000242952	0	0	0	0	ENSG00000242952	RPSAP3
ENSG00000242953	0	0	0.765357	1.53356	ENSG00000242953	AC139453.2
ENSG00000242958	0.347111	1.81874	1.09549	1.94745	ENSG00000242958	AC040975.1
ENSG00000242960	0.141709	0.268524	0	0.302809	ENSG00000242960	FTH1P23
ENSG00000242963	0	0	0	0	ENSG00000242963	AC026336.1
ENSG00000242968	0	0	0	0	ENSG00000242968	AC096992.1
ENSG00000242970	0.304591	0.712467	1.06464	0.827295	ENSG00000242970	AC068522.1
ENSG00000242978	0	0.150454	0	0	ENSG00000242978	AC004534.1
ENSG00000242979	0	0	0.190461	0	ENSG00000242979	AC010285.1
ENSG00000242983	0	0	0	0	ENSG00000242983	CABYRP1
ENSG00000242986	0.195581	0	0	2.90577	ENSG00000242986	RPL21P99
ENSG00000242990	0	0	0	0	ENSG00000242990	RPL13AP23
ENSG00000242991	0.0886047	0.255408	0.0769171	0.0959115	ENSG00000242991	RPL7P40
ENSG00000242992	0.396824	1.84337	2.01777	1.75923	ENSG00000242992	FTH1P4
ENSG00000242993	1.25194	1.64582	0.360325	1.76802	ENSG00000242993	AP000870.1
ENSG00000242995	0	0	0	0.324459	ENSG00000242995	AL161757.1
ENSG00000243000	5.28685	4.84559	8.30655	7.58931	ENSG00000243000	RP11-504P24.3
ENSG00000243003	0.0272928	0.112493	0.0254114	0.0148391	ENSG00000243003	LY6G6F
ENSG00000243007	0	0.150538	0.28535	0	ENSG00000243007	RPL12P35
ENSG00000243009	0	0	0.74619	3.29875	ENSG00000243009	RPP21
ENSG00000243014	0	0	0.240181	0	ENSG00000243014	PTMAP8
ENSG00000243016	0.789183	1.13452	0.596059	1.06424	ENSG00000243016	AC112482.1
ENSG00000243020	0	0	0	0	ENSG00000243020	RPL7P39

ENSG00000243022	0.274922	0.351302	0.181856	0.109592	ENSG00000243022	MARK3P3
ENSG00000243023	0.46069	0.497449	0.198839	0.910344	ENSG00000243023	UBA52P3
ENSG00000243024	1.10237	1.75323	1.97501	3.91522	ENSG00000243024	AC012158.1
ENSG00000243025	0	0.151246	0	0.0853412	ENSG00000243025	MTAPP1
ENSG00000243033	0	0.0594724	0.0537468	0	ENSG00000243033	GAPDHP47
ENSG00000243038	5.0157	7.02609	8.1955	17.0063	ENSG00000243038	AL117692.1
ENSG00000243040	0.262634	0.977366	0.79175	1.5604	ENSG00000243040	RBMY2FP
ENSG00000243044	0	3.85085	0.0912349	1.56296	ENSG00000243044	AC128716.1
ENSG00000243048	0	0	0	0	ENSG00000243048	FTH1P18
ENSG00000243050	0	0	0	0	ENSG00000243050	RPL30P10
ENSG00000243053	3.20431	4.00986	4.42584	5.26672	ENSG00000243053	RPL31P58
ENSG00000243056	2.09979	0.36071	1.84011	4.11076	ENSG00000243056	EIF4EBP3
ENSG00000243058	0	0	1.13112	1.35737	ENSG00000243058	AC015724.1
ENSG00000243063	0	0	0	0	ENSG00000243063	IGKV3-7
ENSG00000243064	1.11469	2.19016	1.72148	4.57476	ENSG00000243064	ABCC13
ENSG00000243067	0	0.67211	0	0.492761	ENSG00000243067	PSMB9
ENSG00000243071	0	0	0.167863	0.222788	ENSG00000243071	AC107032.1
ENSG00000243072	0	0	0	0	ENSG00000243072	AF186996.7
ENSG00000243073	0	0	0	0	ENSG00000243073	PRAMEF4
ENSG00000243085	0.417709	0	0	0	ENSG00000243085	AL390726.1
ENSG00000243094	0.210329	1.00518	0	0.668166	ENSG00000243094	AC079203.1
ENSG00000243095	0	0.0497666	0.089962	0.394874	ENSG00000243095	RPL3P10
ENSG00000243099	0	0	0	0	ENSG00000243099	AC020983.1
ENSG00000243101	0	0.176047	0.715478	0.396218	ENSG00000243101	RPS3P7
ENSG00000243104	0.332664	0.357781	0	0.390809	ENSG00000243104	MTND4LP14
ENSG00000243113	0.118811	0	0	0.0647303	ENSG00000243113	RP11-480I12.9
ENSG00000243116	0.0722093	0.138891	0.0627465	0	ENSG00000243116	AC092943.1
ENSG00000243122	0	0	0	0	ENSG00000243122	AC016304.1
ENSG00000243129	0	0	0.465827	0	ENSG00000243129	AC023790.1
ENSG00000243130	2.68058	0.874845	1.95437	4.43739	ENSG00000243130	PSG11
ENSG00000243135	0.893531	0.515581	0.739713	0	ENSG00000243135	UGT1A3
ENSG00000243137	3.74653	2.40658	3.11037	8.16116	ENSG00000243137	PSG4
ENSG00000243141	0.629368	1.0562	2.35783	3.55032	ENSG00000243141	RPL23AP66
ENSG00000243147	47.9179	38.5142	34.3433	28.7885	ENSG00000243147	MRPL33
ENSG00000243154	0.170508	0.185631	0.175715	0.634201	ENSG00000243154	SYPL1P1
ENSG00000243156	31.8477	49.8938	57.7318	69.8953	ENSG00000243156	MICAL3
ENSG00000243160	0.0822318	0	0	0	ENSG00000243160	AC093270.2
ENSG00000243164	0	0	0	0	ENSG00000243164	AC087879.1
ENSG00000243165	0.828617	0	0	0	ENSG00000243165	AC025033.1
ENSG00000243167	0	0	0	0	ENSG00000243167	RPS10P28
ENSG00000243171	0	0	0	0	ENSG00000243171	AC041039.1
ENSG00000243175	1.70018	3.70772	3.15951	6.15602	ENSG00000243175	RPSAP36
ENSG00000243181	0	0	0	0	ENSG00000243181	AC087343.1
ENSG00000243188	0	0	0	0	ENSG00000243188	HNRNPA1P17
ENSG00000243189	0.438161	0.200969	0.356435	0.33828	ENSG00000243189	HLA-DMA
ENSG00000243195	0	0	0	0	ENSG00000243195	TUBBP11
ENSG00000243199	5.85904	3.83635	2.32491	2.28201	ENSG00000243199	AC115223.1
ENSG00000243207	0.292836	0.751318	1.42599	1.14317	ENSG00000243207	PPAN-P2RY11
ENSG00000243215	0.438161	0.200969	0.356435	0.33828	ENSG00000243215	HLA-DMA
ENSG00000243225	0.340534	0.868051	0.746637	0.846817	ENSG00000243225	AC007686.1
ENSG00000243232	0.485299	2.34072	0.994225	0.736066	ENSG00000243232	PCDHAC2
ENSG00000243234	0	0	0.101523	0	ENSG00000243234	AC010326.1
ENSG00000243236	0.447454	0.660155	1.5376	1.34552	ENSG00000243236	GSTA9P
ENSG00000243238	0	0	0	0	ENSG00000243238	IGKV2-30

ENSG00000243244	0.836023	1.95089	1.78894	3.57783	ENSG00000243244	STON1
ENSG00000243250	0.341286	1.7468	0.706743	0.791295	ENSG00000243250	AP002884.1
ENSG00000243251	4.39762	4.29523	2.66923	4.07637	ENSG00000243251	PGBD3
ENSG00000243256	0.269733	1.02674	0.232192	0.565416	ENSG00000243256	RPL30P14
ENSG00000243257	0.880569	1.66115	2.18081	6.16609	ENSG00000243257	MTCO2P29
ENSG00000243264	0	0	0	0	ENSG00000243264	IGKV2D-29
ENSG00000243265	0.7069	1.86009	1.6793	2.78026	ENSG00000243265	RPL23AP55
ENSG00000243268	0	1.33E-05	0	0	ENSG00000243268	ATP5AP1
ENSG00000243279	2.96738	4.68064	4.53831	5.52521	ENSG00000243279	PRAF2
ENSG00000243280	0.326761	3.70901	4.34458	3.40965	ENSG00000243280	AC093663.2
ENSG00000243284	0.287898	0.572646	0.421545	0.707931	ENSG00000243284	VSIG8
ENSG00000243287	0	0	0	0.230566	ENSG00000243287	AP002088.1
ENSG00000243289	0	0	0	0	ENSG00000243289	AGAP13P
ENSG00000243290	0	0	0	0.476394	ENSG00000243290	IGKV1-12
ENSG00000243297	0.236529	0.282732	0.733843	0.336851	ENSG00000243297	RPL31P61
ENSG00000243302	9.08081	11.6124	20.8471	18.7643	ENSG00000243302	AC018638.4
ENSG00000243303	0.538937	1.7968	0.231885	0.282708	ENSG00000243303	AC103987.1
ENSG00000243304	0	0.0899945	0.220202	0.441854	ENSG00000243304	AC008494.1
ENSG00000243307	0.0814032	0.436417	0.160411	0.775115	ENSG00000243307	POM121L6P
ENSG00000243312	0.147962	0.213582	0.128633	0.160642	ENSG00000243312	AC093827.1
ENSG00000243314	0.476847	0.910158	0.205622	1.50852	ENSG00000243314	AC106707.2
ENSG00000243316	0.0418201	0	0	0.137245	ENSG00000243316	GUCY2GP
ENSG00000243317	11.8764	19.733	19.333	28.9682	ENSG00000243317	C7orf73
ENSG00000243323	0.771629	1.59867	0.934257	1.97551	ENSG00000243323	PTPRVP
ENSG00000243328	0	0	0	0	ENSG00000243328	AC083982.1
ENSG00000243335	9.40103	7.28103	5.90906	8.53682	ENSG00000243335	KCTD7
ENSG00000243336	0	0	0	0.0023022	ENSG00000243336	HLA-J
ENSG00000243353	3.9096	2.08588	6.02875	2.20457	ENSG00000243353	RPS29P19
ENSG00000243355	0	0	0	0	ENSG00000243355	AC012123.2
ENSG00000243364	9.02291	8.31775	7.49014	5.16778	ENSG00000243364	EFNA4
ENSG00000243378	0	0	0.31691	0.858437	ENSG00000243378	AC083801.1
ENSG00000243382	0	0.0446385	0	0	ENSG00000243382	ATP5AP10
ENSG00000243385	0.122072	0.354341	0.105796	0.525016	ENSG00000243385	AC094085.1
ENSG00000243388	0	0	0	0.699525	ENSG00000243388	RPL3P3
ENSG00000243396	0.212028	0.810697	1.46359	0.448757	ENSG00000243396	AC084198.1
ENSG00000243402	0.998034	2.63292	1.83719	3.4845	ENSG00000243402	AC022973.1
ENSG00000243403	0.327258	0.315835	0.301709	2.13912	ENSG00000243403	AC090543.2
ENSG00000243404	1.84336	4.19222	1.9063	8.14473	ENSG00000243404	AC011276.1
ENSG00000243406	6.72087	13.6777	13.0579	17.1322	ENSG00000243406	MRPS31P5
ENSG00000243414	3.0309	1.8572	2.69682	6.3603	ENSG00000243414	TICAM2
ENSG00000243417	0.756419	0.646867	0.292111	0.0977326	ENSG00000243417	AC023424.2
ENSG00000243422	0.677433	2.25096	2.99059	0.182301	ENSG00000243422	RPL23AP49
ENSG00000243423	4.24149	4.41532	3.14794	3.49094	ENSG00000243423	AC004223.1
ENSG00000243429	0	0	0.0651785	0	ENSG00000243429	AF186996.8
ENSG00000243431	0.390355	1.08478	1.2651	0.827158	ENSG00000243431	RPL5P30
ENSG00000243438	0	0.414298	0.498749	0	ENSG00000243438	LARP1BP2
ENSG00000243440	0.0523297	0.453354	0.18211	0.841077	ENSG00000243440	AF130351.1
ENSG00000243441	0	0	0	0.0254603	ENSG00000243441	OR5V1
ENSG00000243444	1.13905	1.74095	2.10885	6.13818	ENSG00000243444	PALM2
ENSG00000243445	0	0	0	0	ENSG00000243445	AC106820.1
ENSG00000243449	16.2521	12.3959	6.11275	8.10977	ENSG00000243449	C4orf48
ENSG00000243452	13.404	31.0604	17.6987	23.4393	ENSG00000243452	NBPF15
ENSG00000243453	0.530978	0	0	0	ENSG00000243453	COX7BP1
ENSG00000243455	0	0	0	0	ENSG00000243455	RPS18P13

ENSG00000243466	0	0	0	0	ENSG00000243466	IGKV1-5
ENSG00000243468	2.88876	4.01194	4.85465	6.85032	ENSG00000243468	INGX
ENSG00000243469	0	0	0	0	ENSG00000243469	RPL7P51
ENSG00000243477	5.09283	8.84713	5.47484	3.15624	ENSG00000243477	NAT6
ENSG00000243478	1.4275	1.14872	1.00707	1.48517	ENSG00000243478	AOX2P
ENSG00000243480	0	0	0.150455	0.237473	ENSG00000243480	AMY2A
ENSG00000243483	0.194136	0.185769	0.168437	0.412163	ENSG00000243483	AC078785.3
ENSG00000243489	0	0	0	0	ENSG00000243489	KRTAP10-11
ENSG00000243492	0.495404	1.60234	0.349705	0.822841	ENSG00000243492	HLA-L
ENSG00000243494	0	0	0.0384919	0	ENSG00000243494	AC011476.1
ENSG00000243495	0	0	4.25204	0	ENSG00000243495	GMFBP1
ENSG00000243496	0	1.90116	0	0	ENSG00000243496	HLA-DOB
ENSG00000243498	3.47319	1.30149	2.31852	0.697022	ENSG00000243498	AC068228.1
ENSG00000243499	0	0.0857199	0.206834	0.0953991	ENSG00000243499	AC117500.1
ENSG00000243500	0	0	0	0	ENSG00000243500	RP11-364B6.2
ENSG00000243501	0.0801045	0.423234	0	0.244832	ENSG00000243501	AL365232.1
ENSG00000243503	0	0	0	0	ENSG00000243503	AC090453.1
ENSG00000243504	0	0.181154	0.16354	0.20134	ENSG00000243504	RPS23P1
ENSG00000243507	0	0	0	0	ENSG00000243507	AC005908.1
ENSG00000243508	0.844405	1.63106	1.63231	4.2879	ENSG00000243508	AC108688.1
ENSG00000243509	34.9294	212.897	10.9238	36.6603	ENSG00000243509	TNFRSF6B
ENSG00000243514	0.219049	0	0.377894	0.462997	ENSG00000243514	RPL32P33
ENSG00000243516	0	0	0	0.168156	ENSG00000243516	RPL12P40
ENSG00000243517	0.292055	0.118073	0	0.12752	ENSG00000243517	AC024940.2
ENSG00000243518	0.152473	0.146608	0.19867	0	ENSG00000243518	AC108729.2
ENSG00000243519	0.295639	0.850239	0.253865	0.927486	ENSG00000243519	IGLVIVOR22-2
ENSG00000243521	0	0.0669533	0	0.0757323	ENSG00000243521	RPL5P33
ENSG00000243531	0	0	0	0	ENSG00000243531	AC079804.2
ENSG00000243536	0	0	0	0	ENSG00000243536	ANTXRLP1
ENSG00000243537	0	0.198023	0	0.219353	ENSG00000243537	KC877373.1
ENSG00000243538	0.83222	1.59065	1.19097	5.54245	ENSG00000243538	RPS26P28
ENSG00000243543	0.112555	0	0.377895	0.12126	ENSG00000243543	WFDC6
ENSG00000243547	0	0	0.0378678	0.0476457	ENSG00000243547	HNRNPKP4
ENSG00000243554	6.46601	7.43016	13.5281	4.01405	ENSG00000243554	AC004967.1
ENSG00000243566	4.75671	7.08463	10.5723	4.62647	ENSG00000243566	UPK3B
ENSG00000243568	4.44297	8.99379	8.17607	12.0447	ENSG00000243568	AC020779.1
ENSG00000243570	0.673506	1.02153	1.99239	0.654293	ENSG00000243570	CFB
ENSG00000243581	0	0	0	0	ENSG00000243581	RPS29P25
ENSG00000243584	0	0.0220599	0.0598967	0.0754177	ENSG00000243584	AC068769.1
ENSG00000243587	1.77881	4.02947	3.93402	5.96621	ENSG00000243587	C6orf183
ENSG00000243592	0	0.127396	0	0.142511	ENSG00000243592	AC016638.1
ENSG00000243594	0.400964	1.56665	0.740797	1.8861	ENSG00000243594	PSMB9
ENSG00000243596	0	0	0	0	ENSG00000243596	AC130509.1
ENSG00000243601	0	0	0	0	ENSG00000243601	RPL12P24
ENSG00000243607	0	0	0.533366	0.736224	ENSG00000243607	AP001318.1
ENSG00000243609	1.58721	2.04419	2.37899	4.34852	ENSG00000243609	AC026470.1
ENSG00000243612	0	0.113748	0.315633	0	ENSG00000243612	HLA-DOB
ENSG00000243621	6.31291	14.5931	18.6166	15.8404	ENSG00000243621	AC003989.2
ENSG00000243627	0.291347	0.112147	0.253385	0.127019	ENSG00000243627	AP000322.1
ENSG00000243635	0	0	0.220646	0	ENSG00000243635	AC091804.1
ENSG00000243641	0.0649073	0.0624281	0.0564162	0.49443	ENSG00000243641	OR13C7
ENSG00000243643	0	0	0	0	ENSG00000243643	TSPY20P
ENSG00000243646	12.1607	22.3019	11.4966	11.132	ENSG00000243646	IL10RB
ENSG00000243648	0	0	0	0	ENSG00000243648	AC109454.1

ENSG00000243649	0.715709	0.908094	3.88551	1.25132	ENSG00000243649	CFB
ENSG00000243658	0.0672138	0.129521	0.237493	0.601405	ENSG00000243658	MTND5P16
ENSG00000243659	0.393154	0.748758	1.33989	2.04345	ENSG00000243659	FO393419.3
ENSG00000243660	4.52178	6.16889	5.41954	11.2787	ENSG00000243660	ZNF487
ENSG00000243661	0	0	0	0.0382885	ENSG00000243661	WBP1LP1
ENSG00000243663	0.669909	0.643195	0.727196	0.819401	ENSG00000243663	RPS4XP14
ENSG00000243664	0	0	0	0	ENSG00000243664	RPS29P12
ENSG00000243667	6.94409	9.14315	9.70743	10.8303	ENSG00000243667	WDR92
ENSG00000243669	0.257421	0	0	0	ENSG00000243669	AP000926.2
ENSG00000243672	0	0	0	0	ENSG00000243672	AC004924.1
ENSG00000243674	0.161083	0.212336	0.18413	0.0799027	ENSG00000243674	AC131233.1
ENSG00000243675	0.307226	2.04112	0.527118	2.56491	ENSG00000243675	AC080013.2
ENSG00000243678	196.753	227.876	144.673	101.5	ENSG00000243678	NME2
ENSG00000243679	9.51327	11.0545	15.8502	16.0844	ENSG00000243679	AC018638.5
ENSG00000243680	0	0	0	0	ENSG00000243680	RPL37P23
ENSG00000243686	0.560348	0	0	0	ENSG00000243686	AC002553.3
ENSG00000243687	0	1.95565	1.01031	2.0507	ENSG00000243687	AC079594.1
ENSG00000243695	0	0.352894	0.855854	0.883765	ENSG00000243695	AL353729.1
ENSG00000243696	0.540238	0.810151	1.03128	0.744913	ENSG00000243696	AC006254.1
ENSG00000243697	0	0.391913	0.0757345	0.0884259	ENSG00000243697	AC009108.1
ENSG00000243705	0	0	0	0	ENSG00000243705	AC010531.2
ENSG00000243708	19.1778	14.3864	11.6379	6.13524	ENSG00000243708	PLA2G4B
ENSG00000243709	0.0436395	0	0.188738	0.157114	ENSG00000243709	LEFTY1
ENSG00000243710	0.611703	2.10247	1.21263	2.50114	ENSG00000243710	CFAP57
ENSG00000243711	0	0	0	0	ENSG00000243711	AC103975.1
ENSG00000243716	103.931	271.216	272.243	298.95	ENSG00000243716	NPIPB5
ENSG00000243719	0.438161	0.200969	0.356435	0.33828	ENSG00000243719	HLA-DMA
ENSG00000243720	0	0	0	0	ENSG00000243720	AP001025.2
ENSG00000243721	1.82408	2.97224	2.3259	6.07143	ENSG00000243721	RPL23AP63
ENSG00000243725	15.1236	15.5143	16.1185	9.06678	ENSG00000243725	TTC4
ENSG00000243729	0	0	0	0.0254603	ENSG00000243729	OR5V1
ENSG00000243730	0	0	0	0	ENSG00000243730	AL079303.1
ENSG00000243742	1.04076	2.87872	4.47306	4.43926	ENSG00000243742	RPLP0P2
ENSG00000243744	0	0	0	0	ENSG00000243744	AC016546.1
ENSG00000243746	0.126672	0.365943	0.183854	0.0485952	ENSG00000243746	EEF1A1P10
ENSG00000243749	14.3556	17.2109	7.76503	6.4339	ENSG00000243749	TMEM35B
ENSG00000243753	2.28735	3.20427	4.14676	4.4427	ENSG00000243753	HLA-L
ENSG00000243758	0	0	0	0	ENSG00000243758	RPL35AP15
ENSG00000243759	0.0585431	0	0.0525142	0.198801	ENSG00000243759	ST13P15
ENSG00000243761	0	0	0	0.442005	ENSG00000243761	AC023194.2
ENSG00000243771	0	0	0	0	ENSG00000243771	AC010618.1
ENSG00000243772	0	0	0.0124249	0.0198593	ENSG00000243772	KIR2DL3
ENSG00000243775	1.09227	2.67396	3.10215	2.4998	ENSG00000243775	OSTCP1
ENSG00000243777	0	0.340085	0.47714	0.103216	ENSG00000243777	AP000942.1
ENSG00000243779	0	0	0	0	ENSG00000243779	AP001086.1
ENSG00000243780	0	0	0	0	ENSG00000243780	AC092754.2
ENSG00000243781	0.182122	0.406016	0.0733619	0.189418	ENSG00000243781	AL590396.1
ENSG00000243789	24.7277	58.8411	27.9807	7.55342	ENSG00000243789	JMJD7
ENSG00000243792	0	0.238848	0	0	ENSG00000243792	OR7E89P
ENSG00000243794	0	0	0	0	ENSG00000243794	SNRPCP10
ENSG00000243802	0	0.988723	0	0.273238	ENSG00000243802	AC090589.1
ENSG00000243804	0	0.112493	0.0254114	0	ENSG00000243804	LY6G6F
ENSG00000243806	0.0903628	0.260279	0	0.0978041	ENSG00000243806	RPL7P18
ENSG00000243811	2.26128	3.30761	2.91387	4.55179	ENSG00000243811	APOBEC3D

ENSG00000243813	1.50623	4.23238	2.60578	8.45358	ENSG00000243813	AC078857.1
ENSG00000243822	0	0	0	0.251572	ENSG00000243822	AC073522.1
ENSG00000243824	0	0.337439	0	0	ENSG00000243824	RPL12P6
ENSG00000243828	0.600023	2.53567	2.39162	3.44781	ENSG00000243828	AL355357.1
ENSG00000243829	0.245481	0.47781	0.320762	0.304948	ENSG00000243829	AC011495.1
ENSG00000243830	0	0	0	0	ENSG00000243830	AC092865.4
ENSG00000243831	0	0	0	0	ENSG00000243831	AL109933.2
ENSG00000243838	0.0451178	0	0.0793819	0.0994643	ENSG00000243838	PSMC1P7
ENSG00000243844	0.131509	0	0.113904	0	ENSG00000243844	AC069181.1
ENSG00000243853	0	0	0	0	ENSG00000243853	ALDH7A1P3
ENSG00000243855	0	0	0	0	ENSG00000243855	RPL12P5
ENSG00000243859	0.0724746	0.139461	0.882261	0.254672	ENSG00000243859	RPL5P17
ENSG00000243864	0	0	0	0	ENSG00000243864	RPS3AP50
ENSG00000243873	0	0.358178	0.323437	0.401119	ENSG00000243873	HMGB1P36
ENSG00000243877	0	0	0.107556	0	ENSG00000243877	HMGB1P38
ENSG00000243886	0	0	0	0	ENSG00000243886	AC117440.1
ENSG00000243889	0	0	0	0	ENSG00000243889	TRBV8-1
ENSG00000243894	0	0	0	0.13724	ENSG00000243894	AC116562.1
ENSG00000243896	11.0155	5.51528	9.40263	1.57007	ENSG00000243896	OR2A7
ENSG00000243897	0.036129	0.0775392	0.255803	0	ENSG00000243897	EGFL8
ENSG00000243899	0	0	0.373846	1.20118	ENSG00000243899	BMS1P7
ENSG00000243904	0.144327	0	0	0	ENSG00000243904	RPSAP5
ENSG00000243910	0.594381	0.549618	0.697376	0.152745	ENSG00000243910	TUBA4B
ENSG00000243914	0.144419	0.138891	0.250986	0.23535	ENSG00000243914	RPL5P14
ENSG00000243915	0	0.0475472	0	0.0817401	ENSG00000243915	THAP12P2
ENSG00000243916	0	0	0	0	ENSG00000243916	AC092183.1
ENSG00000243918	0	0	0	0	ENSG00000243918	EIF4BP8
ENSG00000243920	0	0	0	0	ENSG00000243920	RPS26P24
ENSG00000243925	0	0	0	0	ENSG00000243925	AC091021.1
ENSG00000243927	7.95462	7.78889	8.20958	8.64386	ENSG00000243927	MRPS6
ENSG00000243929	0	0	0	0	ENSG00000243929	AC104784.1
ENSG00000243930	0	0	0	0.142476	ENSG00000243930	AP002884.2
ENSG00000243935	0.149172	0.372222	0.354126	0.597551	ENSG00000243935	RP11-100J16.5
ENSG00000243939	0.433544	1.12653	2.23517	1.79816	ENSG00000243939	AC090142.2
ENSG00000243943	6.33398	12.8458	11.9313	12.8843	ENSG00000243943	ZNF512
ENSG00000243945	0	0	0	0	ENSG00000243945	AC078918.1
ENSG00000243955	0.171961	0.0580916	0.148666	0.0657713	ENSG00000243955	GSTA1
ENSG00000243958	0.169023	0.0380732	1.16434	0.0741571	ENSG00000243958	PSMB9
ENSG00000243964	0	0.179981	0	0	ENSG00000243964	RPL23AP65
ENSG00000243970	1.96798	1.48174	6.88016	3.22263	ENSG00000243970	PPIEL
ENSG00000243974	0	0.0929912	0	0.20744	ENSG00000243974	VTI1BP1
ENSG00000243977	4.11872	7.91128	7.5947	12.6384	ENSG00000243977	AC125604.1
ENSG00000243978	0.0102372	0.0759866	0.120387	0.141035	ENSG00000243978	RTL9
ENSG00000243979	0.130358	0.129548	0.394522	0.500713	ENSG00000243979	AC087752.1
ENSG00000243981	3.35098	4.0664	3.99909	4.98943	ENSG00000243981	AC064862.6
ENSG00000243986	0.341172	0.844641	0.16965	1.33087	ENSG00000243986	ENO1P3
ENSG00000243988	0	0	0.507796	0.416026	ENSG00000243988	AC012181.1
ENSG00000243989	29.7353	41.9039	37.6905	18.0679	ENSG00000243989	ACY1
ENSG00000243995	1.43726	5.47126	3.52607	6.41669	ENSG00000243995	AL035660.2
ENSG00000244000	0	0	0	0	ENSG00000244000	AC006366.1
ENSG00000244002	0	0	0	0	ENSG00000244002	RPSAP39
ENSG00000244004	0	0	0	0	ENSG00000244004	AC097493.2
ENSG00000244005	16.3833	23.4998	23.5518	27.2496	ENSG00000244005	NFS1
ENSG00000244009	0	0.0808958	0	0	ENSG00000244009	B3GAT3P1

ENSG00000244018	0.962351	0.813661	0.82978	3.35086	ENSG00000244018	RPL35P6
ENSG00000244019	0	0.0702399	0.0634593	0	ENSG00000244019	AC010234.1
ENSG00000244020	0	0.606076	0	0	ENSG00000244020	MT1HL1
ENSG00000244021	0.606888	0.94918	0.898888	0.347674	ENSG00000244021	AC093591.1
ENSG00000244024	0	0.138891	0.376479	0.618747	ENSG00000244024	LARP7P4
ENSG00000244025	0	0	0	0	ENSG00000244025	KRTAP19-3
ENSG00000244026	7.26668	9.90287	18.7222	12.0598	ENSG00000244026	FAM86DP
ENSG00000244031	0.084019	0.322992	0.218848	0.182081	ENSG00000244031	RPS3AP17
ENSG00000244038	152.35	197.567	119.365	83.3635	ENSG00000244038	DDOST
ENSG00000244039	0.0519853	0	0.130811	0.0546585	ENSG00000244039	AC008040.3
ENSG00000244043	0	0	0	0	ENSG00000244043	RPS27P27
ENSG00000244045	7.46613	7.21259	8.6673	4.61694	ENSG00000244045	TMEM199
ENSG00000244048	0	0.33155	0.299354	0	ENSG00000244048	RPS18P6
ENSG00000244050	1.93123	1.4199	2.97489	2.75168	ENSG00000244050	DEFB109F
ENSG00000244052	0	0.414137	0.437401	0.390025	ENSG00000244052	RPL5P24
ENSG00000244053	0	0.13442	0	0	ENSG00000244053	AL157792.1
ENSG00000244057	0	0	0	1.09794	ENSG00000244057	LCE3C
ENSG00000244060	0.233735	0.573956	1.13673	1.50931	ENSG00000244060	AC003029.1
ENSG00000244061	0.588315	0.225853	0	0.506441	ENSG00000244061	AC093278.1
ENSG00000244062	0	0	0.0514237	0.0971238	ENSG00000244062	AC080128.1
ENSG00000244065	0.19546	0	0.353857	0.368508	ENSG00000244065	MARK2P17
ENSG00000244067	0	0.0873762	0.118465	0.0991844	ENSG00000244067	GSTA2
ENSG00000244071	0.127461	0	0	0.273779	ENSG00000244071	RPL9P33
ENSG00000244073	0.656463	1.34393	0.924852	1.60119	ENSG00000244073	RPS4XP6
ENSG00000244076	1.37913	1.28182	1.1344	0	ENSG00000244076	AC026410.2
ENSG00000244081	0	0	0	0	ENSG00000244081	AL591379.2
ENSG00000244083	0	0	0	0	ENSG00000244083	AC021205.2
ENSG00000244086	0	0.253466	0	0	ENSG00000244086	AC110749.1
ENSG00000244088	0	0	0	0	ENSG00000244088	RPL23AP44
ENSG00000244089	0.232165	0.222836	0.102347	0.632762	ENSG00000244089	HMGB1P30
ENSG00000244094	0	0	0.0906527	0.222039	ENSG00000244094	SPRR2F
ENSG00000244097	1.13708	0.884237	1.37551	2.31196	ENSG00000244097	RPS4XP17
ENSG00000244099	0	0.364841	0	1.01229	ENSG00000244099	RPS23P3
ENSG00000244101	1.32371	6.1524	4.61494	7.86153	ENSG00000244101	HMGN1P10
ENSG00000244113	0	0.11607	0.314447	0	ENSG00000244113	AC079193.1
ENSG00000244115	1.12381	6.84257	6.54279	0.877565	ENSG00000244115	DNAJC25-GNG10
ENSG00000244116	0	0	0	0	ENSG00000244116	IGKV2-28
ENSG00000244119	0.803381	0.330656	0.475112	0.218726	ENSG00000244119	PDCL3P4
ENSG00000244122	0.404248	0.897762	1.25724	1.12797	ENSG00000244122	UGT1A7
ENSG00000244130	0	0	0	0	ENSG00000244130	UBE2Q2P9
ENSG00000244131	0.320314	0.92291	1.48159	1.70482	ENSG00000244131	RPSAP51
ENSG00000244134	0.696621	2.66139	1.80274	1.2258	ENSG00000244134	RPS12P20
ENSG00000244142	0	0	0	0	ENSG00000244142	ATP6V0CP2
ENSG00000244144	1.72524	0.783134	1.16386	1.14133	ENSG00000244144	AC128688.1
ENSG00000244146	0	0.361852	0.155782	0.191672	ENSG00000244146	AC106872.3
ENSG00000244153	0.0407257	0	0	0	ENSG00000244153	WWP1P1
ENSG00000244155	0	0.378079	0	0.050915	ENSG00000244155	CYP4F34P
ENSG00000244157	0.269939	0.173546	0.312448	0.292139	ENSG00000244157	EIF4E2P2
ENSG00000244159	9.07455	26.0217	8.80444	18.6842	ENSG00000244159	RPS27AP13
ENSG00000244165	5.54841	9.36043	12.7263	10.8121	ENSG00000244165	P2RY11
ENSG00000244167	1.43686	1.37133	0.20654	2.77754	ENSG00000244167	AC005532.2
ENSG00000244171	0.320843	0.936169	0.753856	1.33487	ENSG00000244171	PBX2P1
ENSG00000244176	0.224743	0.648339	0.455653	0.732133	ENSG00000244176	AP003733.1
ENSG00000244183	0	0.308396	0.20206	0.556437	ENSG00000244183	AC104164.4

ENSG00000244187	43.7733	40.0923	32.9644	13.9685	ENSG00000244187	TMEM141
ENSG00000244192	0	0	0.120548	0	ENSG00000244192	AC113367.1
ENSG00000244193	0	0	0.0740232	0	ENSG00000244193	AC008040.4
ENSG00000244196	0	0	0	0	ENSG00000244196	PPIAP15
ENSG00000244199	0.633473	0.60331	0.364599	0.452334	ENSG00000244199	EIF4EP3
ENSG00000244207	0.355728	0.183949	0.490328	0.968502	ENSG00000244207	C4A
ENSG00000244211	0.117285	0.127981	0.116941	0	ENSG00000244211	PDZK1P2
ENSG00000244213	0.0487261	0	0	0	ENSG00000244213	ZFAND6P1
ENSG00000244217	0.181516	0.26164	0.0787921	0.19641	ENSG00000244217	RPS4XP10
ENSG00000244222	0	0	0.0579104	0	ENSG00000244222	OR7E121P
ENSG00000244226	0.361021	0.992352	0.945243	1.40893	ENSG00000244226	ILF2P1
ENSG00000244229	1.03199	2.07089	1.78719	3.29831	ENSG00000244229	AC027575.1
ENSG00000244234	0	0.110877	0	0.163434	ENSG00000244234	GMCL1P1
ENSG00000244235	0.144005	0	0.374062	0.770765	ENSG00000244235	AC103724.1
ENSG00000244237	0	0	0	0	ENSG00000244237	AL133445.1
ENSG00000244242	11.7938	1.62786	3.23374	3.42914	ENSG00000244242	IFITM10
ENSG00000244244	0	0.559426	0	0.450379	ENSG00000244244	AP000805.1
ENSG00000244245	0.259003	0	0	0	ENSG00000244245	AC133134.1
ENSG00000244246	0.101753	0.0977483	0	0	ENSG00000244246	ZNF736P8Y
ENSG00000244249	0	0	0	0	ENSG00000244249	AC063955.1
ENSG00000244251	0.257139	0	0.111456	0.275246	ENSG00000244251	AC013356.1
ENSG00000244253	0	0	0	0	ENSG00000244253	RPS29P24
ENSG00000244255	0	0	0	0	ENSG00000244255	AL645922.1
ENSG00000244257	13.0563	23.3457	51.6076	18.6684	ENSG00000244257	PKD1P1
ENSG00000244259	0	0	0	0	ENSG00000244259	AP000797.2
ENSG00000244266	0.187453	0	0	0.397961	ENSG00000244266	AC090058.1
ENSG00000244267	0.315788	0.299717	0	1.31695	ENSG00000244267	RPL34P22
ENSG00000244270	1.77753	0.191275	0	0	ENSG00000244270	AL139099.1
ENSG00000244273	0	0	0	0	ENSG00000244273	PGBD4P1
ENSG00000244274	18.3808	14.2382	8.85748	4.73665	ENSG00000244274	DBNDD2
ENSG00000244280	0.228447	0.42646	0.121052	0.410584	ENSG00000244280	ECEL1P2
ENSG00000244281	0	0.11451	0.155159	0.324018	ENSG00000244281	AC107302.1
ENSG00000244283	0	0	0	0	ENSG00000244283	RPL23AP73
ENSG00000244289	0	0	0	0	ENSG00000244289	AC068587.2
ENSG00000244291	2.39863	1.71148	2.58675	1.65607	ENSG00000244291	C7orf13
ENSG00000244292	0.145495	0.414776	0.512561	0.813427	ENSG00000244292	OR9N1P
ENSG00000244295	0	0	0	0	ENSG00000244295	RPS20P21
ENSG00000244301	0.573361	0.740762	0.659622	0.970067	ENSG00000244301	AOX3P
ENSG00000244313	1.31266	0.629711	0.753822	2.65755	ENSG00000244313	AC024293.1
ENSG00000244329	0	0	0	0	ENSG00000244329	AC021382.1
ENSG00000244331	0	0	0	0	ENSG00000244331	AC008677.2
ENSG00000244346	0.91533	1.95795	2.9612	3.65231	ENSG00000244346	AC092953.1
ENSG00000244355	0.0302896	0.0578806	0	0.032054	ENSG00000244355	LY6G6D
ENSG00000244361	0	0	0	0	ENSG00000244361	RPL30P7
ENSG00000244362	0.184063	0.52827	0	1.56481	ENSG00000244362	KRTAP19-7
ENSG00000244363	0	0.133427	0.127082	0.154818	ENSG00000244363	RPL7P23
ENSG00000244371	2.12114	3.34031	3.13171	3.29138	ENSG00000244371	PFN1P8
ENSG00000244378	0.81004	1.43654	1.19543	2.09684	ENSG00000244378	RPS2P45
ENSG00000244381	0	0	0	0	ENSG00000244381	AC007849.2
ENSG00000244390	0	0.0439899	0.0909581	0	ENSG00000244390	AC068305.1
ENSG00000244395	0	0	0	0	ENSG00000244395	RBMY1D
ENSG00000244398	106.531	63.9801	79.4901	46.385	ENSG00000244398	AC116533.1
ENSG00000244400	0	0.0906905	0	0	ENSG00000244400	RPS4XP12
ENSG00000244405	12.3285	42.8391	15.4424	24.5301	ENSG00000244405	ETV5

ENSG00000244411	0.0788664	0	0.18316	0	ENSG00000244411	KRTAP5-7
ENSG00000244413	0.176013	0.168485	0	0	ENSG00000244413	RPL23AP56
ENSG00000244414	8.10316	25.287	21.7403	51.041	ENSG00000244414	CFHR1
ENSG00000244422	0	0.639508	0.571284	0	ENSG00000244422	RPL38P3
ENSG00000244427	0	0	0.0960039	0	ENSG00000244427	AC105233.1
ENSG00000244429	0	0.341843	0.204886	1.27173	ENSG00000244429	AC104629.2
ENSG00000244432	0	0	0	0	ENSG00000244432	RPL39P28
ENSG00000244433	0.836396	0.219898	0.20085	0.370012	ENSG00000244433	PGBD4P7
ENSG00000244436	0	0	0.585864	0.711163	ENSG00000244436	AC023050.1
ENSG00000244437	0	0	0	0	ENSG00000244437	IGKV3-15
ENSG00000244441	0	0	0.242239	0.295183	ENSG00000244441	AC126182.2
ENSG00000244444	0.036129	0.0775392	0.255803	0	ENSG00000244444	EGFL8
ENSG00000244451	1.52219	1.46772	1.62361	3.9379	ENSG00000244451	AP003041.1
ENSG00000244456	0	0	0	0	ENSG00000244456	AC090774.1
ENSG00000244457	0	0	0	0	ENSG00000244457	ENO1P1
ENSG00000244462	39.8015	28.7238	23.6415	25.754	ENSG00000244462	RBM12
ENSG00000244470	0	0	0.0664178	0	ENSG00000244470	AC105918.1
ENSG00000244474	0.171609	0.352512	1.11891	0	ENSG00000244474	UGT1A4
ENSG00000244476	0.941241	3.30407	3.37423	4.62807	ENSG00000244476	ERVFRD-1
ENSG00000244480	0.935151	2.89292	2.70716	4.6481	ENSG00000244480	AC005154.3
ENSG00000244482	0.60342	0	0	3.14948	ENSG00000244482	LILRA6
ENSG00000244485	0.330413	0.679995	4.68014	0.205343	ENSG00000244485	RPL18P13
ENSG00000244486	0.582528	0.501148	0.550355	5.44154	ENSG00000244486	SCARF2
ENSG00000244490	1.29141	2.97907	2.23017	8.2398	ENSG00000244490	RWDD4P1
ENSG00000244503	0	0.0424655	0	0	ENSG00000244503	AC108751.5
ENSG00000244509	13.2129	13.8954	12.6284	13.7435	ENSG00000244509	APOBEC3C
ENSG00000244510	0	9.26609	6.55318	7.22081	ENSG00000244510	AC008267.5
ENSG00000244515	0.328468	0.315615	1.04816	0.103014	ENSG00000244515	KRT18P34
ENSG00000244527	0	0	0	0	ENSG00000244527	AC022795.1
ENSG00000244528	0	0	0	0	ENSG00000244528	SEPT14P2
ENSG00000244535	0	0	0	0	ENSG00000244535	AL049714.1
ENSG00000244537	0	0	0.149267	0.186227	ENSG00000244537	KRTAP4-2
ENSG00000244538	0.499165	0	0	0	ENSG00000244538	AC098583.1
ENSG00000244540	1.70007	2.08351	0.816889	0.842152	ENSG00000244540	AC087884.1
ENSG00000244551	0	0	0	0	ENSG00000244551	RPL34P29
ENSG00000244556	1.55532	2.99212	2.84888	3.95587	ENSG00000244556	ODCP
ENSG00000244559	0	0	0	0	ENSG00000244559	AC091179.3
ENSG00000244560	3.70719	7.37523	12.4484	10.7877	ENSG00000244560	AC004890.2
ENSG00000244561	0.13146	0	0.0571285	0	ENSG00000244561	AC092905.1
ENSG00000244563	0	0	0	0	ENSG00000244563	AC006011.1
ENSG00000244565	0	0	0	0	ENSG00000244565	AC073901.1
ENSG00000244571	0	0	0.0752542	0	ENSG00000244571	RPS6P4
ENSG00000244573	2.15317	4.90037	2.92005	9.92616	ENSG00000244573	RPL30P11
ENSG00000244575	0	0	0	0	ENSG00000244575	IGKV1-27
ENSG00000244582	0	0.0811478	0	0	ENSG00000244582	AC233702.1
ENSG00000244585	0	0	0	0	ENSG00000244585	RPL12P33
ENSG00000244588	0.441317	1.30154	0.52275	1.9303	ENSG00000244588	RAD21L1
ENSG00000244593	0	0	0	0	ENSG00000244593	AC025062.1
ENSG00000244604	0.275551	1.34213	1.20738	2.65695	ENSG00000244604	AC025518.1
ENSG00000244607	5.3344	13.6308	14.743	18.8089	ENSG00000244607	CCDC13
ENSG00000244615	0	0	0	0	ENSG00000244615	PSPC1P2
ENSG00000244617	1.47488	0.618841	2.18849	1.8394	ENSG00000244617	ASPRV1
ENSG00000244621	0	0	0	0	ENSG00000244621	RPS17P11
ENSG00000244623	0.28463	0	0.148538	0.434447	ENSG00000244623	OR2AE1

ENSG00000244624	0	0	0	0	ENSG00000244624	KRTAP20-1
ENSG00000244627	22.5419	34.0291	40.4682	41.5596	ENSG00000244627	Z98749.2
ENSG00000244630	0.570061	0.270729	1.22343	0.803882	ENSG00000244630	AC022493.1
ENSG00000244640	0.105479	0.1013	0.0914853	0.1138	ENSG00000244640	AC096922.1
ENSG00000244641	0.387075	0.378758	3.18063	0.795585	ENSG00000244641	AP000926.3
ENSG00000244646	0	0.057919	0.153658	0.182434	ENSG00000244646	XKRY2
ENSG00000244652	0.134194	0.380673	0.790308	0.419699	ENSG00000244652	AC079382.1
ENSG00000244653	0	0	0	0	ENSG00000244653	UBFD1P1
ENSG00000244657	0	2.80518	3.79388	6.13963	ENSG00000244657	AC008267.6
ENSG00000244661	0	0	0	0	ENSG00000244661	TRBV12-1
ENSG00000244662	0.161327	0	0.139568	0.71583	ENSG00000244662	AC087312.1
ENSG00000244668	0	0.539426	0.423891	0.174246	ENSG00000244668	SNRPCP3
ENSG00000244669	0.170508	0.163876	0.148046	0.277087	ENSG00000244669	AC104689.1
ENSG00000244672	2.82455	6.96097	2.92393	8.72912	ENSG00000244672	LY6G5B
ENSG00000244674	0.000919845	0.436036	0	0	ENSG00000244674	RPS3AP15
ENSG00000244681	5.38824	10.8835	9.97116	15.1611	ENSG00000244681	MTHFD2P1
ENSG00000244682	0.619128	0.535968	0.397498	0.470631	ENSG00000244682	FCGR2C
ENSG00000244687	62.476	63.9091	59.882	70.819	ENSG00000244687	UBE2V1
ENSG00000244691	1.60894	4.63588	2.30842	4.06369	ENSG00000244691	RPL10AP1
ENSG00000244693	6.26075	6.9614	4.69294	0.995889	ENSG00000244693	CTAGE8
ENSG00000244694	4.42962	9.18601	8.54424	14.7182	ENSG00000244694	PTCHD4
ENSG00000244699	0	0	0	0	ENSG00000244699	AC139453.3
ENSG00000244703	0	0	0.15067	0	ENSG00000244703	CD46P1
ENSG00000244705	0	0	0.0580289	0	ENSG00000244705	AC020658.1
ENSG00000244708	0	0	0	0.216064	ENSG00000244708	RPL23P10
ENSG00000244712	0.339419	0.65054	0.903672	0.555992	ENSG00000244712	AC084754.1
ENSG00000244716	1.11328	0.965645	1.46049	0.623683	ENSG00000244716	BX679664.3
ENSG00000244717	0	0	0	0	ENSG00000244717	AC145146.1
ENSG00000244720	0	0.250455	0.112832	0.776961	ENSG00000244720	AC055748.1
ENSG00000244721	0.152848	0	0	3.14341	ENSG00000244721	HLA-L
ENSG00000244722	0	0.0705929	0	0	ENSG00000244722	RPSAP29
ENSG00000244723	0.451519	2.90219	1.67894	2.77922	ENSG00000244723	ASLP1
ENSG00000244730	1.50265	3.75345	3.67949	6.4924	ENSG00000244730	AC139451.1
ENSG00000244731	0.204648	1.84907	3.28324	2.1704	ENSG00000244731	C4A
ENSG00000244734	1.2564	1.93192	2.96308	1.98698	ENSG00000244734	HBB
ENSG00000244740	0	0	0	0	ENSG00000244740	AC092991.1
ENSG00000244743	0.96881	3.03038	0.603073	2.33399	ENSG00000244743	AC087588.1
ENSG00000244752	0.492449	0.0767484	0.276904	0	ENSG00000244752	CRYBB2
ENSG00000244753	0	0	0	0	ENSG00000244753	RPL15P21
ENSG00000244754	54.8079	88.2416	106.723	77.2384	ENSG00000244754	N4BP2L2
ENSG00000244756	0	0	0	0	ENSG00000244756	AL049874.2
ENSG00000244921	0.0883218	0	1.85102	0.76613	ENSG00000244921	MTCYBP18
ENSG00000244932	1.63822	1.53362	6.19796	2.27482	ENSG00000244932	AL449212.1
ENSG00000245017	1.72048	2.5917	2.34722	4.23445	ENSG00000245017	LINC02453
ENSG00000245205	0.461239	1.78274	1.49782	0.823358	ENSG00000245205	EEF1A1P4
ENSG00000245317	0.984552	2.10715	2.2051	0.925855	ENSG00000245317	AC008393.1
ENSG00000245680	12.017	14.538	15.6663	13.7594	ENSG00000245680	ZNF585B
ENSG00000245848	9.49871	4.64092	5.67678	1.95073	ENSG00000245848	CEBPA
ENSG00000245888	2.71567	7.82903	6.74807	8.08465	ENSG00000245888	FLJ21408
ENSG00000245958	25.7759	41.4519	39.2811	40.9404	ENSG00000245958	AC093752.1
ENSG00000246082	3.62348	8.28481	6.59632	10.5645	ENSG00000246082	NUDT16P1
ENSG00000246115	0	0	0	0	ENSG00000246115	SUPT4H1P2
ENSG00000246203	2.42664	1.84925	1.93517	1.39461	ENSG00000246203	AL353807.3
ENSG00000246223	4.98303	10.0919	7.21175	13.1561	ENSG00000246223	LINC01550

ENSG00000246366	12.5859	34.6755	26.4197	69.0798	ENSG00000246366	LACTB2-AS1
ENSG00000246575	5.02823	5.30366	11.3013	6.3163	ENSG00000246575	AC093162.2
ENSG00000246596	2.76655	3.87157	3.41362	5.01791	ENSG00000246596	AC139795.1
ENSG00000246705	27.5007	15.5758	11.239	10.2483	ENSG00000246705	H2AFJ
ENSG00000246922	1.28123	2.58838	5.64603	5.29826	ENSG00000246922	UBAP1L
ENSG00000247077	21.7962	21.1803	19.7583	16.6423	ENSG00000247077	PGAM5
ENSG00000247121	8.83051	21.297	21.6547	33.2161	ENSG00000247121	AC009126.1
ENSG00000247270	0.421145	0.925182	0.933311	1.75325	ENSG00000247270	AC132186.1
ENSG00000247315	1.99E-07	0.00256744	0.621291	0	ENSG00000247315	ZCCHC3
ENSG00000247570	0	0	0	0	ENSG00000247570	SDCBPP2
ENSG00000247596	23.0776	39.7229	23.5604	20.7631	ENSG00000247596	TWF2
ENSG00000247626	3.87041	4.38161	6.62532	2.44583	ENSG00000247626	MARS2
ENSG00000247627	0.0853926	0.20562	4.69511	7.49043	ENSG00000247627	MTND4P12
ENSG00000247700	0.185579	0	0.267742	0.271418	ENSG00000247700	HLA-H
ENSG00000247732	0	0	0	0	ENSG00000247732	AC091951.2
ENSG00000247746	0.551279	0.916923	0.521974	1.11905	ENSG00000247746	USP51
ENSG00000247763	0.0431646	0	0	0.143463	ENSG00000247763	AC106800.1
ENSG00000247872	0	0.40114	0	0	ENSG00000247872	SPCS2P3
ENSG00000247911	0.589806	5.40704	4.61503	3.66828	ENSG00000247911	HMGN1P12
ENSG00000248050	0.355764	0.579043	0.65961	1.03214	ENSG00000248050	AC079061.1
ENSG00000248098	13.7652	13.19	13.352	9.54844	ENSG00000248098	BCKDHA
ENSG00000248099	0.783477	1.37455	0.670644	1.285	ENSG00000248099	INSL3
ENSG00000248104	0	0.079708	0	0.0605067	ENSG00000248104	TARS2P1
ENSG00000248105	0	0.330482	2.98175	2.89477	ENSG00000248105	AC008885.1
ENSG00000248106	0	0.2706	0	0.203026	ENSG00000248106	AC116353.2
ENSG00000248113	0.144892	0.184102	0.0419432	0.429472	ENSG00000248113	AC067942.2
ENSG00000248114	1.56395	7.55272	5.91514	7.70592	ENSG00000248114	AC114812.3
ENSG00000248117	0	0	0.812536	0	ENSG00000248117	MINOS1P4
ENSG00000248120	0	0	0	0	ENSG00000248120	AC114967.1
ENSG00000248121	8.93772	14.4161	10.3229	11.7068	ENSG00000248121	SMURF2P1
ENSG00000248122	0.315425	0	0	0.127456	ENSG00000248122	APOOP4
ENSG00000248124	7.1594	15.3252	16.423	18.0324	ENSG00000248124	RRN3P1
ENSG00000248126	0	0	0	0	ENSG00000248126	AC091849.1
ENSG00000248128	1.64181	3.3864	4.75126	8.17902	ENSG00000248128	AC114801.1
ENSG00000248133	0.409731	0	0.348548	0.421769	ENSG00000248133	MTND4LP22
ENSG00000248134	0	0	0	0	ENSG00000248134	AC079395.1
ENSG00000248136	0	0	0	0.183109	ENSG00000248136	MTND6P8
ENSG00000248139	0	0.029377	0.080303	0.134598	ENSG00000248139	CUL4AP1
ENSG00000248144	0	0.443757	0.548307	0.584171	ENSG00000248144	ADH1C
ENSG00000248155	0.419599	1.16347	1.40803	2.2605	ENSG00000248155	CR545473.1
ENSG00000248156	0	0	0	0	ENSG00000248156	BTG4P1
ENSG00000248159	0.059687	0.0575586	0.0520281	0.068052	ENSG00000248159	HSPA8P11
ENSG00000248160	0	0	0	0	ENSG00000248160	AC233724.1
ENSG00000248162	0.625584	1.55059	1.69274	2.22208	ENSG00000248162	AC074198.1
ENSG00000248167	0.32089	0	0	0	ENSG00000248167	TRIM39-RPP21
ENSG00000248170	0	0	0	0	ENSG00000248170	AC117522.1
ENSG00000248180	0.310704	0.76526	0.432256	0.541088	ENSG00000248180	GAPDHP60
ENSG00000248182	0	0	0	0	ENSG00000248182	OR12D1
ENSG00000248185	0	0	0	0	ENSG00000248185	AC025445.1
ENSG00000248188	0	0.215323	0.194496	1.58634	ENSG00000248188	AC005798.1
ENSG00000248191	0.0329031	0	0	0.0360658	ENSG00000248191	PES1P1
ENSG00000248196	0.851272	0.886793	0.246542	0.462509	ENSG00000248196	AC092658.1
ENSG00000248200	0.629566	1.58132	1.28264	1.79546	ENSG00000248200	AC093770.1
ENSG00000248205	0	0	0	0	ENSG00000248205	AC106774.1

ENSG00000248208	0	0	0	0	ENSG00000248208	WDR45P1
ENSG00000248209	0	0	0	0	ENSG00000248209	AC097462.1
ENSG00000248213	0.29301	0.434011	0.329585	0.570169	ENSG00000248213	CICP16
ENSG00000248216	0.10333	0.334484	0.322432	0.952343	ENSG00000248216	KCTD9P5
ENSG00000248229	0	0	0	0	ENSG00000248229	AC106872.4
ENSG00000248230	0	0	0.405988	0.576742	ENSG00000248230	MICE
ENSG00000248231	0.291286	1.23519	0.628048	1.19723	ENSG00000248231	KRT8P4
ENSG00000248234	0	1.22062	0.364463	0	ENSG00000248234	AC091839.1
ENSG00000248235	0	0	0.5948	2.70892	ENSG00000248235	AC037459.1
ENSG00000248236	0	0	0	0	ENSG00000248236	AC008837.1
ENSG00000248237	0	0	0	0	ENSG00000248237	AC105420.1
ENSG00000248249	0.194136	0	0	0	ENSG00000248249	AC110794.1
ENSG00000248257	0	0.145004	0.0406667	0.126168	ENSG00000248257	PSG10P
ENSG00000248259	0	0	0	0	ENSG00000248259	MTND4LP31
ENSG00000248271	0.13066	0	0.113184	0	ENSG00000248271	PGAM1P1
ENSG00000248278	0.187541	0.273521	0.416741	0.614094	ENSG00000248278	SUMO2P17
ENSG00000248280	3.04336	3.4261	7.54447	2.45937	ENSG00000248280	RP11-33B1.2
ENSG00000248281	0	0	0	0	ENSG00000248281	AC106868.1
ENSG00000248282	0.0781907	0	0.067913	0	ENSG00000248282	MTCYBP44
ENSG00000248283	0	0.061665	0.390089	0.139544	ENSG00000248283	CCNL2P1
ENSG00000248286	0	1.60077	0	0	ENSG00000248286	AC140172.1
ENSG00000248287	0	0	0	0	ENSG00000248287	SCGB1D5P
ENSG00000248288	0.988262	2.19171	0.859386	7.53361	ENSG00000248288	AC008868.1
ENSG00000248290	0	0	0	0	ENSG00000248290	TNXA
ENSG00000248293	0	0	0	0	ENSG00000248293	AC008413.1
ENSG00000248295	0.0646977	0.0935105	0.11271	0.354626	ENSG00000248295	DDX43P1
ENSG00000248302	0.496205	1.27867	0.385782	0.482797	ENSG00000248302	BNIP3P41
ENSG00000248305	0	0	0	0	ENSG00000248305	AC105416.1
ENSG00000248308	0	0	0.0723659	0.0903225	ENSG00000248308	AC138938.1
ENSG00000248313	0	0	0	0	ENSG00000248313	CYP4F27P
ENSG00000248315	0	0	0	0	ENSG00000248315	MTND4LP2
ENSG00000248320	0.303723	0.65484	0.644222	1.73562	ENSG00000248320	THAP12P9
ENSG00000248327	0.0154066	0.0151051	0.0134199	0.0171299	ENSG00000248327	NOL8P1
ENSG00000248328	0	0	0	0	ENSG00000248328	MTCO3P28
ENSG00000248333	15.074	13.2468	14.2178	14.7774	ENSG00000248333	CDK11B
ENSG00000248334	2.66994	5.88544	6.70584	8.17046	ENSG00000248334	WHAMMP2
ENSG00000248336	0	0	0	0	ENSG00000248336	HMGN1P11
ENSG00000248337	1.0633	3.04851	5.34347	2.5103	ENSG00000248337	AC233724.2
ENSG00000248340	0.177817	0.948421	1.20365	1.32725	ENSG00000248340	AC106047.2
ENSG00000248345	0	0	0	0	ENSG00000248345	RP11-262D11.1
ENSG00000248347	0.0832147	0.28606	0.186106	0.511523	ENSG00000248347	AC120036.2
ENSG00000248349	0	0	0	0	ENSG00000248349	AC112204.1
ENSG00000248350	2.08392	0.650743	0	1.39404	ENSG00000248350	AC010265.1
ENSG00000248351	0	0	0	0	ENSG00000248351	HSPD1P18
ENSG00000248352	0	0.0103777	0	0	ENSG00000248352	TNXA
ENSG00000248355	0.184682	0	0	0	ENSG00000248355	ARL2BPP6
ENSG00000248364	0	0	0	0	ENSG00000248364	OR7E86P
ENSG00000248365	0.271531	0.260515	0.117572	0.436641	ENSG00000248365	POU5F1P7
ENSG00000248366	0	0	0	0	ENSG00000248366	TRAJ51
ENSG00000248369	0.718371	2.00377	1.83601	3.47568	ENSG00000248369	AC114741.1
ENSG00000248374	0	0.474876	0.186486	0.106816	ENSG00000248374	AC073358.1
ENSG00000248375	2.38082	3.71325	3.88457	5.02003	ENSG00000248375	AC104066.1
ENSG00000248376	0	0	0.0596058	0	ENSG00000248376	AC112698.1
ENSG00000248377	0.408505	0.336599	0.30333	0.747297	ENSG00000248377	HMGN1P9

ENSG00000248383	0.274869	0.248648	0.131412	0.312068	ENSG00000248383	PCDHAC1
ENSG00000248385	0.122457	0.259933	0.247953	0.628477	ENSG00000248385	TARM1
ENSG00000248387	0	0.208065	0.547804	0	ENSG00000248387	AC121161.1
ENSG00000248394	0.161569	0.938852	0.700956	1.23469	ENSG00000248394	FOSL1P1
ENSG00000248396	0	0	0.24594	0.599519	ENSG00000248396	TOMM22P4
ENSG00000248400	0.111614	0	0.104188	0.136355	ENSG00000248400	ST13P12
ENSG00000248401	0.17924	0.114982	0.103914	0.39059	ENSG00000248401	AC114781.1
ENSG00000248403	0	0	0	0	ENSG00000248403	NACAP6
ENSG00000248405	1.80819	2.31789	3.14531	2.21984	ENSG00000248405	PRR5-ARHGAP8
ENSG00000248406	0	0	0	0	ENSG00000248406	AC008758.3
ENSG00000248409	0.449196	0.250721	0.3654	0.382015	ENSG00000248409	AP000344.2
ENSG00000248415	1.0677	2.89768	2.72224	3.21391	ENSG00000248415	GAPDHP61
ENSG00000248418	0	0	0	0	ENSG00000248418	UBL5P1
ENSG00000248419	0	0	0	0	ENSG00000248419	AC110768.1
ENSG00000248420	0	0.0957017	0.172888	0	ENSG00000248420	MTATP6P9
ENSG00000248422	0	0	0	0	ENSG00000248422	AC233724.3
ENSG00000248423	0.529495	2.44108	1.37785	3.32895	ENSG00000248423	AC100850.1
ENSG00000248424	0	0.0631369	0.0570564	0	ENSG00000248424	OR51K1P
ENSG00000248426	0.401326	0	0	0	ENSG00000248426	AC113347.2
ENSG00000248430	0	0	0	0	ENSG00000248430	HMGB3P16
ENSG00000248439	1.066	4.94423	2.57254	3.81261	ENSG00000248439	RPL23AP94
ENSG00000248442	0.0670043	0.257751	0.0582253	0.291522	ENSG00000248442	OR10J7P
ENSG00000248444	0	0.0628648	0	0	ENSG00000248444	HNRNPA1P65
ENSG00000248447	0.0423668	0.262698	0.110645	0	ENSG00000248447	AC107058.1
ENSG00000248448	0	0	0	0	ENSG00000248448	COX5BP1
ENSG00000248449	0.686437	0.926388	1.68126	2.16344	ENSG00000248449	PCDHGB8P
ENSG00000248452	0.293554	0.31834	0.39935	0.500803	ENSG00000248452	AC097714.1
ENSG00000248458	14.2321	38.3093	39.4647	108.186	ENSG00000248458	AL139147.1
ENSG00000248459	0.208657	0.398986	0.72065	1.98902	ENSG00000248459	AC083906.1
ENSG00000248462	0	0	0	0	ENSG00000248462	NENFP3
ENSG00000248466	0	0.58879	0.974901	0.220607	ENSG00000248466	AC098827.1
ENSG00000248469	0	0	0	0	ENSG00000248469	AC139491.1
ENSG00000248471	0	0	0	0	ENSG00000248471	AC233724.4
ENSG00000248472	1.85E-08	0.519358	0.312515	0	ENSG00000248472	DDX11L9
ENSG00000248477	0.150042	0.523627	0.42231	1.15985	ENSG00000248477	AC139495.1
ENSG00000248480	0	0.0560737	0.101354	0	ENSG00000248480	AC093801.2
ENSG00000248483	5.11247	12.0255	11.5665	22.4907	ENSG00000248483	POU5F2
ENSG00000248485	0.123078	0.118542	0.25002	0.314214	ENSG00000248485	PCP4L1
ENSG00000248487	4.84107	8.63758	4.42803	7.79495	ENSG00000248487	ABHD14A
ENSG00000248488	0.092967	0.443801	0.0812201	0.103569	ENSG00000248488	PGAM4P2
ENSG00000248493	0.993736	0.944936	2.0479	1.2774	ENSG00000248493	AC005351.1
ENSG00000248496	1.39304	0.480152	1.07364	0	ENSG00000248496	ZBED9
ENSG00000248498	0.191065	0.21368	0.608341	0.173585	ENSG00000248498	ASNSP1
ENSG00000248503	1.46007	3.43435	3.67765	6.24842	ENSG00000248503	AL356235.1
ENSG00000248506	0.0428217	0.0412398	0.149106	0	ENSG00000248506	AC097474.1
ENSG00000248507	0	0	0	0.0739081	ENSG00000248507	OR5H4P
ENSG00000248511	0.719032	1.38336	1.27778	2.54129	ENSG00000248511	AC112695.1
ENSG00000248521	0.433202	1.20439	0.595835	0.673971	ENSG00000248521	AC092612.1
ENSG00000248522	0	0	0.0165526	0.0732197	ENSG00000248522	SBF1P1
ENSG00000248527	91.2731	68.9425	156.046	214.031	ENSG00000248527	MTATP6P1
ENSG00000248530	0	0	0	0.118598	ENSG00000248530	BCL2L12P1
ENSG00000248531	0	0	0	0	ENSG00000248531	NDUFA5P12
ENSG00000248532	0.839997	1.31481	0	0	ENSG00000248532	AC119751.2
ENSG00000248540	1.01226	1.62812	1.56591	3.47754	ENSG00000248540	AC010931.2

ENSG00000248542	0	0	0	0.127173	ENSG00000248542	AC233724.5
ENSG00000248543	0	0.0743108	0.242177	0	ENSG00000248543	NPM1P41
ENSG00000248546	0.096172	0	0	0	ENSG00000248546	ANP32C
ENSG00000248547	0	0	0	0	ENSG00000248547	AC021146.2
ENSG00000248548	0	0.10544	0	0.0622303	ENSG00000248548	MTND4P8
ENSG00000248552	0	0	0	0	ENSG00000248552	AC074344.1
ENSG00000248553	0	0.336036	0.182177	0.455804	ENSG00000248553	OR52H2P
ENSG00000248557	1.68826	1.62034	1.3385	2.85961	ENSG00000248557	AC024558.1
ENSG00000248560	0	0	0	0	ENSG00000248560	AC008620.2
ENSG00000248563	0	0	0.0206295	0.0258112	ENSG00000248563	RPSAP2
ENSG00000248564	1.53642	2.42545	3.23556	2.2952	ENSG00000248564	AC079140.1
ENSG00000248565	0.0675279	0	0.117357	0	ENSG00000248565	TECRP2
ENSG00000248568	0.0717262	0	0.17089	0.0538479	ENSG00000248568	KRT8P48
ENSG00000248569	0	0	0	0	ENSG00000248569	AC026410.3
ENSG00000248573	0	0	0	0	ENSG00000248573	PRYP6
ENSG00000248574	0.0465928	0.0897263	0.0811001	0.356406	ENSG00000248574	ADAM20P2
ENSG00000248577	0	0	0	0.131254	ENSG00000248577	AC091435.1
ENSG00000248578	0.8626	0.991049	1.63451	0.900533	ENSG00000248578	NPM1P21
ENSG00000248583	0.341309	0	0.744033	0.338214	ENSG00000248583	AC119751.3
ENSG00000248585	0.328621	0.631713	0.499374	0.267174	ENSG00000248585	AC084024.2
ENSG00000248586	0	0	0.0241689	0	ENSG00000248586	AC025470.1
ENSG00000248590	0	0.0667476	0.0426625	0.0488976	ENSG00000248590	GLDCP1
ENSG00000248591	0	0	0	0	ENSG00000248591	AC109445.1
ENSG00000248592	2.82666	3.04378	2.8925	1.45676	ENSG00000248592	TMEM110-MUSTN1
ENSG00000248593	0.909515	1.3716	1.34944	2.09384	ENSG00000248593	DSTNP2
ENSG00000248594	5.96495	8.06191	9.29482	5.15643	ENSG00000248594	AC003029.1
ENSG00000248608	0.102414	0.164456	0	0.0748179	ENSG00000248608	AC133963.1
ENSG00000248610	0.0589323	0.198815	0.154029	0.323225	ENSG00000248610	HSPA8P4
ENSG00000248611	0.254276	0.649668	0.740212	0.454912	ENSG00000248611	AC107385.1
ENSG00000248613	0	0.433294	0	0.46906	ENSG00000248613	AC021146.3
ENSG00000248616	0	0	0.162084	0.504881	ENSG00000248616	AC109439.1
ENSG00000248618	0	0	0	0	ENSG00000248618	ENPP7P3
ENSG00000248621	0	0	1.74704	0	ENSG00000248621	AC108019.1
ENSG00000248625	0	0	0	0.101694	ENSG00000248625	AC079768.1
ENSG00000248626	0	0	0	0	ENSG00000248626	GAPDHP40
ENSG00000248632	2.88309	3.59055	5.02066	5.20434	ENSG00000248632	AC106872.5
ENSG00000248633	0.289395	0	0.250032	0	ENSG00000248633	WRBP1
ENSG00000248635	0	0	0	0	ENSG00000248635	AC147055.1
ENSG00000248637	0	0	0	0	ENSG00000248637	AC108064.1
ENSG00000248639	0.810002	0.581219	0.708446	1.07522	ENSG00000248639	AC098799.1
ENSG00000248640	0	0.101139	0.0568568	0.142506	ENSG00000248640	HNRNPA1P56
ENSG00000248641	2.55349	2.7291	5.92666	6.3131	ENSG00000248641	HMGA1P2
ENSG00000248642	0.12949	0.560454	0.112552	0.775049	ENSG00000248642	OR10J2P
ENSG00000248643	3.14759	3.32126	5.45945	5.99406	ENSG00000248643	RBM14-RBM4
ENSG00000248645	0	0.0421074	0.0380603	0	ENSG00000248645	AC106872.6
ENSG00000248648	0	1.43464	1.75242	1.59465	ENSG00000248648	AC113410.1
ENSG00000248651	0	0.152735	0.137908	0.170155	ENSG00000248651	GCSHP1
ENSG00000248652	0	1.35718	0	0.80449	ENSG00000248652	AC034244.1
ENSG00000248654	0	0.145687	0.121853	0.355535	ENSG00000248654	MTCO3P44
ENSG00000248655	0.164412	0	0.108894	0.250929	ENSG00000248655	NOP56P1
ENSG00000248659	0	0.157512	0.142185	0.175313	ENSG00000248659	AC023162.1
ENSG00000248660	0	0	0	0	ENSG00000248660	SRIP1
ENSG00000248669	0	0	0	0	ENSG00000248669	AC116562.2
ENSG00000248672	0	1.09453	0	0	ENSG00000248672	LY75-CD302

ENSG00000248674	0	0	0	0	ENSG00000248674	RBBP4P6
ENSG00000248684	0.0453697	0.110874	0.157954	0.184491	ENSG00000248684	BIN2P2
ENSG00000248687	0	0	0	0	ENSG00000248687	AC024589.1
ENSG00000248696	1.49137	2.77822	2.77486	2.81392	ENSG00000248696	AC011406.1
ENSG00000248697	0.186498	0.634455	0.457166	0.384862	ENSG00000248697	TOX4P1
ENSG00000248699	0	0	0	0	ENSG00000248699	AC114964.1
ENSG00000248702	0.383041	0	0	0	ENSG00000248702	AC005921.1
ENSG00000248704	0	0	0.0432639	0	ENSG00000248704	MTND4P2
ENSG00000248705	0.400054	1.85259	3.24963	1.58385	ENSG00000248705	AC114812.4
ENSG00000248710	0	0	0.0147691	0	ENSG00000248710	AC079594.2
ENSG00000248711	0.0406621	0.189203	0.174045	0.816997	ENSG00000248711	THUMPD3P1
ENSG00000248712	0.714641	1.75183	1.55575	2.64248	ENSG00000248712	CCDC153
ENSG00000248713	0.0418097	0.0403228	0.141283	0.121053	ENSG00000248713	AC083902.2
ENSG00000248715	0	0	0	0	ENSG00000248715	AC105424.1
ENSG00000248716	0	0	0	0	ENSG00000248716	AC093815.1
ENSG00000248720	0	0.288009	0	0.160624	ENSG00000248720	RFPL4AP5
ENSG00000248722	0	0.234863	0.212088	0.131556	ENSG00000248722	AK3P4
ENSG00000248725	0	0	0	0	ENSG00000248725	AC097488.1
ENSG00000248727	0.208833	0.573457	0.248689	0	ENSG00000248727	LINC01948
ENSG00000248729	0	0.288156	0.106795	0.264938	ENSG00000248729	MTCO1P30
ENSG00000248731	1.3569	2.93786	2.43807	4.63839	ENSG00000248731	AC090103.1
ENSG00000248735	0.0288081	0.194876	0.178687	0.221243	ENSG00000248735	R3HDM2P1
ENSG00000248739	0	0	0	0	ENSG00000248739	AC069306.1
ENSG00000248745	0	0.073304	0.0662234	0	ENSG00000248745	NMNAT1P4
ENSG00000248746	0.401473	0.38042	0.823372	0.765421	ENSG00000248746	ACTN3
ENSG00000248748	0	0.105677	0.0687871	0.0678021	ENSG00000248748	MTND5P9
ENSG00000248750	0.301318	0.519291	0.468831	0.96158	ENSG00000248750	AC020699.1
ENSG00000248751	1.02299	0.55338	0.549971	0.4924	ENSG00000248751	AC004997.1
ENSG00000248755	0.194214	0.0867596	0	0.293136	ENSG00000248755	AC092639.1
ENSG00000248761	0	0	0	0	ENSG00000248761	AC091874.2
ENSG00000248763	0	0	0.229816	0	ENSG00000248763	AC111000.2
ENSG00000248765	0.297323	0.768901	0.32457	1.07213	ENSG00000248765	MTCYBP37
ENSG00000248766	0	0	0	0	ENSG00000248766	AC093303.1
ENSG00000248769	0	0	0	0	ENSG00000248769	AC139495.2
ENSG00000248770	0	0	0	0	ENSG00000248770	AC019235.1
ENSG00000248772	0	14.7392	9.56029	11.9241	ENSG00000248772	AC108729.3
ENSG00000248775	0	0	0	0	ENSG00000248775	AC091951.3
ENSG00000248777	0.150263	0	0.0652811	0	ENSG00000248777	AC006499.1
ENSG00000248778	0	0	0	0	ENSG00000248778	AC105391.1
ENSG00000248780	0	0.135738	0.119093	0.175668	ENSG00000248780	ARL4AP2
ENSG00000248781	0.0903459	0.261818	0.352895	0.146262	ENSG00000248781	PSMC1P4
ENSG00000248785	0	0.781864	0.699579	1.24934	ENSG00000248785	HIGD1AP14
ENSG00000248789	0.198496	0.949625	0.171514	0.210566	ENSG00000248789	LINC02118
ENSG00000248791	0.137189	0.440341	0.35821	0.699745	ENSG00000248791	AC010627.1
ENSG00000248792	0	0	0	0	ENSG00000248792	LINC00266-2P
ENSG00000248794	1.7324	2.39472	5.12894	2.70941	ENSG00000248794	AC026436.1
ENSG00000248795	0	0	0.131227	0.163914	ENSG00000248795	AC098859.1
ENSG00000248796	0	0	0	0.288164	ENSG00000248796	MED15P8
ENSG00000248801	4.68107	11.5392	10.5543	17.6242	ENSG00000248801	C8orf34-AS1
ENSG00000248803	0.991795	1.56721	0.56613	1.03255	ENSG00000248803	AC092349.1
ENSG00000248807	0	0	0	0	ENSG00000248807	KRTAP9-12P
ENSG00000248817	0.0366751	0	0	0	ENSG00000248817	PMPCAP1
ENSG00000248820	0	0	0	0	ENSG00000248820	DYNLL1P6
ENSG00000248821	0	0	0	0	ENSG00000248821	AC009238.3

ENSG00000248822	0.761097	0	0	0	ENSG00000248822	APOBEC3AP1
ENSG00000248824	0	0	0	0	ENSG00000248824	AC108078.1
ENSG00000248826	0	0	0	0	ENSG00000248826	PCBP2P3
ENSG00000248827	0	0	0.0453556	0	ENSG00000248827	AC024587.1
ENSG00000248830	0.0856321	0	0.0699005	0.0772988	ENSG00000248830	ZNF807
ENSG00000248831	0	0	0	0.159523	ENSG00000248831	AC008638.1
ENSG00000248834	0	0	0	0	ENSG00000248834	MARK2P5
ENSG00000248835	1.32025	3.4557	3.20509	5.9162	ENSG00000248835	AL357673.1
ENSG00000248838	0.0872626	0	0	0	ENSG00000248838	PGAM1P13
ENSG00000248840	2.23487	7.21468	5.22849	7.06317	ENSG00000248840	AL645949.1
ENSG00000248843	0.414057	0.636736	0.0719059	0.538537	ENSG00000248843	AL645949.2
ENSG00000248847	0	0	0	0	ENSG00000248847	AC074087.1
ENSG00000248848	0	0.041548	0.0375549	0.0471811	ENSG00000248848	PPBPP2
ENSG00000248850	0	0	0.0470909	0.0590552	ENSG00000248850	AC078867.1
ENSG00000248851	0	0	0.162959	0	ENSG00000248851	AC006427.1
ENSG00000248853	0	0	0	0.110517	ENSG00000248853	AC113352.1
ENSG00000248854	0.0486931	0	0.0424886	0.0531854	ENSG00000248854	HNRNPH1P3
ENSG00000248861	0	0	0	0.00075577	ENSG00000248861	RP11-321E2.2
ENSG00000248863	1.43801	3.18205	2.57692	6.07528	ENSG00000248863	AC097376.1
ENSG00000248867	0	0	0	0	ENSG00000248867	AC010625.1
ENSG00000248871	0	0.0226352	0.000942905	0.000519923	ENSG00000248871	TNFSF12-TNFSF13
ENSG00000248873	0	0.201613	0.305734	0.646697	ENSG00000248873	SERBP1P6
ENSG00000248874	4.07802	9.98556	11.7003	13.9599	ENSG00000248874	C5orf17
ENSG00000248877	0	0	0	0.123072	ENSG00000248877	PGBD4P4
ENSG00000248878	0	0	0	0	ENSG00000248878	AC022447.4
ENSG00000248880	0	0.0296436	0.0267452	0.0341533	ENSG00000248880	ICE2P1
ENSG00000248883	0	0	0	0	ENSG00000248883	B4GALNT2P1
ENSG00000248885	0.218137	0.701518	0.329174	1.23126	ENSG00000248885	AC118465.1
ENSG00000248886	0.0902931	0.173519	0.235148	0.097712	ENSG00000248886	UGT2A3P7
ENSG00000248891	0	0	0	0	ENSG00000248891	AC091860.1
ENSG00000248895	0	0.772435	0	0	ENSG00000248895	AC068531.1
ENSG00000248903	0	0	0	0	ENSG00000248903	AP000867.1
ENSG00000248905	2.37694	6.43637	2.08375	15.8626	ENSG00000248905	FMN1
ENSG00000248907	0.119082	0.0575903	0	0.0717473	ENSG00000248907	MTND2P33
ENSG00000248909	1.73193	1.89376	1.96536	4.91239	ENSG00000248909	HMGB1P21
ENSG00000248911	0	0	0	0	ENSG00000248911	AC009800.1
ENSG00000248913	0	0	0	0.259182	ENSG00000248913	PHBP14
ENSG00000248915	0.172455	0.211497	0.337364	0.305321	ENSG00000248915	ACTR6P1
ENSG00000248916	0.224576	0.428845	0.193664	0.237158	ENSG00000248916	NUP210P3
ENSG00000248919	2.12598	2.28738	2.38879	2.05529	ENSG00000248919	ATP5J2-PTCD1
ENSG00000248920	0.0247832	0.0541723	0	0	ENSG00000248920	USP17L19
ENSG00000248921	0	0.757055	0.180758	0.629384	ENSG00000248921	AC021193.1
ENSG00000248923	0	0.0627891	0.224855	0.173502	ENSG00000248923	MTND5P11
ENSG00000248924	0	0.935448	0.512162	1.12168	ENSG00000248924	AC139713.1
ENSG00000248926	0.251105	0.882531	0.217445	0.361861	ENSG00000248926	AC114801.2
ENSG00000248928	0	0	0	0	ENSG00000248928	AC008837.2
ENSG00000248929	0	0	0	0	ENSG00000248929	HIGD1AP3
ENSG00000248930	0.495006	0.831959	0.861804	2.1195	ENSG00000248930	AC020893.1
ENSG00000248931	0.106377	0.0511973	0.0925445	1.33486	ENSG00000248931	MTCYBP40
ENSG00000248933	0.0247832	0.0541723	0	0	ENSG00000248933	USP17L22
ENSG00000248944	0	0	0	0	ENSG00000248944	FAM90A6P
ENSG00000248946	0	0	0	0.407853	ENSG00000248946	MTND3P22
ENSG00000248950	0	0	0	0	ENSG00000248950	LDHBP3

ENSG00000248951	0	0	0	0	ENSG00000248951	MTCO2P32
ENSG00000248955	0	0	0	0	ENSG00000248955	AC113367.2
ENSG00000248956	0.251241	0.241086	0	0.404901	ENSG00000248956	HMGB1P44
ENSG00000248958	0.0200747	0.0427212	0.0571321	0.120728	ENSG00000248958	ZSWIM5P3
ENSG00000248966	0.041207	0.0197918	0.0358984	0	ENSG00000248966	BCLAF1P1
ENSG00000248967	0.321653	2.75172	1.94794	3.45989	ENSG00000248967	AC022493.2
ENSG00000248971	0.861847	1.2647	1.50019	1.25909	ENSG00000248971	KRT8P46
ENSG00000248977	0	0	0	0	ENSG00000248977	AC095057.1
ENSG00000248978	0	0	0.235859	0	ENSG00000248978	AC009901.1
ENSG00000248979	0	3.89171	1.36365	2.56517	ENSG00000248979	LAMTOR3P2
ENSG00000248987	0.875104	1.1352	0.974957	1.52235	ENSG00000248987	PRDX4P1
ENSG00000248988	0.0937789	0.0908627	0.080918	0	ENSG00000248988	AC093700.1
ENSG00000248989	0	0	1.16875	4.75519	ENSG00000248989	STK19B
ENSG00000248993	0	0	0	0	ENSG00000248993	AL645941.2
ENSG00000248998	0	0.365188	0.076884	0.365852	ENSG00000248998	EFTUD1P2
ENSG00000248999	0	0	0	0	ENSG00000248999	WI2-2373I1.1
ENSG00000249002	0	0	0.627839	0	ENSG00000249002	AC096745.1
ENSG00000249003	0.0944227	0.0439963	0.209861	0.0718973	ENSG00000249003	CLUHP4
ENSG00000249004	0	0	0	0	ENSG00000249004	PRMT5P1
ENSG00000249005	0	0	0	0.181691	ENSG00000249005	FAM90A4P
ENSG00000249006	0	0.0861581	0.0782418	0.130755	ENSG00000249006	AL136360.1
ENSG00000249008	0.487707	1.88411	1.9812	0.783627	ENSG00000249008	AC097518.1
ENSG00000249012	0.950317	4.55425	2.51718	4.99553	ENSG00000249012	AC104819.1
ENSG00000249013	0	0.141357	0	0	ENSG00000249013	FTH1P21
ENSG00000249014	0.738308	0.238691	0.770759	0	ENSG00000249014	HMGN2P4
ENSG00000249016	0.183412	0.17549	0.158466	1.2129	ENSG00000249016	AC112198.3
ENSG00000249018	0	0.0602602	0.0544583	0.0682	ENSG00000249018	GAPDHP56
ENSG00000249019	3.5543	7.94513	10.774	11.8635	ENSG00000249019	AC108471.1
ENSG00000249025	0	2.70928	0	2.13813	ENSG00000249025	ZNF519P4
ENSG00000249026	0.0606145	0.0584509	0.0882788	0.0444773	ENSG00000249026	CTNNA1P1
ENSG00000249030	0	0	0	0	ENSG00000249030	OR12D1
ENSG00000249031	0	0	0	0	ENSG00000249031	SUMO2P6
ENSG00000249034	0.138589	0.159596	0.133905	0.222201	ENSG00000249034	AC005609.1
ENSG00000249038	0	0	0	0	ENSG00000249038	AARSP1
ENSG00000249045	0	0	0	0.932332	ENSG00000249045	MTND3P24
ENSG00000249047	0	0	2.10171	3.04551	ENSG00000249047	COX6B1P5
ENSG00000249048	0	0	0	0	ENSG00000249048	TRAV31
ENSG00000249049	0	0.226601	0	0	ENSG00000249049	AC074124.1
ENSG00000249050	0.082967	0.159925	0.168674	0.182098	ENSG00000249050	AC021242.1
ENSG00000249051	0.194136	0	0	0	ENSG00000249051	AC112518.2
ENSG00000249053	0	0	0	0.0889198	ENSG00000249053	AC106794.1
ENSG00000249055	1.5948	0.842284	2.41993	3.74407	ENSG00000249055	TBCAP3
ENSG00000249056	0	0	0	0	ENSG00000249056	AC099343.1
ENSG00000249064	0	0	0	0	ENSG00000249064	KRT18P25
ENSG00000249065	0.175115	1.20113	0.321779	0.389036	ENSG00000249065	PCNAP1
ENSG00000249068	1.14997	1.96177	2.51728	2.02384	ENSG00000249068	AC008417.1
ENSG00000249072	19074.8	29173.4	4997.88	129.095	ENSG00000249072	AC114801.3
ENSG00000249074	0	0	0	0	ENSG00000249074	NDUFB2P1
ENSG00000249077	0	0.218004	0.196883	0.492435	ENSG00000249077	AL158068.1
ENSG00000249079	0.238423	0	0	0	ENSG00000249079	AC118282.2
ENSG00000249081	0	0.108529	0	0	ENSG00000249081	OR5M14P
ENSG00000249087	3.04101	4.06366	4.28584	2.1219	ENSG00000249087	ZNF436-AS1
ENSG00000249089	1.547	5.72819	4.95507	11.9768	ENSG00000249089	AIG1P1

ENSG00000249092	0	0.292896	0	0.163516	ENSG00000249092	AC008945.1
ENSG00000249098	0.132331	1.10612	1.14635	1.81013	ENSG00000249098	AC055733.1
ENSG00000249101	0	0	0	0	ENSG00000249101	AC008834.1
ENSG00000249103	0	0	0	0	ENSG00000249103	OR12D1
ENSG00000249104	0	0	0	0	ENSG00000249104	USP17L17
ENSG00000249105	0	0	0	0	ENSG00000249105	AC096725.1
ENSG00000249109	0.120833	0.116372	0.332849	0.130606	ENSG00000249109	AC140125.2
ENSG00000249115	6.68611	9.90648	7.14261	6.60037	ENSG00000249115	HAUS5
ENSG00000249119	0.156543	1.29979	2.46713	0.985809	ENSG00000249119	MTND6P4
ENSG00000249123	9.73868	0.48104	0.511296	0.478825	ENSG00000249123	MICE
ENSG00000249127	0	0	0	2.09136	ENSG00000249127	MTND3P3
ENSG00000249129	0.0781097	0.31605	0.206076	0.635149	ENSG00000249129	SUDS3P1
ENSG00000249135	0	0.445263	0.141506	0.305021	ENSG00000249135	AC116347.2
ENSG00000249138	1.75411	0.337136	0.228422	0.284871	ENSG00000249138	SLED1
ENSG00000249139	0	0	0	0	ENSG00000249139	EPPIN-WFDC6
ENSG00000249140	0.852039	1.63255	1.68486	2.36044	ENSG00000249140	PRDX2P3
ENSG00000249141	0.330816	0	0.426335	0	ENSG00000249141	AL159163.1
ENSG00000249142	0	0	0	0.125104	ENSG00000249142	AC074134.1
ENSG00000249148	0.165445	0	0	0.176599	ENSG00000249148	AC006445.2
ENSG00000249149	0	0	0	0	ENSG00000249149	AC099522.1
ENSG00000249156	0.119287	0	0	0	ENSG00000249156	AC233724.6
ENSG00000249157	0	0	0	0	ENSG00000249157	AC093259.1
ENSG00000249158	0.25311	0.0931596	0.0524582	0.0642875	ENSG00000249158	PCDHA11
ENSG00000249160	1.09048	3.03343	2.50405	3.08331	ENSG00000249160	LINC02213
ENSG00000249162	0.133233	0.231158	0.0928737	0.175493	ENSG00000249162	ADAM20P3
ENSG00000249170	0	0	0	0	ENSG00000249170	AC096713.1
ENSG00000249176	0	0	0	0	ENSG00000249176	AC027801.3
ENSG00000249177	0.0855727	0	0.0372458	0	ENSG00000249177	MTND4P29
ENSG00000249183	0	0	0	0	ENSG00000249183	SUMO2P4
ENSG00000249188	0.294924	0.895189	0.481864	2.27538	ENSG00000249188	ENPP7P1
ENSG00000249189	0	0	0.107761	0.129749	ENSG00000249189	AC245052.6
ENSG00000249191	0	0	0	0.525939	ENSG00000249191	UBE2V1P12
ENSG00000249192	0	1.76371	0	7.22421	ENSG00000249192	MTND3P25
ENSG00000249193	0	0.129112	0.233779	0.0733078	ENSG00000249193	HSPD1P5
ENSG00000249197	0	0	0	0	ENSG00000249197	OR10J9P
ENSG00000249200	0.37091	1.1968	1.65111	3.39547	ENSG00000249200	AC110775.1
ENSG00000249206	0	0	0.103143	0	ENSG00000249206	GCNT1P2
ENSG00000249209	0	0	0	0	ENSG00000249209	AP000311.1
ENSG00000249210	0	0.0632015	0.0535839	0.067125	ENSG00000249210	GAPDHP38
ENSG00000249212	0.412104	1.52931	1.85022	2.54663	ENSG00000249212	ATP1B1P1
ENSG00000249213	0.0418538	0	0.0728721	0.228925	ENSG00000249213	AC079097.1
ENSG00000249214	72.8457	169.909	166.394	209.701	ENSG00000249214	AC022558.1
ENSG00000249215	0.0311204	0.0303984	0	0.10706	ENSG00000249215	NCOA4P4
ENSG00000249222	0.8394	3.25686	3.07342	4.45988	ENSG00000249222	ATP5L2
ENSG00000249226	1.88042	3.07318	4.17771	5.87341	ENSG00000249226	SUCLG2P4
ENSG00000249229	0.0543027	0	0.0472383	0.236954	ENSG00000249229	NAMPTP2
ENSG00000249230	1.52915	7.51913	13.1464	15.8915	ENSG00000249230	CDH12P2
ENSG00000249235	0	0	0	0	ENSG00000249235	AC021146.4
ENSG00000249237	0.886958	1.38387	0.672984	0.71693	ENSG00000249237	AL359273.1
ENSG00000249238	0.0215966	0.0416586	0.0188297	0.118662	ENSG00000249238	BCL9P1
ENSG00000249239	0	0.12906	0.237278	0.14977	ENSG00000249239	AC095059.2
ENSG00000249240	0.75404	1.53377	0	2.57959	ENSG00000249240	AC069368.1
ENSG00000249242	1.49284	2.88503	3.94729	6.19168	ENSG00000249242	TMEM150C
ENSG00000249244	0.269807	0.485234	0.359709	0.401387	ENSG00000249244	AC110373.1

ENSG00000249245	0.27414	0.263665	0.475073	0.300142	ENSG00000249245	NCOA4P3
ENSG00000249247	0.0842199	0.276619	0.429389	1.07541	ENSG00000249247	MTCYBP17
ENSG00000249251	0	0	0	0	ENSG00000249251	PGAM1P8
ENSG00000249253	0	0	0	0	ENSG00000249253	AC093004.1
ENSG00000249255	0	0	0	0	ENSG00000249255	PGAM1P9
ENSG00000249256	0	0	0	0	ENSG00000249256	ATP5LP3
ENSG00000249257	0.414064	0.39587	0.715172	0.438707	ENSG00000249257	AC097473.1
ENSG00000249259	0.116376	0.083641	0.180361	0.320427	ENSG00000249259	AC027613.1
ENSG00000249262	0.0889277	0.340544	0.692254	0.671381	ENSG00000249262	AC112250.1
ENSG00000249263	0.321992	0.90385	0	0	ENSG00000249263	PARP4P3
ENSG00000249264	0.221159	0.298838	0.386158	0.0485624	ENSG00000249264	EEF1A1P9
ENSG00000249266	0	0	0	0.196636	ENSG00000249266	MTHFD2P6
ENSG00000249270	0.409192	0.435757	0.200341	0.71422	ENSG00000249270	KATNBL1P4
ENSG00000249271	0	0.139064	0.0626596	0	ENSG00000249271	HNRNPA1P44
ENSG00000249272	0	0	0	0	ENSG00000249272	UNC93B8
ENSG00000249274	0.737152	1.91295	1.33819	2.8365	ENSG00000249274	PDLIM1P4
ENSG00000249277	0	0	0	0	ENSG00000249277	AC092436.3
ENSG00000249278	0	0	0.322482	0.198311	ENSG00000249278	AC112249.1
ENSG00000249282	1.00698	2.25958	0.823526	1.53581	ENSG00000249282	AC233724.7
ENSG00000249283	0	0	0	0.26931	ENSG00000249283	ACTR3BP4
ENSG00000249284	0.0399511	0.0769617	0.0347836	0.307641	ENSG00000249284	AC095050.2
ENSG00000249285	0.29996	0.288179	1.05037	0.540126	ENSG00000249285	AC114981.1
ENSG00000249286	0	0.180814	0.326424	0.413362	ENSG00000249286	AMD1P3
ENSG00000249287	0.200419	0.0967558	0.0871953	0.16413	ENSG00000249287	AC091874.3
ENSG00000249288	2.9834	1.87451	0	0	ENSG00000249288	SLC25A15P5
ENSG00000249289	0.573872	1.01124	1.1904	2.0663	ENSG00000249289	AC010460.1
ENSG00000249301	0	0.344888	0.621935	0.37733	ENSG00000249301	AC108120.2
ENSG00000249302	1.70845	3.10892	4.18525	2.54749	ENSG00000249302	FTH1P24
ENSG00000249305	0	0	0	0	ENSG00000249305	AC048346.1
ENSG00000249311	0.0992425	0.217364	0.129241	0.328286	ENSG00000249311	TERF1P3
ENSG00000249312	0.663899	0.158981	0	0	ENSG00000249312	ARL2BPP4
ENSG00000249316	5.62251	10.3519	10.9833	9.40093	ENSG00000249316	AF131216.2
ENSG00000249319	1.89266	0.774665	1.71291	2.86035	ENSG00000249319	AC068533.4
ENSG00000249320	1.86844	2.26302	0.643806	1.46393	ENSG00000249320	AC133963.2
ENSG00000249321	0	0.389637	0.176035	0.371816	ENSG00000249321	OR5H5P
ENSG00000249329	0	2.04E-06	0	3.10E-09	ENSG00000249329	RP11-432M8.5
ENSG00000249333	0	0	0	0	ENSG00000249333	AC245452.4
ENSG00000249336	0	0	0	0	ENSG00000249336	RP11-133G22.1
ENSG00000249337	0.770736	1.49372	0.313248	0.320984	ENSG00000249337	SNX18P25
ENSG00000249338	0.241351	0.857325	0.104573	0	ENSG00000249338	HMGB1P47
ENSG00000249339	0	0.199302	0	0.00075577	ENSG00000249339	RP11-321E2.7
ENSG00000249347	0	0.304156	0	0	ENSG00000249347	AC073648.2
ENSG00000249351	0	0.0757372	0	0	ENSG00000249351	AC096754.1
ENSG00000249353	0.372543	1.20347	0.946721	1.28384	ENSG00000249353	NPM1P27
ENSG00000249357	0	0.113696	0	0.127456	ENSG00000249357	RP11-432M8.8
ENSG00000249360	0	0	0	0	ENSG00000249360	AC034232.1
ENSG00000249363	0.217233	0.892316	1.44718	1.48108	ENSG00000249363	AC011411.1
ENSG00000249367	0	0	0	0	ENSG00000249367	FABP5P12
ENSG00000249368	0	0	0	0	ENSG00000249368	AC103851.1
ENSG00000249372	0.290366	2.49341	0.248592	2.77228	ENSG00000249372	ATP6V1G1P6
ENSG00000249380	0	0.0751684	0	0.424177	ENSG00000249380	AC138853.1
ENSG00000249386	0	0.0932154	0	0	ENSG00000249386	MTCO2P9
ENSG00000249387	0	0	0	0	ENSG00000249387	KRTAP5-14P
ENSG00000249400	0.317697	0.434695	0.393833	1.13842	ENSG00000249400	HMGB3P17

ENSG00000249410	0	0	0	0	ENSG00000249410	AK4P2
ENSG00000249411	0.35525	0.431946	0.463925	0.632207	ENSG00000249411	AC022325.1
ENSG00000249415	0	0.0415668	0.00939099	0.0470305	ENSG00000249415	BX908738.6
ENSG00000249416	0	0	0	0.380395	ENSG00000249416	AC107393.1
ENSG00000249418	0.189327	0	0	0	ENSG00000249418	AC005741.1
ENSG00000249427	0	0	0	3.10E-09	ENSG00000249427	RP11-432M8.4
ENSG00000249428	0.0418876	0	0.0729309	0.350265	ENSG00000249428	RP11-503N18.3
ENSG00000249433	0	0	0.374228	0.453635	ENSG00000249433	AC008628.1
ENSG00000249434	0	0	0	0.0189286	ENSG00000249434	TRIM26BP
ENSG00000249435	0	0	0	0	ENSG00000249435	AC022137.2
ENSG00000249437	2.78231	7.49632	5.75284	13.9733	ENSG00000249437	NAIP
ENSG00000249438	0	0	0	0	ENSG00000249438	KRT18P45
ENSG00000249439	0.74587	2.18261	2.04782	4.77759	ENSG00000249439	HMGN1P14
ENSG00000249443	0	0	0	0	ENSG00000249443	AC097493.3
ENSG00000249444	0.100733	0.191403	0.0884913	0.217449	ENSG00000249444	AC114324.2
ENSG00000249446	0	0	0	0	ENSG00000249446	TRAJ60
ENSG00000249448	0.111279	0.142932	0.0646015	0.0406205	ENSG00000249448	MTCO1P24
ENSG00000249449	0	0	0	0.346018	ENSG00000249449	MRPL57P6
ENSG00000249452	0	0	0	0	ENSG00000249452	AC093878.1
ENSG00000249454	0	0	0	0.118499	ENSG00000249454	GZMAP1
ENSG00000249459	2.84472	1.96516	5.25496	4.78734	ENSG00000249459	ZNF286B
ENSG00000249462	1.07255	0	0.288116	1.00639	ENSG00000249462	MLLT10P2
ENSG00000249465	0.214689	0.154744	0.27884	0.116961	ENSG00000249465	RBMXP4
ENSG00000249467	0	0	0	0	ENSG00000249467	AL592156.1
ENSG00000249471	5.77197	5.68837	8.05142	4.78828	ENSG00000249471	ZNF324B
ENSG00000249472	3.60842	6.49261	7.49839	9.59232	ENSG00000249472	AC147055.2
ENSG00000249480	0	0	0	0	ENSG00000249480	STK19B
ENSG00000249481	0	0	0	0	ENSG00000249481	SPATS1
ENSG00000249482	0	0	0.128852	0	ENSG00000249482	USP17L14P
ENSG00000249485	0.201085	0.485491	0.496459	0.780902	ENSG00000249485	RBBP4P1
ENSG00000249486	0	0	0	0	ENSG00000249486	AC091912.1
ENSG00000249488	0	0.104472	0.0943368	0	ENSG00000249488	NACAP5
ENSG00000249489	0	0.285198	0.408825	0.127728	ENSG00000249489	GAPDHP70
ENSG00000249493	0	0.240066	0	1.03768	ENSG00000249493	ANKRD20A18P
ENSG00000249495	0	0	0.130398	0	ENSG00000249495	AC117525.1
ENSG00000249501	0.0616151	0	0	0	ENSG00000249501	USP9YP2
ENSG00000249503	0	0	0	0	ENSG00000249503	HMGN1P16
ENSG00000249504	0.0207546	0	0	0	ENSG00000249504	PCDHA14
ENSG00000249505	0	0	0	0	ENSG00000249505	AC108673.1
ENSG00000249506	0.57657	1.5201	1.18394	2.65218	ENSG00000249506	ZEB2P1
ENSG00000249510	0	0.148111	0.0669088	0.083605	ENSG00000249510	AP003478.1
ENSG00000249514	0	0	0	0.329239	ENSG00000249514	TMEM251P1
ENSG00000249516	0	0	0.109461	0.135272	ENSG00000249516	PRELID3BP6
ENSG00000249518	0	0	0	0.0659987	ENSG00000249518	AC011352.2
ENSG00000249520	0	0	0	0.289479	ENSG00000249520	AC093824.1
ENSG00000249522	0	0.73391	0.398487	0	ENSG00000249522	AC147876.1
ENSG00000249525	0	0	0	0	ENSG00000249525	AC034159.1
ENSG00000249531	0.252198	0	0	0	ENSG00000249531	AC098799.2
ENSG00000249539	0	0	0.301653	0	ENSG00000249539	MRPS36P2
ENSG00000249540	0	0.293178	0	0.678696	ENSG00000249540	AC117383.2
ENSG00000249541	0	0	0	0.0616134	ENSG00000249541	AC116359.1
ENSG00000249542	0	0	0	0	ENSG00000249542	EEF1A1P21
ENSG00000249555	0	0	0	0	ENSG00000249555	TMEM248P1
ENSG00000249557	0	0.103775	0.0468957	0.0588126	ENSG00000249557	HSPD1P15

ENSG00000249558	0.406621	0.739829	0.664164	1.28639	ENSG00000249558	RCC2P4
ENSG00000249562	0	0	0	0	ENSG00000249562	AC091885.1
ENSG00000249563	0	0	0	0	ENSG00000249563	AC098976.1
ENSG00000249564	0	0	0	0	ENSG00000249564	AC097510.1
ENSG00000249565	0.202397	0.848248	1.08651	1.15747	ENSG00000249565	SERBP1P5
ENSG00000249571	0	0	0	0	ENSG00000249571	OR12D1
ENSG00000249577	0	0	0.305218	0.371085	ENSG00000249577	AC010424.1
ENSG00000249579	0.257152	2.93749	1.04776	2.23291	ENSG00000249579	AC113420.1
ENSG00000249580	0	0	0.102443	0.890208	ENSG00000249580	MTATP6P22
ENSG00000249581	0	0	0	0	ENSG00000249581	CLRN2
ENSG00000249582	0	0	0.0845352	0	ENSG00000249582	RPL7L1P4
ENSG00000249590	1.55423	2.25503	0.15025	0.778317	ENSG00000249590	AC004832.3
ENSG00000249600	0	0	0	0	ENSG00000249600	AC106806.2
ENSG00000249606	0	0	0	0	ENSG00000249606	TRAPPC2P7
ENSG00000249607	0	0	0	0	ENSG00000249607	AC108103.1
ENSG00000249616	0.675263	1.25793	1.54181	2.42375	ENSG00000249616	CCNB3P1
ENSG00000249617	0	0.957282	0.564349	1.37355	ENSG00000249617	AC106872.7
ENSG00000249619	0	0	0	0	ENSG00000249619	HMGN1P13
ENSG00000249620	0	0	0	0	ENSG00000249620	AC106774.2
ENSG00000249624	0.0302434	0	0	0	ENSG00000249624	AP000295.1
ENSG00000249626	0.27357	1.49134	2.52272	1.80039	ENSG00000249626	AC024560.2
ENSG00000249627	0.165975	0.158981	0	0.176938	ENSG00000249627	AC017037.1
ENSG00000249633	0	0.27028	0.244213	0.311846	ENSG00000249633	OR52V1P
ENSG00000249634	5.91E-06	3.47E-06	0	0	ENSG00000249634	USP9YP5
ENSG00000249646	4.03246	12.537	7.72144	16.7812	ENSG00000249646	OR7E94P
ENSG00000249649	0	0.888097	0.271192	0.644706	ENSG00000249649	MRPS33P2
ENSG00000249654	0	0.0118584	0	0.0133071	ENSG00000249654	VN1R104P
ENSG00000249661	0.37732	0.895195	0.862306	1.8495	ENSG00000249661	TNRC18P1
ENSG00000249663	0	0	0.0540797	0.179459	ENSG00000249663	CR759790.1
ENSG00000249666	1.47E-06	0	0.722845	1.52E-06	ENSG00000249666	RP11-432M8.12
ENSG00000249668	0	0	0	0	ENSG00000249668	KRT18P56
ENSG00000249679	0	0.418511	0.566841	0	ENSG00000249679	AC106897.1
ENSG00000249680	0	0	0	0	ENSG00000249680	TUBA3GP
ENSG00000249681	0	0	0	0.252665	ENSG00000249681	KRT19P3
ENSG00000249686	0	0	0.929354	0.657563	ENSG00000249686	AC108078.2
ENSG00000249689	0	0	0	0	ENSG00000249689	AC138517.1
ENSG00000249691	0.50202	1.24141	1.12167	1.09083	ENSG00000249691	AC026117.1
ENSG00000249692	0.268129	0	0	0	ENSG00000249692	AC009567.2
ENSG00000249693	0	0.0344377	0.109112	0.152526	ENSG00000249693	THEGL
ENSG00000249698	0	0.0802309	0.0760375	0.119151	ENSG00000249698	MTCO3P9
ENSG00000249709	8.97042	18.2382	15.4652	23.6061	ENSG00000249709	ZNF564
ENSG00000249715	1.48773	3.27991	3.47198	4.06873	ENSG00000249715	FER1L5
ENSG00000249721	0	0	0.385716	0.236179	ENSG00000249721	AC112206.3
ENSG00000249726	0	0	0	0.0497214	ENSG00000249726	TUBB1P1
ENSG00000249729	0	0.0578231	0	0.0654704	ENSG00000249729	AC093755.1
ENSG00000249730	0	0	0	0	ENSG00000249730	OR10J4
ENSG00000249735	0	0	0	0	ENSG00000249735	AC021146.5
ENSG00000249741	0	0.16939	0	0.448535	ENSG00000249741	AC093890.1
ENSG00000249744	0	0	0.122628	0.153695	ENSG00000249744	AC010374.2
ENSG00000249745	0	0	0	0	ENSG00000249745	HMGB1P28
ENSG00000249751	0	0.353248	0.318543	0	ENSG00000249751	ECSCR
ENSG00000249754	0	0	0	0	ENSG00000249754	NDUFB4P9
ENSG00000249755	0.104207	0.400337	0.180796	1.79934	ENSG00000249755	AC083829.1
ENSG00000249761	0	0	1.56729	2.84408	ENSG00000249761	AC074133.1

ENSG00000249763	0.0413202	0.0705164	0	0.0452067	ENSG00000249763	AC114786.1
ENSG00000249764	0	0	0	0	ENSG00000249764	AC114811.1
ENSG00000249766	0	0	0	0	ENSG00000249766	AC097535.2
ENSG00000249767	0.468294	0.913911	1.60601	1.6895	ENSG00000249767	ENPP7P10
ENSG00000249768	2.21015	4.96692	6.37126	10.6078	ENSG00000249768	HSPE1P10
ENSG00000249770	0	0	0	0.899558	ENSG00000249770	MTND6P17
ENSG00000249773	0.203016	0.255349	0.268039	0.046437	ENSG00000249773	AC092647.5
ENSG00000249774	1.19462	0	0	3.61625	ENSG00000249774	AC025458.1
ENSG00000249777	0	0	0.192039	0	ENSG00000249777	SAP18P1
ENSG00000249778	0	0	0	0	ENSG00000249778	TRMT112P2
ENSG00000249779	0.110607	0	0.0961808	0.120229	ENSG00000249779	AC106800.2
ENSG00000249780	0	0	0	0	ENSG00000249780	AC093809.1
ENSG00000249795	0.644622	2.16431	0.69927	1.89466	ENSG00000249795	AC097462.2
ENSG00000249798	0	0	0.0898664	0.420485	ENSG00000249798	HSD3BP3
ENSG00000249799	0	0	2.69041	1.24821	ENSG00000249799	SNRPCP13
ENSG00000249811	0	0	0	0	ENSG00000249811	USP17L21
ENSG00000249814	0	0	0.0206295	0.0258112	ENSG00000249814	RPSAP2
ENSG00000249819	0.218975	0	0	0	ENSG00000249819	AC112240.1
ENSG00000249820	0	0	0	0.0772929	ENSG00000249820	AC055753.1
ENSG00000249828	0.453564	0	0.527259	0.123942	ENSG00000249828	AC118282.3
ENSG00000249829	1.5712	2.21382	3.90926	1.57467	ENSG00000249829	AC016559.1
ENSG00000249834	0.49176	0.353956	0.343129	1.0573	ENSG00000249834	PGBD4P3
ENSG00000249838	0	0	0	0	ENSG00000249838	SUMO2P7
ENSG00000249839	1.297	3.99323	0	0	ENSG00000249839	AC011330.1
ENSG00000249840	0	0.0611492	0.110532	0.0691819	ENSG00000249840	GAPDHP76
ENSG00000249843	0.265599	0.758919	0.914505	0.621149	ENSG00000249843	AC112198.4
ENSG00000249844	0	0	0	0	ENSG00000249844	OR7E43P
ENSG00000249848	0.374142	1.08141	0.432279	0.603474	ENSG00000249848	AC112673.1
ENSG00000249850	1.47571	2.60419	2.48707	4.26988	ENSG00000249850	KRT18P31
ENSG00000249851	0	0	0	0.190733	ENSG00000249851	RPS27AP18
ENSG00000249852	0.168724	0.867256	0.68602	3.85708	ENSG00000249852	AC145676.1
ENSG00000249853	0.866532	0.702267	1.41652	3.13731	ENSG00000249853	HS3ST5
ENSG00000249855	0.766907	1.57167	1.10763	0.887129	ENSG00000249855	EEF1A1P19
ENSG00000249858	0	0	0	0	ENSG00000249858	SNX5P1
ENSG00000249860	5.12522	5.25692	6.15767	6.00585	ENSG00000249860	MTRNR2L5
ENSG00000249861	0	0.302066	0.0909429	0.339377	ENSG00000249861	LGALS16
ENSG00000249863	1.155	1.76195	2.02815	1.13312	ENSG00000249863	AC021106.1
ENSG00000249866	0	0	0	0	ENSG00000249866	OR7E83P
ENSG00000249869	0	0	0	0	ENSG00000249869	AC083906.2
ENSG00000249876	0.917949	0.387087	0.715302	0.543366	ENSG00000249876	AC010285.3
ENSG00000249878	0.169475	0.990175	0.294817	0.557555	ENSG00000249878	AC026434.2
ENSG00000249884	2.63325	0.35743	0.629102	0.631393	ENSG00000249884	RNF103-CHMP3
ENSG00000249887	0	0	0	0	ENSG00000249887	AC108210.2
ENSG00000249888	0.334453	0	0.289338	0.347802	ENSG00000249888	AC106800.3
ENSG00000249889	0	0	0	0	ENSG00000249889	ALG1L11P
ENSG00000249890	0	0.473976	0.256878	0	ENSG00000249890	AC107401.1
ENSG00000249891	0	0	0	0	ENSG00000249891	KRT19P6
ENSG00000249893	0	0	0	0	ENSG00000249893	MTND6P16
ENSG00000249904	0	0	0	0	ENSG00000249904	AC010587.1
ENSG00000249908	0	0	0	0	ENSG00000249908	BRD9P2
ENSG00000249909	0.321099	0.304633	0	0	ENSG00000249909	CYCTP
ENSG00000249910	0	0.269518	0	0.0473763	ENSG00000249910	TRIM51CP
ENSG00000249912	0	0	0	0	ENSG00000249912	TRBV26
ENSG00000249915	78.2979	58.6281	65.3822	53.5162	ENSG00000249915	PDCD6

ENSG00000249919	0	0.197155	0.178161	0	ENSG00000249919	FABP5P6
ENSG00000249920	0	0	0	0	ENSG00000249920	HNRNPA1P55
ENSG00000249921	0.477243	2.13587	0.582024	1.09569	ENSG00000249921	AC034207.1
ENSG00000249927	0.43656	1.23648	0.369434	1.34304	ENSG00000249927	AC025768.1
ENSG00000249928	0	1.23902	0.839472	0	ENSG00000249928	UQCRBP3
ENSG00000249930	0.520059	0.48932	2.18459	1.5807	ENSG00000249930	AC007016.1
ENSG00000249931	0.224502	0.276674	0	0	ENSG00000249931	GOLGA8K
ENSG00000249934	0.0313703	0.0604574	0.0546534	0.103302	ENSG00000249934	NCOA4P2
ENSG00000249936	0.250015	0	0	0	ENSG00000249936	RAC1P2
ENSG00000249943	0	0	0	0	ENSG00000249943	AC097486.1
ENSG00000249944	0	0	0	0	ENSG00000249944	AC008628.2
ENSG00000249947	0.948896	1.82681	1.83256	1.70362	ENSG00000249947	XBP1P1
ENSG00000249948	1.2212	2.58691	1.46278	3.18033	ENSG00000249948	GBA3
ENSG00000249950	0	0	0.309411	0	ENSG00000249950	AC010587.2
ENSG00000249956	0	0	0	0	ENSG00000249956	UGT2B24P
ENSG00000249958	0	0.0385996	0.0348909	0.131569	ENSG00000249958	CCT7P2
ENSG00000249960	0	0	0	0	ENSG00000249960	AC067942.3
ENSG00000249961	6.24956	13.1553	12.7065	22.2861	ENSG00000249961	TERB1
ENSG00000249962	1.23927	1.49976	2.34288	2.00778	ENSG00000249962	AL157400.5
ENSG00000249963	0	0	0	0	ENSG00000249963	EEF1A1P20
ENSG00000249965	0	0.492858	0.111236	0.690917	ENSG00000249965	CDC42P4
ENSG00000249967	0	0	0	0	ENSG00000249967	AL355315.1
ENSG00000249970	0	0	0	0	ENSG00000249970	AC074250.1
ENSG00000249973	0	0	0	0.189013	ENSG00000249973	CHCHD2P7
ENSG00000249975	0	0	0	0	ENSG00000249975	OR5H3P
ENSG00000249976	0	0.269559	0.59093	0.146291	ENSG00000249976	AC108157.1
ENSG00000249977	0.22828	0.218029	0.393834	0.964222	ENSG00000249977	AC106748.1
ENSG00000249978	0	0	0	1.10436	ENSG00000249978	TRGV7
ENSG00000249985	0	0	0	0	ENSG00000249985	AC021146.6
ENSG00000249986	0.686329	3.25567	0.979019	5.36195	ENSG00000249986	YWHAQP6
ENSG00000249987	0	0	0	0	ENSG00000249987	RPS4XP20
ENSG00000249990	0.19345	0.185101	0.188838	0.205342	ENSG00000249990	MTCO2P24
ENSG00000249992	3.83864	2.09858	1.16108	17.4787	ENSG00000249992	TMEM158
ENSG00000249995	0.219574	0.317296	0.223458	0.683112	ENSG00000249995	ECM1P2
ENSG00000249997	0	0	0	0	ENSG00000249997	MTCO3P7
ENSG00000250006	0.0933638	0.0897149	0	0.100976	ENSG00000250006	AC008638.2
ENSG00000250011	0.987145	2.29088	1.37846	3.60678	ENSG00000250011	HMGB1P3
ENSG00000250013	0	0	0	0.11268	ENSG00000250013	AC093286.1
ENSG00000250016	0.988577	1.78695	1.53418	2.81619	ENSG00000250016	SNX18P23
ENSG00000250017	9.49915	22.2185	20.5076	33.7526	ENSG00000250017	AC117529.1
ENSG00000250020	0	0	0.161218	0.100445	ENSG00000250020	AC113430.1
ENSG00000250021	7.06885	5.44307	5.02842	3.75814	ENSG00000250021	C15orf38-AP3S2
ENSG00000250026	1.32395	1.74513	1.98084	2.21456	ENSG00000250026	TMPRSS11BNL
ENSG00000250030	0	0.962211	0.313349	0	ENSG00000250030	AC104806.1
ENSG00000250031	0.385905	1.33717	1.26272	0.565031	ENSG00000250031	AC009927.1
ENSG00000250036	0	0	0	0	ENSG00000250036	IGKV1D-37
ENSG00000250037	0	0.569163	0.693616	0.492289	ENSG00000250037	AC091965.2
ENSG00000250038	8.76041	6.60797	5.67728	11.568	ENSG00000250038	AC109588.1
ENSG00000250040	0.0675201	0.227694	0.117617	0.332982	ENSG00000250040	RAF1P1
ENSG00000250045	0.694999	1.06975	2.16697	4.61714	ENSG00000250045	CBX3P3
ENSG00000250050	0.218622	0.0906235	0.152241	0.193032	ENSG00000250050	MTND4P9
ENSG00000250053	0	0	0	0.0850661	ENSG00000250053	RARRES2P4
ENSG00000250055	0	0.199302	0	0.00075577	ENSG00000250055	RP11-321E2.8
ENSG00000250067	2.30671	1.36717	3.60212	1.89987	ENSG00000250067	YJEFN3

ENSG00000250068	2.29809	1.73318	1.61434	2.68826	ENSG00000250068	AL445187.1
ENSG00000250071	0.164381	0.392449	0.527096	0.121766	ENSG00000250071	AC093214.1
ENSG00000250074	0	0.812186	0	0.894684	ENSG00000250074	AC006499.2
ENSG00000250076	0	0	0	0	ENSG00000250076	AC017013.1
ENSG00000250079	0	0	0	0	ENSG00000250079	AC093300.1
ENSG00000250080	0.0329869	0.0635678	0.0574642	0.144627	ENSG00000250080	AC011416.1
ENSG00000250082	0	0	0	0	ENSG00000250082	AC074255.1
ENSG00000250084	0	0	0	0	ENSG00000250084	BX510359.5
ENSG00000250088	0	0	0	0	ENSG00000250088	AC233724.8
ENSG00000250090	2.15004	0	0.0676218	0	ENSG00000250090	AL390198.2
ENSG00000250091	0.598787	0.995889	0.669424	1.43323	ENSG00000250091	DNAH10OS
ENSG00000250099	0	0	0	0	ENSG00000250099	AC091893.1
ENSG00000250100	0	0.119393	0	0	ENSG00000250100	AC111000.3
ENSG00000250111	0	0	0	0	ENSG00000250111	AC107982.1
ENSG00000250113	0	0	0	0.0230077	ENSG00000250113	RP13-221M14.6
ENSG00000250114	0	0.678588	1.20342	0.726007	ENSG00000250114	AC008723.1
ENSG00000250115	0	0	0	0	ENSG00000250115	AK3P2
ENSG00000250118	0	0	0	0	ENSG00000250118	AC114300.1
ENSG00000250120	0.0591208	0.00809258	0.0525104	0.0844322	ENSG00000250120	PCDHA10
ENSG00000250127	14.7324	44.7042	38.0515	64.5332	ENSG00000250127	LINC02108
ENSG00000250130	0.30796	1.19536	0.535559	1.64812	ENSG00000250130	AC090519.1
ENSG00000250138	0.127487	0.425683	0.493158	1.86475	ENSG00000250138	AC139495.3
ENSG00000250140	0	0	0	0.441809	ENSG00000250140	AC026801.2
ENSG00000250144	0	0.0409067	0.221731	0	ENSG00000250144	AC104619.3
ENSG00000250145	0	0	0	0	ENSG00000250145	AC114940.1
ENSG00000250147	0.148541	0.142842	0.129073	0	ENSG00000250147	MORF4L2P1
ENSG00000250148	0.166208	0.280547	0.180871	0.409121	ENSG00000250148	KRT8P31
ENSG00000250151	7.11682	11.7309	11.1273	7.42614	ENSG00000250151	ARPC4-TTLL3
ENSG00000250154	0	0	0.405988	0.576742	ENSG00000250154	MICE
ENSG00000250161	0.868184	1.1001	0.745777	1.21111	ENSG00000250161	TRMT112P5
ENSG00000250162	0	0	0	0.309162	ENSG00000250162	CSNK1A1P3
ENSG00000250169	0	0	0	0	ENSG00000250169	MTND5P13
ENSG00000250173	0	0	0	0	ENSG00000250173	AC122719.2
ENSG00000250182	0.661308	0.639417	0.811906	0.257309	ENSG00000250182	EEF1A1P13
ENSG00000250183	0.0786652	0.453737	0.136646	0.341365	ENSG00000250183	AC097173.1
ENSG00000250185	0	0	0	0	ENSG00000250185	RCC2P8
ENSG00000250189	1.57894	3.80318	3.81314	4.07907	ENSG00000250189	AC097504.1
ENSG00000250191	0	0	0	0	ENSG00000250191	AC105252.1
ENSG00000250194	0	0	0	0	ENSG00000250194	AC109458.1
ENSG00000250197	0	0.687582	1.54551	3.00072	ENSG00000250197	HMGN1P15
ENSG00000250200	0	0	0	0	ENSG00000250200	AC105914.1
ENSG00000250202	0	0	0	1.05991	ENSG00000250202	AC093827.2
ENSG00000250204	0	0	0	0	ENSG00000250204	TTTY23B
ENSG00000250205	0	0	0	0	ENSG00000250205	YWHAEP4
ENSG00000250207	0	0	0	0	ENSG00000250207	AC079776.4
ENSG00000250210	0	1.03381	2.21014	1.44668	ENSG00000250210	FO082796.1
ENSG00000250213	0	0.839408	0	0.891735	ENSG00000250213	AC025554.1
ENSG00000250214	2.50118	1.69263	1.83131	0.741157	ENSG00000250214	AC112225.1
ENSG00000250215	0.0438725	0.126857	0.116395	0.150233	ENSG00000250215	CIR1P2
ENSG00000250219	0.0963009	0.231797	0.0838037	0.157797	ENSG00000250219	LTV1P1
ENSG00000250221	0	0	0	0.131915	ENSG00000250221	KRT8P32
ENSG00000250227	0.0812275	0.248174	0.611251	0.478452	ENSG00000250227	TRIM60P14
ENSG00000250229	0	0	0	0	ENSG00000250229	AC111193.1

ENSG00000250231	0	0	0	0	ENSG00000250231	USP17L16P
ENSG00000250232	0	0	0	0	ENSG00000250232	AF196779.12
ENSG00000250238	0.052067	0.100241	0.181198	0.171326	ENSG00000250238	AC253576.1
ENSG00000250247	0.0517551	0.0996421	0.0902425	0.0565092	ENSG00000250247	SEPHS2P1
ENSG00000250249	0	0	0	0	ENSG00000250249	AC105313.1
ENSG00000250251	19.1484	80.6461	74.7393	55.7293	ENSG00000250251	PKD1P6
ENSG00000250253	0	0	0.105796	0	ENSG00000250253	AC117522.3
ENSG00000250254	0	0	0	0	ENSG00000250254	PTTG2
ENSG00000250257	0	0	0	0.210104	ENSG00000250257	LDHAL6DP
ENSG00000250261	0.622523	0.941093	0.699867	1.10816	ENSG00000250261	CCDC74BP1
ENSG00000250264	5.43974	5.09813	1.7356	2.09379	ENSG00000250264	AL669918.1
ENSG00000250268	0	0	0	0	ENSG00000250268	ALG1L14P
ENSG00000250272	0	0	0	0	ENSG00000250272	TRMT112P1
ENSG00000250273	0	6.05057	0	5.39644	ENSG00000250273	PSMC1P5
ENSG00000250277	0.0842838	0	0	0.182662	ENSG00000250277	AC021146.7
ENSG00000250289	0	0	0	0	ENSG00000250289	VWA8P1
ENSG00000250290	0	0	0.0273102	0.0345077	ENSG00000250290	NCAPGP1
ENSG00000250292	0.0863566	0.0415825	0.188047	0.18888	ENSG00000250292	AC093844.1
ENSG00000250293	0	0	0	0	ENSG00000250293	CRYZP2
ENSG00000250294	0	0	0	0	ENSG00000250294	OR12D1
ENSG00000250296	0	0	0	0	ENSG00000250296	RP11-321E2.9
ENSG00000250299	0.00853781	0	0.226479	0	ENSG00000250299	MRPS31P4
ENSG00000250300	0	0	0	0	ENSG00000250300	AP001960.1
ENSG00000250304	0.0292964	0.0283123	0.178663	0.0642767	ENSG00000250304	ZBED1P1
ENSG00000250305	1.97999	4.6727	4.17086	6.69225	ENSG00000250305	KIAA1456
ENSG00000250306	0	0.924115	0.278304	0.676923	ENSG00000250306	AC091826.1
ENSG00000250307	0	0.0779486	0.0700146	0.0875086	ENSG00000250307	TUBB8P3
ENSG00000250308	0.0610058	0.0881825	0.135359	0.234263	ENSG00000250308	SALL4P1
ENSG00000250315	0.336119	1.61011	0.833433	0.35827	ENSG00000250315	AC110760.3
ENSG00000250316	0	0.0940561	0.0634382	0.0266486	ENSG00000250316	AC068880.1
ENSG00000250317	9.53364	11.2917	10.0561	5.40493	ENSG00000250317	SMIM20
ENSG00000250318	2.67598	2.82857	2.95157	2.23673	ENSG00000250318	AC003072.1
ENSG00000250319	0	0.0962443	0	0	ENSG00000250319	AC010460.2
ENSG00000250321	0	1.48184	0.675563	0	ENSG00000250321	AC079140.2
ENSG00000250322	0	7.39852	5.58905	2.23135	ENSG00000250322	AC026402.1
ENSG00000250324	0	0.109002	0	0	ENSG00000250324	MRPL22P1
ENSG00000250325	0	0	0.0653409	0.239916	ENSG00000250325	IGBP1P4
ENSG00000250327	0.0736377	0.0708144	0	0.194363	ENSG00000250327	RPSAP70
ENSG00000250329	0.0384405	0.222979	0.169836	0.298772	ENSG00000250329	KDELC1P1
ENSG00000250330	0.255422	2.77098	3.55827	1.16726	ENSG00000250330	AC016559.2
ENSG00000250332	0	0.0357336	0.0643592	0.040375	ENSG00000250332	AC010460.3
ENSG00000250339	0	0	0	0	ENSG00000250339	CXCL1P1
ENSG00000250342	0	0	0.733144	0	ENSG00000250342	SNRPCP16
ENSG00000250345	0.102589	0	0.624811	1.11988	ENSG00000250345	AC104090.1
ENSG00000250346	0	0	0.0834097	0	ENSG00000250346	EEF1GP2
ENSG00000250347	0	0	0	0	ENSG00000250347	AC005740.2
ENSG00000250349	0	0	0	0	ENSG00000250349	AF241726.2
ENSG00000250350	2.49452	6.99315	0	2.46665	ENSG00000250350	AC104819.2
ENSG00000250351	0	0	0	0	ENSG00000250351	AC233724.9
ENSG00000250355	35.8574	15.3818	42.9159	4.07211	ENSG00000250355	RP11-79L21.1
ENSG00000250356	0	0	0	0	ENSG00000250356	HSPE1P23
ENSG00000250359	0	0	0	0	ENSG00000250359	PTP4A1P4
ENSG00000250361	0.406903	0.36623	1.46898	1.16456	ENSG00000250361	GYPB

ENSG00000250363	0	0	0	0.05112	ENSG00000250363	KRT18P21
ENSG00000250364	0.0151711	0.0536059	0.0442655	0.0942871	ENSG00000250364	OR12D3
ENSG00000250372	1.05325	2.70056	2.20363	2.69684	ENSG00000250372	MARK2P4
ENSG00000250374	0	0.102602	0	0.0909881	ENSG00000250374	TRIM75P
ENSG00000250376	0	0.0898761	0.0811873	0.101155	ENSG00000250376	AC093720.1
ENSG00000250381	0	0	0	0	ENSG00000250381	UNC93B4
ENSG00000250384	0.759506	2.99353	1.84422	5.21839	ENSG00000250384	UBE2CP3
ENSG00000250386	0.20625	0	0	0	ENSG00000250386	AC233724.10
ENSG00000250389	0	0	0.123005	0.177129	ENSG00000250389	MTND6P2
ENSG00000250391	0	0.0448769	0	0.101005	ENSG00000250391	AC092284.1
ENSG00000250393	0	0	0	0	ENSG00000250393	AC093664.1
ENSG00000250398	0	0	0	0	ENSG00000250398	AC097467.2
ENSG00000250403	0.091246	0.0883958	0.272121	0.40293	ENSG00000250403	AC097460.2
ENSG00000250405	0	0	0	0	ENSG00000250405	AC113367.3
ENSG00000250412	0.851665	1.58205	1.64755	0.461024	ENSG00000250412	KLHL2P1
ENSG00000250416	0.0636027	0.408732	0.179999	0.585696	ENSG00000250416	SEC63P2
ENSG00000250420	2.40422	4.80347	4.89057	7.99212	ENSG00000250420	AACSP1
ENSG00000250422	4.58738	12.3617	10.098	17.8387	ENSG00000250422	AC117529.2
ENSG00000250423	0.170365	0.312426	0.459978	0.654329	ENSG00000250423	KIAA1210
ENSG00000250424	0.0166187	0.0966535	0	0	ENSG00000250424	AC004691.2
ENSG00000250425	0.402349	0.295904	0.314832	0.323114	ENSG00000250425	AC098976.2
ENSG00000250426	0.170493	0.497548	0.605587	0.751583	ENSG00000250426	FTLP10
ENSG00000250428	0.145669	0.424637	0.338032	0.106075	ENSG00000250428	AC100858.1
ENSG00000250430	0.224059	0.239856	0.294912	0.888006	ENSG00000250430	AC106872.8
ENSG00000250439	0.262748	0.803585	1.29579	1.26773	ENSG00000250439	FGD5P1
ENSG00000250441	0	1.87084	1.68051	2.44574	ENSG00000250441	AC109481.1
ENSG00000250442	3.56717	3.52995	5.90628	1.86511	ENSG00000250442	EIF3KP3
ENSG00000250443	0.92311	1.59945	1.33921	3.55081	ENSG00000250443	AC128709.1
ENSG00000250444	0.10695	0.413147	0.43705	0.47094	ENSG00000250444	CCT5P1
ENSG00000250455	0.614452	0	0	0	ENSG00000250455	AC117532.1
ENSG00000250458	0	0	0	0	ENSG00000250458	AC093767.1
ENSG00000250461	0.455772	2.10196	2.10694	7.68844	ENSG00000250461	AC122718.1
ENSG00000250462	7.51309	12.3614	17.4637	12.0389	ENSG00000250462	LRRC37BP1
ENSG00000250464	0	0	0	0.141281	ENSG00000250464	LRRC34P2
ENSG00000250470	0	0	0	0	ENSG00000250470	AC253536.5
ENSG00000250471	0	0	0	0	ENSG00000250471	GMPSP1
ENSG00000250473	0.956638	5.48698	4.79755	5.24362	ENSG00000250473	DUTP7
ENSG00000250474	1.19958	1.13573	0.888594	1.17664	ENSG00000250474	WBP1LP2
ENSG00000250475	0	0	0	0	ENSG00000250475	AC017037.2
ENSG00000250476	0	0	0	0	ENSG00000250476	ENPP7P9
ENSG00000250479	10.3115	11.7515	19.0004	14.1338	ENSG00000250479	CHCHD10
ENSG00000250480	0	0.0714208	0.129073	0.0806605	ENSG00000250480	AC034244.2
ENSG00000250482	0	0.879534	0.246354	0.29832	ENSG00000250482	DUX4L51
ENSG00000250483	0	0.154395	0.231361	0.407741	ENSG00000250483	PPM1AP1
ENSG00000250484	0.316964	1.03738	0.121356	0.621125	ENSG00000250484	AC108075.1
ENSG00000250485	0	0.0526356	0.0237922	0	ENSG00000250485	EXOC7P1
ENSG00000250486	0.798151	1.11676	0.740376	0.565337	ENSG00000250486	FAM218A
ENSG00000250492	0	0	0	0	ENSG00000250492	INTS6P1
ENSG00000250494	0	0	0	0	ENSG00000250494	AC009646.1
ENSG00000250496	0.401057	1.1554	0.640007	1.24973	ENSG00000250496	ABT1P1
ENSG00000250500	0	0.083984	0.151477	0.570877	ENSG00000250500	AC017007.4
ENSG00000250504	0	0	0	0	ENSG00000250504	KRT18P51
ENSG00000250505	0.0881528	0	0	0.0954319	ENSG00000250505	AC006499.3
ENSG00000250506	7.90672	7.10573	12.6353	6.12929	ENSG00000250506	CDK3

ENSG00000250507	0	0	0	0	ENSG00000250507	AC245884.6
ENSG00000250510	0.3066	0.381823	0.618756	1.20775	ENSG00000250510	GPR162
ENSG00000250515	0	0	0	0	ENSG00000250515	AC116353.3
ENSG00000250516	0.0668316	0.192817	0.174227	0.0726955	ENSG00000250516	AC021678.1
ENSG00000250517	1.02573	2.5436	2.35439	3.64766	ENSG00000250517	LDHAL6CP
ENSG00000250523	0	0	0	3.89687	ENSG00000250523	AC093909.3
ENSG00000250526	0.0728505	0	0	0.0398948	ENSG00000250526	CCT6P2
ENSG00000250535	0	0	0	0	ENSG00000250535	STK19B
ENSG00000250536	0	0.726955	0.0516974	0.190776	ENSG00000250536	ABHD17AP3
ENSG00000250537	1.86601	2.15896	3.42082	2.38569	ENSG00000250537	DUX4L8
ENSG00000250539	0.785318	1.82085	2.60256	1.61526	ENSG00000250539	KRT8P33
ENSG00000250540	0	0.691497	0.212192	0	ENSG00000250540	AC104685.1
ENSG00000250547	0	0	0.0531159	0	ENSG00000250547	AC079238.1
ENSG00000250550	0	0	0	0	ENSG00000250550	PPBPP1
ENSG00000250556	0	0	0	0.154988	ENSG00000250556	CCDC34P1
ENSG00000250558	0	2.04E-06	0	3.10E-09	ENSG00000250558	RP11-432M8.3
ENSG00000250560	0	0	0	0	ENSG00000250560	AC093870.1
ENSG00000250561	0.247274	0.144075	0.468926	0.381245	ENSG00000250561	AC079804.3
ENSG00000250562	0	0	0	0	ENSG00000250562	RPL38P4
ENSG00000250563	0	0.0497545	0	0.117804	ENSG00000250563	KNOP1P5
ENSG00000250565	8.69023	11.2077	11.2637	5.86776	ENSG00000250565	ATP6V1E2
ENSG00000250566	0	0.0613625	0	0.138867	ENSG00000250566	UGT2B29P
ENSG00000250568	2.77661	4.28514	1.08054	3.84736	ENSG00000250568	AC098591.2
ENSG00000250569	2.02044	2.92724	2.51288	2.24129	ENSG00000250569	NTAN1P2
ENSG00000250571	18.5458	26.1377	28.1173	19.6891	ENSG00000250571	GLI4
ENSG00000250573	0	0.466077	0.171142	0.629158	ENSG00000250573	AC006499.4
ENSG00000250574	0	0	0	0	ENSG00000250574	AC112173.1
ENSG00000250575	0	0.300149	0.572483	0	ENSG00000250575	AL732372.3
ENSG00000250580	0	0	0	0	ENSG00000250580	SNRPCP8
ENSG00000250587	0	0	0	0	ENSG00000250587	HPRT1P2
ENSG00000250588	4.50274	11.6913	7.93928	9.50709	ENSG00000250588	IQCJ-SCHIP1
ENSG00000250591	0	0	0	0	ENSG00000250591	PRSS3P1
ENSG00000250594	0	0	0	0	ENSG00000250594	AC108145.1
ENSG00000250599	0	0.0509886	0	0	ENSG00000250599	AC064853.3
ENSG00000250606	1.05527	0.630182	0.501614	1.29772	ENSG00000250606	PRSS3P2
ENSG00000250609	0	0	0	0	ENSG00000250609	AC110753.1
ENSG00000250611	1.20107	1.94934	1.29476	1.36471	ENSG00000250611	AC098862.1
ENSG00000250612	0	0	0	0.0445732	ENSG00000250612	AC114786.2
ENSG00000250613	0	0.282417	0	2.17544	ENSG00000250613	AC110768.2
ENSG00000250618	0	0.713498	0	0	ENSG00000250618	AC023141.11
ENSG00000250622	0	0	0.259426	0	ENSG00000250622	AC093325.1
ENSG00000250624	0.0893683	0.686931	0.310306	1.25738	ENSG00000250624	MTCYBP43
ENSG00000250625	0	0.0515975	0.0731079	0.174141	ENSG00000250625	AL031073.1
ENSG00000250627	0	0	0	0	ENSG00000250627	TTC39CP1
ENSG00000250630	0	0	0	0	ENSG00000250630	MTCO1P35
ENSG00000250636	0	0	0	0.0848354	ENSG00000250636	AC019193.1
ENSG00000250637	0	0	0	0	ENSG00000250637	AC134698.1
ENSG00000250640	0.0302363	0.0291002	0.156591	0	ENSG00000250640	AC090835.1
ENSG00000250641	0	0	0	0	ENSG00000250641	AL662899.2
ENSG00000250642	1.85342	0	0	0.393893	ENSG00000250642	AC098799.3
ENSG00000250644	9.92671	0.255564	1.10104	0.383572	ENSG00000250644	AC068580.4
ENSG00000250645	0	0	0.277343	3.30262	ENSG00000250645	AC010442.2
ENSG00000250650	0	0	3.1251	1.89495	ENSG00000250650	AC093534.1
ENSG00000250651	0	0.0123647	0.161969	0.151003	ENSG00000250651	PABPC1P7

ENSG00000250654	1.23145	4.8664	6.35176	3.66123	ENSG00000250654	AC023794.3
ENSG00000250655	0.15736	0.151295	0.204045	0	ENSG00000250655	AC096661.1
ENSG00000250656	1.12619	1.21872	1.20368	0.926117	ENSG00000250656	ST3GAL1P1
ENSG00000250662	0	0.456089	0	0.492976	ENSG00000250662	HNRNPKP5
ENSG00000250667	0	0	0	0	ENSG00000250667	AC106774.3
ENSG00000250669	0	0	0.188336	0.221859	ENSG00000250669	AC112206.4
ENSG00000250672	0	0	0	0	ENSG00000250672	AC010343.2
ENSG00000250673	0	0.206683	0	0.228747	ENSG00000250673	AC097372.1
ENSG00000250677	0	3.14578	0	0	ENSG00000250677	AC114781.3
ENSG00000250678	0	0	0.13833	0	ENSG00000250678	AC008629.2
ENSG00000250684	0	0	0	0	ENSG00000250684	ADI1P2
ENSG00000250687	2.98417	5.74284	6.94881	12.3746	ENSG00000250687	AC146944.2
ENSG00000250688	0	0	0	0	ENSG00000250688	TRAJ55
ENSG00000250693	0	0	0.183656	0.153154	ENSG00000250693	RPF2P2
ENSG00000250703	0	0	0	0	ENSG00000250703	AC113347.3
ENSG00000250705	0	0	0	0	ENSG00000250705	AC008526.1
ENSG00000250709	0.037938	0	0	0.0164675	ENSG00000250709	CCDC169-SOHLH2
ENSG00000250710	0	0	0	0	ENSG00000250710	OR7E99P
ENSG00000250711	0	0.159982	0.29131	0.178021	ENSG00000250711	PRELID3BP7
ENSG00000250712	0.0420575	0.0405054	0	0.0920116	ENSG00000250712	AC106872.9
ENSG00000250715	0	0.402071	0.36307	0	ENSG00000250715	AC233724.11
ENSG00000250721	0	0	0	0	ENSG00000250721	HMGB1P22
ENSG00000250722	8.64616	8.71699	4.20199	7.4473	ENSG00000250722	SELENOP
ENSG00000250725	0	0	0	0	ENSG00000250725	AC080079.1
ENSG00000250726	0	0	0	0	ENSG00000250726	AC107222.1
ENSG00000250727	0	0	0.0349804	0.0437891	ENSG00000250727	AC100871.1
ENSG00000250728	0	0	0	0	ENSG00000250728	AC010468.3
ENSG00000250730	0	0.457876	0.234871	0.129905	ENSG00000250730	HMGB3P3
ENSG00000250731	0.958429	0.644747	0.638574	1.00559	ENSG00000250731	TPM3P6
ENSG00000250732	0.519988	2.39723	0.721741	5.34609	ENSG00000250732	RPEP1
ENSG00000250733	0.450373	1.2542	0.801136	0.991023	ENSG00000250733	C8orf17
ENSG00000250741	0	0	0	0	ENSG00000250741	NT5C1B-RDH14
ENSG00000250745	0.0247832	0.0541723	0.078843	0	ENSG00000250745	USP17L20
ENSG00000250746	0	0	0.0246648	0.0628596	ENSG00000250746	AC105250.1
ENSG00000250747	0	0	0	0	ENSG00000250747	AC116345.2
ENSG00000250749	0.690133	1.98238	2.53566	3.49058	ENSG00000250749	AC122714.1
ENSG00000250750	0	0	0	0	ENSG00000250750	OR5BM1P
ENSG00000250752	0	0.119428	0	0	ENSG00000250752	RPL23AP96
ENSG00000250753	0.773498	2.77577	0.88928	3.9504	ENSG00000250753	AC119751.4
ENSG00000250756	0	2.87737	4.66557	0	ENSG00000250756	AC018645.1
ENSG00000250760	0.0571771	0.0550255	0.198921	0	ENSG00000250760	RP11-440I14.4
ENSG00000250762	0	0.441489	0	0	ENSG00000250762	Z99943.2
ENSG00000250767	0.298235	0.252497	0.14262	1.13915	ENSG00000250767	AC139783.1
ENSG00000250768	0.027274	0	0.0477493	0	ENSG00000250768	DPP3P1
ENSG00000250769	0.254923	1.2712	0.741595	2.51698	ENSG00000250769	AC119751.5
ENSG00000250771	3.52691	7.69808	7.63108	12.7318	ENSG00000250771	AC106865.1
ENSG00000250778	0	1.31923	4.62227	1.96758	ENSG00000250778	AC004980.4
ENSG00000250782	0.237399	0.401812	0	0.381149	ENSG00000250782	AC233724.12
ENSG00000250787	0.361889	0	0	0	ENSG00000250787	HMGN1P17
ENSG00000250788	0	0	0	0	ENSG00000250788	TUBB8P4
ENSG00000250794	0	0.281572	0.199425	0	ENSG00000250794	ALG1L12P
ENSG00000250796	0.554414	1.12967	1.50954	0.932332	ENSG00000250796	AC112484.3
ENSG00000250799	0.0342874	0.131977	0.182435	0.774441	ENSG00000250799	PRODH2
ENSG00000250803	4.98397	7.03626	11.9815	20.3803	ENSG00000250803	AC010255.3

ENSG00000250804	0	0	0	0	ENSG00000250804	AC073648.3
ENSG00000250807	0	2.04E-06	0	3.10E-09	ENSG00000250807	RP11-432M8.2
ENSG00000250808	0	0.372012	0.598409	0	ENSG00000250808	MTCO2P30
ENSG00000250812	0	0	0	0.118745	ENSG00000250812	AC021220.1
ENSG00000250813	0	0	0	0	ENSG00000250813	SERF1AP1
ENSG00000250815	0.215764	0.103607	0.0935566	0.465329	ENSG00000250815	AC105384.2
ENSG00000250816	0.13099	0	0	0	ENSG00000250816	DCAF13P2
ENSG00000250825	0.0882349	0	0	0	ENSG00000250825	PGAM1P12
ENSG00000250826	0	0	0.0937913	0	ENSG00000250826	HNRNPA3P13
ENSG00000250827	0.150273	0.299969	0.167877	0.730434	ENSG00000250827	MFSD4BP1
ENSG00000250828	0	0	0	0	ENSG00000250828	AC108078.3
ENSG00000250830	0	0	0	0	ENSG00000250830	MRPS35P2
ENSG00000250833	0	0	0	0.205342	ENSG00000250833	DNM1P17
ENSG00000250834	0	0	0	0	ENSG00000250834	KRT18P54
ENSG00000250835	4.6552	4.07379	0.93408	9.85228	ENSG00000250835	LSM3P4
ENSG00000250839	0	0	0	0	ENSG00000250839	AC018710.1
ENSG00000250844	0.0247832	0	0	0	ENSG00000250844	USP17L18
ENSG00000250847	0.5775	0	0.484479	0.583785	ENSG00000250847	AC010350.1
ENSG00000250848	0.696931	2.24749	2.85297	3.7972	ENSG00000250848	AC021087.2
ENSG00000250852	0.0192535	0	0	0.021843	ENSG00000250852	AC131180.1
ENSG00000250853	0.312608	1.34828	0.802414	1.95075	ENSG00000250853	RNF138P1
ENSG00000250857	0	0.0902001	0	0	ENSG00000250857	TRIM60P15
ENSG00000250858	0	0	0	0	ENSG00000250858	IGBP1P5
ENSG00000250859	0	0	0	0	ENSG00000250859	HNRNPKP1
ENSG00000250860	0.041552	0.538691	0.561235	0.833457	ENSG00000250860	AC093225.1
ENSG00000250862	0	0	0	0	ENSG00000250862	HMGB1P29
ENSG00000250867	0.0715679	0	0	0	ENSG00000250867	RP11-1415C14.2
ENSG00000250868	0	0.057919	0.153658	0.182434	ENSG00000250868	XKRY
ENSG00000250869	11.2834	24.8937	23.4188	37.6347	ENSG00000250869	AC087359.1
ENSG00000250878	1.91161	3.20371	1.89508	3.8135	ENSG00000250878	METTL21EP
ENSG00000250884	0	0	0	0	ENSG00000250884	OR7E85P
ENSG00000250886	0	0	0	0.185463	ENSG00000250886	AC010368.1
ENSG00000250890	0	1.26165	2.23312	1.33876	ENSG00000250890	AL117351.2
ENSG00000250892	0.196941	0.352475	0.890245	0.332637	ENSG00000250892	AC108475.1
ENSG00000250894	0	0	0	0	ENSG00000250894	PRAMEF31P
ENSG00000250895	0	0.155553	0.421261	0	ENSG00000250895	AC010409.2
ENSG00000250896	0.0867054	0	0	0	ENSG00000250896	RNPS1P1
ENSG00000250897	0	0	0	0	ENSG00000250897	HMGB3P15
ENSG00000250913	0	0	0	0	ENSG00000250913	USP17L23
ENSG00000250914	0	0	0	0	ENSG00000250914	AC139783.2
ENSG00000250918	0.609268	0.869733	0.527327	2.177	ENSG00000250918	RP11-497H16.4
ENSG00000250919	0	0	0	0	ENSG00000250919	UGT2B26P
ENSG00000250922	0	0	0	0	ENSG00000250922	ATP5EP1
ENSG00000250923	0	0	0	0	ENSG00000250923	AC023141.12
ENSG00000250927	0.975855	0.308705	0.167387	1.64523	ENSG00000250927	MESTP3
ENSG00000250928	0.121499	0	0.107239	0	ENSG00000250928	AC008629.3
ENSG00000250933	0	0.0618173	0.111729	0	ENSG00000250933	GAPDHP66
ENSG00000250939	0	0	0	0	ENSG00000250939	AC034198.1
ENSG00000250940	0	0	0	0	ENSG00000250940	AC116562.3
ENSG00000250942	0	0	0	0	ENSG00000250942	ENPP7P11
ENSG00000250946	0	0	0	0	ENSG00000250946	AP004833.1
ENSG00000250951	0.00012314	0	0	0	ENSG00000250951	USP9YP1
ENSG00000250956	0	0	1.2959	0	ENSG00000250956	AC011416.2
ENSG00000250959	6.99668	4.48894	7.19048	8.36768	ENSG00000250959	GLUD1P3

ENSG00000250962	0	0.0716252	0	0	ENSG00000250962	AC090568.1
ENSG00000250966	0	0.650799	0.19352	1.48115	ENSG00000250966	AC023886.2
ENSG00000250972	0	0	0	0	ENSG00000250972	CKS1BP5
ENSG00000250973	0	0	0	0	ENSG00000250973	KRTAP13-6P
ENSG00000250979	0	0.0845682	0.0966731	0.227055	ENSG00000250979	AC022905.1
ENSG00000250980	0.431589	1.67811	1.30296	2.44557	ENSG00000250980	AC113155.1
ENSG00000250982	0.661204	0	0	0.0691913	ENSG00000250982	GAPDHP35
ENSG00000250983	0	0	0	0	ENSG00000250983	AC022296.2
ENSG00000250984	0	0	0	0	ENSG00000250984	AC108082.1
ENSG00000250989	1.04629	4.53413	2.49355	0.751803	ENSG00000250989	AL390726.2
ENSG00000250995	0	0.487093	0.298569	0.214023	ENSG00000250995	AL391280.1
ENSG00000250997	0.16321	1.40967	10.1751	1.87728	ENSG00000250997	AC093853.1
ENSG00000251000	0.812983	1.14006	1.70885	4.71686	ENSG00000251000	AC008592.3
ENSG00000251001	0.137553	0.132352	0	0.147406	ENSG00000251001	AC026427.2
ENSG00000251005	0	0	0	0	ENSG00000251005	AC105758.1
ENSG00000251007	0.0715679	0	0	0	ENSG00000251007	RP11-1415C14.1
ENSG00000251008	0	0	0	0	ENSG00000251008	ORAOV1P1
ENSG00000251012	0	0	0	0	ENSG00000251012	AC083800.1
ENSG00000251013	0	0.592699	0.592747	0.602616	ENSG00000251013	GAPDHP62
ENSG00000251014	0	0.451035	0.614097	0.760285	ENSG00000251014	AC137549.1
ENSG00000251017	0	0	0.177145	0	ENSG00000251017	AC093677.1
ENSG00000251019	0	0	0	0.776877	ENSG00000251019	HIGD1AP13
ENSG00000251025	0.585777	2.19388	2.32016	3.96712	ENSG00000251025	NDUFB5P1
ENSG00000251032	0.0458125	0.133395	0.160088	0.125913	ENSG00000251032	CUL1P1
ENSG00000251035	0	0	0	0	ENSG00000251035	WBP1LP4
ENSG00000251038	1.1952	0.505946	0.914505	0.278665	ENSG00000251038	AC090958.1
ENSG00000251039	0	0	0	0	ENSG00000251039	IGKV2D-40
ENSG00000251046	2.66734	2.83459	1.97981	3.10078	ENSG00000251046	ZNF969P
ENSG00000251050	1.30614	1.23902	1.67894	0.68074	ENSG00000251050	AC112184.1
ENSG00000251051	0	0.0944722	0.402226	0.829514	ENSG00000251051	ELL2P2
ENSG00000251056	0	0.264293	0	0.140407	ENSG00000251056	ANKRD20A17P
ENSG00000251062	1.40116	0	0.913196	1.15427	ENSG00000251062	AC025459.1
ENSG00000251066	0	0.810923	1.22392	0.255867	ENSG00000251066	AC026700.1
ENSG00000251070	0	0	0	0	ENSG00000251070	BMS1P6
ENSG00000251073	0.253055	0.971365	0.438564	0.815487	ENSG00000251073	NUDT19P5
ENSG00000251074	0.0750229	0	0	0.0814638	ENSG00000251074	AC147055.3
ENSG00000251078	0	0	0	0.150339	ENSG00000251078	SLC25A5P9
ENSG00000251079	9.13759	15.6063	22.3603	18.4673	ENSG00000251079	BMS1P2
ENSG00000251087	0	0	0	0	ENSG00000251087	ALG1L3P
ENSG00000251090	0.068322	0.328535	0.181657	0.446113	ENSG00000251090	OR5AC4P
ENSG00000251099	2.30688	0	0	1.23332	ENSG00000251099	AC008967.1
ENSG00000251101	0.177209	0.173175	0.153834	0.383646	ENSG00000251101	AC147055.4
ENSG00000251102	0	0	0.0629039	0	ENSG00000251102	CTBP2P4
ENSG00000251105	0	0.578292	0	0	ENSG00000251105	AC110792.2
ENSG00000251106	0	0	0	0	ENSG00000251106	FAM206BP
ENSG00000251107	0	0	0	0	ENSG00000251107	PDCD5P2
ENSG00000251108	0	0	0	0	ENSG00000251108	YBX1P5
ENSG00000251111	0.130727	0.380743	0.793332	0.569353	ENSG00000251111	FCF1P8
ENSG00000251112	0	0	0	0	ENSG00000251112	AC106794.2
ENSG00000251113	0.0626964	0.120769	0.192647	0.137899	ENSG00000251113	AC092593.1
ENSG00000251118	0	0	0	0	ENSG00000251118	AC008549.3
ENSG00000251122	0	0	0.0652968	0.0815452	ENSG00000251122	NIFKP2
ENSG00000251123	0	0.107596	0	0	ENSG00000251123	AC084752.1
ENSG00000251135	1.98049	2.59965	3.09153	8.855	ENSG00000251135	AC008565.1

ENSG00000251137	0	0.0882903	0	0	ENSG00000251137	RPL7L1P7
ENSG00000251139	2.95097	2.09537	1.17873	0.879181	ENSG00000251139	AC084871.1
ENSG00000251142	0	0	0	0.31886	ENSG00000251142	AC025674.1
ENSG00000251147	0	0	0	0	ENSG00000251147	AC084871.2
ENSG00000251149	0	0	0	0.249331	ENSG00000251149	MTND5P5
ENSG00000251154	0	0.259941	0.397158	0.24516	ENSG00000251154	AC002456.2
ENSG00000251155	0	0	0	0	ENSG00000251155	SEPT14P4
ENSG00000251158	0	0	0	0	ENSG00000251158	AC131392.2
ENSG00000251159	0	0	0	0	ENSG00000251159	AC093852.1
ENSG00000251162	0.466948	2.1963	0.786881	1.42619	ENSG00000251162	AC074198.2
ENSG00000251163	0	0.120834	0.109112	0	ENSG00000251163	PRELID3BP4
ENSG00000251166	0	0	0	0	ENSG00000251166	OR7E163P
ENSG00000251172	0	0.28741	0	0.309162	ENSG00000251172	AC117470.1
ENSG00000251174	0	0	0	0	ENSG00000251174	TSEN2P1
ENSG00000251177	0.0735672	0.295126	0.241784	0.717591	ENSG00000251177	AC093829.1
ENSG00000251178	0.0679767	0.266007	0.518283	0.654215	ENSG00000251178	AC083906.4
ENSG00000251180	1.59932	6.54563	4.09388	2.51615	ENSG00000251180	CU459201.1
ENSG00000251184	0	0	0.472109	0	ENSG00000251184	AL672142.1
ENSG00000251188	0.365268	1.29583	0.805208	0.884098	ENSG00000251188	AC079140.3
ENSG00000251192	6.81395	14.5008	12.84	17.9324	ENSG00000251192	ZNF674
ENSG00000251193	0	0.349137	0.314633	0.727227	ENSG00000251193	AC112203.1
ENSG00000251195	0.385406	0.729783	1.71378	0.79713	ENSG00000251195	AC105417.1
ENSG00000251196	0.243	1.79074	1.42707	1.61181	ENSG00000251196	AC106760.1
ENSG00000251197	0	0.497056	0	0	ENSG00000251197	MICE
ENSG00000251201	4.79408	7.57671	3.61691	3.60688	ENSG00000251201	TMED7-TICAM2
ENSG00000251203	0	0.293245	0.441408	1.34154	ENSG00000251203	AC011726.1
ENSG00000251204	0.0349153	0.202205	0.214132	0.579232	ENSG00000251204	AC027313.1
ENSG00000251209	17.08	35.4458	35.2303	42.9377	ENSG00000251209	LINC00923
ENSG00000251211	0.307629	0.588787	0.201433	0.246888	ENSG00000251211	AC136632.2
ENSG00000251212	0	0	0	0	ENSG00000251212	MTND5P4
ENSG00000251215	0	0	0	0	ENSG00000251215	GOLGA5P1
ENSG00000251220	0	0	0.235192	0	ENSG00000251220	RFPL4AP3
ENSG00000251223	0.0754821	0.0363561	0	0.0413239	ENSG00000251223	MTCO1P9
ENSG00000251228	0	0	0	0	ENSG00000251228	AC104619.4
ENSG00000251229	4.03916	8.65745	8.64508	10.9338	ENSG00000251229	AL645924.2
ENSG00000251234	0.197278	0.85317	0.427997	0.319257	ENSG00000251234	PSMA2P2
ENSG00000251235	0	0	0	0	ENSG00000251235	SNRPCP2
ENSG00000251236	0	0	0	0	ENSG00000251236	AC021146.8
ENSG00000251237	0.375626	0	0	0.388439	ENSG00000251237	B3GNTL1P1
ENSG00000251243	1.65657	1.05654	0.317982	1.17361	ENSG00000251243	AC005178.1
ENSG00000251246	0	1.77E-07	1.12E-07	0	ENSG00000251246	AL691442.1
ENSG00000251247	9.02277	17.1156	20.5286	30.0993	ENSG00000251247	ZNF345
ENSG00000251252	0	0	0	0.122284	ENSG00000251252	MTND2P31
ENSG00000251253	0	0	0	0	ENSG00000251253	MTHFD2P4
ENSG00000251254	0	0	0.351165	2.43484	ENSG00000251254	GTF2F2P1
ENSG00000251258	0.119206	0.172316	0.129813	0.36797	ENSG00000251258	RFPL4B
ENSG00000251261	0	0.379588	0	0	ENSG00000251261	OR7H2P
ENSG00000251271	0	0	0.421596	0	ENSG00000251271	ALG1L7P
ENSG00000251275	0	0	0	0	ENSG00000251275	AC006335.2
ENSG00000251278	0.146003	0	0.126429	0.468769	ENSG00000251278	AC006499.5
ENSG00000251283	0	0	0	0	ENSG00000251283	LINC02272
ENSG00000251284	0.0509416	0.0981982	0	0.111463	ENSG00000251284	AC111000.5
ENSG00000251285	0	0	0	0	ENSG00000251285	AC097484.2
ENSG00000251286	0.0587981	0	0	0	ENSG00000251286	AC097522.1

ENSG00000251287	3.67612	10.0139	11.2033	11.8543	ENSG00000251287	ALG1L2
ENSG00000251288	0.43175	0.699157	0.545719	1.16215	ENSG00000251288	AC018797.3
ENSG00000251296	0	0	0.200814	0.24936	ENSG00000251296	AC006499.6
ENSG00000251297	0.0270024	0	0	0	ENSG00000251297	TUBB7P
ENSG00000251299	0	0.535236	0.934198	0.386138	ENSG00000251299	SLC25A15P3
ENSG00000251300	0	0.0787156	0.14223	0.443909	ENSG00000251300	AC104596.2
ENSG00000251303	0	3.00089	1.97917	3.50985	ENSG00000251303	CAB39P1
ENSG00000251304	0.000585709	0	0	0.00075577	ENSG00000251304	RP11-321E2.5
ENSG00000251306	0.665152	1.76093	0.764911	1.50678	ENSG00000251306	NDUFB4P2
ENSG00000251308	0	0	0	0	ENSG00000251308	MRPS33P3
ENSG00000251312	0	0	0	0	ENSG00000251312	AC004062.1
ENSG00000251313	0.00400839	0	0	0.255387	ENSG00000251313	AC073648.4
ENSG00000251317	0	0	0	0	ENSG00000251317	KLF17P2
ENSG00000251322	2.53369	2.87811	4.34548	4.24128	ENSG00000251322	SHANK3
ENSG00000251332	0.377861	0.633685	0.0817741	0.611247	ENSG00000251332	AC021106.2
ENSG00000251333	0	0	0	0	ENSG00000251333	RTN3P1
ENSG00000251334	0	0.334661	0	0	ENSG00000251334	AC020593.1
ENSG00000251338	0.162568	0.208631	0.0942799	0.413813	ENSG00000251338	AC006499.7
ENSG00000251340	0	0.0573166	0.0937603	0.115854	ENSG00000251340	MTCYBP35
ENSG00000251342	0	0	0	0	ENSG00000251342	AC026774.2
ENSG00000251345	0.0622575	0.179699	0.108265	0.135592	ENSG00000251345	AC093826.1
ENSG00000251347	0.0258753	0.224465	0.157832	0.343328	ENSG00000251347	IRF5P1
ENSG00000251348	0.134515	0.194408	0.14645	1.73298	ENSG00000251348	HSPD1P11
ENSG00000251349	2.68E-07	6.83E-06	1.80E-07	1.86329	ENSG00000251349	MSANTD3-TMEFF1
ENSG00000251352	0	0	0.0822199	0	ENSG00000251352	AC122714.2
ENSG00000251353	0	0	0	0	ENSG00000251353	MTND3P5
ENSG00000251354	0	1.44879	0.436288	2.08973	ENSG00000251354	AC024451.1
ENSG00000251356	0.110788	0.417019	0.188826	0.117445	ENSG00000251356	RAB5CP2
ENSG00000251357	0	0	0	0	ENSG00000251357	AP000350.4
ENSG00000251360	0	0.284788	0	0	ENSG00000251360	KHDC1P1
ENSG00000251366	0	0	0	0.926	ENSG00000251366	DBIP2
ENSG00000251368	0	0	0	0	ENSG00000251368	AC016632.1
ENSG00000251369	6.57421	6.09237	7.92562	5.41196	ENSG00000251369	ZNF550
ENSG00000251373	0	0	0	0	ENSG00000251373	AC092593.2
ENSG00000251374	3.51787	3.31026	5.38935	0	ENSG00000251374	AC010598.1
ENSG00000251378	0.183399	0	0.175262	0	ENSG00000251378	AC096582.2
ENSG00000251380	0	0	0	0	ENSG00000251380	DCANP1
ENSG00000251385	0.0535249	0	0.139682	0	ENSG00000251385	MTCYBP16
ENSG00000251389	0.106314	0.236106	0.304494	0.3441	ENSG00000251389	YTHDF1P1
ENSG00000251394	0.0151711	0.0536059	0.0442655	0.0942871	ENSG00000251394	OR12D3
ENSG00000251395	0.260423	0	0	0	ENSG00000251395	FTH1P9
ENSG00000251400	0.127203	0.163461	0.0362284	0.184193	ENSG00000251400	ALDH7A1P1
ENSG00000251401	12.733	33.7339	11.5976	10.0988	ENSG00000251401	AC093729.1
ENSG00000251402	0	0.328775	0.237471	0.161496	ENSG00000251402	FAM90A25P
ENSG00000251407	0	0	0	0	ENSG00000251407	MTND1P22
ENSG00000251411	0.277643	0.213125	0.333697	0.599828	ENSG00000251411	AC093827.3
ENSG00000251418	0	0	0	0	ENSG00000251418	ASS1P8
ENSG00000251419	0	0	0	0.0841048	ENSG00000251419	AC108120.3
ENSG00000251424	0	0	0	0	ENSG00000251424	AC021146.9
ENSG00000251427	0	0	0	0	ENSG00000251427	AC111000.6
ENSG00000251429	1.57911	3.13766	3.29576	4.13313	ENSG00000251429	AC098679.3
ENSG00000251430	0	0	0	0	ENSG00000251430	MTCO3P27
ENSG00000251431	0.103648	0.148175	0	0.0544578	ENSG00000251431	AC245884.7
ENSG00000251433	0	0	0.173534	0	ENSG00000251433	CCNHP1

ENSG00000251435	0	0	0	0.0599205	ENSG00000251435	C1GALT1P2
ENSG00000251436	0.0328614	0.0316632	0.0330438	0.0720408	ENSG00000251436	NUP58P1
ENSG00000251437	0	0	0	0	ENSG00000251437	NDUFS5P4
ENSG00000251439	0	0	0	0	ENSG00000251439	AC006070.1
ENSG00000251440	0	0	0	0	ENSG00000251440	STMN1P2
ENSG00000251441	0.133242	0.770667	0.598952	0.558516	ENSG00000251441	RTEL1P1
ENSG00000251447	0.202152	0	0	0	ENSG00000251447	AC107027.2
ENSG00000251449	0	0	0	0	ENSG00000251449	MTND1P19
ENSG00000251451	1.57705	4.36275	6.25877	3.0708	ENSG00000251451	GTF2IP9
ENSG00000251452	0	0	0	0.187898	ENSG00000251452	AC109811.2
ENSG00000251453	0	0.29964	0	0	ENSG00000251453	HAUS1P1
ENSG00000251463	0.175281	0.0843861	0.191841	0.191818	ENSG00000251463	FKBP4P1
ENSG00000251464	0	0	0	0	ENSG00000251464	RPL7L1P13
ENSG00000251467	0.464709	0.993355	0.574633	1.85369	ENSG00000251467	AC020893.2
ENSG00000251468	0.0431388	0.040145	0.108797	0.137617	ENSG00000251468	AC135352.1
ENSG00000251470	0	0	0	0	ENSG00000251470	ASNSP4
ENSG00000251473	0.0543596	0	0	0.0592999	ENSG00000251473	AC004069.2
ENSG00000251474	11.7073	22.0161	30.7599	29.0693	ENSG00000251474	RPL32P3
ENSG00000251476	0	0.298219	0.403918	1.16342	ENSG00000251476	MTCO1P31
ENSG00000251477	0	0	0	0	ENSG00000251477	AC114322.1
ENSG00000251478	0	0	0.161044	0.0405363	ENSG00000251478	AC008817.1
ENSG00000251482	0.264299	0	0	0	ENSG00000251482	AKIRIN2P1
ENSG00000251483	0	0	0	0	ENSG00000251483	LYPLA1P2
ENSG00000251484	1.21393	1.67271	2.56177	1.2414	ENSG00000251484	AL356488.1
ENSG00000251485	1.19407	1.61081	2.55711	1.153	ENSG00000251485	AC068134.3
ENSG00000251489	0	0	0	0	ENSG00000251489	AC108941.1
ENSG00000251491	0	0	0.0674134	0	ENSG00000251491	OR7E28P
ENSG00000251492	0	0.209255	0	0	ENSG00000251492	AC104136.1
ENSG00000251493	1.54745	9.29078	3.77904	2.46225	ENSG00000251493	FOXD1
ENSG00000251495	1.66857	1.88682	1.9615	2.36249	ENSG00000251495	PPIAP11
ENSG00000251498	0	0.182372	0	0.102605	ENSG00000251498	AC021146.10
ENSG00000251501	0	0	0	0	ENSG00000251501	AC114774.1
ENSG00000251503	0	0.12654	0.0754996	0.167039	ENSG00000251503	CENPS-CORT
ENSG00000251508	1.14382	0.470289	0.759415	1.6208	ENSG00000251508	AL133380.1
ENSG00000251515	0	0.049821	0	0	ENSG00000251515	CCDC11P1
ENSG00000251516	0.538248	3.52177	3.28683	2.70905	ENSG00000251516	AC098583.2
ENSG00000251520	1.23482	4.3015	4.31324	3.05316	ENSG00000251520	AL162431.3
ENSG00000251521	0.304051	0.0730898	0.789534	0.391637	ENSG00000251521	IMPA1P1
ENSG00000251525	0	0	0	0	ENSG00000251525	TCP11X3P
ENSG00000251529	0	0	0.135028	0.333374	ENSG00000251529	AC021146.11
ENSG00000251535	0.490444	0.134444	0.606778	0.150111	ENSG00000251535	AC079140.4
ENSG00000251537	1.1091	1.37882	1.235	1.52088	ENSG00000251537	AC005324.3
ENSG00000251539	0	0	0	0	ENSG00000251539	SNX18P24
ENSG00000251544	0	0.038749	0.0700519	0.0880559	ENSG00000251544	MTND5P12
ENSG00000251545	0	0	0	0	ENSG00000251545	AC136628.2
ENSG00000251546	0	0	0	0	ENSG00000251546	IGKV1D-39
ENSG00000251547	0	0	0	0	ENSG00000251547	OR12D1
ENSG00000251548	0	0	0	0	ENSG00000251548	AC106760.2
ENSG00000251549	0	0	0	0	ENSG00000251549	AC091965.3
ENSG00000251550	0	0.634378	0.585914	1.04341	ENSG00000251550	AC091133.4
ENSG00000251552	0.367536	1.0853	0.818801	1.20194	ENSG00000251552	COQ10BP2
ENSG00000251553	0	0.0422025	0.193861	0.265365	ENSG00000251553	DDX18P4
ENSG00000251557	0.244951	1.13238	1.05593	1.16941	ENSG00000251557	HNRNPKP3
ENSG00000251563	0.556576	0.99204	1.22808	1.83455	ENSG00000251563	IARS2P1

ENSG00000251564	0	0	1.45843	0	ENSG00000251564	AC012441.1
ENSG00000251566	0.136001	0.52692	1.07122	0	ENSG00000251566	HMGB1P35
ENSG00000251568	0.0543596	0.470893	0.0951994	0.296499	ENSG00000251568	ALG3P1
ENSG00000251569	0	0.0827714	0	0	ENSG00000251569	AC093899.2
ENSG00000251571	0.0283046	0.0550186	0.0740671	0.0934197	ENSG00000251571	DDX3P3
ENSG00000251572	0	0	0.121289	0	ENSG00000251572	AF213884.2
ENSG00000251578	0	0	0	0	ENSG00000251578	TRBV21-1
ENSG00000251579	0.42731	0.956332	1.48008	1.83013	ENSG00000251579	AC055733.3
ENSG00000251581	3.35204	1.75446	0.0958732	1.89217	ENSG00000251581	MICE
ENSG00000251583	0	0	0	0	ENSG00000251583	AC008427.1
ENSG00000251585	0.928765	1.12465	1.58315	1.74758	ENSG00000251585	AC026444.1
ENSG00000251587	0.0623608	0	0	0.0678765	ENSG00000251587	LDHAP1
ENSG00000251588	0	0	0.0169484	0.0427513	ENSG00000251588	AC125336.1
ENSG00000251590	0	0.147893	0.20043	0.335321	ENSG00000251590	NIFKP7
ENSG00000251591	0	0	0	0	ENSG00000251591	AC016612.1
ENSG00000251593	0.0339855	0.0325613	0	0	ENSG00000251593	MSNP1
ENSG00000251595	2.00188	2.45461	3.62439	1.74328	ENSG00000251595	ABCA11P
ENSG00000251596	0.122479	0.0942355	0.170553	0.457154	ENSG00000251596	HADHAP1
ENSG00000251597	0	0	0	0	ENSG00000251597	RPL37P25
ENSG00000251605	0.417675	1.22833	1.82247	2.98729	ENSG00000251605	AC104108.1
ENSG00000251606	0.67535	2.86497	1.7134	2.76037	ENSG00000251606	CTD-2215E18.1
ENSG00000251608	0	0	0	0	ENSG00000251608	OR12D1
ENSG00000251609	0.372769	0.81707	0.718223	1.92133	ENSG00000251609	SETP12
ENSG00000251610	0	0	0	0	ENSG00000251610	AC083906.5
ENSG00000251614	0.347079	0.884604	0.723051	1.27549	ENSG00000251614	HSPA8P19
ENSG00000251617	0.430889	0	0	0	ENSG00000251617	RP11-382F24.1
ENSG00000251618	0	0	0	0	ENSG00000251618	AC007322.4
ENSG00000251624	0.478777	0	0	0	ENSG00000251624	UNC93B7
ENSG00000251627	0	0	0.0605631	0	ENSG00000251627	AC010395.2
ENSG00000251630	0	3.13009	3.23885	4.0903	ENSG00000251630	AC119751.6
ENSG00000251633	0	0	0	0	ENSG00000251633	GYG1P1
ENSG00000251634	0.360197	0	0	0	ENSG00000251634	AC145138.1
ENSG00000251638	0	0	0	0	ENSG00000251638	AC006390.1
ENSG00000251639	0	0	0.0432961	0	ENSG00000251639	AC092535.2
ENSG00000251643	0	0	0	0.106569	ENSG00000251643	AC093763.2
ENSG00000251644	0	0	0	0	ENSG00000251644	HPRT1P1
ENSG00000251647	0	0	0	0.233138	ENSG00000251647	AC114781.4
ENSG00000251648	0	1.03329	0	1.15841	ENSG00000251648	AC008958.1
ENSG00000251655	0.966185	0	0.526429	1.43154	ENSG00000251655	PRB1
ENSG00000251656	0	0	0	0.183127	ENSG00000251656	PRELID3BP5
ENSG00000251663	0	0	0	0	ENSG00000251663	SUMO2P5
ENSG00000251664	0.312453	0.162931	0.105318	0.0865265	ENSG00000251664	PCDHA12
ENSG00000251667	0.425289	0.556688	0.860978	1.20638	ENSG00000251667	BRCC3P1
ENSG00000251668	0	0	0	0	ENSG00000251668	AC113404.2
ENSG00000251669	1.62853	3.90088	6.09192	1.91746	ENSG00000251669	FAM86EP
ENSG00000251682	1.20116	3.57329	2.08185	6.58824	ENSG00000251682	AC122718.2
ENSG00000251685	0	0.0375548	0.227006	0.206812	ENSG00000251685	UGT2B27P
ENSG00000251686	0	0	0	0	ENSG00000251686	OR10J8P
ENSG00000251689	1.21075	1.44437	0.319386	1.07726	ENSG00000251689	AC079140.5
ENSG00000251691	0	0.0208363	0	0	ENSG00000251691	AC114786.3
ENSG00000251692	0.0541892	0.0521578	0	0.0899164	ENSG00000251692	PTX4
ENSG00000251694	0	0	0	0	ENSG00000251694	USP17L9P
ENSG00000251695	0.369356	0.618789	0.595226	0.894225	ENSG00000251695	AC124890.1
ENSG00000253107	0	0.158707	0.189898	0.364975	ENSG00000253107	AC090819.1

ENSG00000253109	0	0.150003	0.136424	0	ENSG00000253109	RPL12P22
ENSG00000253110	0	0.0913527	0.165039	0.102789	ENSG00000253110	AC011410.1
ENSG00000253114	0	0.192106	0	0.296007	ENSG00000253114	AC090151.1
ENSG00000253117	0	0	0	0	ENSG00000253117	OC90
ENSG00000253118	0	0	0	0	ENSG00000253118	AC022695.1
ENSG00000253119	0.189431	0.43263	0.0549457	0.280138	ENSG00000253119	HNRNPA3P7
ENSG00000253120	0	0	0	0	ENSG00000253120	IGLV2-34
ENSG00000253124	0	0	0	0	ENSG00000253124	TRAPPC2P2
ENSG00000253126	0	0	0	0	ENSG00000253126	IGLVI-56
ENSG00000253127	0	0	0	0	ENSG00000253127	IGKV2D-36
ENSG00000253128	0	0	0	0	ENSG00000253128	IGHV4-80
ENSG00000253131	0	0	0	0	ENSG00000253131	IGHV7-56
ENSG00000253132	0	0	0	0	ENSG00000253132	IGHV3-62
ENSG00000253135	0	0	0	0	ENSG00000253135	AC103724.2
ENSG00000253137	0.0585987	0.338338	0.203849	0.255455	ENSG00000253137	AC092709.1
ENSG00000253144	0	0.51017	1.26999	0	ENSG00000253144	AC104117.2
ENSG00000253146	0.28506	0.475132	0.109638	0.305044	ENSG00000253146	CIR1P1
ENSG00000253148	0	0.214058	0.0552877	0.139178	ENSG00000253148	RGS21
ENSG00000253149	0	0	0	0	ENSG00000253149	AC245166.1
ENSG00000253152	0	0	0	0	ENSG00000253152	IGLV3-17
ENSG00000253153	0.164554	1.89366	1.41892	0.693114	ENSG00000253153	AP001207.1
ENSG00000253155	0	0	0	0.19898	ENSG00000253155	AC008676.3
ENSG00000253156	0	0	0.723139	0.881184	ENSG00000253156	AC022360.1
ENSG00000253158	0	0	0	0	ENSG00000253158	IGKV3-31
ENSG00000253159	3.24067	2.98867	5.02151	7.749	ENSG00000253159	PCDHGA12
ENSG00000253160	0	0	0	0	ENSG00000253160	AC105185.1
ENSG00000253166	0	3.19701	1.15142	0	ENSG00000253166	AC131281.1
ENSG00000253169	0	0	0	0	ENSG00000253169	IGHVII-65-1
ENSG00000253173	0	0	0	0.243078	ENSG00000253173	AC084251.1
ENSG00000253175	0	0	0	0.751037	ENSG00000253175	AC023632.1
ENSG00000253176	0	0	0	0	ENSG00000253176	AC104997.1
ENSG00000253178	0	0	0	0	ENSG00000253178	AC022559.1
ENSG00000253179	0	0	0	0	ENSG00000253179	CALCP
ENSG00000253180	0.946965	1.63396	0.500751	1.81235	ENSG00000253180	AC104986.1
ENSG00000253183	1.52399	2.29272	3.10384	5.70295	ENSG00000253183	AC005531.1
ENSG00000253186	0	0.997622	0	0.364036	ENSG00000253186	AC022616.2
ENSG00000253188	0	0	0	0	ENSG00000253188	TRBV6-7
ENSG00000253191	0	0	0	0	ENSG00000253191	IGKV1D-32
ENSG00000253193	0.0774896	0	0.184282	0.0560641	ENSG00000253193	FCGR1C
ENSG00000253195	0	0	0	0	ENSG00000253195	AC134698.2
ENSG00000253198	0	0.879534	0	0	ENSG00000253198	AC139365.1
ENSG00000253202	0	0.456089	0	2.46488	ENSG00000253202	IGKV3-25
ENSG00000253203	6.97921	17.1447	13.9002	23.3416	ENSG00000253203	GUSBP3
ENSG00000253204	0	0	0	0	ENSG00000253204	AC090281.1
ENSG00000253206	1.38842	3.05054	6.43052	8.72043	ENSG00000253206	AC090155.1
ENSG00000253207	0.473404	0.681151	0.551246	2.2221	ENSG00000253207	AC103993.1
ENSG00000253208	0	0	0.141784	0.0885074	ENSG00000253208	AC015743.1
ENSG00000253209	0	0	0	0	ENSG00000253209	IGHV3-65
ENSG00000253213	0	0.439923	0.378787	0.364273	ENSG00000253213	AC010306.1
ENSG00000253216	0	1.39809	0.618958	0.747674	ENSG00000253216	AC022790.1
ENSG00000253218	0.120325	0.579961	0.994033	1.31475	ENSG00000253218	KLF3P1
ENSG00000253219	0.0464503	0.0447486	0.0404052	0.0507347	ENSG00000253219	KRT18P41
ENSG00000253223	0.027757	0.0804102	0.0242192	0.091884	ENSG00000253223	AC110998.1

ENSG00000253224	0	0	0	0	ENSG00000253224	PGAM5P1
ENSG00000253225	0	0	0	0	ENSG00000253225	AC103833.1
ENSG00000253226	0	0	0.179008	0	ENSG00000253226	HAUS1P3
ENSG00000253228	0	0	0	0	ENSG00000253228	NRBF2P4
ENSG00000253229	0	0	0	0	ENSG00000253229	HIGD1AP6
ENSG00000253231	0	0	0	0	ENSG00000253231	COX6CP8
ENSG00000253232	0	0	0	0	ENSG00000253232	AC091144.1
ENSG00000253233	0	0	0	0	ENSG00000253233	AP005902.1
ENSG00000253234	0.406903	0	0	0.419162	ENSG00000253234	IGLV2-5
ENSG00000253237	0	0	0	0	ENSG00000253237	AC034114.1
ENSG00000253239	0	0	0	0	ENSG00000253239	IGLVI-70
ENSG00000253240	0	0	0	0.112631	ENSG00000253240	IGHV3-36
ENSG00000253241	0	0	0	0	ENSG00000253241	IGHV3-50
ENSG00000253242	0	0	0	0	ENSG00000253242	IGLVIV-64
ENSG00000253245	0.0668316	0.194219	0.290379	0.961848	ENSG00000253245	MTND1P36
ENSG00000253247	0.180945	0	0	0	ENSG00000253247	IGHV3-76
ENSG00000253250	1.9949	4.35973	1.7607	2.52226	ENSG00000253250	C8orf88
ENSG00000253251	2.88276	3.28047	2.59366	2.34203	ENSG00000253251	AC008560.1
ENSG00000253257	0	1.90765	0	5.8323	ENSG00000253257	MTND4P7
ENSG00000253261	0	0	0.242239	0	ENSG00000253261	AC008410.1
ENSG00000253262	0	0	0	0	ENSG00000253262	AC019176.1
ENSG00000253265	0	0.515702	0	0	ENSG00000253265	IGKV2-14
ENSG00000253271	0	0	0	0	ENSG00000253271	AC027419.1
ENSG00000253273	2.91088	4.08066	3.82804	7.19848	ENSG00000253273	AC022826.1
ENSG00000253274	0	0	0	0	ENSG00000253274	IGHV1-67
ENSG00000253276	6.0833	6.143	5.11772	4.90394	ENSG00000253276	CCDC71L
ENSG00000253278	0	0	0	0	ENSG00000253278	IGKV2-10
ENSG00000253283	0.376862	0	0.217699	0.404901	ENSG00000253283	AC091175.1
ENSG00000253290	0	1.50954	0.65279	1.12416	ENSG00000253290	AC069113.1
ENSG00000253291	0	0	0	0	ENSG00000253291	TRBV7-7
ENSG00000253292	0	0.29535	0.0667116	0.0833616	ENSG00000253292	MIOXP1
ENSG00000253293	2.92398	5.53424	9.02107	5.83049	ENSG00000253293	HOXA10
ENSG00000253294	0	0	0	0	ENSG00000253294	IGHVII-40-1
ENSG00000253299	0	0	0	0	ENSG00000253299	AC025647.1
ENSG00000253303	0	0	0	0	ENSG00000253303	IGHVIII-82
ENSG00000253304	1.06444	4.7785	0.865916	3.51111	ENSG00000253304	TMEM200B
ENSG00000253305	1.29435	0.810933	1.3293	1.6134	ENSG00000253305	PCDHGB6
ENSG00000253309	3.6043	3.92721	3.44503	4.18327	ENSG00000253309	SERPINE3
ENSG00000253310	0	0	0	0	ENSG00000253310	IGHVIII-76-1
ENSG00000253312	0	0	1.23877	0	ENSG00000253312	AC022616.3
ENSG00000253313	5.58752	6.14042	4.48077	3.32196	ENSG00000253313	C1orf210
ENSG00000253318	0.056983	0.0550961	0.0496465	0.125044	ENSG00000253318	TMCC1P1
ENSG00000253319	0	0.633378	0	0	ENSG00000253319	AC134698.3
ENSG00000253320	8.81833	19.6827	19.9068	25.8425	ENSG00000253320	AZIN1-AS1
ENSG00000253325	0	0	0	0	ENSG00000253325	IGHV7-34-1
ENSG00000253326	0.660768	0.295094	0.818181	0.5562	ENSG00000253326	AL606534.5
ENSG00000253328	1.84096	3.28122	2.37819	3.91103	ENSG00000253328	SUMO2P19
ENSG00000253329	0	0	0	0	ENSG00000253329	IGLV3-30
ENSG00000253330	0.717036	1.60561	1.19707	2.52681	ENSG00000253330	AC024451.2
ENSG00000253332	0	0	0	0	ENSG00000253332	AP005902.2
ENSG00000253333	0	0	0	0	ENSG00000253333	AC146944.3
ENSG00000253336	0.0782777	0.0502568	0.182073	0.143511	ENSG00000253336	AC018992.1
ENSG00000253338	0	0	0	0	ENSG00000253338	IGLV3-29
ENSG00000253340	0	0	0	0.148553	ENSG00000253340	AC087272.1

ENSG00000253341	0	0	0	0	ENSG00000253341	AC115837.1
ENSG00000253345	0	0	0	0	ENSG00000253345	IGHVII-22-1
ENSG00000253346	0	0	0	0	ENSG00000253346	AC109329.1
ENSG00000253349	0	0	0	0.485812	ENSG00000253349	COX6B1P6
ENSG00000253350	0.954807	1.96043	1.72948	3.24521	ENSG00000253350	RP11-127H5.1
ENSG00000253359	0	0	0	0	ENSG00000253359	IGHV3-37
ENSG00000253362	0.231241	0.662479	0.618763	1.22057	ENSG00000253362	AC012400.1
ENSG00000253365	0	0	0	0	ENSG00000253365	IGKV1D-22
ENSG00000253366	0.251553	0.746617	0.775822	0.912713	ENSG00000253366	AC139272.1
ENSG00000253367	0	0.250391	0	0	ENSG00000253367	IGHVIII-25-1
ENSG00000253368	70.9356	35.1482	27.2513	39.108	ENSG00000253368	TRNP1
ENSG00000253370	0	0	0	2.86255	ENSG00000253370	AC027308.1
ENSG00000253379	0.41603	0.930875	1.11468	1.94167	ENSG00000253379	AC099805.1
ENSG00000253382	0	0	0.067913	0	ENSG00000253382	POU5F1P2
ENSG00000253383	0	0.626885	0.283065	0.344184	ENSG00000253383	AC100784.1
ENSG00000253384	0.752504	1.53202	1.84038	2.03428	ENSG00000253384	AC124242.2
ENSG00000253386	0	0	0	0	ENSG00000253386	IGHVII-49-1
ENSG00000253387	0	0	0	0	ENSG00000253387	IGHVIII-5-1
ENSG00000253391	0	0	0	0	ENSG00000253391	AC100870.1
ENSG00000253393	0.848298	0.400474	0.749414	0.871344	ENSG00000253393	RANP9
ENSG00000253401	0	0	0	0.225468	ENSG00000253401	VTA1P2
ENSG00000253409	0	0	0	0	ENSG00000253409	TRBV7-4
ENSG00000253410	81.5375	45.1075	6.72966	36.7053	ENSG00000253410	AC068228.3
ENSG00000253412	0	0	0	0	ENSG00000253412	IGHVIII-13-1
ENSG00000253413	0	0	0	0	ENSG00000253413	AC107934.1
ENSG00000253415	0	0	0	0	ENSG00000253415	AC016877.2
ENSG00000253418	0.183686	0.083584	0.376987	0.109673	ENSG00000253418	SNX18P27
ENSG00000253421	0	0	0	0	ENSG00000253421	ZNHIT1P1
ENSG00000253422	0	0	0.0901141	0.110517	ENSG00000253422	AC008677.3
ENSG00000253423	0	0	0	0	ENSG00000253423	AC090132.1
ENSG00000253425	0	0	0	0	ENSG00000253425	HSPA8P13
ENSG00000253426	2.44077	5.97154	6.28221	8.42462	ENSG00000253426	AC022784.3
ENSG00000253429	0.732875	1.38811	0.312793	0.37956	ENSG00000253429	AP005660.1
ENSG00000253431	0	0	0	0	ENSG00000253431	SRPK2P
ENSG00000253435	0	0.266808	0	0	ENSG00000253435	IGKV2-4
ENSG00000253439	0.267523	0.386522	0.394511	0.86657	ENSG00000253439	CDC42P5
ENSG00000253440	0	0	0	0	ENSG00000253440	IGHV3-33-2
ENSG00000253441	0	0	0	0	ENSG00000253441	IGHV3-25
ENSG00000253448	0	0	0	0	ENSG00000253448	IGLV3-6
ENSG00000253451	0	0.324658	0.292932	0	ENSG00000253451	IGLV2-28
ENSG00000253454	0.557911	1.32576	1.6721	2.59272	ENSG00000253454	NDUFA5P2
ENSG00000253457	0.765666	1.47262	0.907232	1.13499	ENSG00000253457	SMIM18
ENSG00000253458	0	0	0	0	ENSG00000253458	IGHVII-15-1
ENSG00000253459	1.75942	1.86129	2.30587	2.65733	ENSG00000253459	AL139099.1
ENSG00000253460	0	0	0	0	ENSG00000253460	IGKV2OR22-3
ENSG00000253461	0	0	0	0	ENSG00000253461	IGKV1-35
ENSG00000253462	0	0.233448	0	0	ENSG00000253462	IGHVIII-26-1
ENSG00000253463	0.496468	0.476994	0.215112	0.666974	ENSG00000253463	HMGB1P19
ENSG00000253464	0	0	0	0	ENSG00000253464	IGHV3-29
ENSG00000253465	0.141779	0	0	0	ENSG00000253465	IGHVIV-44-1
ENSG00000253467	0	0	0	0	ENSG00000253467	IGHV7-40
ENSG00000253468	0.242455	0	0.210871	0.398292	ENSG00000253468	AP003355.1
ENSG00000253472	0	0	0	0	ENSG00000253472	AC034205.1
ENSG00000253480	0	0	0	0	ENSG00000253480	AC122713.1

ENSG00000253481	0	0	0.348933	0	ENSG00000253481	IGKV1OR22-1
ENSG00000253482	0	0	0	0	ENSG00000253482	IGHVII-26-2
ENSG00000253483	0.435715	0.285177	0.39949	1.39928	ENSG00000253483	AC104561.2
ENSG00000253485	0.246456	0.188948	0.505933	0.731085	ENSG00000253485	PCDHGA5
ENSG00000253486	1.02428	0.914223	0.844637	2.64197	ENSG00000253486	RP11-726G23.7
ENSG00000253487	0	0	0	0	ENSG00000253487	IGKV2-36
ENSG00000253488	0.111953	0.738525	0.320326	0.78712	ENSG00000253488	FAM60DP
ENSG00000253491	0	0	0	0	ENSG00000253491	IGHVII-30-1
ENSG00000253492	0	0	0.845031	0	ENSG00000253492	CDH12P3
ENSG00000253493	0	0	0	0	ENSG00000253493	AC087808.1
ENSG00000253495	0	0	0	0.338461	ENSG00000253495	CYCSP23
ENSG00000253497	0	0	0	0	ENSG00000253497	IGKV1-13
ENSG00000253499	0	0	0	0	ENSG00000253499	AC025881.1
ENSG00000253501	0	0	0	0	ENSG00000253501	IGKV3D-34
ENSG00000253502	0	0	0	0	ENSG00000253502	ATP6V1G1P2
ENSG00000253504	0	0.10356	0	0	ENSG00000253504	MTCYBP19
ENSG00000253506	0	0	0	0	ENSG00000253506	NACA2
ENSG00000253512	0	0	0	0	ENSG00000253512	AC008562.1
ENSG00000253516	0.184063	0.35218	0.323445	0.978005	ENSG00000253516	HMGB1P41
ENSG00000253517	0	0.0262185	0.0711883	0.179191	ENSG00000253517	XRCC6P4
ENSG00000253520	0	0.353248	0	0	ENSG00000253520	AC136628.3
ENSG00000253525	0.0397673	0.261276	0.17312	0.342961	ENSG00000253525	AC104966.1
ENSG00000253528	0	1.49847	1.79097	1.32972	ENSG00000253528	AC087752.2
ENSG00000253534	0.139575	0	0	0.146159	ENSG00000253534	TRBV6-8
ENSG00000253536	0.066712	0.585986	0.859493	0.644447	ENSG00000253536	AC138832.1
ENSG00000253537	0.724679	0.317057	1.35427	0.961118	ENSG00000253537	PCDHGA7
ENSG00000253540	2.79506	2.68929	13.1155	3.67187	ENSG00000253540	FAM86HP
ENSG00000253541	0	0	0	0.119853	ENSG00000253541	SEPT10P1
ENSG00000253542	0.236125	0.220459	0.908547	0.594448	ENSG00000253542	SDR16C6P
ENSG00000253543	1.25048	0.348799	0.893785	1.92838	ENSG00000253543	AC083923.1
ENSG00000253544	0.524659	0.0810153	0.508032	0.731664	ENSG00000253544	C1GALT1P3
ENSG00000253545	0	0	0	0	ENSG00000253545	IGHV3-52
ENSG00000253546	0	0.650743	0	1.39404	ENSG00000253546	IGLVVI-22-1
ENSG00000253547	0.0877449	0.0422496	0	0.0959434	ENSG00000253547	AP001858.1
ENSG00000253548	0	0	0	0	ENSG00000253548	PYDC2
ENSG00000253550	1.80272	2.72362	2.27272	2.00186	ENSG00000253550	AC016065.2
ENSG00000253555	0.0418445	0	0.145589	0.232642	ENSG00000253555	AC011978.1
ENSG00000253556	0.124961	0	0.145179	0.275251	ENSG00000253556	MTCO1P4
ENSG00000253558	1.0709	2.25909	1.47819	3.50485	ENSG00000253558	AC024568.1
ENSG00000253560	0	0	0	0	ENSG00000253560	AC013643.1
ENSG00000253564	0.222177	0.495587	0.33373	0.738152	ENSG00000253564	AC100823.2
ENSG00000253568	0	0	0	0	ENSG00000253568	AC090572.1
ENSG00000253569	0	0	0.0770618	0	ENSG00000253569	VENTXP5
ENSG00000253570	0	0	0	0.207767	ENSG00000253570	AC069120.2
ENSG00000253571	0.124068	0.11937	0.053939	0.202669	ENSG00000253571	AC087369.1
ENSG00000253578	0	0	0	0	ENSG00000253578	IGKV1-22
ENSG00000253579	0.891882	0.841373	1.5063	0.456727	ENSG00000253579	SUMO2P16
ENSG00000253580	0	0.446954	0.17322	1.15288	ENSG00000253580	TRMT10BP1
ENSG00000253581	0	0	0	0	ENSG00000253581	AC105031.1
ENSG00000253587	0	0	0	0	ENSG00000253587	IGHV3-30-2
ENSG00000253588	0	0	0	0	ENSG00000253588	IGHVIII-44
ENSG00000253590	0	0	0	0	ENSG00000253590	IGLV3-13
ENSG00000253592	0	0	0	0	ENSG00000253592	IGKV2-38
ENSG00000253597	0	0	0	0	ENSG00000253597	IGHVII-43-1

ENSG00000253598	0.474856	1.8558	2.54998	0.622237	ENSG00000253598	SLC10A5
ENSG00000253600	0	0	0	0.190797	ENSG00000253600	AC008446.1
ENSG00000253605	0	0	0	0	ENSG00000253605	HNRNPA1P38
ENSG00000253606	0	0.0624046	0	0.0360508	ENSG00000253606	AFG3L2P1
ENSG00000253610	0	0	0	0	ENSG00000253610	AP006245.1
ENSG00000253611	0	0.0722457	0.0652811	0	ENSG00000253611	VN1R46P
ENSG00000253612	0	0	0	0.181354	ENSG00000253612	WBP1LP3
ENSG00000253615	0	0	0	0	ENSG00000253615	AC069113.3
ENSG00000253617	0	0	0	0	ENSG00000253617	AC109479.2
ENSG00000253620	0	2.51282	6.49327	0	ENSG00000253620	AC144568.1
ENSG00000253621	0	0.630338	0.37961	0.464783	ENSG00000253621	RPSAP74
ENSG00000253623	1.25932	4.14201	5.1733	9.10503	ENSG00000253623	AC009879.1
ENSG00000253625	0	0	0	0	ENSG00000253625	IGKV2-23
ENSG00000253626	2.24322	5.7174	7.62875	6.43793	ENSG00000253626	EIF5AL1
ENSG00000253630	1.49109	1.39809	0	0	ENSG00000253630	AC026407.1
ENSG00000253631	0	0.266808	0	0	ENSG00000253631	IGLV7-35
ENSG00000253633	0.957035	1.77823	1.60617	3.36192	ENSG00000253633	AP002852.2
ENSG00000253635	0	0	0	0	ENSG00000253635	IGHVIII-67-3
ENSG00000253637	0	0	0	0	ENSG00000253637	IGLVV-58
ENSG00000253638	0	0.61843	0.139568	0.825134	ENSG00000253638	AF186190.1
ENSG00000253639	0	0.464465	0	0.504029	ENSG00000253639	SUMO2P18
ENSG00000253646	0	0	0	0	ENSG00000253646	AC010476.1
ENSG00000253650	0.540575	0	0	0	ENSG00000253650	SMARCE1P4
ENSG00000253651	0	0	0	0.373346	ENSG00000253651	SOD1P3
ENSG00000253654	0	0.0977483	0	0.10988	ENSG00000253654	AC105029.1
ENSG00000253655	0	0	0	0	ENSG00000253655	IGJP1
ENSG00000253657	0	0	0	0	ENSG00000253657	AC022634.1
ENSG00000253663	0	0.0726653	0.13132	0.164095	ENSG00000253663	NPM1P52
ENSG00000253667	0.548608	1.8073	1.67292	2.62232	ENSG00000253667	AC100821.1
ENSG00000253668	0	0	0	0	ENSG00000253668	AC103778.1
ENSG00000253670	0.2614	2.74057	1.252	2.22492	ENSG00000253670	AC073581.1
ENSG00000253674	0	0	0	0	ENSG00000253674	IGHVII-78-1
ENSG00000253676	0.2591	1.61987	0.692918	1.13798	ENSG00000253676	TAGLN2P1
ENSG00000253677	0	0	0	0	ENSG00000253677	UBE2HP1
ENSG00000253680	0	0	0	0	ENSG00000253680	AC093331.1
ENSG00000253683	0	0	0	0	ENSG00000253683	AC027309.2
ENSG00000253684	0.255422	0.487005	0.220223	0.934065	ENSG00000253684	BUD31P1
ENSG00000253685	0	0	0	0	ENSG00000253685	MTND5P41
ENSG00000253689	0	0.518268	0.468047	0.285297	ENSG00000253689	IGHV3-54
ENSG00000253691	0.738603	0.469411	0.424362	0.259182	ENSG00000253691	IGKV2OR22-4
ENSG00000253692	0	0	0	0	ENSG00000253692	IGHEP1
ENSG00000253697	0	2.62726	0	0	ENSG00000253697	AC103834.1
ENSG00000253703	0	0	0	0	ENSG00000253703	IGHV1-68
ENSG00000253705	0	0	0	0	ENSG00000253705	IGHV3-41
ENSG00000253707	0	0	0	0	ENSG00000253707	AC022616.4
ENSG00000253709	0	0	0	0	ENSG00000253709	IGHV1-14
ENSG00000253710	7.49917	9.09439	10.1706	10.0743	ENSG00000253710	ALG11
ENSG00000253714	0	0	0	0	ENSG00000253714	IGHVII-53-1
ENSG00000253719	15.8057	13.7366	21.503	12.388	ENSG00000253719	ATXN7L3B
ENSG00000253721	0	0	0	0	ENSG00000253721	SUMO2P20
ENSG00000253723	0	1.56721	1.13226	0.688367	ENSG00000253723	AC107934.2
ENSG00000253725	0	0	0	0.0643664	ENSG00000253725	AC126915.1
ENSG00000253729	50.3165	95.1923	86.8301	94.6438	ENSG00000253729	PRKDC
ENSG00000253731	0.85199	0.302146	1.07913	1.18041	ENSG00000253731	PCDHGA6

ENSG00000253732	0	0	0	0	ENSG00000253732	IGKV2-19
ENSG00000253742	0.293894	0	0.487728	0.274764	ENSG00000253742	IGHV3-60
ENSG00000253743	0.0686829	0.0661737	0.0299096	0.150834	ENSG00000253743	MARK2P11
ENSG00000253747	0	0	0	0	ENSG00000253747	IGHVII-62-1
ENSG00000253748	0.407758	0	0	0.165149	ENSG00000253748	CYP4F44P
ENSG00000253750	0	0.504774	0	0	ENSG00000253750	AC090136.1
ENSG00000253752	0	0	0	0	ENSG00000253752	IGLVI-63
ENSG00000253755	0	0	0	0	ENSG00000253755	IGHGP
ENSG00000253756	0	0	0	0	ENSG00000253756	CARSP2
ENSG00000253759	0	0	0	0	ENSG00000253759	IGHV3-57
ENSG00000253760	0	0	0	0	ENSG00000253760	AC009812.2
ENSG00000253763	0	0	0	0	ENSG00000253763	IGHV3-6
ENSG00000253765	0	0	0	0	ENSG00000253765	IGKV2D-19
ENSG00000253767	0.496287	0.417445	0.59432	0.793727	ENSG00000253767	PCDHGA8
ENSG00000253770	0.253674	0	0.659443	0.817428	ENSG00000253770	HMGB1P23
ENSG00000253771	3.30453	4.6653	4.60202	5.0504	ENSG00000253771	TPTE2P1
ENSG00000253772	1.70548	3.19993	2.96863	5.0027	ENSG00000253772	AC112191.1
ENSG00000253777	0	0	0	0	ENSG00000253777	AC026616.1
ENSG00000253779	0	0	0	0	ENSG00000253779	IGLVVI-25-1
ENSG00000253780	0	0	0	0	ENSG00000253780	IGHVIII-2-1
ENSG00000253781	0	0	0	0	ENSG00000253781	ZNF317P1
ENSG00000253785	0.0785059	0	0	0	ENSG00000253785	AC008429.2
ENSG00000253786	0	0	0	0	ENSG00000253786	IGLV3-15
ENSG00000253787	1.15382	1.80963	0.517979	4.77088	ENSG00000253787	LINC02219
ENSG00000253789	0	0	0	0.215644	ENSG00000253789	NARSP2
ENSG00000253790	0	0.422255	0	0.236998	ENSG00000253790	AC007991.1
ENSG00000253793	0	0	0	0	ENSG00000253793	AC008066.1
ENSG00000253794	0	0	0	0	ENSG00000253794	IGLV10-67
ENSG00000253795	0	0.0639437	0	0	ENSG00000253795	MTND1P5
ENSG00000253797	6.2304	8.01137	8.67761	7.65772	ENSG00000253797	UTP14C
ENSG00000253800	0	0	0	0.209795	ENSG00000253800	AC090136.2
ENSG00000253801	0	0	0	0	ENSG00000253801	AC010376.1
ENSG00000253803	0	0	0	0	ENSG00000253803	AC091163.3
ENSG00000253808	0	0	0	0	ENSG00000253808	IGHVII-46-1
ENSG00000253810	0.109639	0.159236	0.0955936	0.120239	ENSG00000253810	PSAT1P1
ENSG00000253813	0.318687	0.30547	0.281929	0.510464	ENSG00000253813	COX6B1P4
ENSG00000253814	2.04144	9.53825	0	2.69561	ENSG00000253814	MRPS36P3
ENSG00000253816	0	0.913968	0.584623	0.386953	ENSG00000253816	AC138866.1
ENSG00000253817	0	0	0	0.381896	ENSG00000253817	AC120036.3
ENSG00000253818	0	0.463987	0.599177	0	ENSG00000253818	IGLV1-41
ENSG00000253820	0	0	0	0	ENSG00000253820	IGHVII-67-1
ENSG00000253822	0	0	0	0	ENSG00000253822	IGLV3-24
ENSG00000253823	0	0.35098	0.475398	0.77974	ENSG00000253823	IGLV1-62
ENSG00000253826	0	0	0	0	ENSG00000253826	WBP1LP10
ENSG00000253828	0.0510605	0.0976968	0.0883007	0.110796	ENSG00000253828	MTND2P38
ENSG00000253831	0.0881366	0.11273	0.0802024	0.29431	ENSG00000253831	ETV3L
ENSG00000253833	0	0.919936	0.806674	0	ENSG00000253833	AC022868.1
ENSG00000253840	0	0	0	0	ENSG00000253840	AC044836.1
ENSG00000253841	0.15792	1.34897	0.277205	0.590448	ENSG00000253841	AC024681.1
ENSG00000253843	0	0	0	0	ENSG00000253843	AC104989.1
ENSG00000253845	0	0	0	0	ENSG00000253845	AC139365.2
ENSG00000253846	7.32537	2.53617	5.2713	5.5176	ENSG00000253846	PCDHGA10
ENSG00000253857	0	0.147353	0	0	ENSG00000253857	AC022679.1
ENSG00000253860	0	0	0	0	ENSG00000253860	IGKV3-34

ENSG00000253861	0.69204	4.2365	1.45422	0	ENSG00000253861	SLC2A3P1
ENSG00000253862	0	0.139689	0.252577	0	ENSG00000253862	IGHVIII-47-1
ENSG00000253866	0	0	0	0	ENSG00000253866	TMEM97P2
ENSG00000253869	0	0.203973	0.0916712	0.115025	ENSG00000253869	PIGFP1
ENSG00000253870	0	0	0	0	ENSG00000253870	IGKV1-32
ENSG00000253873	4.74218	3.35702	3.44397	5.1399	ENSG00000253873	PCDHGA11
ENSG00000253874	0	0	0	0	ENSG00000253874	IGLVIV-66-1
ENSG00000253881	0	0	0	0	ENSG00000253881	AC105233.2
ENSG00000253882	1.56933	1.50502	2.98464	6.1893	ENSG00000253882	AC099548.2
ENSG00000253883	0	0	0	0	ENSG00000253883	IGHV3-19
ENSG00000253884	3.88946	0	0	0	ENSG00000253884	AC022616.5
ENSG00000253885	0	0	0	0	ENSG00000253885	ARF1P3
ENSG00000253886	0	0.049976	0	0.116098	ENSG00000253886	AC026688.1
ENSG00000253889	0	0	0	0	ENSG00000253889	IGLVI-38
ENSG00000253895	0	0	0	0	ENSG00000253895	IGHVII-44-2
ENSG00000253896	1.33009	1.83974	2.07928	3.28462	ENSG00000253896	AC144568.2
ENSG00000253897	0	0.0982723	0	0.223301	ENSG00000253897	AC034205.2
ENSG00000253899	0.0961916	0.0472826	0.259183	0.271695	ENSG00000253899	AC067904.2
ENSG00000253900	0	0	0	0	ENSG00000253900	CDH12P4
ENSG00000253903	0	0	0	0	ENSG00000253903	AC090150.2
ENSG00000253906	0	0	0	0	ENSG00000253906	IGKV2D-10
ENSG00000253907	0	0	0	0	ENSG00000253907	AC021678.3
ENSG00000253908	0.589686	1.03881	1.10905	2.9742	ENSG00000253908	AC104115.2
ENSG00000253910	0.648444	0.234422	0.97906	0.909334	ENSG00000253910	PCDHGB2
ENSG00000253912	0	0.890424	2.35094	3.00363	ENSG00000253912	AC018442.3
ENSG00000253913	0	0	0	0	ENSG00000253913	IGLV3-26
ENSG00000253915	0.325526	0.394333	0	0.79719	ENSG00000253915	AC104371.1
ENSG00000253916	0	0.0776168	0	0	ENSG00000253916	MTCO1P49
ENSG00000253919	0.0332503	0.223974	0.0864163	0.181607	ENSG00000253919	THAP12P7
ENSG00000253920	0	0	0	0	ENSG00000253920	IGLV3-31
ENSG00000253923	2.92694	6.22356	7.11153	10.3378	ENSG00000253923	AP002981.1
ENSG00000253934	0	0	0	0	ENSG00000253934	MRPL49P2
ENSG00000253935	0	0	0	0	ENSG00000253935	IGLVIV-53
ENSG00000253936	0	0	0	0	ENSG00000253936	IGHV3-63
ENSG00000253937	0	0	0	0	ENSG00000253937	NATP
ENSG00000253940	0	0	0	0	ENSG00000253940	AC026421.1
ENSG00000253941	0	0.436607	0.196053	0.47213	ENSG00000253941	IGHVII-51-2
ENSG00000253942	0	0.10512	0	0	ENSG00000253942	AP001330.3
ENSG00000253943	0.231217	0.356128	0.241495	0.101022	ENSG00000253943	KRT18P37
ENSG00000253945	0	0	0	0	ENSG00000253945	AC024995.1
ENSG00000253946	0	0	0.13833	0	ENSG00000253946	AC008489.1
ENSG00000253951	0	0	0	0	ENSG00000253951	AC087360.1
ENSG00000253952	0.404243	0.381924	0	0	ENSG00000253952	HIGD1AP18
ENSG00000253953	8.85779	3.64469	5.48817	5.39571	ENSG00000253953	PCDHGB4
ENSG00000253954	0.806574	1.46684	1.6331	1.83343	ENSG00000253954	HMGN1P38
ENSG00000253957	0	0	0	0	ENSG00000253957	IGHV3-22
ENSG00000253958	1.26475	1.09476	0.675551	0.342948	ENSG00000253958	CLDN23
ENSG00000253963	0	0	0	0	ENSG00000253963	IGLV3-2
ENSG00000253964	0.239476	0.228556	0	0.252503	ENSG00000253964	AC103783.1
ENSG00000253966	0.0440589	0.680747	0.232418	0.529908	ENSG00000253966	AC008514.2
ENSG00000253970	0	0	0	0.129892	ENSG00000253970	MTND2P7
ENSG00000253971	0	0.211576	0.456446	0.169569	ENSG00000253971	CDC42P3
ENSG00000253975	0.0356642	0.0687181	0.124237	0.273477	ENSG00000253975	AC018861.1
ENSG00000253976	0	0	0	0	ENSG00000253976	AC022679.2

ENSG00000253977	0	0	0	0	ENSG00000253977	MTCO2P4
ENSG00000253981	1.34596	5.34685	9.8613	3.30441	ENSG00000253981	ALG1L13P
ENSG00000253989	0	0	0	13.8969	ENSG00000253989	IGHVIII-38-1
ENSG00000253991	0.13648	1.44033	1.08511	0.877745	ENSG00000253991	AP001207.2
ENSG00000253993	0	0	0	0	ENSG00000253993	AC104027.1
ENSG00000253994	0	0	0	0	ENSG00000253994	NDUFB9P3
ENSG00000253995	0	0	0	0	ENSG00000253995	RPL10P18
ENSG00000253996	4.59877	8.17626	9.08404	17.371	ENSG00000253996	IGHVII-20-1
ENSG00000253997	0	0.434253	0	0.240045	ENSG00000253997	AC090142.3
ENSG00000253998	0	0	0	0	ENSG00000253998	IGKV2-29
ENSG00000253999	0	0	0	0	ENSG00000253999	IGKV3D-31
ENSG00000254004	13.3951	11.5292	13.7279	11.7901	ENSG00000254004	ZNF260
ENSG00000254009	1.0741	1.00955	0.900869	0	ENSG00000254009	IGKV2D-38
ENSG00000254012	0	0	0	0	ENSG00000254012	RPL10P8
ENSG00000254013	0.0518133	0.0497155	0	0.223535	ENSG00000254013	AC044849.1
ENSG00000254014	0	0	0	0	ENSG00000254014	AC009902.1
ENSG00000254015	0	0	0	0	ENSG00000254015	MTND4LP26
ENSG00000254016	0	0.498652	1.03866	0.456126	ENSG00000254016	ALG1L10P
ENSG00000254017	0.0946311	0.410017	0.205887	1.08563	ENSG00000254017	IGHEP2
ENSG00000254019	0	0.35147	0.554142	0.525016	ENSG00000254019	AC011676.2
ENSG00000254023	0	0	0	0	ENSG00000254023	PKMP4
ENSG00000254025	0	0.0666699	0.0602406	0	ENSG00000254025	BRIX1P1
ENSG00000254029	0	0	0	0	ENSG00000254029	IGLC4
ENSG00000254030	0	0.694056	0	0.37956	ENSG00000254030	IGLC5
ENSG00000254036	0	0	0	0	ENSG00000254036	IGHVIII-67-2
ENSG00000254037	0	0	0	0	ENSG00000254037	AC021733.2
ENSG00000254045	0	0	0	0	ENSG00000254045	IGHVIII-22-2
ENSG00000254046	0	0	0	0	ENSG00000254046	IGHV1-17
ENSG00000254047	0	0.0643549	0.116301	0.0744697	ENSG00000254047	AC025437.6
ENSG00000254051	0.175417	0.33584	0.303281	0.186673	ENSG00000254051	AC011853.1
ENSG00000254052	0	0	0	0	ENSG00000254052	IGHVIII-67-4
ENSG00000254053	0	0	0	0	ENSG00000254053	IGHVIII-5-2
ENSG00000254056	0	0	0	0	ENSG00000254056	IGHV3-71
ENSG00000254061	1.42797	1.46697	2.04477	8.75894	ENSG00000254061	AC091144.2
ENSG00000254063	0	0	0	0	ENSG00000254063	DUXAP2
ENSG00000254065	0	0.65612	0	0.731366	ENSG00000254065	AC024451.3
ENSG00000254069	0	0.0786508	0.207237	0.0898876	ENSG00000254069	AC134698.4
ENSG00000254070	0	0	0	0	ENSG00000254070	AC104576.1
ENSG00000254073	0	0	0	0	ENSG00000254073	IGLVVII-41-1
ENSG00000254075	0.27915	1.06189	1.19945	0.292317	ENSG00000254075	IGLVV-66
ENSG00000254076	0.205587	0.265329	0.292441	0.703549	ENSG00000254076	AC110053.1
ENSG00000254077	0	0	0	0	ENSG00000254077	IGLV3-7
ENSG00000254079	0	0.168485	0.15215	0	ENSG00000254079	AC012339.2
ENSG00000254087	6.73985	6.43484	4.30232	3.47997	ENSG00000254087	LYN
ENSG00000254088	0.889918	1.67533	1.63768	1.03671	ENSG00000254088	SLC2A3P4
ENSG00000254090	0	0.32191	0.393327	0.65787	ENSG00000254090	MTND2P32
ENSG00000254091	0	0	0	0	ENSG00000254091	AC022784.5
ENSG00000254093	13.086	14.2144	16.5834	12.2374	ENSG00000254093	PINX1
ENSG00000254097	0	0	0	0	ENSG00000254097	IGKV3D-25
ENSG00000254098	0	0	0	0	ENSG00000254098	IGKV2-26
ENSG00000254103	0	0.157705	0.315553	0	ENSG00000254103	AC009927.2
ENSG00000254104	0	0	0	0.539772	ENSG00000254104	AC136777.2
ENSG00000254105	1.29174	1.3556	2.37005	1.00972	ENSG00000254105	VENTXP6
ENSG00000254106	0	0	0	0.154569	ENSG00000254106	LINC01848

ENSG00000254112	1.29663	7.05246	2.15497	7.07894	ENSG00000254112	AP003467.2
ENSG00000254114	0	0.23877	1.07789	0.526943	ENSG00000254114	HMGN1P28
ENSG00000254117	0	0	0.239891	0	ENSG00000254117	IGHV2-10
ENSG00000254118	0	0	0	0	ENSG00000254118	MTCYBP20
ENSG00000254122	2.29041	1.91061	2.66778	4.36362	ENSG00000254122	PCDHGB7
ENSG00000254124	0	0	0.162084	0	ENSG00000254124	EEF1A1P37
ENSG00000254126	0	0	0	0	ENSG00000254126	CD8B2
ENSG00000254127	0	0	0	0	ENSG00000254127	IGLCOR22-1
ENSG00000254131	3.60128	3.29071	3.13556	3.50655	ENSG00000254131	AC093367.1
ENSG00000254132	0	0.130266	0.154442	0	ENSG00000254132	MTND6P3
ENSG00000254133	0	0	0	0	ENSG00000254133	RP11-1198D22.3
ENSG00000254134	0	0	0	0	ENSG00000254134	IGHVII-74-1
ENSG00000254145	0	0	0	0.299759	ENSG00000254145	AC134698.5
ENSG00000254146	0	0.110434	0	0.371613	ENSG00000254146	HMGB1P46
ENSG00000254150	0	0	0	0	ENSG00000254150	AC087664.3
ENSG00000254151	0.12761	0.338282	0.343989	0.0525014	ENSG00000254151	NIPA2P4
ENSG00000254152	0	0	0	0	ENSG00000254152	AC109329.2
ENSG00000254156	0	0	0	0	ENSG00000254156	MTND6P20
ENSG00000254157	0	0	0	0	ENSG00000254157	IGKV2-18
ENSG00000254158	0.0754596	0.0725599	0.13201	0	ENSG00000254158	AC104117.4
ENSG00000254161	0.254273	0.244199	0	0	ENSG00000254161	IGLVIV-65
ENSG00000254167	0	0	0	0	ENSG00000254167	IGHVIII-51-1
ENSG00000254170	0	0.0819192	0	0.267629	ENSG00000254170	AC008802.1
ENSG00000254174	0	0	0	0	ENSG00000254174	IGHV1-12
ENSG00000254175	0	0	0	0.244114	ENSG00000254175	IGLVI-42
ENSG00000254176	0	0	0	0	ENSG00000254176	IGHV3-75
ENSG00000254181	0	0	0	0	ENSG00000254181	SLC25A51P3
ENSG00000254182	0	0	0	0	ENSG00000254182	AC106038.2
ENSG00000254183	0	0.253633	0.153207	0.379828	ENSG00000254183	AC104417.1
ENSG00000254184	1.47517	1.93349	3.12063	2.11357	ENSG00000254184	TYW1B
ENSG00000254185	0	0	0.119498	0.0748342	ENSG00000254185	AC021001.1
ENSG00000254189	0.0729129	0.640131	0.617562	0.954906	ENSG00000254189	AC090095.1
ENSG00000254190	0	0	0	0	ENSG00000254190	AC023632.3
ENSG00000254193	2.1214	0	0	13.1303	ENSG00000254193	AC131281.2
ENSG00000254195	0.523368	0	0.225439	0	ENSG00000254195	TPM3P3
ENSG00000254198	41.6631	48.8514	32.4058	28.9554	ENSG00000254198	AC113191.1
ENSG00000254200	0	1.19998	0.425561	0.520246	ENSG00000254200	AC008412.1
ENSG00000254203	0	0	0	0	ENSG00000254203	IGHVII-33-1
ENSG00000254206	0.273004	0.526855	0.614046	0.65313	ENSG00000254206	NPIPB11
ENSG00000254210	0	0	0	0	ENSG00000254210	IGHVIII-16-1
ENSG00000254212	0	0	0	0	ENSG00000254212	AC009901.2
ENSG00000254213	0	0.0951558	0.171903	0.214031	ENSG00000254213	FAM213AP2
ENSG00000254214	0	0	0	0	ENSG00000254214	IGHVII-28-1
ENSG00000254215	0	0	0	0	ENSG00000254215	IGHVIII-11-1
ENSG00000254216	1.13117	3.23737	0.611433	2.55875	ENSG00000254216	AC107952.1
ENSG00000254220	0	0	0	0	ENSG00000254220	IGKV2D-18
ENSG00000254221	0.504219	0.264878	0.597268	0.729489	ENSG00000254221	PCDHGB1
ENSG00000254225	0	0.148266	0	0	ENSG00000254225	BTF3P1
ENSG00000254228	0	0	0.149087	0.180923	ENSG00000254228	IGHV3-42
ENSG00000254229	0	0.055885	0	0	ENSG00000254229	FAM90A12P
ENSG00000254240	0	0	0	0	ENSG00000254240	IGLVI-20
ENSG00000254241	0	0	0	0	ENSG00000254241	MTCO1P47
ENSG00000254244	0	0	0	0.114039	ENSG00000254244	PAICSP4
ENSG00000254245	0.26336	0.0509257	0.320312	0.831501	ENSG00000254245	PCDHGA3

ENSG00000254247	0	0	0	0	ENSG00000254247	AC107953.1
ENSG00000254252	0	0.0851527	0	0	ENSG00000254252	RPL7P20
ENSG00000254253	0.308895	1.68129	0.357309	1.22276	ENSG00000254253	AC022861.1
ENSG00000254255	0	0	0	0	ENSG00000254255	AC060788.1
ENSG00000254256	0	0	0	0	ENSG00000254256	RPSAP71
ENSG00000254264	0	0	0	0.338461	ENSG00000254264	IGKV3OR22-2
ENSG00000254265	0	0.0650239	0	0	ENSG00000254265	AC100810.2
ENSG00000254268	0	0	0	0	ENSG00000254268	RFPL4AP7
ENSG00000254270	0	0	0	0	ENSG00000254270	ERHP1
ENSG00000254272	1.01154	1.54207	0.705038	3.39404	ENSG00000254272	AC087854.1
ENSG00000254273	0.699684	1.33662	1.60939	1.7235	ENSG00000254273	AC018620.1
ENSG00000254274	0.528038	1.98692	2.06001	4.40951	ENSG00000254274	TDGF1P5
ENSG00000254276	0	2.68227	1.10658	0.473635	ENSG00000254276	RP11-1198D22.2
ENSG00000254279	0	0	0	0	ENSG00000254279	IGHVII-1-1
ENSG00000254283	0	0	0	0	ENSG00000254283	AC023632.4
ENSG00000254284	0	0	0	0	ENSG00000254284	IGHV3-79
ENSG00000254285	0.180073	0.833068	0.209164	0.777905	ENSG00000254285	KRT8P3
ENSG00000254289	0	0	0	0	ENSG00000254289	IGHV3-32
ENSG00000254292	0	0	0	0	ENSG00000254292	IGKV2D-14
ENSG00000254294	0.079531	0.0739172	0.100723	0.0424396	ENSG00000254294	AC021305.1
ENSG00000254305	0	0	0	0	ENSG00000254305	AC011716.1
ENSG00000254308	0	0	0	0	ENSG00000254308	IGLVIV-59
ENSG00000254309	0	0	0	0	ENSG00000254309	AC124290.2
ENSG00000254310	0	0	0	0	ENSG00000254310	AC025755.1
ENSG00000254311	0	0	0	0	ENSG00000254311	SNRPCP17
ENSG00000254312	0	0	0	0	ENSG00000254312	MRPL57P7
ENSG00000254313	0	0	0	0	ENSG00000254313	AC090821.2
ENSG00000254316	0	0	0	0	ENSG00000254316	AC090820.1
ENSG00000254318	0	0.11607	0.104816	0.616217	ENSG00000254318	C8orf87
ENSG00000254320	0	0	0	0	ENSG00000254320	AP006245.2
ENSG00000254326	0.147819	0.280889	0.126933	0	ENSG00000254326	IGHV7-27
ENSG00000254328	1.9347	9.16154	12.1384	5.96858	ENSG00000254328	AC008429.4
ENSG00000254329	0	0	0	0	ENSG00000254329	IGHVII-60-1
ENSG00000254331	0	0	0	0	ENSG00000254331	CKS1BP7
ENSG00000254332	0.0991748	0.0949476	0	0.110517	ENSG00000254332	AF201337.1
ENSG00000254335	0	0	0.845031	0	ENSG00000254335	CDH12P1
ENSG00000254336	0	0	0	0	ENSG00000254336	AC008694.2
ENSG00000254342	0	2.36711	0	0	ENSG00000254342	AC022616.6
ENSG00000254345	0	0	0	0	ENSG00000254345	IGKV2D-23
ENSG00000254346	0	0.126914	0.29511	0.717511	ENSG00000254346	MTND1P6
ENSG00000254348	0	0	0	0	ENSG00000254348	AC120036.4
ENSG00000254349	19.4606	83.4196	38.5225	67.218	ENSG00000254349	MIR2052HG
ENSG00000254351	0	0	0	0	ENSG00000254351	ARL2BPP5
ENSG00000254352	0.800544	6.15839	2.20518	5.14113	ENSG00000254352	AC100854.1
ENSG00000254355	0	0.260377	0	0	ENSG00000254355	IGLVI-68
ENSG00000254358	0	1.08021	1.95773	1.47591	ENSG00000254358	CYCSP22
ENSG00000254373	0	0	0.530828	0.359887	ENSG00000254373	AC112191.2
ENSG00000254374	0	0	0	0	ENSG00000254374	GOLGA6L21P
ENSG00000254376	0.107257	0.206479	0.0957987	0.351072	ENSG00000254376	SOX5P1
ENSG00000254381	0	0	0	0	ENSG00000254381	TUBB8P5
ENSG00000254384	0	0	0	0	ENSG00000254384	MTND6P19
ENSG00000254387	0	0	0	0.157163	ENSG00000254387	MYL12AP1
ENSG00000254388	0.442935	2.17505	1.20655	1.11108	ENSG00000254388	DUTP2
ENSG00000254392	0	0	0.0879384	0.218942	ENSG00000254392	AC090539.2

ENSG00000254395	0	0	0	0	ENSG00000254395	IGHV4-55
ENSG00000254398	0.171762	0.897374	0.839811	2.83277	ENSG00000254398	AC055876.2
ENSG00000254399	0	0.066848	0	0.0755651	ENSG00000254399	GLYATL1P4
ENSG00000254402	0.0704279	0	0.0669445	0.274527	ENSG00000254402	LRRC24
ENSG00000254403	0.254844	0	0.110783	0.59972	ENSG00000254403	OR10Y1P
ENSG00000254405	0	3.21927	0.192683	3.22555	ENSG00000254405	MSH5-SAPCD1
ENSG00000254406	0	0.0748312	0.0676086	0	ENSG00000254406	AP001994.1
ENSG00000254407	0	0	0	0	ENSG00000254407	PHBP17
ENSG00000254408	0	0.0984311	0.118587	0	ENSG00000254408	OR4A1P
ENSG00000254411	0	0.302675	0	0	ENSG00000254411	AP002512.1
ENSG00000254412	0.022526	0.175681	0.0616614	0.0653839	ENSG00000254412	AC118273.1
ENSG00000254413	1.43494	5.31391	4.9381	0.684953	ENSG00000254413	CHKB-CPT1B
ENSG00000254415	0.250686	0.872419	0.665774	1.39076	ENSG00000254415	SIGLEC14
ENSG00000254423	0	0.113499	0.134992	0.432863	ENSG00000254423	AC087203.1
ENSG00000254424	1.11762	0	0.920175	1.10229	ENSG00000254424	AP003733.2
ENSG00000254425	0.403551	0.587196	0.725684	1.9279	ENSG00000254425	AC022690.1
ENSG00000254430	0.191873	0.184388	0.416395	0.10372	ENSG00000254430	OR6M3P
ENSG00000254436	0	0	0	0.245983	ENSG00000254436	AP000648.1
ENSG00000254437	0	0	0	0	ENSG00000254437	AP003398.1
ENSG00000254440	0.335301	0.99894	0.885122	1.708	ENSG00000254440	PBOV1
ENSG00000254441	0.207026	0.91032	0.776798	1.72551	ENSG00000254441	AP001646.1
ENSG00000254442	0	0	0.28791	0	ENSG00000254442	AP000859.1
ENSG00000254445	0	0	0	0	ENSG00000254445	HSPB2-C11orf52
ENSG00000254447	0	0	0	0.0867058	ENSG00000254447	OR7E11P
ENSG00000254449	0	0	0.10199	0	ENSG00000254449	AP002765.1
ENSG00000254454	0.0408403	0	0.0686739	0.0825864	ENSG00000254454	RCC2P6
ENSG00000254455	0	0	0	0	ENSG00000254455	HIGD1AP10
ENSG00000254457	0.65188	0.292979	0.135116	0.326234	ENSG00000254457	OR5D2P
ENSG00000254462	0.314183	0	0	0	ENSG00000254462	TMX2-CTNND1
ENSG00000254463	1.14122	2.35028	2.29552	4.00868	ENSG00000254463	AC087276.1
ENSG00000254464	0	0	0.0633615	0	ENSG00000254464	OR4A3P
ENSG00000254465	0.0492706	0.0474793	0.0643707	0.162233	ENSG00000254465	THAP12P4
ENSG00000254466	0.120047	0.0577564	0.0521969	0.130791	ENSG00000254466	OR4D10
ENSG00000254469	4.10337	9.87157	11.5161	12.3991	ENSG00000254469	AP002495.1
ENSG00000254470	8.15433	10.1353	13.4285	7.3764	ENSG00000254470	AP5B1
ENSG00000254471	0.348368	0.281192	0	0.498051	ENSG00000254471	AP001284.1
ENSG00000254472	0.11261	0.409722	0.159338	0.540028	ENSG00000254472	OR4A49P
ENSG00000254475	0.0889086	0.25628	0.0771795	0.0962339	ENSG00000254475	OR2AT1P
ENSG00000254478	1.73811	0	0	0	ENSG00000254478	AP004609.2
ENSG00000254479	0.0690081	0.195677	0.117509	0.147057	ENSG00000254479	SLC25A1P1
ENSG00000254481	0	0.145136	0.26155	0.816676	ENSG00000254481	AP000911.2
ENSG00000254482	0	0.69715	0.179362	0.338478	ENSG00000254482	AP003102.1
ENSG00000254483	5.7644	0.253708	0.653817	0	ENSG00000254483	AL590705.4
ENSG00000254487	0	0.0841566	0	0	ENSG00000254487	AC130364.1
ENSG00000254490	0	0	0	0	ENSG00000254490	OR5M7P
ENSG00000254491	0	0	0	0	ENSG00000254491	AC022832.1
ENSG00000254492	0	0	0	0	ENSG00000254492	AP001328.1
ENSG00000254496	0	0	0	0.612691	ENSG00000254496	CBX3P8
ENSG00000254498	0.0717171	0.068967	0.0628645	0.233749	ENSG00000254498	AC104042.1
ENSG00000254500	0.819462	0.774617	1.04564	0.421769	ENSG00000254500	RANP3
ENSG00000254502	0.216764	0	0.142096	0.293278	ENSG00000254502	AP003097.1
ENSG00000254503	4.15752	8.16509	6.93653	13.9302	ENSG00000254503	AC010319.1
ENSG00000254505	21.414	25.591	30.9637	32.6094	ENSG00000254505	CHMP4A
ENSG00000254506	0.0707919	0.409206	0.18515	0.571044	ENSG00000254506	AP003080.1

ENSG00000254507	0	0.837227	1.20281	1.11053	ENSG00000254507	DEFB131E
ENSG00000254509	2.1685	9.94114	3.52911	4.58489	ENSG00000254509	AP000866.3
ENSG00000254512	0.647889	3.0505	2.6479	4.70757	ENSG00000254512	PHBP2
ENSG00000254515	0	0	0	0	ENSG00000254515	AP001124.1
ENSG00000254517	0	0	0	0	ENSG00000254517	AC027369.2
ENSG00000254521	0	0.0392435	0.177297	1.24708	ENSG00000254521	SIGLEC12
ENSG00000254522	0.383041	0.65586	0.652632	1.56856	ENSG00000254522	AP001767.1
ENSG00000254524	0	0	0	0	ENSG00000254524	AC068339.1
ENSG00000254527	0.809811	3.87424	4.17986	8.22074	ENSG00000254527	ENPP7P12
ENSG00000254529	0.0654811	0	0	0.213744	ENSG00000254529	AC023078.1
ENSG00000254531	8.4143	5.40192	4.05026	3.33486	ENSG00000254531	FLJ20021
ENSG00000254534	0.0347058	0	0.0751822	0.113412	ENSG00000254534	AP000776.1
ENSG00000254535	0.368562	0.512286	0.683014	0.585832	ENSG00000254535	PABPC4L
ENSG00000254536	0.425775	0.745578	0.572947	0.19311	ENSG00000254536	AL360181.3
ENSG00000254537	8.04586	16.9522	12.4825	31.6703	ENSG00000254537	AL137161.1
ENSG00000254541	0	0	0	0	ENSG00000254541	AC023078.2
ENSG00000254543	0	0	0	0	ENSG00000254543	AC130365.1
ENSG00000254544	0	0	0	0	ENSG00000254544	PCNAP4
ENSG00000254546	0.100664	0.389543	0.695501	1.21447	ENSG00000254546	AC090099.2
ENSG00000254547	0	0	0	0	ENSG00000254547	AC036111.1
ENSG00000254550	0.155519	0	0	0	ENSG00000254550	OMP
ENSG00000254553	0.94734	0.464701	0.694017	0.652311	ENSG00000254553	AL033529.1
ENSG00000254555	0	0	0	0	ENSG00000254555	AP003730.1
ENSG00000254558	0	0	0	0	ENSG00000254558	AP005435.1
ENSG00000254564	0	2.17601	0	0.310814	ENSG00000254564	AC100767.1
ENSG00000254565	0.179034	0.467543	0.59724	1.41497	ENSG00000254565	MTND2P26
ENSG00000254567	0.439714	0.390687	0.331016	0.708368	ENSG00000254567	UBTFL9
ENSG00000254569	0	0	0	0	ENSG00000254569	AP002004.2
ENSG00000254572	0	0	0	0	ENSG00000254572	AP002469.1
ENSG00000254576	0.0672651	0.194063	0.409156	0.157642	ENSG00000254576	OR4C1P
ENSG00000254579	2.74613	5.07563	3.61773	6.70081	ENSG00000254579	AC013488.1
ENSG00000254581	0	0	0	0	ENSG00000254581	AC068587.3
ENSG00000254582	0.426207	0.513812	0.554462	1.37931	ENSG00000254582	PSMA2P1
ENSG00000254583	0	0	0.0825197	0.102789	ENSG00000254583	AC021269.1
ENSG00000254585	0	0	0	0.222198	ENSG00000254585	MAGEL2
ENSG00000254589	0.0581901	0	0	0.190514	ENSG00000254589	EIF4A2P3
ENSG00000254590	0.139663	0.628881	0.715228	0.947524	ENSG00000254590	AP003396.2
ENSG00000254591	0	0	0	0	ENSG00000254591	AP003532.1
ENSG00000254593	0.754351	1.78419	2.29671	2.37148	ENSG00000254593	OR7E126P
ENSG00000254595	1.22354	3.72788	4.31213	7.28295	ENSG00000254595	AC084337.1
ENSG00000254596	0	0	0.231885	0.282708	ENSG00000254596	AP002748.2
ENSG00000254597	0	0	0	0	ENSG00000254597	FAM90A10P
ENSG00000254598	0.47665	0.446036	1.1596	0.994242	ENSG00000254598	CSNK2A3
ENSG00000254601	0	0.296471	0	0.651451	ENSG00000254601	CYCSP26
ENSG00000254603	0.0667455	0	0.0580014	0.0726033	ENSG00000254603	OR5M6P
ENSG00000254608	0	1.06994	0.26403	0.898654	ENSG00000254608	RP11-56A10.1
ENSG00000254609	0	0	0	0	ENSG00000254609	AC136443.1
ENSG00000254612	0.174531	0.170122	0	0	ENSG00000254612	AP001000.1
ENSG00000254613	0.0729129	0	0	0	ENSG00000254613	OR6M2P
ENSG00000254614	26.7677	7.13569	4.84846	7.81076	ENSG00000254614	AP003068.2
ENSG00000254616	0.121499	0.466442	0.421214	1.45437	ENSG00000254616	AP001775.1
ENSG00000254617	0	0.0781405	0	0	ENSG00000254617	AP005435.2
ENSG00000254618	0.572436	0.636209	0.948914	0.900147	ENSG00000254618	TMED10P1
ENSG00000254621	0	0	0	0	ENSG00000254621	SETP16

ENSG00000254623	0	0	0.450435	0	ENSG00000254623	DEFB108E
ENSG00000254624	0	0.0735194	0.0332089	0	ENSG00000254624	OR4R3P
ENSG00000254629	0	0	0	0.11886	ENSG00000254629	AP002370.1
ENSG00000254633	0	0	0	0	ENSG00000254633	AL512590.2
ENSG00000254634	6.0343	15.0503	18.1449	11.7405	ENSG00000254634	SMG1P6
ENSG00000254636	0.236358	0.30585	0.619318	0.256406	ENSG00000254636	ARMS2
ENSG00000254637	0	0	0	0	ENSG00000254637	OR4A18P
ENSG00000254640	7.64842	11.8709	10.2123	16.271	ENSG00000254640	RP11-384C21.9
ENSG00000254642	0.592544	0	0	1.24494	ENSG00000254642	COX6CP5
ENSG00000254644	0.239116	2.48162	0.823765	0	ENSG00000254644	AC007751.1
ENSG00000254646	0	0	0	0	ENSG00000254646	OR8B10P
ENSG00000254647	0	0	0	0.145347	ENSG00000254647	INS
ENSG00000254650	0.215406	0.495607	0.665982	0.646274	ENSG00000254650	MTCYBP41
ENSG00000254655	0	0	0	0	ENSG00000254655	AP004607.1
ENSG00000254656	0.244281	0.111604	0.0336362	1.42978	ENSG00000254656	RTL1
ENSG00000254658	0	0	0	0	ENSG00000254658	OR8J2
ENSG00000254660	0	0	0.193929	0.120494	ENSG00000254660	AP002512.2
ENSG00000254663	0.0719174	0.66848	0.302007	0.302265	ENSG00000254663	OR4A11P
ENSG00000254667	0	0	0.0478376	0.659816	ENSG00000254667	AP000783.1
ENSG00000254668	0	0	0	0	ENSG00000254668	AC023442.1
ENSG00000254672	0.275278	1.05333	1.52842	1.43277	ENSG00000254672	AL136146.1
ENSG00000254673	0	0	0	0	ENSG00000254673	AC110275.1
ENSG00000254674	0	0.0641076	0	0	ENSG00000254674	OR4A42P
ENSG00000254677	0.0972386	0	0	0.265188	ENSG00000254677	OSBPL9P2
ENSG00000254678	0.348685	0.991445	1.78905	0.361847	ENSG00000254678	AP005018.1
ENSG00000254681	9.9476	57.2317	56.0973	49.8091	ENSG00000254681	PKD1P5
ENSG00000254683	0	0	0	0	ENSG00000254683	SNRPCP6
ENSG00000254684	0	0.146505	0	0	ENSG00000254684	AP002803.1
ENSG00000254685	9.84616	8.89827	9.70421	6.27446	ENSG00000254685	FPGT
ENSG00000254692	1.08511	0.398995	0.631215	0	ENSG00000254692	AL136295.1
ENSG00000254696	0.49008	1.40874	0.98908	0.324623	ENSG00000254696	RP11-72M10.7
ENSG00000254697	0	0.153673	0	0.171172	ENSG00000254697	COPS8P3
ENSG00000254700	0	0	0	0	ENSG00000254700	DEFB131C
ENSG00000254701	0.251553	14.7495	0.340343	0.912713	ENSG00000254701	AC138866.2
ENSG00000254702	0.109876	0	0	0.0808304	ENSG00000254702	AP002353.1
ENSG00000254704	0.0276825	0	0	0	ENSG00000254704	AP002358.2
ENSG00000254706	0	0	0	0	ENSG00000254706	AL512785.2
ENSG00000254708	0.642787	0.137622	0.935458	1.26424	ENSG00000254708	AL139174.1
ENSG00000254709	0	0	0	0.0780225	ENSG00000254709	IGLL5
ENSG00000254712	0.185367	0.498527	0.398842	1.55058	ENSG00000254712	AC087280.1
ENSG00000254713	0.0645099	0.0628976	0.167594	0.643296	ENSG00000254713	HNRNPA1P72
ENSG00000254714	0.0884616	0.0360169	0.172136	0.132047	ENSG00000254714	AP006587.1
ENSG00000254715	0.627555	0.141438	0.761414	0.728161	ENSG00000254715	OR7E154P
ENSG00000254717	0.358845	0.624592	0	0.897733	ENSG00000254717	GLYATL1P2
ENSG00000254719	0	2.91791	0	0	ENSG00000254719	AC080023.2
ENSG00000254720	0	0	0	0.0707201	ENSG00000254720	AC023078.3
ENSG00000254722	0	0	0	0	ENSG00000254722	FAM8A2P
ENSG00000254723	0	0	0	0	ENSG00000254723	OR4A12P
ENSG00000254724	0.0624074	0.300216	0.0578837	0.0712772	ENSG00000254724	OR7E10P
ENSG00000254725	0	0	0	0	ENSG00000254725	AC009643.1
ENSG00000254726	1.16564	1.73672	3.02489	2.32858	ENSG00000254726	MEX3A
ENSG00000254727	0.162337	0	0	0	ENSG00000254727	PTP4A1P6
ENSG00000254728	0	0	0	0.0238689	ENSG00000254728	AC027369.3
ENSG00000254730	0.937391	3.71328	3.91797	2.09844	ENSG00000254730	AP002453.2

ENSG00000254732	2.23086	4.59823	5.07877	5.01788	ENSG00000254732	AP001931.1
ENSG00000254735	0.131655	0.384497	0	0	ENSG00000254735	HMGB1P42
ENSG00000254736	0	0	0	0.138882	ENSG00000254736	BRD9P1
ENSG00000254737	0.0668316	0	0.0580758	0	ENSG00000254737	OR10G4
ENSG00000254738	0	0	0	0	ENSG00000254738	AC023078.4
ENSG00000254743	0.956856	1.84015	2.28992	4.46895	ENSG00000254743	OR10V3P
ENSG00000254747	0	0	0	0	ENSG00000254747	MTND4LP18
ENSG00000254748	0	0.0685694	0	0	ENSG00000254748	HNRNPCP8
ENSG00000254749	0.0789046	0	0.0685301	0.256789	ENSG00000254749	OR5BD1P
ENSG00000254750	1.8831	0.971107	5.18547	0.645692	ENSG00000254750	CASP1P2
ENSG00000254751	0	0	0	0	ENSG00000254751	TRIM64DP
ENSG00000254752	0	0	0	0	ENSG00000254752	OR5M2P
ENSG00000254755	0	0	0	0	ENSG00000254755	AP001189.2
ENSG00000254758	0.210635	0.203886	0.187519	0.364957	ENSG00000254758	AP000889.1
ENSG00000254759	0	0	0	0.062889	ENSG00000254759	NAP1L1P1
ENSG00000254764	0	0.0836516	0	0.0474942	ENSG00000254764	TRIM53CP
ENSG00000254765	0	0	0	0	ENSG00000254765	AC011092.1
ENSG00000254767	0	0	0	0	ENSG00000254767	OR2AL1P
ENSG00000254769	0.0673525	0.0647714	0.175579	0.0732535	ENSG00000254769	OR4A4P
ENSG00000254770	0.198947	0	0.288146	0.43367	ENSG00000254770	OR4D7P
ENSG00000254771	0.760948	0	0.662944	1.6673	ENSG00000254771	AP001893.2
ENSG00000254772	497.618	379.048	351.531	242.507	ENSG00000254772	EEF1G
ENSG00000254776	0	0.0738374	0	0	ENSG00000254776	AC084121.1
ENSG00000254778	0	0.6267	0	0.632152	ENSG00000254778	AL662828.1
ENSG00000254779	0	0.479658	0.432364	0.872131	ENSG00000254779	EGLN1P1
ENSG00000254780	0	0	0	0	ENSG00000254780	AC023232.1
ENSG00000254781	0.154556	0.221976	0.222153	0.479323	ENSG00000254781	AC091564.4
ENSG00000254783	0.534368	1.28359	0.471376	2.3135	ENSG00000254783	AP003084.1
ENSG00000254784	0	0	0	0.0777048	ENSG00000254784	LRRC6P1
ENSG00000254785	0	0	0	0	ENSG00000254785	AP005435.3
ENSG00000254786	0.107815	0.103775	0	0.0588126	ENSG00000254786	AP001636.1
ENSG00000254788	0.609585	1.67423	0.764439	1.70334	ENSG00000254788	CKLF-CMTM1
ENSG00000254792	19.1926	29.6254	27.0521	32.2863	ENSG00000254792	AP003716.2
ENSG00000254793	0.366378	0.596288	0.44607	0.437483	ENSG00000254793	FDPSP4
ENSG00000254794	0	38.0313	35.4139	20.4482	ENSG00000254794	AP000676.1
ENSG00000254795	0	0	0	0.0723281	ENSG00000254795	OR5AP1P
ENSG00000254796	0	0	0	0	ENSG00000254796	AC134684.1
ENSG00000254798	0	0.0960994	0	0.10351	ENSG00000254798	AP001981.1
ENSG00000254799	0.606926	0	0	0	ENSG00000254799	SLC25A47P1
ENSG00000254800	0	0	0.13424	0	ENSG00000254800	AP006587.2
ENSG00000254801	0	0	0	0	ENSG00000254801	AC084851.1
ENSG00000254803	0	0	0	0	ENSG00000254803	AP004607.2
ENSG00000254805	0	0.725114	0	0	ENSG00000254805	SNRPCP14
ENSG00000254806	1.25561	1.65238	1.76929	0.569143	ENSG00000254806	SYS1-DBNDD2
ENSG00000254807	0	0	0	0	ENSG00000254807	AP003033.1
ENSG00000254811	1.18745	1.55345	1.44295	2.2935	ENSG00000254811	AP002001.1
ENSG00000254816	0.222669	0	0	0	ENSG00000254816	AC090857.1
ENSG00000254817	0	0	0	0	ENSG00000254817	AC107918.1
ENSG00000254818	0.095067	0.0418867	0.0266816	0.18302	ENSG00000254818	AP004607.3
ENSG00000254824	0	5.05656	4.44026	15.1367	ENSG00000254824	AP003461.1
ENSG00000254825	0.0360044	0	0	0	ENSG00000254825	OR9G2P
ENSG00000254827	0.719327	1.54277	0.80318	0.751284	ENSG00000254827	SLC22A18AS
ENSG00000254828	0	0	0	0	ENSG00000254828	AP005597.1
ENSG00000254831	0	0.0542404	0.141325	0.176801	ENSG00000254831	KRT18P58

ENSG00000254832	0	0	0	0.235912	ENSG00000254832	OR4A40P
ENSG00000254834	0	0	0.0505638	0	ENSG00000254834	OR5M10
ENSG00000254838	0.247119	0.397753	0.527968	0.916411	ENSG00000254838	GVINP1
ENSG00000254840	1.85299	3.27744	4.03289	3.60068	ENSG00000254840	AC024405.2
ENSG00000254841	0.0529172	0	0	0.173388	ENSG00000254841	OR4V1P
ENSG00000254843	1.4422	2.78178	1.95112	4.7524	ENSG00000254843	XIAPP2
ENSG00000254845	0.071134	0.136803	0.0618038	0.187235	ENSG00000254845	OR8G7P
ENSG00000254848	0	0	0.0673069	0.252289	ENSG00000254848	OR5BN1P
ENSG00000254850	0	0	0	0	ENSG00000254850	AC004923.2
ENSG00000254851	0	0	0	0.900835	ENSG00000254851	AP005018.2
ENSG00000254852	1.17174	2.75167	3.01948	1.12783	ENSG00000254852	NPIPA2
ENSG00000254853	0.0938897	0.176915	0	0.301206	ENSG00000254853	AP004247.1
ENSG00000254856	2.86216	4.84271	10.3611	13.1351	ENSG00000254856	NDUFA3P2
ENSG00000254857	0	0	0	0	ENSG00000254857	AC090099.3
ENSG00000254858	8.51479	6.25743	7.68147	4.72562	ENSG00000254858	MPV17L2
ENSG00000254866	0.537051	2.65465	2.39273	0.604256	ENSG00000254866	DEFB109D
ENSG00000254867	0	0.201783	0.273351	0	ENSG00000254867	AP006287.1
ENSG00000254870	0	0	0.367462	0	ENSG00000254870	ATP6V1G2-DDX39B
ENSG00000254871	0	0	0	0	ENSG00000254871	AC024475.2
ENSG00000254873	0.395641	0.563398	0.777601	0.638155	ENSG00000254873	AP001267.1
ENSG00000254875	0	0.6267	0	0	ENSG00000254875	AL845464.1
ENSG00000254877	0.193284	0.278608	1.00676	1.67163	ENSG00000254877	AP001636.2
ENSG00000254883	0.30551	0.724313	0.392305	0.95658	ENSG00000254883	AP003385.4
ENSG00000254884	1.25881	2.73481	3.2941	4.38247	ENSG00000254884	PRR13P2
ENSG00000254886	0	0	0	0	ENSG00000254886	OR4A10P
ENSG00000254888	0	0	0	0	ENSG00000254888	AP000827.1
ENSG00000254889	0	0	0	0	ENSG00000254889	AC084121.2
ENSG00000254890	0	0.332559	0.150146	0.739532	ENSG00000254890	AP003049.1
ENSG00000254891	0	0	0.0574856	0	ENSG00000254891	OR4A9P
ENSG00000254892	0	0	0.0332284	1.21949	ENSG00000254892	AP003396.4
ENSG00000254893	0.718799	2.3461	0.410464	0.291228	ENSG00000254893	AC113404.3
ENSG00000254895	0.209037	0.546536	0.541643	1.87264	ENSG00000254895	MTCO3P15
ENSG00000254897	0.123763	0.119292	0.143815	0.135838	ENSG00000254897	AP003035.1
ENSG00000254899	0	0	0	0	ENSG00000254899	BX248516.1
ENSG00000254901	9.95297	7.32026	9.84653	12.4008	ENSG00000254901	BORCS8
ENSG00000254903	0	0	0	0	ENSG00000254903	OR8L1P
ENSG00000254909	12.9107	11.2233	14.1902	6.42151	ENSG00000254909	AP003392.2
ENSG00000254912	0.400573	0.175386	0	0	ENSG00000254912	AC135983.3
ENSG00000254914	0	0	0	0	ENSG00000254914	AC109810.1
ENSG00000254915	1.34566	2.86994	0.863729	4.89648	ENSG00000254915	AP003168.1
ENSG00000254916	0	4.67E-06	0	0.1791	ENSG00000254916	AP004607.4
ENSG00000254917	0.0656188	0	0.0561379	0	ENSG00000254917	OR7E15P
ENSG00000254920	0	0	0	0	ENSG00000254920	AC027369.4
ENSG00000254923	0.100501	0.421202	0.436367	0.344985	ENSG00000254923	AC130366.1
ENSG00000254924	0.937391	0.889413	1.60699	1.95435	ENSG00000254924	AP000867.2
ENSG00000254925	0	0	0	0	ENSG00000254925	OR4C9P
ENSG00000254926	0.08321	0.0799736	0.0722503	0	ENSG00000254926	AP000445.2
ENSG00000254931	0.101984	0.43682	0.200135	0.833616	ENSG00000254931	MTATP6P15
ENSG00000254935	0	0	0	0	ENSG00000254935	AP002469.2
ENSG00000254937	0	0.147675	0	0	ENSG00000254937	AP000916.1
ENSG00000254939	0	0	0.0575956	0	ENSG00000254939	AP003038.1
ENSG00000254940	0	0	0	0	ENSG00000254940	OR4A19P
ENSG00000254941	0.358067	0	0.309411	0.571192	ENSG00000254941	AP000866.4
ENSG00000254943	0	0	0.258018	0	ENSG00000254943	AP003501.2

ENSG00000254944	0.425754	0.469916	0.535425	0.479731	ENSG00000254944	ATP5F1P5
ENSG00000254947	0.0728105	0.140057	0.189819	0.184549	ENSG00000254947	OR8K4P
ENSG00000254948	0	0	0	0	ENSG00000254948	OR7E158P
ENSG00000254949	0	0	0.625175	0.726007	ENSG00000254949	AP001781.1
ENSG00000254953	0	0	0	0	ENSG00000254953	AP001803.1
ENSG00000254954	0.308931	0.293178	0	0.644706	ENSG00000254954	SLC2A13P1
ENSG00000254957	0.139131	0.272575	0.204837	0.720792	ENSG00000254957	AC111188.2
ENSG00000254959	0	0	0	0	ENSG00000254959	INMT-MINDY4
ENSG00000254961	0	0.324658	0	0	ENSG00000254961	TUBB4BP4
ENSG00000254962	2.98591	4.87133	5.35978	8.68676	ENSG00000254962	OR4A14P
ENSG00000254965	0	0	0.197758	0	ENSG00000254965	C1DP5
ENSG00000254974	0	0	0.157716	0	ENSG00000254974	AP001372.4
ENSG00000254976	0.142402	0.286734	0.614675	0.502286	ENSG00000254976	AP001804.1
ENSG00000254978	0	0.806556	0.268197	0.5119	ENSG00000254978	ALG1L9P
ENSG00000254979	0.0581678	0.60862	0.423975	1.43868	ENSG00000254979	AP000781.2
ENSG00000254982	1.37717	4.9448	3.1776	6.16405	ENSG00000254982	HMGB1P24
ENSG00000254984	6.27578	12.9522	15.6159	25.4653	ENSG00000254984	FTLP6
ENSG00000254986	39.7135	31.0265	25.5783	21.5435	ENSG00000254986	DPP3
ENSG00000254992	0	0	0	0	ENSG00000254992	AP001582.1
ENSG00000254993	0	0	0.0470419	0.0589944	ENSG00000254993	TRIM77BP
ENSG00000254995	7.73669	3.13771	13.1623	4.28543	ENSG00000254995	STX16-NPEPL1
ENSG00000254996	0.502126	1.57026	1.61405	3.72563	ENSG00000254996	ANKHD1-EIF4EBP3
ENSG00000254997	0	0.0971279	0	0.0550785	ENSG00000254997	KRTAP5-9
ENSG00000254999	38.3682	21.9982	20.3911	21.1026	ENSG00000254999	BRK1
ENSG00000255000	0.476874	0.344155	0.207352	0.129901	ENSG00000255000	AC139103.1
ENSG00000255001	0	15.9462	9.43344	12.9762	ENSG00000255001	AC109635.3
ENSG00000255003	0.310687	0.294845	0.799175	0	ENSG00000255003	CYCSP28
ENSG00000255006	0	0	0	0	ENSG00000255006	ELOCP22
ENSG00000255009	0	0	0	0	ENSG00000255009	UBTFL1
ENSG00000255010	0.230238	0	0	0.246388	ENSG00000255010	AP001767.2
ENSG00000255011	0.398503	0	0	0	ENSG00000255011	AP004607.5
ENSG00000255012	0	0	0	0	ENSG00000255012	OR5M1
ENSG00000255014	0	0	0	0	ENSG00000255014	ARL6IP1P3
ENSG00000255016	0	0	0	0	ENSG00000255016	AC107918.2
ENSG00000255018	0	0	0	0	ENSG00000255018	AC022878.1
ENSG00000255019	0	0	0	0	ENSG00000255019	OR5D15P
ENSG00000255022	0	0.381252	0.298175	0	ENSG00000255022	AP000676.2
ENSG00000255025	0	0	0	0	ENSG00000255025	AF228730.5
ENSG00000255030	0.139403	0.353423	0.436441	1.42827	ENSG00000255030	AP001804.2
ENSG00000255033	0	0	0	0	ENSG00000255033	SERPINA15P
ENSG00000255035	0	0	0	0	ENSG00000255035	SDHCP4
ENSG00000255037	0.646766	0	0	0	ENSG00000255037	AC136443.2
ENSG00000255038	0.444284	1.14593	1.10168	0.410275	ENSG00000255038	AP006287.2
ENSG00000255040	0	0.279336	0.23176	0.30972	ENSG00000255040	MORF4L1P3
ENSG00000255042	0	0	0	0	ENSG00000255042	AC109635.4
ENSG00000255046	4.7459	5.48211	12.7755	21.1605	ENSG00000255046	AC069185.1
ENSG00000255047	0	0.172951	0.154359	0.673637	ENSG00000255047	HNRNPRP2
ENSG00000255048	0	0.140634	0.381237	0.476577	ENSG00000255048	OR8X1P
ENSG00000255051	0	0.105341	0.193848	0.122779	ENSG00000255051	BCAS2P1
ENSG00000255053	0	0	0	0	ENSG00000255053	OR4A44P
ENSG00000255054	0.420085	0	0.588841	0	ENSG00000255054	AL020996.2
ENSG00000255055	0	0	0	0	ENSG00000255055	MTND1P35
ENSG00000255057	0.786952	0.97666	1.60618	2.52595	ENSG00000255057	AP003041.2
ENSG00000255058	0	0	0	0.88087	ENSG00000255058	PDCL2P2

ENSG00000255059	0	0	0.136468	0	ENSG00000255059	AP000620.1
ENSG00000255062	0.796533	1.00335	1.72959	2.29592	ENSG00000255062	AP001318.3
ENSG00000255063	0	0	0	0	ENSG00000255063	AP001646.2
ENSG00000255065	0	0	0	0.0867161	ENSG00000255065	AP002001.2
ENSG00000255070	0	0	0.103636	0	ENSG00000255070	OSBPL9P3
ENSG00000255072	8.55611	2.1406	5.17809	0	ENSG00000255072	PIGY
ENSG00000255073	0.852723	1.31074	0.814903	0.857252	ENSG00000255073	ZFP91-CNTF
ENSG00000255074	0.440567	0.140791	0.381459	0.663405	ENSG00000255074	AC018523.1
ENSG00000255075	0	0	0	0	ENSG00000255075	CENPUP1
ENSG00000255077	0	1.60057	0.702421	0.850648	ENSG00000255077	AP005639.1
ENSG00000255078	0.128051	0.184767	0.111317	0.557497	ENSG00000255078	OR4A6P
ENSG00000255083	0	0	0	0	ENSG00000255083	OR5AK1P
ENSG00000255085	1.03677	1.12397	1.34008	1.79	ENSG00000255085	AF186192.2
ENSG00000255086	1.00583	0.53932	0.129759	0.40794	ENSG00000255086	AC024341.1
ENSG00000255088	0	0	0	0	ENSG00000255088	AC013828.2
ENSG00000255093	0	0.121421	0	0.135915	ENSG00000255093	AP002008.2
ENSG00000255095	0	0	0	0	ENSG00000255095	OR1D4
ENSG00000255096	0.21487	0	0	0	ENSG00000255096	OR5B10P
ENSG00000255098	2.99561	4.43663	11.2276	3.08082	ENSG00000255098	RP11-481A20.11
ENSG00000255099	0.0184006	0	0.0160412	0.0404698	ENSG00000255099	AC023245.2
ENSG00000255103	10.4241	10.2112	5.49526	17.3883	ENSG00000255103	KIAA0754
ENSG00000255104	0.0881342	0.118185	0.060932	0.139622	ENSG00000255104	AC005324.4
ENSG00000255105	1.88559	2.80997	1.58257	0.767811	ENSG00000255105	AC007751.2
ENSG00000255106	0	0	0	0	ENSG00000255106	AC010768.3
ENSG00000255107	0	0	0	0.0511147	ENSG00000255107	AC079089.2
ENSG00000255110	0	0	0	0	ENSG00000255110	AP005597.2
ENSG00000255111	0.212401	0.136814	0.316843	0.098387	ENSG00000255111	AP006587.3
ENSG00000255112	35.65	23.8839	27.0717	22.2448	ENSG00000255112	CHMP1B
ENSG00000255113	0	0	0	0	ENSG00000255113	OR4A48P
ENSG00000255115	1.53216	2.71513	1.8903	1.82066	ENSG00000255115	AP002812.4
ENSG00000255116	0.486373	0.560374	0.11048	1.30431	ENSG00000255116	SLC5A4P1
ENSG00000255122	0.912684	0	1.77598	2.08841	ENSG00000255122	AC068587.4
ENSG00000255123	0.0155926	0.424534	0.779839	0.633872	ENSG00000255123	MTND5P21
ENSG00000255127	0	0	0	0	ENSG00000255127	AP003171.2
ENSG00000255128	0.0371972	0	0	0	ENSG00000255128	AC130360.2
ENSG00000255131	0.269542	0.129042	0.174901	0.583788	ENSG00000255131	OR9L1P
ENSG00000255134	2.65595	4.12034	7.53407	12.6733	ENSG00000255134	OR8K2P
ENSG00000255138	0	0	0	0	ENSG00000255138	GLTPP1
ENSG00000255140	0	0.325587	0.294044	0.565894	ENSG00000255140	AC068339.2
ENSG00000255141	0.979549	1.69555	1.27779	1.39854	ENSG00000255141	HNRNPA1P76
ENSG00000255144	0	0.449269	0.202938	0	ENSG00000255144	AC025857.1
ENSG00000255147	0	0	0	0	ENSG00000255147	AP003385.6
ENSG00000255149	0	2.64303	2.32141	0.938081	ENSG00000255149	AP002963.1
ENSG00000255150	1.72109	6.12873	2.49306	7.87193	ENSG00000255150	EID3
ENSG00000255151	0	0	0	1.28E-06	ENSG00000255151	GLYATL1P3
ENSG00000255152	0.224861	0.426415	0.240836	0	ENSG00000255152	MSH5-SAPCD1
ENSG00000255154	0	0	0.414761	0	ENSG00000255154	HTD2
ENSG00000255155	0	0	0	0.678971	ENSG00000255155	AP004371.1
ENSG00000255157	0	1.64178	0.4614	0	ENSG00000255157	DEFB130C
ENSG00000255161	0	0.0855727	0	0	ENSG00000255161	AC113192.3
ENSG00000255162	0	0.0771944	0	0	ENSG00000255162	AP004833.2
ENSG00000255163	0	0	0.3425	0	ENSG00000255163	HSPE1P18
ENSG00000255166	1.77731	0	0	0	ENSG00000255166	AC022616.7
ENSG00000255168	3.96677	3.27074	2.20282	3.16151	ENSG00000255168	RP11-458D21.5

ENSG00000255170	0	0	1.20635	0	ENSG00000255170	AP003122.3
ENSG00000255172	0.0594725	0.116657	0.370978	0.131892	ENSG00000255172	OR5AM1P
ENSG00000255174	0	0.219856	0	0	ENSG00000255174	AC107918.3
ENSG00000255181	0.0579115	0	0	0	ENSG00000255181	CCDC166
ENSG00000255184	0	0.0958259	0.0433053	0.271733	ENSG00000255184	AP004607.6
ENSG00000255185	22.5485	39.443	35.6454	37.4528	ENSG00000255185	PDXDC2P
ENSG00000255188	0	2.02395	0	0	ENSG00000255188	AP003327.1
ENSG00000255189	0	0.06905	0	0	ENSG00000255189	GLYATL1P1
ENSG00000255190	0	0	0	0	ENSG00000255190	TRIM51DP
ENSG00000255192	0.151456	0.382148	0.525456	0.66039	ENSG00000255192	NANOGP8
ENSG00000255194	0	0	0	0	ENSG00000255194	SSU72P2
ENSG00000255196	0	0.0670271	0.0605631	0	ENSG00000255196	OR4A17P
ENSG00000255199	1.01606	0.55764	0	1.73996	ENSG00000255199	GTF2IP11
ENSG00000255200	3.41933	4.63783	4.12444	6.01133	ENSG00000255200	PGAM1P8
ENSG00000255203	0.0947884	0.410408	1.72237	0.695636	ENSG00000255203	OR7E2P
ENSG00000255204	0	0	0	0.45641	ENSG00000255204	AC036111.2
ENSG00000255205	0	0	0	0	ENSG00000255205	MED28P5
ENSG00000255207	1.42034	1.3464	0.622185	2.57842	ENSG00000255207	AL133399.1
ENSG00000255210	0.109465	0.420481	0.0959065	0.118011	ENSG00000255210	AP001889.1
ENSG00000255211	0	0	0.0506732	0	ENSG00000255211	AC130365.2
ENSG00000255213	0	0	0	0.119866	ENSG00000255213	NPM1P35
ENSG00000255214	0	0	0	0	ENSG00000255214	AP006587.4
ENSG00000255215	0	0	0	0	ENSG00000255215	OR4R1P
ENSG00000255217	0	0.187862	0.169585	0.41662	ENSG00000255217	AP003034.1
ENSG00000255218	0.0895226	0	0	0.0968853	ENSG00000255218	OR5BC1P
ENSG00000255220	0.644192	1.41467	0.971695	1.27093	ENSG00000255220	DDX18P5
ENSG00000255221	2.79134	2.99035	3.46137	0.359394	ENSG00000255221	CARD17
ENSG00000255222	0.0789046	0	0.216086	0.342385	ENSG00000255222	SETP17
ENSG00000255223	0	0.117135	0.0529295	0	ENSG00000255223	OR5M11
ENSG00000255225	0.288035	0.210114	0.128739	0.258343	ENSG00000255225	AP001804.3
ENSG00000255230	0	0	0	0	ENSG00000255230	AC004923.3
ENSG00000255231	0	0	0.646502	0	ENSG00000255231	MRPS36P4
ENSG00000255232	0.452622	1.45786	1.54018	2.60921	ENSG00000255232	AC087441.2
ENSG00000255235	0	0	0	0	ENSG00000255235	AP005435.4
ENSG00000255238	0.0751316	0.144491	0.130562	0	ENSG00000255238	RFPL4AP1
ENSG00000255239	0	0.0810189	0.0731318	0.139085	ENSG00000255239	TREHP1
ENSG00000255245	0	0	0	0	ENSG00000255245	FXYD6-FXYD2
ENSG00000255251	0	0.0350081	0.0316456	0	ENSG00000255251	PRR23D1
ENSG00000255253	0	0	0	0	ENSG00000255253	AC068587.5
ENSG00000255254	0	0	0	0	ENSG00000255254	HIGD1AP5
ENSG00000255255	0	0.371539	0.861364	0.824326	ENSG00000255255	PPP1R1AP1
ENSG00000255259	0.0500563	0	0.0871108	0.0546578	ENSG00000255259	ZNF123P
ENSG00000255261	0	0	0	0	ENSG00000255261	OR7E4P
ENSG00000255262	0	0	0	0	ENSG00000255262	ELOBP2
ENSG00000255265	0	0	0	0.121776	ENSG00000255265	TMA16P1
ENSG00000255266	1.00757	0.933793	0.834589	0.503476	ENSG00000255266	AP003484.1
ENSG00000255268	0	0	0	0	ENSG00000255268	AC130364.2
ENSG00000255273	0	0	0	0	ENSG00000255273	AF238378.1
ENSG00000255275	0.155912	0.38562	0.250605	0.264681	ENSG00000255275	AL080251.1
ENSG00000255277	0	0.178308	0	0.136376	ENSG00000255277	ABCC6P2
ENSG00000255280	0	0	0.318543	0	ENSG00000255280	AP001922.4
ENSG00000255281	0.0685467	0.0330214	0.0597007	0.225337	ENSG00000255281	AC090124.3
ENSG00000255282	1.0633	1.90773	1.81877	2.49982	ENSG00000255282	WTAPP1
ENSG00000255283	0	1.73416	2.00973	0.948281	ENSG00000255283	AP005597.3

ENSG00000255284	9.0206	14.5958	11.1422	15.8543	ENSG00000255284	AP006621.3
ENSG00000255285	0	0	0	0	ENSG00000255285	AP004833.3
ENSG00000255286	0	0.250517	0.274541	0	ENSG00000255286	AP000907.2
ENSG00000255287	0	0	0	0	ENSG00000255287	SNRPGP16
ENSG00000255288	0	0	0	0	ENSG00000255288	AL358944.1
ENSG00000255291	0	0	0.299368	0.18194	ENSG00000255291	HMGB1P40
ENSG00000255292	0.0958798	0.431136	0.67994	0.207456	ENSG00000255292	SDHD
ENSG00000255293	0	0.0234117	0	0	ENSG00000255293	WIZP1
ENSG00000255294	0.158386	0.455425	0	0.169149	ENSG00000255294	OR4A50P
ENSG00000255295	0	0	0	0	ENSG00000255295	AP002404.1
ENSG00000255296	0.521608	0.248277	0.13992	0.834237	ENSG00000255296	AP002490.2
ENSG00000255297	0	0	0	0	ENSG00000255297	OR4A41P
ENSG00000255298	0	0	0	0	ENSG00000255298	OR8G5
ENSG00000255302	32.7736	19.5578	21.6786	27.0619	ENSG00000255302	EID1
ENSG00000255303	2.46054	0.242771	1.04229	0.961576	ENSG00000255303	OR5BA1P
ENSG00000255304	0	0	0	0	ENSG00000255304	OR4A46P
ENSG00000255305	0.0790817	0	0.120246	0.039227	ENSG00000255305	AP004607.7
ENSG00000255307	0.0564303	0.162927	0.294498	0.246121	ENSG00000255307	OR52B2
ENSG00000255309	0.290989	0	0.249965	1.21718	ENSG00000255309	AC131935.1
ENSG00000255312	0	0	0	0	ENSG00000255312	OR4C7P
ENSG00000255315	0	0	0	0	ENSG00000255315	AP000916.2
ENSG00000255316	0	0.139238	0	0	ENSG00000255316	MTND6P25
ENSG00000255319	3.17533	10.3985	26.4275	39.813	ENSG00000255319	ENPP7P8
ENSG00000255329	0.959989	3.51388	2.30191	2.5344	ENSG00000255329	H2AFZP4
ENSG00000255330	0.0122903	0.863489	1.24935	3.75809	ENSG00000255330	SOGA3
ENSG00000255331	0.0898238	0.172621	0	0.291643	ENSG00000255331	AP000790.1
ENSG00000255333	0	0	0	0	ENSG00000255333	AP000435.1
ENSG00000255336	0	0	0	0	ENSG00000255336	AP003181.2
ENSG00000255338	0	0	0	0	ENSG00000255338	AC118273.2
ENSG00000255339	0.679848	2.20594	1.31516	2.44036	ENSG00000255339	AL133352.1
ENSG00000255341	0	0	0	0	ENSG00000255341	OR8Q1P
ENSG00000255342	0.350834	0.50376	0.606562	4.1068	ENSG00000255342	AP000926.4
ENSG00000255346	2.01487	3.83275	3.85672	5.9347	ENSG00000255346	NOX5
ENSG00000255347	0.160001	0	0	0.433819	ENSG00000255347	AC021820.1
ENSG00000255349	0	0	0	0	ENSG00000255349	OR4A7P
ENSG00000255350	0.0759265	0.146274	0.218617	0.806599	ENSG00000255350	MTCO1P15
ENSG00000255352	0.126863	0.183366	0.110508	0.243512	ENSG00000255352	PPP1R10P1
ENSG00000255353	0.14367	0.0466528	0.0418683	0	ENSG00000255353	AP003057.1
ENSG00000255356	0	0	0	0	ENSG00000255356	AC007536.1
ENSG00000255358	0.442999	1.55747	2.17315	3.19601	ENSG00000255358	AC019227.1
ENSG00000255359	0.284524	0.157928	0.205622	0.340478	ENSG00000255359	CCDC179
ENSG00000255360	0	0	0	0	ENSG00000255360	AP004607.8
ENSG00000255361	0	0.480924	0.0888452	0.708563	ENSG00000255361	AC103843.2
ENSG00000255365	0	0	0.457612	0	ENSG00000255365	AC040926.1
ENSG00000255368	0.15605	0	0	0	ENSG00000255368	AC087373.1
ENSG00000255369	0	1.04653	0.472746	0.288081	ENSG00000255369	AP000920.1
ENSG00000255370	0	0	0	0	ENSG00000255370	CYCSP25
ENSG00000255374	0	1.71026	0	0	ENSG00000255374	TAS2R43
ENSG00000255376	0.13099	0	0	0.140587	ENSG00000255376	AP003066.2
ENSG00000255377	0	0	0	0	ENSG00000255377	DUXAP5
ENSG00000255378	0	0.0350081	0.0316456	0	ENSG00000255378	PRR23D2
ENSG00000255379	0	0.304565	1.37843	2.63391	ENSG00000255379	CYCSP29
ENSG00000255380	0	0	0	0	ENSG00000255380	AP001317.1
ENSG00000255381	0	0	0.406295	0.167174	ENSG00000255381	AP001258.2

ENSG00000255384	1.20598	1.78072	1.68939	2.75395	ENSG00000255384	AP001267.2
ENSG00000255385	0	0	0	0.138211	ENSG00000255385	UBTFL10
ENSG00000255386	0.088645	0.128046	0.154318	0.0969178	ENSG00000255386	OR5BR1P
ENSG00000255387	0	0	0.0287746	0.0724166	ENSG00000255387	AC015689.2
ENSG00000255391	0	0.123519	0.11151	0	ENSG00000255391	AP003497.1
ENSG00000255394	1.64406	1.38412	0.917277	1.8193	ENSG00000255394	C8orf49
ENSG00000255396	0	0.647914	0.116976	0.434433	ENSG00000255396	AP000857.1
ENSG00000255397	0	0.0800029	0.0238349	0.0292507	ENSG00000255397	AC022182.3
ENSG00000255398	3.61829	2.66076	1.4134	0.317474	ENSG00000255398	HCAR3
ENSG00000255401	0	0.561779	0.253865	0	ENSG00000255401	AC021269.2
ENSG00000255403	0	0	0.0305352	0	ENSG00000255403	AP000641.1
ENSG00000255408	0	0.0228668	0.0488055	0.0861342	ENSG00000255408	PCDHA3
ENSG00000255413	0	0	0	0	ENSG00000255413	AC022880.1
ENSG00000255415	0	0	0	0	ENSG00000255415	AP000867.3
ENSG00000255416	0	0.0772573	0	0	ENSG00000255416	AP003033.2
ENSG00000255417	0	0.300855	0.260938	1.17949	ENSG00000255417	MTCO2P15
ENSG00000255419	0.679768	1.82221	0.626018	0.33876	ENSG00000255419	MSH5-SAPCD1
ENSG00000255423	3.20066	6.04326	4.02452	5.65338	ENSG00000255423	EBLN2
ENSG00000255424	3.74057	2.73833	0.773114	7.48165	ENSG00000255424	AC027026.1
ENSG00000255425	0	0	0	0	ENSG00000255425	OR8G3P
ENSG00000255430	0	0	0	0	ENSG00000255430	CASP1P1
ENSG00000255431	0	0	0	0	ENSG00000255431	OR5B19P
ENSG00000255432	0	0.438949	0	0	ENSG00000255432	AP001458.2
ENSG00000255436	0	0	0	0	ENSG00000255436	Z95704.2
ENSG00000255437	0	0	0	0	ENSG00000255437	AC023538.1
ENSG00000255439	0.820984	1.03709	0.674858	1.07221	ENSG00000255439	AC135050.2
ENSG00000255442	0	0	0	0	ENSG00000255442	AC109635.5
ENSG00000255444	0	0	0	0	ENSG00000255444	CYCSP27
ENSG00000255445	0.401495	1.06073	1.21941	1.19278	ENSG00000255445	AP003072.2
ENSG00000255450	0	0.265618	0	0.0750709	ENSG00000255450	AC110056.1
ENSG00000255452	0.249555	0	0	0	ENSG00000255452	AC084851.2
ENSG00000255454	0	0	0.264967	2.90118	ENSG00000255454	AC100770.1
ENSG00000255457	0	0	0	0.438644	ENSG00000255457	AC022880.2
ENSG00000255459	1.54437	2.09713	3.28834	5.27275	ENSG00000255459	AC105233.3
ENSG00000255460	0	0	0	0.334005	ENSG00000255460	ZDHHC20P3
ENSG00000255461	0	0	0	0	ENSG00000255461	OR8I1P
ENSG00000255463	0	0	0	0	ENSG00000255463	AC011979.2
ENSG00000255464	4.74348	0	0	0	ENSG00000255464	SEPT14P8
ENSG00000255466	0	0.0656208	0	0.148391	ENSG00000255466	OR5AL2P
ENSG00000255468	21.7591	48.2897	48.9969	103.783	ENSG00000255468	AP001107.9
ENSG00000255469	0	0	0	0	ENSG00000255469	BOLA3P1
ENSG00000255470	0.0719043	0.1184	0.106912	0	ENSG00000255470	AC090099.4
ENSG00000255472	0.554896	1.10408	0.361042	1.77684	ENSG00000255472	AL161668.2
ENSG00000255481	0	0.127724	0	0	ENSG00000255481	OR56A7P
ENSG00000255482	0	0	0.133856	0	ENSG00000255482	AP001830.2
ENSG00000255483	0	0	0	0	ENSG00000255483	AP000889.2
ENSG00000255485	0	0	0	0	ENSG00000255485	OR5G4P
ENSG00000255486	0	0	0	0	ENSG00000255486	AP003122.4
ENSG00000255489	0	0	0	0	ENSG00000255489	AC115990.1
ENSG00000255490	0	0	0	0	ENSG00000255490	EIF4A2P5
ENSG00000255492	0.242767	4.63037	1.88352	2.3023	ENSG00000255492	AC104383.1
ENSG00000255493	0	0	0	0	ENSG00000255493	AP005639.2
ENSG00000255497	0	0	0	0	ENSG00000255497	AC022616.8
ENSG00000255499	17.5261	6.42184	6.11891	1.78535	ENSG00000255499	AC036111.3

ENSG00000255500	0	0	0	0	ENSG00000255500	AC109635.6
ENSG00000255501	20.6053	3.53834	4.66896	6.33129	ENSG00000255501	CARD18
ENSG00000255504	1.61882	3.88386	1.88228	6.22936	ENSG00000255504	AP001533.1
ENSG00000255505	0	0	0	0	ENSG00000255505	AC079064.1
ENSG00000255508	1.14827	1.28181	2.0021	1.59639	ENSG00000255508	AP002990.1
ENSG00000255510	0	0	0.0569129	0.0712481	ENSG00000255510	OR8A2P
ENSG00000255511	0.0665666	0.0962072	0	0.0730592	ENSG00000255511	AC023078.6
ENSG00000255513	0.996861	0	0.579528	0	ENSG00000255513	AC005363.1
ENSG00000255514	0	0	0	0	ENSG00000255514	OR4B2P
ENSG00000255515	0	0	0	0	ENSG00000255515	AP003499.1
ENSG00000255519	0	0	0	0	ENSG00000255519	AC103855.4
ENSG00000255522	0	0	0	0	ENSG00000255522	SNRPCP5
ENSG00000255524	0.302437	0.321756	0.487421	0.465933	ENSG00000255524	NPIPB8
ENSG00000255526	0.794472	0.708337	0.648223	0	ENSG00000255526	NEDD8-MDP1
ENSG00000255527	0	0	0	0	ENSG00000255527	AC027369.5
ENSG00000255529	14.942	12.9258	17.3933	9.48728	ENSG00000255529	POLR2M
ENSG00000255530	0.544375	0	0	0.285297	ENSG00000255530	AF235103.2
ENSG00000255531	0	0	0	0	ENSG00000255531	NDUFS5P6
ENSG00000255532	0	0	0.0515429	0.0672494	ENSG00000255532	AC118942.1
ENSG00000255533	0	0	0	0	ENSG00000255533	AC136475.6
ENSG00000255534	0	0.0666699	0.120481	0.128527	ENSG00000255534	OR4A43P
ENSG00000255535	0.0947284	0	0.16444	0.102421	ENSG00000255535	AP003041.3
ENSG00000255536	0	0.0622727	0	0	ENSG00000255536	AC023078.7
ENSG00000255537	3.75784	7.73445	7.52159	11.8901	ENSG00000255537	AP000708.1
ENSG00000255538	0.0858183	0.0824781	0.149021	0.0929622	ENSG00000255538	OR10V2P
ENSG00000255540	0	0	0.0625993	0	ENSG00000255540	AP003122.5
ENSG00000255541	0	0.601635	0.464677	0	ENSG00000255541	AP000873.5
ENSG00000255543	0	0	0	0	ENSG00000255543	AP005597.4
ENSG00000255544	0	0	0	0	ENSG00000255544	DEFB108D
ENSG00000255547	0	0	0	0	ENSG00000255547	RPA2P3
ENSG00000255549	0	0.605504	0	0.863007	ENSG00000255549	ENPP7P6
ENSG00000255550	0	0	0	0	ENSG00000255550	AP006587.5
ENSG00000255551	0	0	0	0	ENSG00000255551	AC027369.6
ENSG00000255552	0.0327519	0.873338	0.449344	1.54458	ENSG00000255552	LY6G6E
ENSG00000255554	0.0649887	0	0	0	ENSG00000255554	OR7E1P
ENSG00000255556	0	0.0722485	0.19864	0.281279	ENSG00000255556	AC087203.2
ENSG00000255560	0	0	0	0	ENSG00000255560	OR4R2P
ENSG00000255561	1.44115	1.34663	0.940187	1.12964	ENSG00000255561	FDXACB1
ENSG00000255562	0.0582034	0	0.0880466	0.141741	ENSG00000255562	UNC93B6
ENSG00000255563	0.912979	3.73742	1.55092	2.12515	ENSG00000255563	AC021006.3
ENSG00000255566	0.459727	7.23527	6.49431	5.61774	ENSG00000255566	AC135279.1
ENSG00000255569	0	0	0	0	ENSG00000255569	TRAV1-1
ENSG00000255575	0	2.95175	2.55011	0	ENSG00000255575	AC004812.1
ENSG00000255581	0	0.0996883	0	0.111959	ENSG00000255581	AC006511.2
ENSG00000255582	0	0	0	0	ENSG00000255582	OR10G2
ENSG00000255583	0	0	0	0	ENSG00000255583	AC084357.3
ENSG00000255585	0.240371	0.932308	1.35613	2.87703	ENSG00000255585	AL590627.1
ENSG00000255587	0.200437	0.271621	0.209756	0.264405	ENSG00000255587	RAB44
ENSG00000255591	0.6829	0	0.817892	0	ENSG00000255591	AL590762.1
ENSG00000255594	0	0	0	3.19807	ENSG00000255594	Z82188.1
ENSG00000255619	0	0	0.0106603	0	ENSG00000255619	CT476828.3
ENSG00000255622	0.0379028	0.0873755	0	0.0405402	ENSG00000255622	PCDHB17P
ENSG00000255624	1.97404	4.22263	2.43337	1.55452	ENSG00000255624	AC073585.1
ENSG00000255627	0.554513	0.269364	0.734204	0.44566	ENSG00000255627	AC092862.1

ENSG00000255633	17018.3	16320.5	18959	17904	ENSG00000255633	MTRNR2L9
ENSG00000255637	0	0	0	14.6739	ENSG00000255637	AC109992.1
ENSG00000255638	0	0	0.0106603	0	ENSG00000255638	CT476828.4
ENSG00000255639	0	0.319988	0.245663	0.468866	ENSG00000255639	AC005833.3
ENSG00000255641	0	0	0.245181	0	ENSG00000255641	AC068775.2
ENSG00000255642	0.091193	0.393047	0.44926	0.199195	ENSG00000255642	PABPC1P4
ENSG00000255647	0.30951	1.18912	0.626527	0.445461	ENSG00000255647	AC093510.1
ENSG00000255653	0	0	0.0436344	0	ENSG00000255653	AP002383.2
ENSG00000255663	0	0.239614	0.743908	0.685699	ENSG00000255663	AP002373.1
ENSG00000255664	0.115052	0	0	0	ENSG00000255664	ARL6IP1P1
ENSG00000255674	0	0	0	0	ENSG00000255674	AC013718.1
ENSG00000255681	15.3566	9.26589	12.4535	38.5609	ENSG00000255681	AC084125.1
ENSG00000255690	0.0318107	0.0920548	0.138724	0.213851	ENSG00000255690	TRIL
ENSG00000255692	0.194218	0.515166	0.15318	0.56555	ENSG00000255692	AC002563.1
ENSG00000255700	0.121499	0	0	0.130655	ENSG00000255700	APOOP3
ENSG00000255701	0.486162	1.08918	0.215959	0.947681	ENSG00000255701	AC090953.1
ENSG00000255703	0.227325	0	0.400519	0.48009	ENSG00000255703	AC127070.4
ENSG00000255704	0	0	0	0	ENSG00000255704	AC140063.1
ENSG00000255707	0	0	0.0106603	0	ENSG00000255707	CT476828.5
ENSG00000255710	0.178828	1.14718	0.933086	1.10416	ENSG00000255710	AP003170.1
ENSG00000255713	0.0678815	0.326392	0.294921	0.664315	ENSG00000255713	OR4D2
ENSG00000255725	0	0	0	0	ENSG00000255725	TDGP1
ENSG00000255726	0	1.82617	0.803968	0	ENSG00000255726	AL662844.1
ENSG00000255729	1.73125	1.38235	2.34936	1.62111	ENSG00000255729	AC005618.1
ENSG00000255730	2.89797	1.82928	2.73014	2.33848	ENSG00000255730	AC011462.1
ENSG00000255734	0	0.088638	0.0801036	0	ENSG00000255734	HNRNPABP1
ENSG00000255735	0.843555	0.87964	1.48622	0.36687	ENSG00000255735	AC110619.1
ENSG00000255737	2.66472	3.70086	2.45808	4.36605	ENSG00000255737	AGAP2-AS1
ENSG00000255743	0	15.8772	0	2.93479	ENSG00000255743	AL360078.1
ENSG00000255748	1.12711	1.08114	1.34211	1.05632	ENSG00000255748	AC226150.4
ENSG00000255749	0	0	0.275371	0	ENSG00000255749	GNAI2P1
ENSG00000255752	0	0	0	0	ENSG00000255752	AL451105.1
ENSG00000255753	0.62076	3.20674	0.63046	1.50849	ENSG00000255753	AC009533.2
ENSG00000255757	30.5696	68.3273	66.1134	168.994	ENSG00000255757	AC087894.1
ENSG00000255763	0	0.542565	0	0	ENSG00000255763	MRPS18CP4
ENSG00000255767	3.03921	6.59927	4.13194	3.76289	ENSG00000255767	AC108488.2
ENSG00000255769	4.17829	6.08673	4.93245	3.83736	ENSG00000255769	GOLGA2P10
ENSG00000255776	0	0	0	0.152137	ENSG00000255776	VDAC2P2
ENSG00000255780	0.962428	2.26449	2.11138	2.69188	ENSG00000255780	AC020611.1
ENSG00000255782	0	0	0	0	ENSG00000255782	Z83840.1
ENSG00000255783	2.84538	8.69829	0	0	ENSG00000255783	AC018692.3
ENSG00000255786	0	0.865657	0.521683	2.85558	ENSG00000255786	AP000763.1
ENSG00000255798	0.554251	0.665257	0.184789	0.103515	ENSG00000255798	RP11-817J15.3
ENSG00000255800	0.0529713	0	0	0.0578032	ENSG00000255800	OR13C5
ENSG00000255804	0.058665	0.16936	0.255099	0.575416	ENSG00000255804	OR6J1
ENSG00000255807	0	0	0.15164	0	ENSG00000255807	PTP4A1P2
ENSG00000255813	1.55742	5.02932	5.30207	5.22535	ENSG00000255813	AL162497.1
ENSG00000255815	0.115367	0.0500812	0.101279	0	ENSG00000255815	KRT8P11
ENSG00000255819	0.0290979	0.412709	0.192155	0.461204	ENSG00000255819	KLRC4-KLRK1
ENSG00000255823	84710.6	84804.2	135921	136478	ENSG00000255823	MTRNR2L8
ENSG00000255824	0	2.37837	2.06665	0.73786	ENSG00000255824	AL590369.1
ENSG00000255830	0	0	0	0	ENSG00000255830	AC069240.1
ENSG00000255831	1.69781	1.24554	2.29737	4.08263	ENSG00000255831	AL139385.1
ENSG00000255833	0.0809752	0.191003	0.2257	0.285966	ENSG00000255833	TIFAB

ENSG00000255835	0.143077	0.162907	0.132862	0	ENSG00000255835	AL117348.2
ENSG00000255836	0.0544647	0.10213	0	0.298938	ENSG00000255836	AC131206.1
ENSG00000255837	0.0990988	1.0311	0.455987	0.727775	ENSG00000255837	TAS2R20
ENSG00000255838	0	0	0	0	ENSG00000255838	AC069262.1
ENSG00000255840	15.3961	18.3676	24.1213	0	ENSG00000255840	AC022555.1
ENSG00000255851	26.1545	53.4718	62.6701	76.1163	ENSG00000255851	AC061975.9
ENSG00000255853	0	0	0.0701231	0.0875599	ENSG00000255853	AC006065.1
ENSG00000255854	0.42727	0	0.950324	0.16126	ENSG00000255854	PPIAL4B
ENSG00000255855	0	0	0	0	ENSG00000255855	KDM4F
ENSG00000255860	0.237264	0	0.572684	0.106543	ENSG00000255860	AP000812.2
ENSG00000255863	0	0	0	0	ENSG00000255863	AC073610.2
ENSG00000255870	0	0.0853194	0.215718	0	ENSG00000255870	AP003170.2
ENSG00000255872	0.16336	0.696558	0.598219	1.80267	ENSG00000255872	AL138752.2
ENSG00000255874	0	0.116883	0.422196	0.392862	ENSG00000255874	LINC00346
ENSG00000255875	0.357596	0.344691	0.752472	0.468525	ENSG00000255875	AC008813.1
ENSG00000255883	0.200854	0.137905	0.428276	0	ENSG00000255883	FUNDC2P1
ENSG00000255885	0	0	0	0	ENSG00000255885	AC124891.1
ENSG00000255892	0	0.543508	0.613358	0.151702	ENSG00000255892	NDFIP1P1
ENSG00000255899	0	0	0	0	ENSG00000255899	AL662844.2
ENSG00000255900	0	0	1.15926	0	ENSG00000255900	AC006065.2
ENSG00000255902	0	0	0.583333	0.227797	ENSG00000255902	AP001062.1
ENSG00000255903	0	0	0	0	ENSG00000255903	RPL12P46
ENSG00000255905	0	0.197752	0	0.0934497	ENSG00000255905	AL391319.1
ENSG00000255909	0	0.687258	0.304157	0.448106	ENSG00000255909	PDCD5P1
ENSG00000255913	155.385	215.579	244.121	471.688	ENSG00000255913	AL805909.1
ENSG00000255915	0.770811	0.729783	1.64222	0.397773	ENSG00000255915	AC113134.1
ENSG00000255919	0.168606	0.969089	0.728962	2.15636	ENSG00000255919	AC226150.1
ENSG00000255923	0	0	0	0	ENSG00000255923	AC078878.1
ENSG00000255927	0	0	0	0	ENSG00000255927	AC005000.1
ENSG00000255940	0	0	0	0	ENSG00000255940	REXO1L10P
ENSG00000255951	0.262644	0.377982	0.455011	0.992728	ENSG00000255951	AC022364.2
ENSG00000255960	0	0.947246	0.982942	0.692836	ENSG00000255960	AC092851.1
ENSG00000255963	0.42727	0	0.950324	0.16126	ENSG00000255963	PPIAL4A
ENSG00000255964	0	0	0	0	ENSG00000255964	HSPD1P12
ENSG00000255965	7.34531	3.8153	7.30769	33.0497	ENSG00000255965	AC073916.1
ENSG00000255967	0.424314	0.07133	0.236238	0.271079	ENSG00000255967	HADHAP2
ENSG00000255972	0	0	0	0	ENSG00000255972	AC026333.1
ENSG00000255973	0	0.35558	0	0.388439	ENSG00000255973	AC137627.1
ENSG00000255974	0.294548	0.492044	0.0893977	0.485108	ENSG00000255974	CYP2A6
ENSG00000255976	0.648577	1.76497	1.03125	0	ENSG00000255976	RAB11AP2
ENSG00000255977	0	0	0	0	ENSG00000255977	AC006927.1
ENSG00000255982	0.0915595	0.0879799	0.0794762	0.198109	ENSG00000255982	NXPE2P1
ENSG00000255986	0.444371	4.32097	0.658907	2.73898	ENSG00000255986	MT1JP
ENSG00000255987	0	0	0	0	ENSG00000255987	TOMM20P2
ENSG00000255988	3.03454	1.99476	1.96854	3.1338	ENSG00000255988	TUBB4BP1
ENSG00000255990	0	0	0	2.53877	ENSG00000255990	AC034102.1
ENSG00000255991	0	0	0	0	ENSG00000255991	AC121334.1
ENSG00000255993	0	0	0.0411244	0.151518	ENSG00000255993	PSMC1P9
ENSG00000255994	0.222516	0	0	0	ENSG00000255994	CCDC177
ENSG00000255995	0	0	4.25893	0	ENSG00000255995	AP002795.1
ENSG00000255996	0	0.135439	0.238472	0.888879	ENSG00000255996	AC005906.1
ENSG00000256004	0	0	0	0.134967	ENSG00000256004	AC092490.3
ENSG00000256005	2.10209	1.33449	1.34112	0.934402	ENSG00000256005	AC093734.1
ENSG00000256014	8.77E-05	0	0	0	ENSG00000256014	AL031390.1

ENSG00000256018	12.7725	80.0468	15.1801	16.4804	ENSG00000256018	HIST1H3G
ENSG00000256019	0	0.578065	0.0765797	0.111705	ENSG00000256019	AC018630.1
ENSG00000256021	1.68059	1.47105	1.89658	0.896659	ENSG00000256021	ELOCP31
ENSG00000256024	0	0	0.0106603	0	ENSG00000256024	CT476828.6
ENSG00000256029	0.357576	0	0.437164	0.255231	ENSG00000256029	AL590560.1
ENSG00000256030	0.195581	0.563072	0	0.41511	ENSG00000256030	CBX3P4
ENSG00000256035	0	0.061665	0.111479	0.0697721	ENSG00000256035	AP000619.2
ENSG00000256037	0.233209	0.575769	0.90972	0.3765	ENSG00000256037	MRPL40P1
ENSG00000256040	0.219009	0.065927	0.599265	3.01523	ENSG00000256040	PAPPA-AS1
ENSG00000256041	0.117397	0	0	0	ENSG00000256041	AP001858.2
ENSG00000256043	1.40907	1.84426	2.00618	1.97625	ENSG00000256043	CTSO
ENSG00000256044	0	0	0	0	ENSG00000256044	AC026333.2
ENSG00000256045	6374.99	6087.32	8998.46	8658.09	ENSG00000256045	MTRNR2L10
ENSG00000256053	18.852	22.029	26.4809	31.4234	ENSG00000256053	APOPT1
ENSG00000256056	1.80731	2.92969	1.40145	7.37338	ENSG00000256056	AC087257.2
ENSG00000256060	9.74184	4.25379	5.67512	2.13838	ENSG00000256060	AC003002.1
ENSG00000256061	3.1765	3.86826	3.92491	6.72932	ENSG00000256061	DNAAF4
ENSG00000256062	2.80799	4.89155	4.53177	8.94956	ENSG00000256062	ABO
ENSG00000256066	0	0	0	0	ENSG00000256066	AC013269.1
ENSG00000256069	0.149183	0.76275	1.181	1.20748	ENSG00000256069	A2MP1
ENSG00000256070	0	0	0.178788	0.0889563	ENSG00000256070	AC016956.1
ENSG00000256073	2.13384	2.82533	3.38164	0.771521	ENSG00000256073	URB1-AS1
ENSG00000256075	0	0.0506286	0	0	ENSG00000256075	AC008033.1
ENSG00000256079	0.836797	0.903606	1.00529	0.946704	ENSG00000256079	AC092451.2
ENSG00000256081	0	0	0	0	ENSG00000256081	AC243972.2
ENSG00000256087	22.3829	10.5625	13.7412	20.25	ENSG00000256087	ZNF432
ENSG00000256091	0	0.456383	0.565611	1.67914	ENSG00000256091	MTRF1LP1
ENSG00000256093	0	0	0	0	ENSG00000256093	AC122688.1
ENSG00000256097	2.24027	1.62772	2.96207	1.66203	ENSG00000256097	LINC00696
ENSG00000256098	1.44089	2.01385	1.19225	1.46019	ENSG00000256098	AP002392.1
ENSG00000256100	0	0	0	0	ENSG00000256100	AP000721.1
ENSG00000256103	0	0	0	0	ENSG00000256103	ATP5J2P5
ENSG00000256108	0.750089	0.959721	1.73769	2.015	ENSG00000256108	AC135586.1
ENSG00000256121	0	0	0	0	ENSG00000256121	AC010296.1
ENSG00000256122	8.37701	0	18.0036	13.558	ENSG00000256122	AC093334.1
ENSG00000256125	0	0.558757	0.757731	0.615065	ENSG00000256125	AC005868.1
ENSG00000256134	0.74032	1.60052	2.57032	2.80262	ENSG00000256134	EGLN3P1
ENSG00000256136	0	0	0	0	ENSG00000256136	AC092865.5
ENSG00000256138	0.20192	0.0969904	0.0876067	0.218108	ENSG00000256138	ZKSCAN7P1
ENSG00000256142	0.503754	0.187984	0.785246	0.987809	ENSG00000256142	AL513327.1
ENSG00000256143	0	0	0	0	ENSG00000256143	Z95704.5
ENSG00000256148	1.25108	2.15227	4.10319	12.2826	ENSG00000256148	AP000763.2
ENSG00000256157	0	0	0	0	ENSG00000256157	AC011604.1
ENSG00000256159	0.160329	0.46102	0.27748	1.02703	ENSG00000256159	AC022080.3
ENSG00000256162	0.0661395	0.233796	0.134508	0.411817	ENSG00000256162	SMLR1
ENSG00000256167	0	0.115219	0.207277	0.130815	ENSG00000256167	ATF4P4
ENSG00000256171	0	0	0	0.392543	ENSG00000256171	GCSHP4
ENSG00000256176	1.59659	1.51519	4.65584	4.82192	ENSG00000256176	AC024940.3
ENSG00000256178	7.18628	4.38898	2.49621	0	ENSG00000256178	AC004889.1
ENSG00000256181	0	0	0	0	ENSG00000256181	AP001880.1
ENSG00000256182	0.0558027	0.368731	0.553969	0.323113	ENSG00000256182	AL590325.1
ENSG00000256186	6.70507	27.6016	27.7353	41.112	ENSG00000256186	AL732372.1
ENSG00000256188	0.197502	1.38946	1.02511	4.09197	ENSG00000256188	TAS2R30
ENSG00000256189	0	0.13514	0.122107	0.152745	ENSG00000256189	AP003717.2

ENSG00000256192	0	0.118218	0	0.133625	ENSG00000256192	AC012158.2
ENSG00000256206	0	0	0.145953	0	ENSG00000256206	AC018523.2
ENSG00000256210	0	0	0	0	ENSG00000256210	AC005255.1
ENSG00000256211	0	0	0	0	ENSG00000256211	AC023512.1
ENSG00000256212	0.295129	0.117613	0.186791	0.134129	ENSG00000256212	AL773602.1
ENSG00000256221	0	0	0	0	ENSG00000256221	AC244502.2
ENSG00000256222	10136.6	10151.1	14115.1	12430.8	ENSG00000256222	MTRNR2L3
ENSG00000256223	3.29475	6.11866	10.436	8.51174	ENSG00000256223	ZNF10
ENSG00000256225	0	0	0	0	ENSG00000256225	AL590710.1
ENSG00000256229	4.33032	8.16227	7.08387	9.18678	ENSG00000256229	ZNF486
ENSG00000256235	0	0	0	0.310885	ENSG00000256235	SMIM3
ENSG00000256238	0.0556201	0.305628	1.69131	1.37431	ENSG00000256238	SUPT16HP1
ENSG00000256239	0.056629	0.0897227	0.0588977	0.15832	ENSG00000256239	AL589642.1
ENSG00000256240	0	0	0	0	ENSG00000256240	AC010620.1
ENSG00000256243	0.496335	0.537476	0.42947	0.52918	ENSG00000256243	AL121594.2
ENSG00000256252	0	0	0.0106603	0	ENSG00000256252	CT476828.7
ENSG00000256254	0.107257	0.10324	0.0933078	0.0586138	ENSG00000256254	AP000619.3
ENSG00000256261	1.65928	0.393637	0	0.190327	ENSG00000256261	AC104698.1
ENSG00000256263	0	0.253197	0.117158	0.086778	ENSG00000256263	DDX11L8
ENSG00000256269	3.2642	5.05223	4.40826	4.68916	ENSG00000256269	HMBS
ENSG00000256274	0.505397	1.88944	0.933925	2.38092	ENSG00000256274	AC018630.2
ENSG00000256280	0.406903	0	0.346175	0	ENSG00000256280	AP006289.1
ENSG00000256282	0.917402	2.59454	2.60591	3.01821	ENSG00000256282	AC112694.1
ENSG00000256283	0	0	0	0	ENSG00000256283	METTL8P1
ENSG00000256285	0	2.08588	0.920175	0	ENSG00000256285	OSBPL9P5
ENSG00000256293	0	0.223166	0.0989065	0.122503	ENSG00000256293	AC135279.2
ENSG00000256294	6.13068	10.5447	8.3809	12.7683	ENSG00000256294	ZNF225
ENSG00000256295	26.7168	40.0466	46.0798	63.6991	ENSG00000256295	AC005086.2
ENSG00000256301	6.70507	27.6016	27.7353	41.112	ENSG00000256301	AC138031.2
ENSG00000256304	1.60631	1.50798	2.33432	2.54896	ENSG00000256304	CCDC150P1
ENSG00000256305	0	0	0	0	ENSG00000256305	AL359757.1
ENSG00000256309	0.0341159	0	0.472279	2.71385	ENSG00000256309	AC009469.1
ENSG00000256310	0	0	0	0	ENSG00000256310	NDUFA5P6
ENSG00000256316	15.9054	101.067	23.0352	20.383	ENSG00000256316	HIST1H3F
ENSG00000256323	12.7043	36.5942	18.3993	32.6164	ENSG00000256323	AL049542.1
ENSG00000256331	0	0	0	0	ENSG00000256331	NIFKP3
ENSG00000256338	1.81231	1.09761	0.845892	2.0398	ENSG00000256338	RPL41P2
ENSG00000256340	0.018632	0.0538962	0.218966	0.108434	ENSG00000256340	ABCC6P1
ENSG00000256344	0	0	0.0106603	0	ENSG00000256344	CT476828.8
ENSG00000256346	0	0	0	0	ENSG00000256346	AC092470.1
ENSG00000256347	0.686546	0.41239	0	0.185924	ENSG00000256347	OR8R1P
ENSG00000256349	0.34301	0.443793	0.337464	0.603088	ENSG00000256349	AP002748.4
ENSG00000256350	0	0	0	0	ENSG00000256350	AC243972.3
ENSG00000256351	8.77667	15.7245	13.2445	17.8331	ENSG00000256351	AC007834.2
ENSG00000256352	0	1.99173	0	2.93479	ENSG00000256352	AL109922.2
ENSG00000256353	0	0	0	0	ENSG00000256353	AC087258.2
ENSG00000256354	0	0	0	0	ENSG00000256354	AC104304.1
ENSG00000256355	0.0933638	0	0.243126	0.201952	ENSG00000256355	NTAN1P3
ENSG00000256356	0.0819859	0	0	0.030894	ENSG00000256356	HSPA8P5
ENSG00000256358	0	0	3.03E-06	1.70E-06	ENSG00000256358	AC016489.1
ENSG00000256361	1.70214	2.01784	2.26935	3.36339	ENSG00000256361	AC027544.1
ENSG00000256371	0.068684	0	0.0596844	0.0746793	ENSG00000256371	LRRC34P1
ENSG00000256372	0	0	0	0	ENSG00000256372	AC023050.2
ENSG00000256374	0	0.243112	0.118486	0.198619	ENSG00000256374	PPIAL4D

ENSG00000256378	0	0	0	0	ENSG00000256378	AC008011.1
ENSG00000256379	22.5871	70.0626	53.7243	87.1792	ENSG00000256379	TRAV8-5
ENSG00000256383	3.63489	7.27704	6.46217	7.38086	ENSG00000256383	AC020910.2
ENSG00000256385	0	0	0.598598	0.557402	ENSG00000256385	UBE2NP1
ENSG00000256386	0	0	0.169983	0	ENSG00000256386	AP000244.1
ENSG00000256390	0	0.0574239	0	0.0930877	ENSG00000256390	AC092143.1
ENSG00000256391	0.31076	1.05245	0.672237	1.43496	ENSG00000256391	SDIM1
ENSG00000256393	0	0	0	0	ENSG00000256393	AC138123.1
ENSG00000256394	0	0.0652249	0.0442213	0.0556408	ENSG00000256394	ASIC5
ENSG00000256399	0.733842	3.41177	2.3405	5.41284	ENSG00000256399	AC079866.1
ENSG00000256400	4.05648	15.0618	10.8265	8.25606	ENSG00000256400	AC018630.3
ENSG00000256404	8.77E-05	27.1546	0	0	ENSG00000256404	AC109133.1
ENSG00000256407	0.312094	0.250917	0.339535	0.788525	ENSG00000256407	AL357673.1
ENSG00000256420	0.190625	0.308146	0.413144	0.348432	ENSG00000256420	OSBPL9P4
ENSG00000256425	0	0	0	2.93479	ENSG00000256425	AC092989.1
ENSG00000256436	0.406569	0.794118	0.450554	1.72035	ENSG00000256436	TAS2R31
ENSG00000256439	0.66814	1.33253	1.19329	1.84553	ENSG00000256439	AC008731.1
ENSG00000256441	0	0	0	0.200187	ENSG00000256441	AP001888.1
ENSG00000256450	0.391651	0.220597	1.22041	0.735284	ENSG00000256450	AC007552.1
ENSG00000256453	0.0827473	0.0742519	0.531475	0.0942684	ENSG00000256453	DND1
ENSG00000256456	0	0	0.0106603	0	ENSG00000256456	CT476828.9
ENSG00000256463	0.114691	0.0735194	0.132836	0.0228737	ENSG00000256463	SALL3
ENSG00000256464	0.374805	1.23329	1.28428	1.01578	ENSG00000256464	YWHABP2
ENSG00000256465	0	0	0	0	ENSG00000256465	AC023050.3
ENSG00000256466	0.445533	0.506291	0.780287	0.651853	ENSG00000256466	AP003026.1
ENSG00000256474	0	0	0.484477	0	ENSG00000256474	TRAV11
ENSG00000256480	0	0	0	0	ENSG00000256480	AC018653.2
ENSG00000256490	0	0	0.0106603	0	ENSG00000256490	CT476828.10
ENSG00000256492	0	0	0	0	ENSG00000256492	AL118508.1
ENSG00000256496	0	0.0663165	0	0.149945	ENSG00000256496	AC073913.1
ENSG00000256498	0	0	0	0	ENSG00000256498	AL928654.1
ENSG00000256500	0.426345	0.366077	0.121184	0.11608	ENSG00000256500	AL139300.1
ENSG00000256502	0	0	1.29412	0	ENSG00000256502	AC073913.2
ENSG00000256515	0	0	0	0	ENSG00000256515	CCL3L3
ENSG00000256518	0.27433	0.00448056	0.0999635	0	ENSG00000256518	AP000812.3
ENSG00000256521	0	0	0.0106603	0	ENSG00000256521	CT476828.11
ENSG00000256525	6.9646	11.1391	12.1772	14.6738	ENSG00000256525	POLG2
ENSG00000256527	0.0772586	0.148552	0.268429	0	ENSG00000256527	AP002833.1
ENSG00000256528	0.0284134	0	0.0495379	0	ENSG00000256528	AP006285.1
ENSG00000256530	0.0519548	0.659444	0.222493	0.433834	ENSG00000256530	AC019294.1
ENSG00000256533	0.518597	0.392393	1.6037	0.628129	ENSG00000256533	AP002373.2
ENSG00000256537	6.91909	10.7667	7.35604	8.33192	ENSG00000256537	SMIM10L1
ENSG00000256545	14.6628	41.5349	4.29515	38.5461	ENSG00000256545	AL139819.1
ENSG00000256552	0.487819	0.216121	0.48796	0.840219	ENSG00000256552	AC092745.2
ENSG00000256553	0.236959	0.202582	0.372563	0.897513	ENSG00000256553	TRAV1-2
ENSG00000256557	3.20877	8.28859	7.47097	17.0979	ENSG00000256557	AC009509.3
ENSG00000256563	0.267476	1.13681	1.49738	2.56945	ENSG00000256563	NANOGNBP2
ENSG00000256566	0.273238	0.587735	0.238591	0.504243	ENSG00000256566	AL049650.1
ENSG00000256574	0.139169	0.024544	0.0242512	0.0610878	ENSG00000256574	OR13A1
ENSG00000256579	31.1364	36.6345	36.2053	35.9613	ENSG00000256579	AC135776.1
ENSG00000256581	0.0422608	0.0801852	0.109567	0.114352	ENSG00000256581	NLRP9P1
ENSG00000256586	0	0	1.66693	0.693216	ENSG00000256586	AC091171.1
ENSG00000256589	0	0.176361	0.348549	0.673435	ENSG00000256589	ENPP7P5
ENSG00000256590	0	0	0.167733	0.206081	ENSG00000256590	TRDV3

ENSG00000256591	5.79065	2.84003	2.34513	2.43227	ENSG00000256591	AP003108.2
ENSG00000256594	3.39567	15.8177	11.6061	10.8095	ENSG00000256594	AC010186.2
ENSG00000256599	0	0	0	0	ENSG00000256599	AC020663.1
ENSG00000256604	6.4816	8.48436	10.2656	12.3917	ENSG00000256604	AC093668.2
ENSG00000256612	1.48251	3.03525	3.3085	6.0181	ENSG00000256612	CYP2B7P
ENSG00000256614	0	0	0	0	ENSG00000256614	AK6P1
ENSG00000256616	0.692378	2.06475	1.04141	2.18719	ENSG00000256616	AP002414.2
ENSG00000256618	20773.7	20228.2	27988	23798.5	ENSG00000256618	MTRNR2L1
ENSG00000256619	0	0	0.0106603	0	ENSG00000256619	CT476828.12
ENSG00000256625	0.491443	0.46775	0.952224	0.72429	ENSG00000256625	AC092747.2
ENSG00000256626	0	0	0	0	ENSG00000256626	AC024224.1
ENSG00000256627	0.103582	0	0.179719	0.1118	ENSG00000256627	AC073651.2
ENSG00000256629	0	0.560349	0.857421	0.802771	ENSG00000256629	TAS2R67P
ENSG00000256630	0	0	0	0	ENSG00000256630	AC090424.1
ENSG00000256631	0	0	0.0106603	0	ENSG00000256631	CT476828.13
ENSG00000256632	0	0	0	0	ENSG00000256632	AC135586.2
ENSG00000256640	0.174316	0.658619	0.598466	0.549382	ENSG00000256640	AC023051.2
ENSG00000256646	7.52244	5.71141	6.07127	4.76976	ENSG00000256646	AC010132.3
ENSG00000256651	0.066234	0.360964	0.327636	0.504386	ENSG00000256651	AC006518.1
ENSG00000256655	0.964688	1.78789	3.74833	4.74985	ENSG00000256655	TMEM75
ENSG00000256657	0	0.471671	0.717475	0.824969	ENSG00000256657	AC244131.1
ENSG00000256660	0.650206	1.11055	1.10013	2.14909	ENSG00000256660	CLEC12B
ENSG00000256663	7.67792	11.3182	3.89624	16.5895	ENSG00000256663	AC112777.1
ENSG00000256664	28.7993	9.23941	19.2206	9.72619	ENSG00000256664	AC025423.2
ENSG00000256667	2.35884	4.42631	4.8285	5.91916	ENSG00000256667	KLRA1P
ENSG00000256671	0	0.00772512	0	0.824323	ENSG00000256671	LIMS4
ENSG00000256673	0.166866	1.94595	0	0.793198	ENSG00000256673	AC141557.1
ENSG00000256674	0.040513	0.0780419	0.141087	0.132995	ENSG00000256674	AC020549.1
ENSG00000256678	0.166994	0.319963	0	0	ENSG00000256678	AC025423.3
ENSG00000256681	0.567982	0	0.817698	0	ENSG00000256681	CCDC58P5
ENSG00000256682	0.199466	0.64254	0.388092	0.647228	ENSG00000256682	AC006518.2
ENSG00000256683	15.4605	14.6542	14.7508	11.3626	ENSG00000256683	ZNF350
ENSG00000256692	6.70507	27.6016	27.7353	41.112	ENSG00000256692	AC139099.1
ENSG00000256704	0.10553	0.0558579	0.0924047	0.235449	ENSG00000256704	SDCCAG3P1
ENSG00000256708	0	0	0	0	ENSG00000256708	AC007458.1
ENSG00000256709	0	0	0	0	ENSG00000256709	AL133271.1
ENSG00000256713	0.153995	0.635171	0.659307	0.85959	ENSG00000256713	PGA5
ENSG00000256715	0	5.84964	2.88878	1.83563	ENSG00000256715	AL050302.1
ENSG00000256720	0.14926	0.427182	0	0.317929	ENSG00000256720	BTG1P1
ENSG00000256723	0.0508416	0	0.13271	0.111011	ENSG00000256723	AP003717.3
ENSG00000256731	5.7607	14.1685	14.2713	21.3964	ENSG00000256731	AL591069.1
ENSG00000256734	0	0.0896074	0	0.282064	ENSG00000256734	AC027544.3
ENSG00000256737	0	0	0	0	ENSG00000256737	RBBP4P5
ENSG00000256745	0.448738	0.143343	0.655745	0.167233	ENSG00000256745	AP002784.2
ENSG00000256748	0.0408321	0.196638	0.177744	0.139755	ENSG00000256748	AC005832.2
ENSG00000256752	0	0	0	0	ENSG00000256752	HPRT1P3
ENSG00000256756	0	0	0	0	ENSG00000256756	TIMM17BP1
ENSG00000256761	0	0	0	0	ENSG00000256761	AL008733.1
ENSG00000256762	0	0	0.156277	0.193946	ENSG00000256762	STH
ENSG00000256771	3.85634	6.38725	6.85182	3.36267	ENSG00000256771	ZNF253
ENSG00000256774	0	0	0	0	ENSG00000256774	AC087241.2
ENSG00000256777	0	0	0	0.101513	ENSG00000256777	PDCL3P7
ENSG00000256779	0.0321967	0.092864	0.0836896	0	ENSG00000256779	AP002383.4
ENSG00000256786	0	0	0	0	ENSG00000256786	AP001029.1

ENSG00000256797	0	0	0	0.098205	ENSG00000256797	KLRF2
ENSG00000256799	0	0.107342	0	0	ENSG00000256799	AC005832.3
ENSG00000256804	0	0	2.48581	0.506267	ENSG00000256804	AC138466.2
ENSG00000256806	0	0	0	3.09698	ENSG00000256806	C17orf100
ENSG00000256812	11.4504	3.62364	18.5385	3.98383	ENSG00000256812	CAPNS2
ENSG00000256815	0	0	1.29349	3.14232	ENSG00000256815	AL590325.2
ENSG00000256817	0.466745	1.044	1.61567	0.997219	ENSG00000256817	TPT1P12
ENSG00000256818	0	0	0	0	ENSG00000256818	AP001069.1
ENSG00000256822	15.8509	56.562	43.9118	74.7333	ENSG00000256822	AC084125.2
ENSG00000256825	0	0	0	0	ENSG00000256825	AC026786.1
ENSG00000256826	0.43656	1.23648	0.745297	0.671518	ENSG00000256826	ATP5J2P4
ENSG00000256827	0	0.7444	2.0193	1.64088	ENSG00000256827	AC068790.1
ENSG00000256835	0	0	0	0	ENSG00000256835	AC005294.1
ENSG00000256840	0	0	0.0106603	0	ENSG00000256840	CT476828.14
ENSG00000256843	2.52815	0	1.70353	0	ENSG00000256843	AC023157.2
ENSG00000256844	0	0	0	0	ENSG00000256844	MEF2BNBP1
ENSG00000256845	1.22955	2.66409	2.31684	3.29702	ENSG00000256845	AC007401.1
ENSG00000256847	0	0	0	0	ENSG00000256847	CCND2P1
ENSG00000256849	0.117008	0.0375986	0.170468	0.0850145	ENSG00000256849	TCP1P3
ENSG00000256851	0	0	0	0	ENSG00000256851	AL663061.2
ENSG00000256852	0	0	0	0.0690886	ENSG00000256852	KNOP1P1
ENSG00000256861	0.455436	0	0	0	ENSG00000256861	AC048338.1
ENSG00000256863	0	0	0	0	ENSG00000256863	AP001880.2
ENSG00000256868	0	0	0.0106603	0	ENSG00000256868	CT476828.15
ENSG00000256870	0	0	0.0627871	0.207469	ENSG00000256870	SLC5A8
ENSG00000256873	0	0	0	0	ENSG00000256873	AL021977.1
ENSG00000256874	0	0	0	0	ENSG00000256874	AL080274.1
ENSG00000256878	0	0	0	2.93479	ENSG00000256878	AC087897.1
ENSG00000256882	0	1.99173	0	2.93479	ENSG00000256882	AC091320.1
ENSG00000256885	9.34456	19.902	19.155	26.8338	ENSG00000256885	AP001877.1
ENSG00000256889	0.880569	9.96688	7.9963	9.68957	ENSG00000256889	AC093847.1
ENSG00000256892	1.01474	0.635299	1.23473	1.49166	ENSG00000256892	MTRNR2L7
ENSG00000256896	0.0457238	0	0.198656	0.0498947	ENSG00000256896	PSMC1P8
ENSG00000256898	0	0.53425	0.387094	0.725255	ENSG00000256898	AP002770.2
ENSG00000256902	0	0	0	0	ENSG00000256902	IQSEC3P1
ENSG00000256905	3.61919	1.67999	0	1.73273	ENSG00000256905	AC090571.1
ENSG00000256912	0	0.41681	0.18818	0.461133	ENSG00000256912	AC007068.2
ENSG00000256913	0.0240636	0	0.0411359	0	ENSG00000256913	AC005840.4
ENSG00000256917	0	0.961255	1.69826	0	ENSG00000256917	AC008033.2
ENSG00000256920	42.7634	70.6152	65.3466	113.267	ENSG00000256920	CR753846.1
ENSG00000256929	0	0	0	0	ENSG00000256929	AC067852.1
ENSG00000256937	0	0.212793	0	0.0800963	ENSG00000256937	KRT17P8
ENSG00000256950	0.0621159	0.348474	0.258948	0.920337	ENSG00000256950	AC069503.2
ENSG00000256951	0	0	0	0	ENSG00000256951	AC055876.3
ENSG00000256963	0.781289	1.10912	3.32824	0	ENSG00000256963	AC079602.2
ENSG00000256966	1.04587	0.489815	0.781986	0.531336	ENSG00000256966	AL513165.2
ENSG00000256968	0	0	0.415362	0	ENSG00000256968	SNRPEP2
ENSG00000256974	2.84538	8.69829	34.3952	8.60823	ENSG00000256974	AC018692.4
ENSG00000256975	0.0277039	0.159331	0.048132	0.185342	ENSG00000256975	AC092821.2
ENSG00000256977	0.580822	0.748134	0.39052	4.13103	ENSG00000256977	LIMS3
ENSG00000256980	0.127148	0.122013	0.624184	0.629422	ENSG00000256980	KHDC1L
ENSG00000256981	0.230473	1.51745	0.560753	1.61834	ENSG00000256981	AC134349.2
ENSG00000256986	0	0	0	0	ENSG00000256986	AC140847.3
ENSG00000256987	0.456449	0.923286	1.3221	1.94322	ENSG00000256987	AC023050.4

ENSG00000256989	0.374134	2.29404	1.91545	2.33356	ENSG00000256989	AC010335.1
ENSG00000257005	0	0	0	0	ENSG00000257005	AC027667.1
ENSG00000257008	0.0910771	0	0	0	ENSG00000257008	GPR142
ENSG00000257010	0	0	0	0	ENSG00000257010	AC140481.1
ENSG00000257012	0	0	0	0	ENSG00000257012	AP002383.5
ENSG00000257016	0	0	0	0	ENSG00000257016	SLC25A39P2
ENSG00000257017	4.15151	6.24993	5.61272	7.21817	ENSG00000257017	HP
ENSG00000257019	0	0	0.0519571	0	ENSG00000257019	OR13C2
ENSG00000257021	0	0	0	0.626398	ENSG00000257021	HSPE1P20
ENSG00000257026	0.719494	0.397448	0.481598	0.960143	ENSG00000257026	AC040173.1
ENSG00000257028	0.757225	0.0156863	0	0	ENSG00000257028	C15orf37
ENSG00000257033	5.83917	5.65899	8.74189	6.63093	ENSG00000257033	AL391357.1
ENSG00000257034	0	0	0.203102	0	ENSG00000257034	AL021707.2
ENSG00000257035	0	0	0	0.167693	ENSG00000257035	AC025252.2
ENSG00000257037	0.519742	1.40413	0.572368	1.43687	ENSG00000257037	RARSP1
ENSG00000257040	0.543122	0.899977	1.23304	2.26193	ENSG00000257040	AC005477.1
ENSG00000257043	0	0	0.269338	0	ENSG00000257043	AP006296.1
ENSG00000257046	0	0	0	0	ENSG00000257046	AC011604.2
ENSG00000257053	0	0	5.85434	0	ENSG00000257053	Z98941.1
ENSG00000257062	0	0.23651	0.509905	1.07907	ENSG00000257062	AC022335.1
ENSG00000257065	0.395946	0.102824	0.277402	0.274022	ENSG00000257065	AL049844.1
ENSG00000257070	0.575927	1.36803	2.7251	0.903736	ENSG00000257070	AP003170.5
ENSG00000257073	0	1.02242	0	1.03E-05	ENSG00000257073	AC011933.1
ENSG00000257074	0.996683	0.775284	0.247845	0.461654	ENSG00000257074	RPL29P33
ENSG00000257075	0.44443	1.06678	0.867108	1.5566	ENSG00000257075	RPEP6
ENSG00000257078	0.079193	0.227713	0.0685364	0	ENSG00000257078	AC006512.2
ENSG00000257087	0	0	0	0.310816	ENSG00000257087	AP003174.3
ENSG00000257088	0.0693968	0	0	0.1276	ENSG00000257088	PNMA6D
ENSG00000257093	3.40166	2.84355	3.68908	2.89477	ENSG00000257093	KIAA1147
ENSG00000257094	0	0	0.2847	0.346018	ENSG00000257094	AC016957.1
ENSG00000257101	0	0	0	0	ENSG00000257101	LRRC37A13P
ENSG00000257103	11.8016	12.3787	12.6353	10.9784	ENSG00000257103	LSM14A
ENSG00000257108	0.225301	0.280267	0.37362	0.820203	ENSG00000257108	NHLRC4
ENSG00000257109	0	0	0	0.106362	ENSG00000257109	OR4F28P
ENSG00000257110	60.4541	113.13	91.2973	151.63	ENSG00000257110	AL354808.1
ENSG00000257113	0	0	0	0	ENSG00000257113	AC090502.2
ENSG00000257115	0	0	0	0	ENSG00000257115	OR11H12
ENSG00000257119	0	0.40098	0	0	ENSG00000257119	EEF1B2P4
ENSG00000257121	0.966166	2.94011	3.72749	3.58412	ENSG00000257121	AC126615.2
ENSG00000257122	3.52326	4.68058	5.67914	5.40002	ENSG00000257122	RRN3P3
ENSG00000257123	7.2782	7.76551	5.59229	4.36636	ENSG00000257123	BX927168.1
ENSG00000257125	0	0	0	0	ENSG00000257125	KRT127P
ENSG00000257127	1.66827	3.78021	3.34409	5.77991	ENSG00000257127	CLLU1
ENSG00000257128	0	0	0	0	ENSG00000257128	AC006197.1
ENSG00000257129	0	0.0243523	0.0440814	0.0829977	ENSG00000257129	AC126177.1
ENSG00000257138	0.0527557	0.0507817	0	0.0575707	ENSG00000257138	TAS2R38
ENSG00000257142	0	0	0	0	ENSG00000257142	AL512310.1
ENSG00000257146	0	0	0.997822	0.515099	ENSG00000257146	AC079905.2
ENSG00000257147	22.5042	60.3381	0	202.663	ENSG00000257147	AL663093.1
ENSG00000257148	0	0	0	0	ENSG00000257148	CR753819.1
ENSG00000257149	4.29205	16.5337	8.29951	11.7756	ENSG00000257149	AC127032.1
ENSG00000257150	0.585054	1.20168	1.1725	1.19022	ENSG00000257150	PGAM1P5
ENSG00000257153	137.516	413.723	205.819	814.202	ENSG00000257153	BX088523.1
ENSG00000257154	11.2977	19.9007	12.7719	36.2645	ENSG00000257154	AL662822.1

ENSG00000257157	0	0	0	0	ENSG00000257157	AC018659.1
ENSG00000257158	21.9025	58.5115	42.9039	81.3871	ENSG00000257158	BX284927.1
ENSG00000257159	0.219637	0.434342	0.391014	0.315767	ENSG00000257159	AC084033.1
ENSG00000257160	1.23107	4.11192	1.9704	8.55182	ENSG00000257160	AL662822.2
ENSG00000257162	0	0	0	0	ENSG00000257162	MED15P6
ENSG00000257168	18.6228	35.8578	29.8837	38.7151	ENSG00000257168	BX927214.1
ENSG00000257169	2.58775	5.61586	3.65289	19.1152	ENSG00000257169	AC125612.1
ENSG00000257170	0	3.14696	2.28701	0	ENSG00000257170	CR382280.1
ENSG00000257171	0.0819873	0.26735	0	0.16381	ENSG00000257171	CR383658.2
ENSG00000257172	3.01995	11.4488	4.71324	21.277	ENSG00000257172	AL662822.3
ENSG00000257173	0	0	0	0	ENSG00000257173	AK6P2
ENSG00000257175	0	0	0	0	ENSG00000257175	CR383656.2
ENSG00000257177	11.2977	19.9007	12.7719	36.2645	ENSG00000257177	BX936369.1
ENSG00000257179	0	0	0	0	ENSG00000257179	HMGN2P6
ENSG00000257182	1.23107	4.11192	1.9704	8.55182	ENSG00000257182	BX927220.1
ENSG00000257184	0.218753	0.417533	0.870018	0.229856	ENSG00000257184	AC004080.3
ENSG00000257187	0	0	0.0899446	0	ENSG00000257187	BX248519.1
ENSG00000257188	19.3529	48.1127	45.066	106.775	ENSG00000257188	BX005432.1
ENSG00000257189	2.48236	7.82834	8.59891	10.0475	ENSG00000257189	AC139677.1
ENSG00000257190	2.09289	4.24442	1.66567	3.21291	ENSG00000257190	BX927220.2
ENSG00000257192	0	0	1.49594	0	ENSG00000257192	AL662866.1
ENSG00000257195	1.11521	0.814693	1.10541	1.19988	ENSG00000257195	HNRNPA1P50
ENSG00000257198	0.208657	2.1197	0.798718	1.12543	ENSG00000257198	FAM205BP
ENSG00000257199	0	0	0	0	ENSG00000257199	AC025161.1
ENSG00000257206	8.60188	14.7077	16.6893	24.9024	ENSG00000257206	CR762481.1
ENSG00000257207	0.48953	0.560876	0.830041	3.30559	ENSG00000257207	AC112229.3
ENSG00000257210	0	0	0	0	ENSG00000257210	NACAP3
ENSG00000257211	0	4.24E-07	1.44732	3.49473	ENSG00000257211	AC138688.1
ENSG00000257212	44.9816	60.3664	68.3359	89.2653	ENSG00000257212	BX248419.1
ENSG00000257213	0	0	0	0	ENSG00000257213	AL773543.1
ENSG00000257215	3.50046	9.33161	9.33714	10.1998	ENSG00000257215	CR847794.2
ENSG00000257216	36.5908	88.7587	75.7909	126.135	ENSG00000257216	AL845450.1
ENSG00000257217	0	0.403128	0	0	ENSG00000257217	CR759904.1
ENSG00000257218	12.5954	10.8957	13.9306	11.6729	ENSG00000257218	GATC
ENSG00000257220	1.12148	0.881456	0	2.6422	ENSG00000257220	FAM213AP1
ENSG00000257223	11.4161	26.4914	26.2241	55.7534	ENSG00000257223	CR753309.1
ENSG00000257224	0	0	0	0	ENSG00000257224	CR383656.3
ENSG00000257227	0	0	0	0	ENSG00000257227	DUXAP10
ENSG00000257230	0	0	0	0	ENSG00000257230	LINC02448
ENSG00000257231	0	0.830008	0.743508	0	ENSG00000257231	DYNLL1P4
ENSG00000257232	0	0	0	0	ENSG00000257232	DPCR1
ENSG00000257233	0	0	0	0	ENSG00000257233	CR936921.1
ENSG00000257236	11.7638	0	21.472	0	ENSG00000257236	AL773541.1
ENSG00000257237	0	0	0	0	ENSG00000257237	AC018448.1
ENSG00000257238	0.967847	5.36006	6.48123	31.5001	ENSG00000257238	BX511262.1
ENSG00000257240	33.1037	17.9146	36.3363	31.0239	ENSG00000257240	CR753309.2
ENSG00000257242	5.48205	3.38041	3.24139	6.05555	ENSG00000257242	LINC01619
ENSG00000257243	0	0.390772	1.64601	1.60102	ENSG00000257243	AC020612.1
ENSG00000257245	1.77202	16.3321	15.8156	15.8388	ENSG00000257245	CR388229.1
ENSG00000257246	0.959889	3.00968	1.9639	3.83969	ENSG00000257246	PHBP19
ENSG00000257247	59.5468	79.595	164.19	127.506	ENSG00000257247	BX294158.1
ENSG00000257248	4.88094	9.52805	14.3918	16.063	ENSG00000257248	BX294158.2
ENSG00000257249	4.88094	9.52805	14.3918	16.063	ENSG00000257249	CR759890.1
ENSG00000257251	1.23107	4.11192	1.9704	8.55182	ENSG00000257251	AL844213.1

ENSG00000257254	0	0	0	0.221859	ENSG00000257254	AC010202.1
ENSG00000257255	0	4.82892	0	0	ENSG00000257255	CR759772.1
ENSG00000257260	0	0	0	0	ENSG00000257260	CR847794.2
ENSG00000257263	3.75543	10.1541	7.43986	17.3849	ENSG00000257263	CR938714.1
ENSG00000257266	15.0632	30.1214	32.6485	54.7169	ENSG00000257266	BX248408.1
ENSG00000257267	4.67616	3.90813	6.06196	5.17901	ENSG00000257267	ZNF271P
ENSG00000257273	11.2977	19.9007	12.7719	36.2645	ENSG00000257273	CR382280.2
ENSG00000257276	0	23.2982	18.9241	26.8168	ENSG00000257276	CR759737.1
ENSG00000257278	0	0	0.780934	8.2061	ENSG00000257278	AC139677.2
ENSG00000257281	0.0582457	0.206495	0.231835	0.290777	ENSG00000257281	AC009729.1
ENSG00000257287	0	0.249319	0.225439	0.274764	ENSG00000257287	AC016256.1
ENSG00000257288	0	0.0249062	0.109997	0.0552529	ENSG00000257288	AC068305.2
ENSG00000257289	0.645454	0	0	0.904503	ENSG00000257289	AC025423.5
ENSG00000257292	0	0	0	0	ENSG00000257292	AC117372.1
ENSG00000257295	4.88094	9.52805	14.3918	16.063	ENSG00000257295	BX927214.2
ENSG00000257296	0.191366	0.565436	0.330631	1.44226	ENSG00000257296	AC093027.1
ENSG00000257299	0	9.89929	0	11.3894	ENSG00000257299	AL773535.1
ENSG00000257300	0	0	0.117267	0	ENSG00000257300	HAUS8P1
ENSG00000257301	1.83169	4.13359	4.81581	12.29	ENSG00000257301	CR762481.2
ENSG00000257302	0.0668462	0	0	0	ENSG00000257302	FAHD2P1
ENSG00000257305	16.4876	40.9438	54.8938	85.8506	ENSG00000257305	AC225613.1
ENSG00000257307	0.193734	0.093666	0.255821	0	ENSG00000257307	AL162311.2
ENSG00000257308	0	0.0308626	0.055799	0.0702293	ENSG00000257308	AC090017.1
ENSG00000257311	3.89041	11.6695	7.22999	18.1559	ENSG00000257311	AC225613.2
ENSG00000257313	0	0.267134	22.1637	41.2445	ENSG00000257313	CR753846.2
ENSG00000257314	33.1037	17.9146	36.3363	31.0239	ENSG00000257314	CR753835.1
ENSG00000257315	21.073	27.9713	26.3036	24.0589	ENSG00000257315	ZBED6
ENSG00000257316	0	0.0470529	0	0	ENSG00000257316	AC087311.1
ENSG00000257318	7.24018	16.7535	14.267	24.6271	ENSG00000257318	AC138688.2
ENSG00000257320	6.01054	14.0535	16.6311	21.5665	ENSG00000257320	AL662834.1
ENSG00000257321	0.251476	4.97607	0.335085	5.3242	ENSG00000257321	AL662822.4
ENSG00000257323	0	0	0	0	ENSG00000257323	AC123904.2
ENSG00000257324	1.64273	5.32831	2.80046	7.93452	ENSG00000257324	AL844213.2
ENSG00000257326	1.38E-07	0	7.84318	0	ENSG00000257326	CR936880.1
ENSG00000257327	0	0.251795	0.0874374	0	ENSG00000257327	AC012555.1
ENSG00000257328	0	0	0	0	ENSG00000257328	AL049543.1
ENSG00000257331	0	0	0	0	ENSG00000257331	RACGAP1P
ENSG00000257332	0	0.258083	0	0	ENSG00000257332	HNRNPA1P69
ENSG00000257333	2.09289	4.24442	1.66567	3.21291	ENSG00000257333	BX248518.1
ENSG00000257334	18.6228	35.8578	29.8837	38.7151	ENSG00000257334	CR759281.1
ENSG00000257335	1.51716	0.957301	0.780802	1.28436	ENSG00000257335	MGAM
ENSG00000257336	0	0	0	0.361847	ENSG00000257336	PRELID2P1
ENSG00000257338	4.85452	4.14585	3.47307	6.37901	ENSG00000257338	BX936369.2
ENSG00000257339	0.367849	1.46528	3.66202	6.87901	ENSG00000257339	PLEKHM1
ENSG00000257340	3.51171	10.9233	9.70791	18.1345	ENSG00000257340	CR762481.3
ENSG00000257341	0.342873	0.218115	0.375649	0.0612136	ENSG00000257341	AL928654.4
ENSG00000257343	0	0	0.133714	0	ENSG00000257343	AC055716.1
ENSG00000257348	49.252	98.4983	82.814	148.899	ENSG00000257348	AC217779.1
ENSG00000257350	0.0427139	0.317609	0.36511	0.327068	ENSG00000257350	AC027287.1
ENSG00000257351	13.4938	25.0794	15.5744	50.6737	ENSG00000257351	AL773544.1
ENSG00000257355	0	0.446979	0	0	ENSG00000257355	AC008770.2
ENSG00000257356	0.152411	0	0.131905	0.325786	ENSG00000257356	BNIP3P6
ENSG00000257360	0.0942013	0.138939	0.0823907	0.0518553	ENSG00000257360	AC123567.1
ENSG00000257361	11.4161	26.4914	26.2241	55.7534	ENSG00000257361	CR753835.2

ENSG00000257362	7.0693	11.3685	15.0646	14.9909	ENSG00000257362	BX927220.3
ENSG00000257363	18.6228	35.8578	29.8837	38.7151	ENSG00000257363	AL662831.1
ENSG00000257364	0.544682	0	0.0773252	0.189346	ENSG00000257364	VENTXP3
ENSG00000257365	7.75087	10.8386	11.4186	12.1476	ENSG00000257365	FNTB
ENSG00000257368	0.103648	0.290971	0.963674	0.654324	ENSG00000257368	AC063924.1
ENSG00000257369	1.41446	5.43235	6.18395	5.82457	ENSG00000257369	CR812479.1
ENSG00000257374	0.849731	1.48321	0.800734	0	ENSG00000257374	AC217778.1
ENSG00000257376	0.254618	0.664509	0.973252	1.11009	ENSG00000257376	AC079601.2
ENSG00000257377	6.53881	4.15564	7.25295	13.0821	ENSG00000257377	AC217775.1
ENSG00000257382	0.394301	0.398814	2.44774	5.26096	ENSG00000257382	AC217772.1
ENSG00000257383	3.62936	8.40096	10.3302	13.505	ENSG00000257383	CR759784.1
ENSG00000257384	0	1.10912	0.332824	0.402831	ENSG00000257384	AC009779.1
ENSG00000257389	0	0	0	0	ENSG00000257389	AC107016.1
ENSG00000257390	4.14256	4.85503	6.29117	4.04159	ENSG00000257390	AC023055.1
ENSG00000257392	0.294285	0.0942596	0.425756	0.106025	ENSG00000257392	AC126177.3
ENSG00000257393	7.0693	11.3685	15.0646	14.9909	ENSG00000257393	AL662822.5
ENSG00000257394	4.88094	9.52805	14.3918	16.063	ENSG00000257394	CR759281.2
ENSG00000257396	0	0	0	0	ENSG00000257396	CR759815.1
ENSG00000257399	1.23107	4.11192	1.9704	8.55182	ENSG00000257399	CR388372.1
ENSG00000257402	0	0	0	0	ENSG00000257402	KRT126P
ENSG00000257403	3.06842	3.25518	6.98999	5.87457	ENSG00000257403	AC008740.1
ENSG00000257404	0	0	0	0	ENSG00000257404	AC107016.2
ENSG00000257405	0	0	0	0	ENSG00000257405	AC079600.1
ENSG00000257408	0.317552	0.610518	0.275791	0.430557	ENSG00000257408	AC092375.1
ENSG00000257411	3.59035	0	0	0	ENSG00000257411	AC034102.2
ENSG00000257412	2.64618	2.5088	2.88249	9.73402	ENSG00000257412	BX927178.1
ENSG00000257413	0.000863665	0.00235394	0.00142445	0.00120458	ENSG00000257413	YTHDC1
ENSG00000257414	0	0	0	0	ENSG00000257414	OR6C73P
ENSG00000257415	0.279394	1.18111	0.588163	1.39183	ENSG00000257415	AC084364.1
ENSG00000257416	1.64273	5.32831	2.80046	7.93452	ENSG00000257416	CR759912.1
ENSG00000257418	33.9066	85.2208	72.85	65.1963	ENSG00000257418	CR759787.1
ENSG00000257420	0	23.2982	18.9241	26.8168	ENSG00000257420	AL845557.1
ENSG00000257421	2.87207	6.53563	6.34001	10.8786	ENSG00000257421	CR354443.1
ENSG00000257423	0.251476	4.97607	0.335085	5.3242	ENSG00000257423	AL844213.3
ENSG00000257425	3.51171	10.9233	9.70791	18.1345	ENSG00000257425	AL844213.4
ENSG00000257426	0	0	0	1.00697	ENSG00000257426	AC126177.5
ENSG00000257427	0	0	0	0	ENSG00000257427	AL731683.1
ENSG00000257428	3.01995	11.4488	4.71324	21.277	ENSG00000257428	BX248096.1
ENSG00000257432	0	0.30307	0.192202	0.289267	ENSG00000257432	AL512310.3
ENSG00000257436	1.14823	4.4163	11.0589	7.21207	ENSG00000257436	AC217778.2
ENSG00000257437	0.0437403	0.226371	0.160163	0.232487	ENSG00000257437	AC217779.2
ENSG00000257440	0	3.14696	2.28701	0	ENSG00000257440	AL662822.6
ENSG00000257444	0	0.505456	0.423112	0.189933	ENSG00000257444	SETP7
ENSG00000257446	0.397762	0.70477	0.203127	0.442936	ENSG00000257446	ZNF878
ENSG00000257451	7.0693	11.3685	15.0646	14.9909	ENSG00000257451	CR388372.2
ENSG00000257457	8.60188	14.7077	16.6893	24.9024	ENSG00000257457	BX936369.3
ENSG00000257461	2.74E-07	0	6.92639	12.0368	ENSG00000257461	AL844203.1
ENSG00000257464	0.587321	4.41333	0.492855	11.363	ENSG00000257464	AC125611.1
ENSG00000257465	0.611019	0.892042	0.792059	2.24292	ENSG00000257465	ELOCP32
ENSG00000257468	0	0	0	0	ENSG00000257468	AC225613.3
ENSG00000257469	3.51171	10.9233	9.70791	18.1345	ENSG00000257469	BX936375.1
ENSG00000257473	0.0443433	0	0	0	ENSG00000257473	HLA-DQA2
ENSG00000257478	4.88094	9.52805	14.3918	16.063	ENSG00000257478	AL773535.2
ENSG00000257480	0	0	0.0596752	0	ENSG00000257480	MRPL2P1

ENSG00000257482	0	0	0	0	ENSG00000257482	ZNF727
ENSG00000257485	2.74E-07	0	6.92639	12.0368	ENSG00000257485	CR812479.2
ENSG00000257489	2.09713	10.3056	6.31975	9.77781	ENSG00000257489	AC010203.1
ENSG00000257493	0	0.598631	0.530359	1.0843	ENSG00000257493	AL512310.4
ENSG00000257501	0.295609	0.985702	0.784602	1.67095	ENSG00000257501	AC007424.1
ENSG00000257502	0	0	0	0	ENSG00000257502	BX248406.1
ENSG00000257503	0	0	0	0	ENSG00000257503	CYB5AP5
ENSG00000257506	0	1.65126	0	0	ENSG00000257506	AC133555.1
ENSG00000257511	1.19079	3.09935	2.00116	4.55963	ENSG00000257511	AC084824.1
ENSG00000257512	0.500105	0.801206	2.06021	2.20531	ENSG00000257512	AC124947.2
ENSG00000257513	0	0	0.0777356	0	ENSG00000257513	NPIPB1P
ENSG00000257516	0	0	0	0	ENSG00000257516	CR354443.2
ENSG00000257528	0	0	0	0.0442282	ENSG00000257528	KRT8P19
ENSG00000257529	1.16942	1.1865	1.66521	1.59657	ENSG00000257529	RPL36A-HNRNPH2
ENSG00000257531	7.85345	15.2657	3.99477	9.83727	ENSG00000257531	AC008147.3
ENSG00000257535	1.41446	5.43235	6.18395	5.82457	ENSG00000257535	CR759890.2
ENSG00000257536	9.64873	14.9546	9.62966	27.1205	ENSG00000257536	AL845509.1
ENSG00000257537	75.1959	187.988	178.254	250.844	ENSG00000257537	AC139677.3
ENSG00000257538	0	0	0	0	ENSG00000257538	AL935026.1
ENSG00000257539	0.282417	0.31955	0.482525	0.764844	ENSG00000257539	HSPA8P14
ENSG00000257542	0.206609	0.173213	0.396854	0.502698	ENSG00000257542	OR7E47P
ENSG00000257544	2.69953	16.7277	12.8568	13.2465	ENSG00000257544	CR847849.1
ENSG00000257545	3.45459	5.72855	6.12841	5.93171	ENSG00000257545	AC079385.1
ENSG00000257549	2.72466	3.85605	5.26352	14.2934	ENSG00000257549	AL662822.7
ENSG00000257554	1.23107	4.11192	1.9704	8.55182	ENSG00000257554	CR751550.1
ENSG00000257558	0	0	0	0	ENSG00000257558	CR383656.4
ENSG00000257559	2.72466	3.85605	5.26352	14.2934	ENSG00000257559	CR382280.3
ENSG00000257560	2.10655	5.6499	8.59112	17.5874	ENSG00000257560	BX247900.2
ENSG00000257561	16.3756	20.4435	24.1407	30.0933	ENSG00000257561	AC138688.3
ENSG00000257562	0	0	0	0	ENSG00000257562	AL671859.1
ENSG00000257564	0	0.118733	0	0.134403	ENSG00000257564	AC068993.1
ENSG00000257565	19.003	41.1814	29.133	57.6428	ENSG00000257565	AC217770.1
ENSG00000257569	0.3141	1.49058	0.269371	1.96473	ENSG00000257569	GSTP1P1
ENSG00000257570	0	0	0	0	ENSG00000257570	AC020612.2
ENSG00000257571	19.3529	48.1127	45.066	106.775	ENSG00000257571	CR933842.1
ENSG00000257572	0.113354	0.278257	0.220994	1.01278	ENSG00000257572	AC008127.2
ENSG00000257573	0	0	0	0	ENSG00000257573	RP11-496I2.5
ENSG00000257575	0.967847	5.36006	6.48123	31.5001	ENSG00000257575	AL805934.1
ENSG00000257576	0	0.0672426	0.0915745	0.0760198	ENSG00000257576	HSPD1P4
ENSG00000257578	0	0	0	0	ENSG00000257578	AC074378.1
ENSG00000257580	0	0	0	0	ENSG00000257580	AC008055.1
ENSG00000257586	0	0	0	0	ENSG00000257586	AC018448.2
ENSG00000257589	2.69953	16.7277	12.8568	13.2465	ENSG00000257589	AL805913.1
ENSG00000257590	22.9542	35.6859	32.8435	51.4254	ENSG00000257590	CR759772.2
ENSG00000257591	4.27021	3.76587	4.67765	2.79616	ENSG00000257591	ZNF625
ENSG00000257593	29.6671	57.8883	59.4732	105.377	ENSG00000257593	CR759793.1
ENSG00000257594	6.07825	9.98544	5.99139	4.33107	ENSG00000257594	GALNT4
ENSG00000257599	63.8088	48.0975	66.6765	47.214	ENSG00000257599	OVCH1-AS1
ENSG00000257600	6.01054	14.0535	16.6311	21.5665	ENSG00000257600	CR388219.1
ENSG00000257601	28.3557	65.8332	56.4624	112.592	ENSG00000257601	CR759784.2
ENSG00000257602	1.64273	5.32831	2.80046	7.93452	ENSG00000257602	BX927220.4
ENSG00000257604	0	0.493003	1.35383	0	ENSG00000257604	AC027288.2
ENSG00000257608	1.71887	3.2175	2.48787	6.51675	ENSG00000257608	GRAMD4P3
ENSG00000257609	0	0.191751	0.173201	0.107822	ENSG00000257609	AC091515.1

ENSG00000257611	0.0456056	0.0442712	0.0608008	0.0759087	ENSG00000257611	AC010182.1
ENSG00000257615	0	0	0.944927	1.06066	ENSG00000257615	AC139677.4
ENSG00000257616	0.227505	0.376483	0.07949	0.126032	ENSG00000257616	AC055716.2
ENSG00000257618	7.0693	11.3685	15.0646	14.9909	ENSG00000257618	BX000357.1
ENSG00000257624	1.03448	0	0.460578	0.540391	ENSG00000257624	AC004024.1
ENSG00000257626	1.38E-07	0	7.84318	0	ENSG00000257626	CR753819.2
ENSG00000257629	0	0	0	0.774578	ENSG00000257629	AC006199.1
ENSG00000257630	0	3.14696	2.28701	0	ENSG00000257630	CR388372.3
ENSG00000257632	0	1.08801	0.896307	0	ENSG00000257632	CR759828.1
ENSG00000257635	0	6.89E-06	3.08E-06	2.42E-06	ENSG00000257635	CR383656.5
ENSG00000257637	0	0.403128	0	0	ENSG00000257637	CR759795.1
ENSG00000257639	0	0	0	0	ENSG00000257639	AC005632.1
ENSG00000257643	0.820371	1.56226	2.11673	1.43319	ENSG00000257643	AC084824.2
ENSG00000257644	0	0	0.188947	0	ENSG00000257644	CR383656.6
ENSG00000257645	0	0	3.05247	0	ENSG00000257645	AC087897.1
ENSG00000257646	0.251476	4.97607	0.335085	5.3242	ENSG00000257646	BX936369.4
ENSG00000257648	0	0	0	0	ENSG00000257648	CYCSP30
ENSG00000257649	0	0	0.133069	0	ENSG00000257649	METTL7AP1
ENSG00000257651	17.5019	62.0693	34.3903	79.9988	ENSG00000257651	CR759890.3
ENSG00000257652	18.8	0	0.423861	0	ENSG00000257652	AC019173.1
ENSG00000257656	2.72466	3.85605	5.26352	14.2934	ENSG00000257656	AL844213.5
ENSG00000257658	0.938721	0.977471	1.00394	1.13239	ENSG00000257658	AC004217.3
ENSG00000257659	3.01995	11.4488	4.71324	21.277	ENSG00000257659	CR759912.2
ENSG00000257661	0	2.15576	0	4.47839	ENSG00000257661	AL845509.2
ENSG00000257662	0	0	0	0	ENSG00000257662	EIF4A1P12
ENSG00000257664	0.3121	0.600902	0.135028	0.166687	ENSG00000257664	AC078814.3
ENSG00000257665	1.41446	5.43235	6.18395	5.82457	ENSG00000257665	AL773535.3
ENSG00000257666	0.286447	1.62228	1.63908	2.90826	ENSG00000257666	CBX3P5
ENSG00000257668	0	0	0.0292392	0	ENSG00000257668	AC084033.2
ENSG00000257670	14.9558	27.0618	28.4798	45.2721	ENSG00000257670	BX511262.2
ENSG00000257672	0	0	0	0	ENSG00000257672	CR383656.7
ENSG00000257674	0.0707063	0	0	0.0801529	ENSG00000257674	AC020629.1
ENSG00000257675	0.0441825	0.171038	0.117676	0	ENSG00000257675	BTBD10P1
ENSG00000257679	0.000435758	0	0.000769214	0.000385772	ENSG00000257679	UGT2A3
ENSG00000257680	0.391603	3.18203	0.583928	3.29432	ENSG00000257680	AC016144.1
ENSG00000257686	0	3.14696	2.28701	0	ENSG00000257686	CR759912.3
ENSG00000257687	0	0	0	0	ENSG00000257687	AC079600.2
ENSG00000257690	0	0	4.82644	0	ENSG00000257690	CR759890.4
ENSG00000257691	0	0	0	0	ENSG00000257691	AC133555.2
ENSG00000257693	2.09289	4.24442	1.66567	3.21291	ENSG00000257693	CR759912.4
ENSG00000257697	9.64873	14.9546	9.62966	27.1205	ENSG00000257697	BX927180.1
ENSG00000257701	15.0457	24.3198	15.5275	38.1622	ENSG00000257701	BX247900.3
ENSG00000257704	2.67614	2.86726	5.25767	5.72693	ENSG00000257704	INAFM1
ENSG00000257705	0.58346	0	1.95134	2.59831	ENSG00000257705	AL844853.1
ENSG00000257707	2.18712	2.37204	1.71669	4.18271	ENSG00000257707	AL662890.2
ENSG00000257709	1.38E-07	0	7.84318	0	ENSG00000257709	BX927139.1
ENSG00000257712	2.72466	3.85605	5.26352	14.2934	ENSG00000257712	BX936369.5
ENSG00000257713	1.64273	5.32831	2.80046	7.93452	ENSG00000257713	AL662822.8
ENSG00000257717	0	0	0	0	ENSG00000257717	AC225613.4
ENSG00000257720	0	0	0	0	ENSG00000257720	ILF2P2
ENSG00000257721	0	0	0	0	ENSG00000257721	CR383656.8
ENSG00000257723	0	0.207644	0.187501	0.349707	ENSG00000257723	CHCHD3P2
ENSG00000257726	0.151803	0.21895	0.199623	0.164804	ENSG00000257726	AC078880.2

ENSG00000257727	67.4635	82.0903	78.9171	97.3057	ENSG00000257727	CNPY2
ENSG00000257730	0	0.961255	2.54739	3.05851	ENSG00000257730	LSM6P2
ENSG00000257731	0	0	0.188333	0.245355	ENSG00000257731	CR383656.9
ENSG00000257733	6.01054	14.0535	16.6311	21.5665	ENSG00000257733	CR759782.1
ENSG00000257736	3.62936	8.40096	10.3302	13.505	ENSG00000257736	CR933877.1
ENSG00000257738	0.360544	0.259828	0.391236	0.585273	ENSG00000257738	AC009248.1
ENSG00000257739	16.0994	28.6638	30.3074	44.8447	ENSG00000257739	CR753819.3
ENSG00000257743	0.0502905	0.110428	0.0870295	0.155932	ENSG00000257743	MGAM2
ENSG00000257744	1.77202	16.3321	15.8156	15.8388	ENSG00000257744	AL662833.1
ENSG00000257745	0.163766	0.58256	0.465088	0.705763	ENSG00000257745	UGT2B10
ENSG00000257749	1.52146	1.20756	2.65471	8.43705	ENSG00000257749	CTD-2314B22.2
ENSG00000257751	0	0.162782	0	0	ENSG00000257751	AL512310.5
ENSG00000257752	0	1.19194	0.579753	1.54739	ENSG00000257752	AC091516.1
ENSG00000257757	0.0670043	0	0	0	ENSG00000257757	OR6C7P
ENSG00000257758	0	0	0	0	ENSG00000257758	KRT18P20
ENSG00000257763	0	0.300674	0.339565	0.169671	ENSG00000257763	OR5BK1P
ENSG00000257767	0	0	0	0.0206374	ENSG00000257767	AC002996.1
ENSG00000257770	0	0	0	0	ENSG00000257770	GPX5
ENSG00000257773	0.120614	0.114473	0	0	ENSG00000257773	AC011595.2
ENSG00000257774	0	0.0553131	0	1.78956	ENSG00000257774	AC139677.5
ENSG00000257775	11.4845	15.2953	19.8384	28.716	ENSG00000257775	AC127032.2
ENSG00000257777	0	0.224334	0.0674715	0.253244	ENSG00000257777	AC022507.1
ENSG00000257778	12.2979	19.7225	35.2826	47.0983	ENSG00000257778	AL390196.1
ENSG00000257779	0	0	0	0.314092	ENSG00000257779	AC078814.4
ENSG00000257780	0.101953	0.0979396	0.176908	0.220183	ENSG00000257780	GLYCAM1
ENSG00000257782	33.9066	85.2208	72.85	65.1963	ENSG00000257782	CR354443.3
ENSG00000257783	16.0994	28.6638	30.3074	44.8447	ENSG00000257783	AL773544.2
ENSG00000257786	0	0	0	0.577782	ENSG00000257786	AKIRIN1P1
ENSG00000257790	0.498469	1.34713	1.39198	0.109253	ENSG00000257790	EIF4A1P4
ENSG00000257791	1.41446	5.43235	6.18395	5.82457	ENSG00000257791	BX294158.3
ENSG00000257792	0	0.068967	0	0.155833	ENSG00000257792	AC090115.2
ENSG00000257793	0.0755051	0.212444	0.194669	0.120412	ENSG00000257793	CRHR1
ENSG00000257794	0.584155	0.269839	0.485899	1.97014	ENSG00000257794	RP11-125N22.4
ENSG00000257796	19.3529	48.1127	45.066	106.775	ENSG00000257796	CR936918.1
ENSG00000257798	1.64273	5.32831	2.80046	7.93452	ENSG00000257798	CR751550.2
ENSG00000257800	1.00732	1.44364	2.85591	3.08556	ENSG00000257800	FNBP1P1
ENSG00000257802	0.0996317	0.43163	0.567872	0.543982	ENSG00000257802	AC089984.2
ENSG00000257803	0.0400746	0.44933	0.139564	0.811803	ENSG00000257803	AC010200.1
ENSG00000257805	19.3529	48.1127	45.066	106.775	ENSG00000257805	BX908738.1
ENSG00000257806	5.97055	28.366	23.6536	62.7926	ENSG00000257806	AC225613.5
ENSG00000257807	0	0	0.0516016	0	ENSG00000257807	AC003686.1
ENSG00000257811	16.0994	28.6638	30.3074	44.8447	ENSG00000257811	AL662867.1
ENSG00000257813	0	0.0715742	0.0433504	0.109147	ENSG00000257813	AC090525.2
ENSG00000257814	0	0	0	0	ENSG00000257814	ARL17
ENSG00000257818	0.281914	0.778348	0.854026	0.806015	ENSG00000257818	C1GALT1P1
ENSG00000257819	2.18825	16.025	7.95823	10.3835	ENSG00000257819	BX927214.3
ENSG00000257820	0	0	0.326316	0	ENSG00000257820	AC024909.2
ENSG00000257822	208.149	521.777	419.739	637.776	ENSG00000257822	AC217770.2
ENSG00000257823	0	0	0.0604014	0.151133	ENSG00000257823	AC092552.1
ENSG00000257825	1.2058	1.16375	3.15706	1.33151	ENSG00000257825	CR383656.10
ENSG00000257832	0.699302	2.15878	0.871935	2.01468	ENSG00000257832	AL671879.1
ENSG00000257834	17.308	54.3949	0	0	ENSG00000257834	AL662822.9
ENSG00000257838	0.499487	0.523148	0	1.87765	ENSG00000257838	AC106788.1
ENSG00000257841	9.85036	12.5591	11.4887	11.2534	ENSG00000257841	BX294158.4

ENSG00000257843	20.2253	77.3892	73.8842	139.73	ENSG00000257843	AL845450.2
ENSG00000257844	0.0716181	0.137756	0.06223	0	ENSG00000257844	KRT90P
ENSG00000257846	0	0	0	0	ENSG00000257846	AL512310.6
ENSG00000257847	1.25381	4.34677	1.42137	5.58868	ENSG00000257847	LSM3P2
ENSG00000257848	0	0.112906	0.0510198	0.128008	ENSG00000257848	AC074029.1
ENSG00000257850	3.01995	11.4488	4.71324	21.277	ENSG00000257850	CR388372.4
ENSG00000257851	0	0.105826	0	0.368145	ENSG00000257851	HNRNPA3P10
ENSG00000257852	0	0	0	0	ENSG00000257852	AC048344.2
ENSG00000257853	0	0	0	0	ENSG00000257853	MED15P1
ENSG00000257854	2.09289	4.24442	1.66567	3.21291	ENSG00000257854	BX000357.2
ENSG00000257855	0	0	0	0.265076	ENSG00000257855	AC126471.1
ENSG00000257856	1.45378	3.08411	3.05253	8.15553	ENSG00000257856	CR759792.1
ENSG00000257858	0	0	0	0	ENSG00000257858	MTND1P24
ENSG00000257860	0	0	0	0.120748	ENSG00000257860	AC068643.2
ENSG00000257862	9.85036	12.5591	11.4887	11.2534	ENSG00000257862	CR759281.3
ENSG00000257864	0.755228	1.8038	0.868708	0.673248	ENSG00000257864	AC025030.1
ENSG00000257865	0	0	0	0.342266	ENSG00000257865	AC090022.1
ENSG00000257867	0	0	0	0	ENSG00000257867	CR753815.1
ENSG00000257868	0	0	0	0	ENSG00000257868	CTD-2311B13.8
ENSG00000257872	0.208336	0	0	0	ENSG00000257872	AC233290.1
ENSG00000257873	0	0	0	0	ENSG00000257873	AC127032.3
ENSG00000257874	0	0	0.0899446	0	ENSG00000257874	BX927320.1
ENSG00000257875	0.465348	0.538339	0.80544	0.331444	ENSG00000257875	AC089998.3
ENSG00000257882	0	0	0.011168	0.0140709	ENSG00000257882	AC217770.3
ENSG00000257884	0	0	0.0222326	0	ENSG00000257884	AL512310.7
ENSG00000257885	0	0.0782486	0.0713654	0.172223	ENSG00000257885	PHBP18
ENSG00000257887	0	0	0	5.44718	ENSG00000257887	AC138688.4
ENSG00000257888	1.49827	1.53425	2.83478	1.35914	ENSG00000257888	AC127032.4
ENSG00000257889	26.786	46.2078	65.0388	110.567	ENSG00000257889	AC225613.6
ENSG00000257892	8.60188	14.7077	16.6893	24.9024	ENSG00000257892	AL844213.6
ENSG00000257895	0.0192667	0	0	0	ENSG00000257895	BX511262.3
ENSG00000257896	5.3983	13.6829	8.60477	14.1351	ENSG00000257896	AC093012.1
ENSG00000257897	0.0886047	0.170272	0	0.20704	ENSG00000257897	AC139697.1
ENSG00000257899	1.17828	6.01467	4.63108	6.42788	ENSG00000257899	RP11-125N22.3
ENSG00000257901	2.74E-07	0	6.92639	12.0368	ENSG00000257901	CR759890.5
ENSG00000257902	0	4.15237	0	0	ENSG00000257902	BX936369.6
ENSG00000257905	0	0	0	0	ENSG00000257905	AC004486.1
ENSG00000257907	0.325883	0.901925	0.405208	0.817552	ENSG00000257907	EEF1A1P17
ENSG00000257911	3.01995	11.4488	4.71324	21.277	ENSG00000257911	CR382280.4
ENSG00000257914	0.58346	0	1.95134	2.59831	ENSG00000257914	AL662834.2
ENSG00000257915	0.256223	0.779077	0.824611	0.65207	ENSG00000257915	GLULP5
ENSG00000257916	8.60188	14.7077	16.6893	24.9024	ENSG00000257916	AL662822.10
ENSG00000257917	24.6137	112.347	68.3013	279.617	ENSG00000257917	AL901607.1
ENSG00000257921	0.335292	0.797102	1.08764	1.23613	ENSG00000257921	AC025165.3
ENSG00000257923	17.6676	16.8632	19.6286	21.1595	ENSG00000257923	CUX1
ENSG00000257927	0	0	0	0	ENSG00000257927	MRPS36P5
ENSG00000257933	0	0	0	0	ENSG00000257933	RP11-125N22.1
ENSG00000257934	2.74E-07	0	6.92639	12.0368	ENSG00000257934	BX927214.4
ENSG00000257936	1.19694	6.90658	10.0207	22.7539	ENSG00000257936	AC139677.6
ENSG00000257937	0.146719	4.25928	1.4041	4.78195	ENSG00000257937	AL844213.7
ENSG00000257939	41.5854	72.8141	67.1033	135.305	ENSG00000257939	AC019319.1
ENSG00000257941	0.802349	4.05488	1.28973	3.86104	ENSG00000257941	AC011611.5
ENSG00000257944	3.62936	8.40096	10.3302	13.505	ENSG00000257944	AL844853.2
ENSG00000257945	7.0693	11.3685	15.0646	14.9909	ENSG00000257945	CR759912.5

ENSG00000257949	17.9415	11.3695	13.8959	8.63267	ENSG00000257949	TEN1
ENSG00000257950	1.37695	2.7123	2.34012	4.15175	ENSG00000257950	P2RX5-TAX1BP3
ENSG00000257951	0	0	0.0571285	0	ENSG00000257951	AC126177.6
ENSG00000257954	0.857008	2.92868	1.93873	9.15508	ENSG00000257954	AC125611.2
ENSG00000257955	0.258658	0.684148	1.1278	1.68894	ENSG00000257955	AC004801.3
ENSG00000257956	1.53594	0.792488	9.27265	6.40443	ENSG00000257956	NOP56P3
ENSG00000257957	0.453741	1.57669	1.48373	1.23226	ENSG00000257957	QRSL1P3
ENSG00000257961	8.21686	12.4235	6.96212	4.03502	ENSG00000257961	AC003070.1
ENSG00000257962	0.770811	1.09467	0.656889	0	ENSG00000257962	AC011773.2
ENSG00000257966	6.69979	13.2992	13.0018	22.0431	ENSG00000257966	OLA1P3
ENSG00000257967	0	1.08801	0.896307	0	ENSG00000257967	BX927178.2
ENSG00000257972	20.4213	20.6538	30.9788	33.6704	ENSG00000257972	AL663093.2
ENSG00000257975	1.45378	3.08411	3.05253	8.15553	ENSG00000257975	CR547132.1
ENSG00000257976	0	0	0	0	ENSG00000257976	AL079352.1
ENSG00000257977	0	0	0	0	ENSG00000257977	RP11-496I2.6
ENSG00000257978	10.6365	7.17451	10.9191	16.7489	ENSG00000257978	BX927180.2
ENSG00000257979	7.44052	19.0013	13.3882	31.5414	ENSG00000257979	SNRPGP18
ENSG00000257980	3.01995	11.4488	4.71324	21.277	ENSG00000257980	AL844213.8
ENSG00000257981	7.68775	14.5997	30.6927	59.0503	ENSG00000257981	CR547129.1
ENSG00000257984	20.4481	76.4981	46.9564	33.9458	ENSG00000257984	BX927220.5
ENSG00000257987	0.221647	0.67698	0.832877	0.706349	ENSG00000257987	TEX49
ENSG00000257990	0.234205	0.476435	0.353741	0.513395	ENSG00000257990	NF1P4
ENSG00000257991	0.631133	3.11818	1.86181	2.08757	ENSG00000257991	AC089984.3
ENSG00000257993	13.4938	25.0794	15.5744	50.6737	ENSG00000257993	AL662867.2
ENSG00000257994	0.218076	0	0	0	ENSG00000257994	AC084364.2
ENSG00000257998	0	0	0	0	ENSG00000257998	AC123904.3
ENSG00000258002	3.50046	9.33161	9.33714	10.1998	ENSG00000258002	CR759815.2
ENSG00000258003	0.254355	0.145807	1.84977	3.4792	ENSG00000258003	AC139677.7
ENSG00000258004	0.146719	4.25928	1.4041	4.78195	ENSG00000258004	BX248096.2
ENSG00000258008	10.6365	7.17451	10.9191	16.7489	ENSG00000258008	AL845509.3
ENSG00000258009	99.7037	198.23	176.078	326.899	ENSG00000258009	AL662833.2
ENSG00000258011	0.310082	0	0	0	ENSG00000258011	AC144548.1
ENSG00000258012	0.935465	2.02722	1.52306	2.75278	ENSG00000258012	AC026111.1
ENSG00000258013	0	1.48327	0.629057	1.33415	ENSG00000258013	RPL3P13
ENSG00000258014	7.91263	28.5993	7.88199	47.0926	ENSG00000258014	CR759747.1
ENSG00000258015	0	0	0	0	ENSG00000258015	CR753846.3
ENSG00000258016	0	0	0	0	ENSG00000258016	HIGD1AP1
ENSG00000258020	99.7037	198.23	176.078	326.899	ENSG00000258020	CR759814.1
ENSG00000258021	0	0	0	0	ENSG00000258021	AC025259.2
ENSG00000258022	4.85452	4.14585	3.47307	6.37901	ENSG00000258022	AL662822.11
ENSG00000258023	0	0	0	0	ENSG00000258023	BX296568.1
ENSG00000258024	0.150481	0.0723501	0	0	ENSG00000258024	AC090115.3
ENSG00000258025	0.146719	4.25928	1.4041	4.78195	ENSG00000258025	CR759912.6
ENSG00000258027	0	0.130538	0	0	ENSG00000258027	NF1P4
ENSG00000258030	2.09289	4.24442	1.66567	3.21291	ENSG00000258030	AL662825.1
ENSG00000258032	9.85036	12.5591	11.4887	11.2534	ENSG00000258032	BX927214.5
ENSG00000258033	1.04651	2.80926	1.02672	2.58243	ENSG00000258033	AC063947.2
ENSG00000258036	0	0.0867596	0	0.195424	ENSG00000258036	KRT125P
ENSG00000258037	6.14623	13.9711	10.5784	28.5052	ENSG00000258037	AC127032.5
ENSG00000258040	7.91381	8.66338	10.3284	19.7138	ENSG00000258040	AC005086.3
ENSG00000258045	6.72931	15.8363	12.9253	26.9019	ENSG00000258045	CR382280.5
ENSG00000258049	2.97342	12.5323	3.21547	17.6442	ENSG00000258049	AC217775.2
ENSG00000258051	0.327704	0.105273	0.0947318	0.71524	ENSG00000258051	AC074029.2
ENSG00000258052	0.0749597	0	0.214752	0	ENSG00000258052	AC025263.2

ENSG00000258053	2.41841	5.72487	4.52794	10.9562	ENSG00000258053	AC025575.2
ENSG00000258054	4.85452	4.14585	3.47307	6.37901	ENSG00000258054	CR382280.6
ENSG00000258058	2.64618	2.5088	2.88249	9.73402	ENSG00000258058	CR759828.2
ENSG00000258059	2.0766	0	1.26063	10.351	ENSG00000258059	AL662857.1
ENSG00000258060	0	0	0	0	ENSG00000258060	AL662833.3
ENSG00000258062	0	0	0	0	ENSG00000258062	BX927168.2
ENSG00000258064	0	0	0	0	ENSG00000258064	AC073612.1
ENSG00000258065	0	0	0	0	ENSG00000258065	AL122126.1
ENSG00000258067	18.6228	35.8578	29.8837	38.7151	ENSG00000258067	AL773535.4
ENSG00000258069	19.3529	48.1127	45.066	106.775	ENSG00000258069	CR753509.1
ENSG00000258070	3.51171	10.9233	9.70791	18.1345	ENSG00000258070	CR774188.1
ENSG00000258071	0	0	0	0.182606	ENSG00000258071	ARL2BPP2
ENSG00000258072	0	0	0	0	ENSG00000258072	AC126177.7
ENSG00000258073	0	1.4997	0	0	ENSG00000258073	AC128657.1
ENSG00000258074	0.108776	0	0.0943368	0	ENSG00000258074	VTI1BP3
ENSG00000258075	2.72466	3.85605	5.26352	14.2934	ENSG00000258075	CR762481.4
ENSG00000258076	0	0.818814	1.87311	1.49584	ENSG00000258076	CR383656.12
ENSG00000258080	0.185682	1.06092	0.687787	1.66127	ENSG00000258080	ARHGAP42P4
ENSG00000258083	0	0	0.0483487	0	ENSG00000258083	OR9A4
ENSG00000258085	0.222637	0.598247	0.231535	0.891883	ENSG00000258085	UGT2B15
ENSG00000258090	0	0.0902338	0.319025	0.102859	ENSG00000258090	AC093014.1
ENSG00000258091	0.955223	1.79786	0.402115	0	ENSG00000258091	AC011611.6
ENSG00000258093	3.74555	7.23554	10.579	12.8347	ENSG00000258093	AC005086.4
ENSG00000258094	24.4156	100.748	90.1078	105.952	ENSG00000258094	CR759912.7
ENSG00000258097	2.87207	6.53563	6.34001	10.8786	ENSG00000258097	AL670886.1
ENSG00000258103	23.8652	49.8788	33.2454	64.8609	ENSG00000258103	CT009481.1
ENSG00000258104	0	0	0.341744	0	ENSG00000258104	HIGD1AP9
ENSG00000258110	2.18825	16.025	7.95823	10.3835	ENSG00000258110	CR812479.3
ENSG00000258111	0	2.15197	3.00537	2.81919	ENSG00000258111	AC079316.1
ENSG00000258112	0	0.0594018	0	0.0672388	ENSG00000258112	CCNG2P1
ENSG00000258113	3.75026	11.1488	19.2962	26.8252	ENSG00000258113	CR847852.1
ENSG00000258116	0	0	0	0	ENSG00000258116	AC008083.2
ENSG00000258118	0	0	0	0	ENSG00000258118	AC010198.2
ENSG00000258120	0.102965	0.43456	0	0	ENSG00000258120	KRT128P
ENSG00000258124	1.41446	5.43235	6.18395	5.82457	ENSG00000258124	BX927214.6
ENSG00000258126	0.58346	0	1.95134	2.59831	ENSG00000258126	CR933877.2
ENSG00000258128	0.894013	1.99575	2.35572	3.26441	ENSG00000258128	AC079598.2
ENSG00000258130	6.70019	10.3726	11.9165	15.2275	ENSG00000258130	AC106782.1
ENSG00000258133	0	0	0	0	ENSG00000258133	AC025578.1
ENSG00000258134	0.886047	0.852735	1.07769	1.34276	ENSG00000258134	AC016954.1
ENSG00000258138	3.03177	1.91015	7.15037	5.71422	ENSG00000258138	AL935156.1
ENSG00000258141	0.146719	4.25928	1.4041	4.78195	ENSG00000258141	CR388372.5
ENSG00000258142	0.297878	0.571087	0.25785	0.477851	ENSG00000258142	AC093023.1
ENSG00000258143	17.901	28.822	36.0095	80.5577	ENSG00000258143	AC225613.7
ENSG00000258145	33.5078	46.2322	35.1603	35.972	ENSG00000258145	BX927168.3
ENSG00000258146	3.51171	10.9233	9.70791	18.1345	ENSG00000258146	AL662822.12
ENSG00000258147	0.251476	4.97607	0.335085	5.3242	ENSG00000258147	CR762481.5
ENSG00000258148	0.562648	1.05834	0	0.568928	ENSG00000258148	AC007115.1
ENSG00000258149	2.18825	16.025	7.95823	10.3835	ENSG00000258149	CR759890.6
ENSG00000258150	1.17705	0.769523	0.804567	0.363686	ENSG00000258150	AC133555.3
ENSG00000258151	2.87207	6.53563	6.34001	10.8786	ENSG00000258151	CR759761.1
ENSG00000258153	0	0.374807	0.369021	0	ENSG00000258153	HSPE1P4
ENSG00000258154	0	0	0	0	ENSG00000258154	AL512356.2
ENSG00000258155	7.83657	10.9232	33.388	11.1286	ENSG00000258155	BX927220.6

ENSG00000258158	1.41446	5.43235	6.18395	5.82457	ENSG00000258158	AL662822.13
ENSG00000258159	0	0.149109	0	0.332406	ENSG00000258159	IMMP1LP2
ENSG00000258160	0	0	0	0	ENSG00000258160	AL713890.1
ENSG00000258164	0.51877	1.63312	1.78633	1.87821	ENSG00000258164	AL845454.1
ENSG00000258165	11.2977	19.9007	12.7719	36.2645	ENSG00000258165	CR762481.6
ENSG00000258166	2.87207	6.53563	6.34001	10.8786	ENSG00000258166	CR753842.1
ENSG00000258173	0	0	0	0	ENSG00000258173	AC079598.3
ENSG00000258179	0	0.443705	0	0	ENSG00000258179	AC079598.4
ENSG00000258182	0	0	0	0	ENSG00000258182	CR759848.1
ENSG00000258184	0	0	0	0	ENSG00000258184	AC087883.1
ENSG00000258186	14.7927	17.5153	6.02204	9.03546	ENSG00000258186	SLC7A5P2
ENSG00000258191	22.5042	60.3381	141.096	1.57E-06	ENSG00000258191	AL805909.2
ENSG00000258192	0	0	0	0	ENSG00000258192	AL670886.2
ENSG00000258193	0	0.279378	0.505154	0	ENSG00000258193	AC011602.1
ENSG00000258194	18.6228	35.8578	29.8837	38.7151	ENSG00000258194	BX294158.5
ENSG00000258195	0	0	1.49594	0	ENSG00000258195	BX005439.1
ENSG00000258198	0	0	0	0	ENSG00000258198	RP11-146E13.3
ENSG00000258200	6.93945	14.2272	13.3873	24.2046	ENSG00000258200	BX247900.4
ENSG00000258202	0	0	0	0	ENSG00000258202	AC026371.1
ENSG00000258204	0	0.318002	0	0	ENSG00000258204	AC008126.1
ENSG00000258205	0	0	0	0	ENSG00000258205	AC079598.5
ENSG00000258206	0	1.0105	0.342118	0	ENSG00000258206	AC137768.1
ENSG00000258207	0	44.822	2.30693	27.1057	ENSG00000258207	AL662831.2
ENSG00000258208	15.4746	27.9335	17.3937	22.1049	ENSG00000258208	AL805909.3
ENSG00000258209	45.676	141.009	133.76	196.102	ENSG00000258209	AL845450.3
ENSG00000258211	2.18825	16.025	7.95823	10.3835	ENSG00000258211	BX294158.6
ENSG00000258212	0.729753	0.958429	0.908919	1.34172	ENSG00000258212	ZNF75BP
ENSG00000258213	7.68775	0	0	10.568	ENSG00000258213	AL844527.1
ENSG00000258215	0	0	0	0.281866	ENSG00000258215	AC078886.1
ENSG00000258218	4.85452	4.14585	3.47307	6.37901	ENSG00000258218	CR762481.7
ENSG00000258219	3.51171	10.9233	9.70791	18.1345	ENSG00000258219	BX927143.1
ENSG00000258221	2.64618	2.5088	2.88249	9.73402	ENSG00000258221	BX322539.1
ENSG00000258223	0	0.0662287	0.0299851	0.224624	ENSG00000258223	PRSS58
ENSG00000258224	0	0	0	0	ENSG00000258224	AC090049.2
ENSG00000258226	0.0192667	0	0	0	ENSG00000258226	AL805934.2
ENSG00000258227	0.666052	1.07505	1.30724	2.726	ENSG00000258227	CLEC5A
ENSG00000258228	0	0	0	0	ENSG00000258228	AL805934.2
ENSG00000258230	0.588127	0.852011	0.439629	1.89071	ENSG00000258230	AC063950.1
ENSG00000258231	1.35342	2.51985	3.28504	5.7736	ENSG00000258231	AC020637.1
ENSG00000258233	0.515808	0.887607	0.735279	0.548674	ENSG00000258233	ARHGAP42P5
ENSG00000258238	34.2596	48.1107	46.6687	75.1841	ENSG00000258238	AL662867.3
ENSG00000258239	0	0	0	0.350416	ENSG00000258239	MTND2P17
ENSG00000258241	47.3465	70.3689	57.6773	106.808	ENSG00000258241	BX571801.1
ENSG00000258243	1.23107	4.11192	1.9704	8.55182	ENSG00000258243	CR759912.8
ENSG00000258244	0.345924	0.664071	0.499818	0.496558	ENSG00000258244	AC069240.2
ENSG00000258245	0.692996	4.65618	0.885814	1.48504	ENSG00000258245	RPL10P13
ENSG00000258247	0	0	0	0	ENSG00000258247	RP11-167N24.6
ENSG00000258248	0	0	0	0	ENSG00000258248	AL773544.3
ENSG00000258251	0	0	0	0	ENSG00000258251	YPEL5P3
ENSG00000258256	5.02192	10.1154	8.81993	13.5211	ENSG00000258256	AC011773.3
ENSG00000258259	0.0192667	0	0	0	ENSG00000258259	CR759761.2
ENSG00000258261	6.94969	27.1319	23.6015	35.999	ENSG00000258261	CR753803.1
ENSG00000258262	0	0	0	0	ENSG00000258262	AC063949.1
ENSG00000258263	2.18825	16.025	7.95823	10.3835	ENSG00000258263	AL773535.5

ENSG00000258264	100.288	36.2557	0	0	ENSG00000258264	CR753651.1
ENSG00000258269	0	3.14696	2.28701	0	ENSG00000258269	BX248096.3
ENSG00000258270	0	0	0.341744	0	ENSG00000258270	AC138688.5
ENSG00000258271	0	0	0	0	ENSG00000258271	AC025260.1
ENSG00000258273	0	2.42546	0	0	ENSG00000258273	AC024257.2
ENSG00000258275	0.136231	0.784975	0.177186	0.676015	ENSG00000258275	OR7K1P
ENSG00000258278	0	0	0	0	ENSG00000258278	CLUHP8
ENSG00000258281	15.1086	18.6749	16.054	21.9854	ENSG00000258281	CR753819.4
ENSG00000258282	0	0	0	0.168651	ENSG00000258282	AL121766.1
ENSG00000258284	0	5.43209	0.958274	2.2971	ENSG00000258284	POLR2KP1
ENSG00000258286	1.83169	4.13359	4.81581	12.29	ENSG00000258286	AL844213.10
ENSG00000258287	0	0	0.117771	0.206812	ENSG00000258287	AC021146.1
ENSG00000258288	0	0	0.158991	0.391202	ENSG00000258288	NENFP2
ENSG00000258289	27.1358	30.8465	21.9247	23.1979	ENSG00000258289	CHURC1
ENSG00000258290	0	0	0	0	ENSG00000258290	BRWD1P2
ENSG00000258291	31.6305	68.237	56.3874	129.568	ENSG00000258291	BX248321.1
ENSG00000258292	1.53901	1.47079	3.60396	2.7887	ENSG00000258292	LINC02410
ENSG00000258296	0	0	0	0	ENSG00000258296	BX927168.4
ENSG00000258298	3.75543	10.1541	7.43986	17.3849	ENSG00000258298	BX927139.2
ENSG00000258299	4.85452	4.14585	3.47307	6.37901	ENSG00000258299	AL844213.11
ENSG00000258300	0.230479	0	0.615783	0.241055	ENSG00000258300	NUTF2P2
ENSG00000258304	0	0.217013	0	0.515476	ENSG00000258304	AC233290.2
ENSG00000258311	1.76091	2.68033	2.68812	4.08314	ENSG00000258311	AC009779.3
ENSG00000258315	16.1845	24.0032	11.9957	12.2595	ENSG00000258315	C17orf49
ENSG00000258316	0.161053	0.206692	0.326914	0.425833	ENSG00000258316	KLF17P1
ENSG00000258318	2.74E-07	0	6.92639	12.0368	ENSG00000258318	BX294158.7
ENSG00000258320	0	0	0	0	ENSG00000258320	AC090502.4
ENSG00000258321	0.146719	4.25928	1.4041	4.78195	ENSG00000258321	AL662822.14
ENSG00000258322	13.5125	32.0351	30.5529	40.998	ENSG00000258322	AC138688.6
ENSG00000258324	0	0	0	0	ENSG00000258324	AL512310.8
ENSG00000258326	4.88094	23.8201	0	16.063	ENSG00000258326	AL662831.3
ENSG00000258330	0.0192667	0	0	0	ENSG00000258330	CR753842.2
ENSG00000258333	1.83169	4.13359	4.81581	12.29	ENSG00000258333	AL662822.15
ENSG00000258336	0	0	0.188947	0	ENSG00000258336	DUX4L52
ENSG00000258348	9.85036	12.5591	11.4887	11.2534	ENSG00000258348	AL662831.4
ENSG00000258349	0	4.82892	0	0	ENSG00000258349	AL663093.3
ENSG00000258350	0	0.716897	0	0.430504	ENSG00000258350	SYF2P1
ENSG00000258352	1.82606	13.262	12.7657	8.99297	ENSG00000258352	AC119044.1
ENSG00000258353	0.251476	4.97607	0.335085	5.3242	ENSG00000258353	CR382280.7
ENSG00000258356	1.64273	5.32831	2.80046	7.93452	ENSG00000258356	CR388372.6
ENSG00000258357	0.173453	0.0828892	0.157034	0.112074	ENSG00000258357	AC023161.2
ENSG00000258358	0.0474021	0.0456406	0.172099	0.103581	ENSG00000258358	AC087888.1
ENSG00000258359	0.603733	1.70408	1.27898	1.41792	ENSG00000258359	PCNPP1
ENSG00000258360	0	0	0	0	ENSG00000258360	NF1P12
ENSG00000258361	9.64873	14.9546	9.62966	27.1205	ENSG00000258361	BX284927.2
ENSG00000258363	3.40249	10.8935	11.3699	21.1572	ENSG00000258363	GRAMD4P4
ENSG00000258365	1.88939	5.29598	6.42845	7.81008	ENSG00000258365	AC073655.2
ENSG00000258366	11.3695	17.7592	17.0163	21.0523	ENSG00000258366	RTEL1
ENSG00000258367	70.4369	158.882	143.855	371.685	ENSG00000258367	CR383656.14
ENSG00000258368	0.708862	2.38227	2.64552	1.48992	ENSG00000258368	ZNF970P
ENSG00000258369	0	0.318976	0	0	ENSG00000258369	ADI1P3
ENSG00000258370	9.02704	22.3148	11.142	35.1254	ENSG00000258370	AL845443.1
ENSG00000258372	1.88814	4.48346	10.3396	12.6795	ENSG00000258372	ARL17A
ENSG00000258373	0.0720338	0.762108	0.250292	0.313321	ENSG00000258373	SLC25A3P2

ENSG00000258374	18.6228	35.8578	29.8837	38.7151	ENSG00000258374	CR759928.1
ENSG00000258375	1.03221	2.0594	2.2209	2.82286	ENSG00000258375	AC079363.1
ENSG00000258381	0	0	0	0	ENSG00000258381	AL512360.1
ENSG00000258385	0.253382	0.625579	0.689199	0.831383	ENSG00000258385	AL391516.1
ENSG00000258386	0.409731	0	0	0	ENSG00000258386	AL352984.1
ENSG00000258387	0	2.25979	0	0	ENSG00000258387	AL358913.1
ENSG00000258388	0.192247	0.814442	1.33219	0.254934	ENSG00000258388	PPT2-EGFL8
ENSG00000258389	0.000272154	0	0	0	ENSG00000258389	DUX4
ENSG00000258392	0	0	0.0801803	0.0999188	ENSG00000258392	RPA2P1
ENSG00000258397	0	0	0	0	ENSG00000258397	BCAR1P1
ENSG00000258401	0.199629	0	0	0	ENSG00000258401	AL512361.1
ENSG00000258405	4.57059	4.13493	5.25368	4.20144	ENSG00000258405	ZNF578
ENSG00000258406	0	0	0	0.157765	ENSG00000258406	AL445383.1
ENSG00000258408	0	0.247648	0	0	ENSG00000258408	NT5CP2
ENSG00000258411	0	0	0	0	ENSG00000258411	AL161670.1
ENSG00000258415	0	0	0	0	ENSG00000258415	AC060814.1
ENSG00000258417	0.211442	0.374547	0.430666	0.984028	ENSG00000258417	AC100868.1
ENSG00000258420	0	0	0.119434	0.147787	ENSG00000258420	AC012414.1
ENSG00000258421	0	0	0	0	ENSG00000258421	FXNP1
ENSG00000258423	0	0	0.18643	0	ENSG00000258423	OR7E105P
ENSG00000258427	0	0	0	0	ENSG00000258427	RBM8B
ENSG00000258429	5.07555	5.22295	7.82651	2.21202	ENSG00000258429	PDF
ENSG00000258431	0	0	0.105303	0.130655	ENSG00000258431	AC004825.1
ENSG00000258434	0	0	0	0	ENSG00000258434	DUX4L11
ENSG00000258436	0	0	0	0	ENSG00000258436	RNASE12
ENSG00000258438	0	0	0	0	ENSG00000258438	AL512310.9
ENSG00000258439	1.76034	2.85822	2.34535	4.701	ENSG00000258439	AC007956.1
ENSG00000258440	0	0	0	0	ENSG00000258440	AL118557.1
ENSG00000258445	0.361577	1.86453	0.887106	0.685301	ENSG00000258445	AL132777.1
ENSG00000258446	0	0	0	0	ENSG00000258446	AL133153.1
ENSG00000258448	0.99613	1.82771	1.7564	1.89043	ENSG00000258448	AL442663.2
ENSG00000258452	0.421508	0.40235	0	1.81068	ENSG00000258452	AC022404.1
ENSG00000258453	0.190664	0.122275	0.110513	0.138364	ENSG00000258453	OR11H2
ENSG00000258456	0.214941	0.30687	0.14157	0.178465	ENSG00000258456	PTCD2P1
ENSG00000258462	0	1.01518	1.79208	0	ENSG00000258462	AL591767.2
ENSG00000258463	0	0	0	0	ENSG00000258463	AC138701.2
ENSG00000258465	0.392144	0.543405	0.459897	0.949485	ENSG00000258465	AL139011.2
ENSG00000258466	1.29931	1.2585	1.65162	2.95549	ENSG00000258466	AL049779.1
ENSG00000258467	0	0.0908551	0	0	ENSG00000258467	AL132857.1
ENSG00000258468	0	0.185223	0	0.0698572	ENSG00000258468	OR11G1P
ENSG00000258469	1.95112	1.99496	1.10081	2.57085	ENSG00000258469	CHMP4BP1
ENSG00000258472	4.00139	8.03041	7.07349	10.4585	ENSG00000258472	AC005726.2
ENSG00000258474	0.530663	0.509103	0.344724	0.56928	ENSG00000258474	LINC02313
ENSG00000258475	0	0	0	0	ENSG00000258475	U85056.3
ENSG00000258477	0	0.170845	0.317941	0.576743	ENSG00000258477	PPIAP6
ENSG00000258482	0	0	0	0	ENSG00000258482	TRAV15
ENSG00000258484	2.63042	9.44818	6.47165	2.01612	ENSG00000258484	SPESP1
ENSG00000258485	0.480152	2.63867	2.26985	3.66442	ENSG00000258485	SRMP2
ENSG00000258488	1.72484	0	3.5629	3.16607	ENSG00000258488	AC023310.1
ENSG00000258491	0.102792	0.148429	0	0	ENSG00000258491	AL606834.1
ENSG00000258493	0	4.71868	4.04265	3.28023	ENSG00000258493	AL121603.1
ENSG00000258494	0	0	0	0	ENSG00000258494	OR11J5P
ENSG00000258500	2.06918	4.0038	6.14498	7.9709	ENSG00000258500	AL845552.1
ENSG00000258501	0	0	0.0302307	0.114203	ENSG00000258501	EIF3LP1

ENSG00000258503	0	0	0	0	ENSG00000258503	AL352979.1
ENSG00000258505	0.188424	0.362106	0	0.203749	ENSG00000258505	AL442163.2
ENSG00000258506	0	0	0	0	ENSG00000258506	AL163642.1
ENSG00000258509	0	0	0	0	ENSG00000258509	AL049870.1
ENSG00000258510	0	1.48226	1.33856	1.65244	ENSG00000258510	AC007954.1
ENSG00000258512	0.131237	0.236247	0.825753	0.41103	ENSG00000258512	LINC00239
ENSG00000258513	0	0	0.468273	0	ENSG00000258513	AC006349.1
ENSG00000258514	0	0	0	0	ENSG00000258514	DUX4L14
ENSG00000258519	0	0	0	0	ENSG00000258519	AL121579.1
ENSG00000258524	0.148088	0	0.384583	0.633609	ENSG00000258524	NT5CP1
ENSG00000258527	0.182584	0.393578	0.412565	0	ENSG00000258527	ASB9P1
ENSG00000258529	0	0	0	0	ENSG00000258529	AP001781.3
ENSG00000258531	6.74135	11.6044	8.04922	19.0067	ENSG00000258531	BANF1P1
ENSG00000258536	0	0	0	0.634573	ENSG00000258536	FKBP1BP1
ENSG00000258539	0.371356	1.44998	0.979072	1.14144	ENSG00000258539	AC068896.1
ENSG00000258540	0	0	0	0	ENSG00000258540	AC107958.1
ENSG00000258541	0.098843	0.284925	0	0	ENSG00000258541	OR4K4P
ENSG00000258542	3.12543	0	0	0	ENSG00000258542	AC068831.4
ENSG00000258543	0	0	0	0	ENSG00000258543	CR354443.1
ENSG00000258544	0.310687	0	0	0.324046	ENSG00000258544	GLRXP2
ENSG00000258546	0	0.0489127	0.0439787	0.0551847	ENSG00000258546	CENPUP2
ENSG00000258549	0	0	0	0	ENSG00000258549	AL161713.1
ENSG00000258550	0	0.0600452	0.235829	0	ENSG00000258550	OR7E106P
ENSG00000258552	0.123821	0	0	0	ENSG00000258552	AC007375.1
ENSG00000258555	0.224513	0.557638	0.412027	0.622321	ENSG00000258555	SPECC1L-ADORA2A
ENSG00000258557	0	0	0	0	ENSG00000258557	AC245505.1
ENSG00000258562	0	0	0	0	ENSG00000258562	AC106028.1
ENSG00000258563	0	0.10468	0.189068	0.235052	ENSG00000258563	PSMA3P
ENSG00000258564	0	0.0659668	0.0596058	0.074582	ENSG00000258564	OR4N1P
ENSG00000258565	0.916229	2.97992	1.57519	7.05511	ENSG00000258565	BLZF2P
ENSG00000258566	0.116605	0	0	0	ENSG00000258566	AC007376.1
ENSG00000258567	0	0	0	0	ENSG00000258567	DUX4L16
ENSG00000258568	1.30624	3.03075	1.97883	1.29558	ENSG00000258568	RHOQP1
ENSG00000258570	0.42237	0.623572	1.17398	0.228573	ENSG00000258570	AC110027.1
ENSG00000258571	2.37869	2.01401	4.74603	5.27058	ENSG00000258571	PTTG4P
ENSG00000258572	0.124515	0.179699	0.108265	0.135592	ENSG00000258572	AL133467.1
ENSG00000258577	0	0	0	0	ENSG00000258577	SNRPGP1
ENSG00000258578	0.169156	0.810189	1.02385	0.901314	ENSG00000258578	AC008015.1
ENSG00000258581	1.10881	4.15117	7.91833	3.63807	ENSG00000258581	AL157871.3
ENSG00000258585	0	0	0	0	ENSG00000258585	ZNF519P3
ENSG00000258587	0	0	0	0.270545	ENSG00000258587	AC006530.1
ENSG00000258588	0	0	0	0	ENSG00000258588	TRIM6-TRIM34
ENSG00000258589	0	0	0	0	ENSG00000258589	CR753842.1
ENSG00000258590	0.305338	0.917959	0.967199	1.5831	ENSG00000258590	NBEAP1
ENSG00000258591	0	0	0	0	ENSG00000258591	AL109628.1
ENSG00000258595	0	0	0	0	ENSG00000258595	AL110118.1
ENSG00000258597	0	0.0887601	0.0801803	0.0999188	ENSG00000258597	SERPINA2
ENSG00000258599	0	0	0	0	ENSG00000258599	AL355922.3
ENSG00000258605	0	0	0.73498	1.31593	ENSG00000258605	DYNLL1P2
ENSG00000258608	0	0	0	0	ENSG00000258608	DNAJC19P9
ENSG00000258611	0.433079	0.351987	0.394207	0.262482	ENSG00000258611	AC087641.1
ENSG00000258613	0	0	0	0	ENSG00000258613	RPL21P7
ENSG00000258615	0	2.73926	0	0.969422	ENSG00000258615	AL117187.1
ENSG00000258617	0	0.240101	0	0.259865	ENSG00000258617	DUX4L13

ENSG00000258618	0	0	0	0	ENSG00000258618	RPL21P9
ENSG00000258619	0.152229	0.212577	0.549599	0.891209	ENSG00000258619	AL136298.2
ENSG00000258622	0	0	0	2.71474	ENSG00000258622	AL442163.3
ENSG00000258624	0	0	0	0.408027	ENSG00000258624	SERPINE4P
ENSG00000258625	0	0	0	0	ENSG00000258625	OR11H5P
ENSG00000258626	0.642199	1.52317	0.826112	0.669283	ENSG00000258626	AL049779.2
ENSG00000258627	0	0	0	3.39096	ENSG00000258627	AC103996.1
ENSG00000258628	0.0777708	0.382308	0.32157	0.761679	ENSG00000258628	AC126603.1
ENSG00000258629	0	0.114116	0.0687812	0.216019	ENSG00000258629	AL391261.1
ENSG00000258632	0.561827	1.79226	1.13272	1.19388	ENSG00000258632	AC135626.1
ENSG00000258635	0	0	0	0	ENSG00000258635	CR354443.2
ENSG00000258638	0	0	0.410807	0	ENSG00000258638	AL389895.1
ENSG00000258639	0	0.109468	0.296614	0.122808	ENSG00000258639	AL359212.1
ENSG00000258640	1.00735	0.821009	1.31292	1.21854	ENSG00000258640	RPL21P5
ENSG00000258641	0	0	0	0	ENSG00000258641	OR4T1P
ENSG00000258643	12.0785	9.50869	19.6977	10.2376	ENSG00000258643	BCL2L2-PABPN1
ENSG00000258645	0	0.714407	0.36535	1.26591	ENSG00000258645	HSPE1P2
ENSG00000258648	1.83851	3.42205	2.81634	5.53471	ENSG00000258648	UBE2CP1
ENSG00000258650	0	1.11524	1.96415	2.36202	ENSG00000258650	HSBP1P1
ENSG00000258652	0.137553	0	0.476478	0.742466	ENSG00000258652	OR4Q1P
ENSG00000258653	2.20655	4.5038	3.42919	5.41871	ENSG00000258653	AC005520.1
ENSG00000258656	0	0	0	0	ENSG00000258656	AL160236.1
ENSG00000258659	4.60737	5.5327	2.93187	4.06972	ENSG00000258659	TRIM34
ENSG00000258664	24.1279	11.292	19.6207	3.40289	ENSG00000258664	IFRG15
ENSG00000258665	0	0	0.256667	0	ENSG00000258665	AC068831.5
ENSG00000258668	0	2.20666	2.95713	0.716529	ENSG00000258668	COX6CP11
ENSG00000258671	0	0	0	0	ENSG00000258671	AL132639.1
ENSG00000258674	0.727964	0.500296	1.01829	0.469963	ENSG00000258674	AC011448.1
ENSG00000258677	0.667964	0	0.228417	0	ENSG00000258677	AC022826.2
ENSG00000258679	1.74592	1.94187	2.34812	3.74735	ENSG00000258679	AC121758.1
ENSG00000258680	0	0	0	0	ENSG00000258680	AL132994.1
ENSG00000258681	0.073084	0	0.0636288	0.238253	ENSG00000258681	AL355836.1
ENSG00000258684	0.859451	0.310137	0.108923	0.932209	ENSG00000258684	BMS1P16
ENSG00000258685	0.134009	0.257751	0.310906	0.10505	ENSG00000258685	AL359219.1
ENSG00000258691	0.578931	1.25492	3.14081	2.39108	ENSG00000258691	AL355102.2
ENSG00000258692	0.0175178	0	0	0	ENSG00000258692	SALL4P7
ENSG00000258697	0.000272154	0	0	0	ENSG00000258697	DUX4L6
ENSG00000258705	0.0179111	0	0	0	ENSG00000258705	AC245505.2
ENSG00000258706	0	0	0	0	ENSG00000258706	AC127381.1
ENSG00000258707	0	0	0	0	ENSG00000258707	AC023310.2
ENSG00000258708	0.976537	1.70499	2.66258	1.25243	ENSG00000258708	SLC25A21-AS1
ENSG00000258712	0.0585893	0	0	0	ENSG00000258712	AC060814.2
ENSG00000258713	0	0	0	0	ENSG00000258713	C20orf141
ENSG00000258721	0	0	0	0	ENSG00000258721	OR11H3P
ENSG00000258722	0.0274507	0.185199	0.231906	0.30126	ENSG00000258722	CKAP2P1
ENSG00000258724	0	0.506846	0.248237	0.0448308	ENSG00000258724	AC105001.2
ENSG00000258726	0	0	0	0	ENSG00000258726	DUXAP6
ENSG00000258728	0	0	0	0	ENSG00000258728	AL162231.3
ENSG00000258729	0.034222	0.297911	0.297522	0.264478	ENSG00000258729	AL355102.3
ENSG00000258732	0	0	0.231413	0	ENSG00000258732	AC025884.1
ENSG00000258734	0	0	0	0	ENSG00000258734	AL049873.2
ENSG00000258737	0	0	0	0	ENSG00000258737	SUB1P2
ENSG00000258739	0	0	0	0.346748	ENSG00000258739	ENO1P2
ENSG00000258740	0	0.0960595	0.0867668	0.218694	ENSG00000258740	AL691403.1

ENSG00000258741	0.163451	0.330405	0.281245	0.342344	ENSG00000258741	AC091544.3
ENSG00000258744	0.192585	0.647746	2.61198	0.521185	ENSG00000258744	AL132800.1
ENSG00000258746	0	0.20501	0	0	ENSG00000258746	AL162632.2
ENSG00000258750	0	0	0	0	ENSG00000258750	AL358335.1
ENSG00000258755	1.52854	0.258033	0.392105	0	ENSG00000258755	DUX4L7
ENSG00000258758	0.0718166	0.0684362	0.104538	0.269994	ENSG00000258758	AL137100.1
ENSG00000258759	0.132293	0.629763	0.79321	0	ENSG00000258759	AL049779.3
ENSG00000258762	0	0	0	0	ENSG00000258762	MTND4P33
ENSG00000258764	0	0	0	0	ENSG00000258764	AL049874.4
ENSG00000258767	0	0	0	0	ENSG00000258767	AC060814.3
ENSG00000258769	1.11584	1.79565	0.958789	0.386563	ENSG00000258769	AC005479.1
ENSG00000258771	0	0	0	0	ENSG00000258771	BCAR1P2
ENSG00000258774	0.266625	0	0.420706	0.0890122	ENSG00000258774	NANOGP7
ENSG00000258778	1.1434	2.77248	2.12295	5.88438	ENSG00000258778	AL161670.2
ENSG00000258780	0.360263	0.16043	0.563971	0.856313	ENSG00000258780	BMS1P15
ENSG00000258781	0	0	0	0	ENSG00000258781	AL589743.2
ENSG00000258783	0.0469551	0.135666	0.490114	0.129568	ENSG00000258783	KRT18P6
ENSG00000258786	0	0	0	0	ENSG00000258786	AC183089.1
ENSG00000258787	0	0.25238	0.112341	0	ENSG00000258787	AC091078.2
ENSG00000258788	0.599505	6.71567	3.14519	4.77415	ENSG00000258788	CKS1BP1
ENSG00000258790	3.5119	2.91853	4.49153	4.07282	ENSG00000258790	AL121594.3
ENSG00000258792	1.91637	8.166	9.88038	14.6782	ENSG00000258792	AL137230.1
ENSG00000258794	0.0471007	0.228132	0.0411375	0	ENSG00000258794	DUX4L27
ENSG00000258796	0.15792	1.06423	0.686403	1.18056	ENSG00000258796	AL133241.1
ENSG00000258797	0	0	0	0	ENSG00000258797	AC023310.3
ENSG00000258799	0	0	0	0	ENSG00000258799	ZNF519P2
ENSG00000258802	0	2.49394	0	1.41303	ENSG00000258802	AL139317.2
ENSG00000258804	1.06997	2.64485	2.9092	3.95047	ENSG00000258804	LINC01148
ENSG00000258805	0	0	0	0	ENSG00000258805	ADIPOR1P2
ENSG00000258806	0.199466	1.15099	0.577792	1.30191	ENSG00000258806	OR11H7
ENSG00000258812	0	0	0	0	ENSG00000258812	TRAV33
ENSG00000258816	0	0	0	0	ENSG00000258816	AC121758.2
ENSG00000258817	0	0.0291324	0	0.0650243	ENSG00000258817	OR4C13
ENSG00000258818	4.01583	6.34252	1.29739	2.41553	ENSG00000258818	RNASE4
ENSG00000258822	0	0.061665	0	0	ENSG00000258822	OR4K16P
ENSG00000258823	0.0853943	0	0	0	ENSG00000258823	AL160314.3
ENSG00000258828	0	0.0637094	0.172457	0.0879719	ENSG00000258828	KRT8P2
ENSG00000258830	0.053182	0.0950276	0.100892	0.156215	ENSG00000258830	AC137834.1
ENSG00000258834	0	7.80E-10	0	0.276159	ENSG00000258834	DUX4L4
ENSG00000258835	0	0.291589	0	0	ENSG00000258835	TRAV28
ENSG00000258836	0	0.462134	0.834659	0.136668	ENSG00000258836	AL121579.2
ENSG00000258838	2.81393	2.77043	1.4795	2.80396	ENSG00000258838	ERCC6-PGBD3
ENSG00000258839	3.2849	5.68885	8.23397	6.32835	ENSG00000258839	MC1R
ENSG00000258841	0	0	0	0.22047	ENSG00000258841	EEF1A1P2
ENSG00000258846	0.129488	0.041571	0.52602	0.0944027	ENSG00000258846	EEF1A1P33
ENSG00000258847	2.47338	5.51343	3.99882	6.61466	ENSG00000258847	AL391261.2
ENSG00000258848	0	0	0	0	ENSG00000258848	GRAMD4P6
ENSG00000258849	0	0	0	0.736691	ENSG00000258849	OR7E159P
ENSG00000258855	0	0	0.0603209	0	ENSG00000258855	OR11J2P
ENSG00000258856	0.173983	0	0.0755175	0.0494169	ENSG00000258856	AL136520.1
ENSG00000258863	0	0.146953	0.0677445	0.0821653	ENSG00000258863	SETP1
ENSG00000258864	0.729969	0	0	0	ENSG00000258864	AC008575.1
ENSG00000258869	0.665897	0.478463	1.15184	0.532407	ENSG00000258869	LINC02312
ENSG00000258870	0.837449	2.38926	2.00391	4.67708	ENSG00000258870	EIF4EBP1P1

ENSG00000258872	0.292741	0.516205	0.452072	0.526478	ENSG00000258872	FDPSP3
ENSG00000258873	0.404811	1.31624	1.29793	3.02737	ENSG00000258873	DUXA
ENSG00000258875	0.896838	1.39312	1.21167	1.29468	ENSG00000258875	AL135818.1
ENSG00000258877	0	0	0	0.0393095	ENSG00000258877	ATP5A1P4
ENSG00000258878	0	0	0	0	ENSG00000258878	AL355076.3
ENSG00000258880	0	0	0	0	ENSG00000258880	BX248244.1
ENSG00000258881	1.52278	4.51389	3.4346	6.32105	ENSG00000258881	AC007040.2
ENSG00000258883	0	0.236116	0.205904	0	ENSG00000258883	AC068446.3
ENSG00000258886	2.45838	5.10468	4.8443	1.97523	ENSG00000258886	HIGD1AP17
ENSG00000258887	0	0.282417	0	0	ENSG00000258887	AL160237.2
ENSG00000258890	20.8462	43.4768	40.8256	55.4084	ENSG00000258890	CEP95
ENSG00000258893	0.067824	0.0850561	0.177134	0.301179	ENSG00000258893	SETP2
ENSG00000258894	0.0750877	0	0	0.0409106	ENSG00000258894	AL358913.2
ENSG00000258895	0	0	0	0.469809	ENSG00000258895	AC104390.1
ENSG00000258896	1.89179	1.80595	2.16473	2.81347	ENSG00000258896	SCOCP1
ENSG00000258899	0	0.198949	0.119843	0.0749726	ENSG00000258899	OR4U1P
ENSG00000258900	0.858801	2.0353	0.849102	1.39923	ENSG00000258900	HNRNPCP1
ENSG00000258901	0	0	0	0	ENSG00000258901	AL121821.2
ENSG00000258905	0	0	0	0	ENSG00000258905	TRAV32
ENSG00000258906	0.112799	0.108294	0.097803	0.121517	ENSG00000258906	AL157687.1
ENSG00000258907	0.114797	0	0	0	ENSG00000258907	AC009779.4
ENSG00000258911	0	0	0	0	ENSG00000258911	DUX4L10
ENSG00000258915	0.0695582	0.0670156	0	0.0772628	ENSG00000258915	BHLHB9P1
ENSG00000258916	0	0.0312674	0.00941177	0.0715873	ENSG00000258916	SPATA31E2P
ENSG00000258917	0.425223	1.82771	0.873126	1.25462	ENSG00000258917	ZMYND19P1
ENSG00000258923	0	0.247528	0.0868581	0.251569	ENSG00000258923	MTND5P35
ENSG00000258925	0	0	0.0887808	0	ENSG00000258925	NPM1P5
ENSG00000258928	0.140127	0	0	0.470126	ENSG00000258928	AL358333.2
ENSG00000258930	1.62509	7.10278	5.4027	6.93438	ENSG00000258930	AC005230.1
ENSG00000258932	2.81171	8.53093	8.74151	15.1074	ENSG00000258932	AL390334.1
ENSG00000258934	0.450681	0	0.391236	0.682819	ENSG00000258934	AL356800.1
ENSG00000258941	0	0	0	0	ENSG00000258941	RP11-407N17.3
ENSG00000258945	1.92983	2.73177	2.39381	1.3599	ENSG00000258945	AL049775.3
ENSG00000258947	53.2422	32.0587	12.9202	27.0784	ENSG00000258947	TUBB3
ENSG00000258948	0	0	0.0441828	0	ENSG00000258948	KRT8P1
ENSG00000258951	0.589624	1.42328	1.25243	1.46753	ENSG00000258951	KRT18P7
ENSG00000258956	0.148088	0	0	0	ENSG00000258956	COX4I1P1
ENSG00000258960	0	0	0	0	ENSG00000258960	AL391261.3
ENSG00000258962	0.305725	0.34094	0.587704	0.386665	ENSG00000258962	AL121839.1
ENSG00000258963	0	0	0	0	ENSG00000258963	EDDM3DP
ENSG00000258965	0	0	0.575508	0.938346	ENSG00000258965	AC044913.1
ENSG00000258966	2.19851	3.32003	1.85877	3.60357	ENSG00000258966	GTF3AP2
ENSG00000258967	3.03565	3.41686	0.170765	8.54957	ENSG00000258967	AL117694.1
ENSG00000258968	2.34318	7.91074	8.9911	9.42834	ENSG00000258968	AL049830.4
ENSG00000258971	1.14487	1.61424	1.44098	0.584904	ENSG00000258971	AC112693.2
ENSG00000258972	0	0	0.116386	0	ENSG00000258972	AC005225.4
ENSG00000258973	0	0.304129	0.46636	0	ENSG00000258973	AL096870.1
ENSG00000258978	1.05524	0	0.89955	1.09013	ENSG00000258978	HIF1AP1
ENSG00000258980	0.203081	1.16539	0.350867	1.72202	ENSG00000258980	EIF1AXP2
ENSG00000258981	0.218975	0	0	0.700179	ENSG00000258981	COX5AP2
ENSG00000258984	0.885983	2.04623	1.65703	1.11442	ENSG00000258984	UBE2F-SCLY
ENSG00000258986	0.321059	0.448589	0.727342	0.669724	ENSG00000258986	TMEM179
ENSG00000258987	0	0	0.114039	0.141281	ENSG00000258987	AL132642.1
ENSG00000258988	0	0.0461575	0.0435237	0.104448	ENSG00000258988	AL135978.1

ENSG00000258989	0	2.34494	1.16882	1.40375	ENSG00000258989	AL355916.3
ENSG00000258990	0	0	0	0.123459	ENSG00000258990	MPPE1P1
ENSG00000258991	0	0	0.0410906	0	ENSG00000258991	DUX4L19
ENSG00000258992	0	0	0	0	ENSG00000258992	TSPY1
ENSG00000258993	0	1.43464	0.853937	1.5453	ENSG00000258993	AL352979.3
ENSG00000258995	0	0	0	0	ENSG00000258995	PARP1P2
ENSG00000258996	0	0	0	0	ENSG00000258996	AL359219.2
ENSG00000258997	0	0	0	0	ENSG00000258997	NF1P2
ENSG00000259000	0.0179671	0.0264696	0.0237175	0.0606948	ENSG00000259000	DOCK11P1
ENSG00000259003	0.166956	0.16046	0.144964	0	ENSG00000259003	AC243965.1
ENSG00000259009	0.126335	0.121533	0.109842	0.206299	ENSG00000259009	TPRX2P
ENSG00000259010	0	0	0	0	ENSG00000259010	AL049869.1
ENSG00000259012	0	0	0	0.381861	ENSG00000259012	MTCYBP27
ENSG00000259013	1.63673	1.53806	4.37286	0.575397	ENSG00000259013	AL118558.2
ENSG00000259015	2.20302	3.72586	3.20466	2.89945	ENSG00000259015	AL442663.4
ENSG00000259016	0	0	0	0	ENSG00000259016	AL391156.1
ENSG00000259019	0	0	0	0	ENSG00000259019	EIF4BP1
ENSG00000259020	0	0	1.59486	0.975504	ENSG00000259020	AL049872.1
ENSG00000259021	0.3141	0	0	0	ENSG00000259021	TPRX1P1
ENSG00000259022	1.18555	5.11586	2.93427	3.38043	ENSG00000259022	DNAJC8P1
ENSG00000259024	3.02761	6.86695	3.90479	0.962846	ENSG00000259024	TVP23C-CDRT4
ENSG00000259025	0	0	0	0	ENSG00000259025	AC037471.1
ENSG00000259029	0	0	0	0	ENSG00000259029	DUX4L18
ENSG00000259030	1.5709	2.72255	2.12024	3.51906	ENSG00000259030	FPGT-TNNI3K
ENSG00000259032	0	0	0	0	ENSG00000259032	ENSAP2
ENSG00000259034	0.000272154	0	0	0	ENSG00000259034	DUX4L3
ENSG00000259040	0.2631	1.04726	1.22256	0.723875	ENSG00000259040	BLOC1S5-TXNDC5
ENSG00000259043	0.228402	0.608242	0.507512	0.796329	ENSG00000259043	BRD7P1
ENSG00000259045	0	0	0.0828559	0.103174	ENSG00000259045	MTCO1P2
ENSG00000259046	0	0	0	0	ENSG00000259046	AL049870.4
ENSG00000259047	1.17193	0.739411	1.53984	0.402831	ENSG00000259047	AL163153.1
ENSG00000259050	0.282606	0.110118	0.0988072	0.367009	ENSG00000259050	CHORDC2P
ENSG00000259051	0	0	0	0	ENSG00000259051	HNRNPUP1
ENSG00000259056	0	0	0	0	ENSG00000259056	DUXAP1
ENSG00000259057	0	0	0.0472383	0.296193	ENSG00000259057	AC105109.1
ENSG00000259059	0	0	0.127832	0.157981	ENSG00000259059	PEBP1P1
ENSG00000259060	0.123821	0	0	0	ENSG00000259060	AL163195.3
ENSG00000259063	0.000272154	0	0	0	ENSG00000259063	DUX4L5
ENSG00000259064	0	0	0	0	ENSG00000259064	AC091544.4
ENSG00000259066	0.510895	0.88079	0.717414	1.969	ENSG00000259066	AL110118.2
ENSG00000259068	0	0	0	0	ENSG00000259068	TRAV37
ENSG00000259074	0.292006	1.26016	1.01143	0.337392	ENSG00000259074	PSMB7P1
ENSG00000259075	1.14102	0.000361499	0.296943	0.874034	ENSG00000259075	POC1B-GALNT4
ENSG00000259078	0	0	0	0	ENSG00000259078	PTBP1P
ENSG00000259079	1.14356	3.01379	5.07605	6.29675	ENSG00000259079	AC005476.1
ENSG00000259086	0	0	0	0	ENSG00000259086	AL136298.3
ENSG00000259089	0	0	0	0	ENSG00000259089	GRAMD4P5
ENSG00000259090	0.469235	0.518891	0.962228	1.3448	ENSG00000259090	AL121594.4
ENSG00000259092	0	0	0.244685	0	ENSG00000259092	TRAV30
ENSG00000259095	0	0	0	0	ENSG00000259095	GTF2IP22
ENSG00000259096	0	0.110751	0.141197	0.127092	ENSG00000259096	FAM35CP
ENSG00000259098	1.02562	2.28773	2.57151	4.38933	ENSG00000259098	AC025884.2
ENSG00000259099	0	0	0	0	ENSG00000259099	AC025574.1

ENSG00000259100	0.035839	0.935591	0.995989	1.37724	ENSG00000259100	AL157791.1
ENSG00000259101	0	0	0	0	ENSG00000259101	CR936239.1
ENSG00000259102	0	0.0588863	0	0.10594	ENSG00000259102	SMARCE1P3
ENSG00000259105	0.0860828	0	0.0746454	0.0930813	ENSG00000259105	RPS3AP4
ENSG00000259109	0	2.48457	2.66011	1.60472	ENSG00000259109	AC004858.1
ENSG00000259112	0	0.989712	0	1.78053	ENSG00000259112	NDUFC2-KCTD14
ENSG00000259117	0	0	0	0	ENSG00000259117	AL121576.1
ENSG00000259120	0.585632	1.66233	2.00242	2.27898	ENSG00000259120	SMIM6
ENSG00000259121	3.59907	2.16625	3.03501	6.94917	ENSG00000259121	AL109628.2
ENSG00000259122	0.778375	1.04779	1.21122	0.974657	ENSG00000259122	TVP23BP1
ENSG00000259128	0.000272154	0	0	0.0452164	ENSG00000259128	DUX4L2
ENSG00000259132	0.401581	0	0.378663	0	ENSG00000259132	AL132780.3
ENSG00000259133	2.20674	1.92121	2.63844	3.13561	ENSG00000259133	AL161757.5
ENSG00000259136	0	0	0.457067	0.0646478	ENSG00000259136	AL137100.2
ENSG00000259137	0	0	0	0.159872	ENSG00000259137	AL109766.1
ENSG00000259139	0	0	0	0	ENSG00000259139	DUX4L12
ENSG00000259140	0.219111	1.28334	0.88233	2.15157	ENSG00000259140	AL049839.1
ENSG00000259144	0	0.0514187	0.0465106	0.0602837	ENSG00000259144	RANBP20P
ENSG00000259145	0	0	0	0	ENSG00000259145	RP11-566K19.9
ENSG00000259148	0	0	0	0	ENSG00000259148	YWHAZP1
ENSG00000259151	0.16864	0.609061	1.62194	1.19904	ENSG00000259151	CAP2P1
ENSG00000259154	0	0	0	0	ENSG00000259154	DUX4L17
ENSG00000259155	0.44936	2.42706	2.39295	2.25191	ENSG00000259155	AL591767.3
ENSG00000259156	0	0.202553	0.257574	0.553077	ENSG00000259156	CHEK2P2
ENSG00000259157	0	0	0	0	ENSG00000259157	AL079307.3
ENSG00000259159	0	0.0588901	0	0.112305	ENSG00000259159	MFRP
ENSG00000259160	0	0.947149	0	1.22724	ENSG00000259160	AL049869.4
ENSG00000259161	0.36441	1.49735	0.892708	1.50702	ENSG00000259161	AL137779.3
ENSG00000259162	0.332721	0.34154	0.185159	0.231566	ENSG00000259162	AL355075.5
ENSG00000259164	0.291263	0.666598	0	0	ENSG00000259164	AC007375.2
ENSG00000259165	0.731674	1.84959	1.6992	2.11949	ENSG00000259165	AL391262.1
ENSG00000259167	0	0.0696388	0.062921	0.0786656	ENSG00000259167	NMNAT1P1
ENSG00000259169	0	0	0	0	ENSG00000259169	GNRHR2P1
ENSG00000259171	0	3.16502	1.03297	2.0577	ENSG00000259171	AL163636.2
ENSG00000259173	0	0	0	0	ENSG00000259173	AC090515.3
ENSG00000259174	0	0	0.0832328	0	ENSG00000259174	RP11-1180F24.1
ENSG00000259179	0	0	0.119434	0	ENSG00000259179	UBE2CP4
ENSG00000259183	0	0	0	0	ENSG00000259183	MED28P6
ENSG00000259184	0	0	0	0	ENSG00000259184	RP11-566K19.4
ENSG00000259186	0.0881656	0	0	0	ENSG00000259186	AC009660.1
ENSG00000259191	0.209254	1.90924	0.363042	1.7677	ENSG00000259191	AC027237.1
ENSG00000259192	1.61528	1.87803	1.10869	2.30476	ENSG00000259192	AC109631.1
ENSG00000259195	0	2.25294	2.65442	4.25118	ENSG00000259195	AC021739.1
ENSG00000259202	1.8199	7.44919	2.57552	7.58491	ENSG00000259202	AC012568.1
ENSG00000259205	0.419879	0.444305	0.480296	1.69798	ENSG00000259205	PRKXP1
ENSG00000259207	0.229852	0.143444	0.475856	7.34084	ENSG00000259207	ITGB3
ENSG00000259208	0	0	0	0	ENSG00000259208	AC023968.1
ENSG00000259214	0	0.850251	0	0.902559	ENSG00000259214	AC012414.2
ENSG00000259216	0.162631	2.34331	0	0.848604	ENSG00000259216	AC084757.1
ENSG00000259217	0	0	0	0.87125	ENSG00000259217	AC068867.1
ENSG00000259224	0.144391	0.3397	0.529308	0.558226	ENSG00000259224	SLC35G6
ENSG00000259227	0	0	0	0	ENSG00000259227	AC087699.1
ENSG00000259228	0.261925	0.763699	0.227783	0.284992	ENSG00000259228	HNRNPA1P62
ENSG00000259229	0	0	0	0	ENSG00000259229	AC026826.2

ENSG00000259231	0	0	0	0	ENSG00000259231	AC090888.1
ENSG00000259232	0.357311	2.85205	3.66262	3.63031	ENSG00000259232	AC105129.1
ENSG00000259233	0	0	0	0	ENSG00000259233	RP11-467N20.6
ENSG00000259236	0.0359038	0.155625	0.120512	0.161784	ENSG00000259236	GOLGA8VP
ENSG00000259239	0.323164	0.893821	0.527065	1.20669	ENSG00000259239	AC021755.1
ENSG00000259243	0	0.223713	0.298816	0.741248	ENSG00000259243	GOLGA6L19
ENSG00000259246	0	0	0	0	ENSG00000259246	HMGN2P47
ENSG00000259247	0.0385549	0.148554	0.102208	0.126622	ENSG00000259247	TTTY25P
ENSG00000259257	0.445384	1.18418	1.17029	1.0866	ENSG00000259257	AC037479.1
ENSG00000259258	0	1.23741	2.25912	4.83378	ENSG00000259258	AC013553.1
ENSG00000259259	0	0.147198	0.259662	0.413348	ENSG00000259259	NPM1P42
ENSG00000259261	0	0	0	0	ENSG00000259261	IGHV4OR15-8
ENSG00000259262	0	0.466896	0	0	ENSG00000259262	NDUFA3P4
ENSG00000259266	1.50045	0	3.64304	1.45548	ENSG00000259266	AC022523.2
ENSG00000259270	0	0	0	0	ENSG00000259270	AC044860.2
ENSG00000259271	0.0354448	0	0	0.0420445	ENSG00000259271	ANKRD62P1
ENSG00000259273	0	0	0	0	ENSG00000259273	AC027176.1
ENSG00000259286	0.0682321	0.0679403	0.242768	0.22454	ENSG00000259286	AC087639.1
ENSG00000259288	0.505768	1.523	0.435111	1.72963	ENSG00000259288	BUB1B-PAK6
ENSG00000259295	8.25709	9.71752	16.4771	18.2826	ENSG00000259295	CSPG4P12
ENSG00000259299	0	0	0	0	ENSG00000259299	AC061965.1
ENSG00000259300	0	0	0.0420967	0.0528418	ENSG00000259300	TUBBP8
ENSG00000259301	0	0	0	0	ENSG00000259301	AC084759.1
ENSG00000259302	0	0	0	0	ENSG00000259302	AC048382.3
ENSG00000259303	0	0.351246	0	0	ENSG00000259303	IGHV2OR16-5
ENSG00000259304	0	0	0	0	ENSG00000259304	AC090888.2
ENSG00000259305	1.56761	2.81537	2.33724	3.27884	ENSG00000259305	ZHX1-C8orf76
ENSG00000259308	0.652332	1.02591	0.779201	1.77288	ENSG00000259308	AC024270.1
ENSG00000259315	4.6429	10.9169	10.2266	16.9428	ENSG00000259315	ACTG1P17
ENSG00000259316	1.16048	3.74341	2.74689	4.85706	ENSG00000259316	AC087632.1
ENSG00000259317	0	0	0	0	ENSG00000259317	AC044860.3
ENSG00000259318	3.81259	5.40325	4.33568	5.68355	ENSG00000259318	AL356801.1
ENSG00000259323	6.35488	13.5817	0	0	ENSG00000259323	RP13-608F4.5
ENSG00000259324	0	0	0	0	ENSG00000259324	OR11K1P
ENSG00000259325	0.0127944	0	0	0	ENSG00000259325	SPATA31E3P
ENSG00000259328	7.58499	12.3415	21.161	10.1065	ENSG00000259328	RP11-152F13.7
ENSG00000259332	1.14082	2.14122	1.29617	0.249289	ENSG00000259332	ST20-MTHFS
ENSG00000259333	0	0	0	0	ENSG00000259333	AC127029.1
ENSG00000259335	0.290234	0.341807	0.2809	0.318178	ENSG00000259335	HNRNPMP1
ENSG00000259337	0	0	0	0	ENSG00000259337	IGHV1OR15-2
ENSG00000259338	0	0	0	0	ENSG00000259338	AC051619.2
ENSG00000259339	0.0809636	0.311771	0.774123	0.616276	ENSG00000259339	TGIF1P1
ENSG00000259340	0	0	0	0	ENSG00000259340	AC110588.1
ENSG00000259344	0.194481	1.26005	0.591531	2.33948	ENSG00000259344	RP11-566K19.6
ENSG00000259346	0	0	0	0	ENSG00000259346	AC105129.2
ENSG00000259350	0.512827	0.731688	0.584767	0.564356	ENSG00000259350	AC067805.1
ENSG00000259358	0.0752025	0.0469527	0.0616752	0.476154	ENSG00000259358	AC026951.1
ENSG00000259363	1.23392	2.53443	1.72035	7.31531	ENSG00000259363	AC090825.1
ENSG00000259369	0	0	0	0	ENSG00000259369	AC009997.1
ENSG00000259371	0	0.180478	0.0394708	0	ENSG00000259371	AL136295.3
ENSG00000259374	0.365685	1.1103	0.602336	2.4949	ENSG00000259374	NDUFB4P11
ENSG00000259378	0.27262	2.01068	1.69825	1.74555	ENSG00000259378	DCAF13P3
ENSG00000259379	0.252644	0.177316	0.0331317	0.31515	ENSG00000259379	MTND5P32
ENSG00000259381	0.585968	1.26934	1.0623	0.960013	ENSG00000259381	AC090695.1

ENSG00000259384	0	0.0743862	0	0	ENSG00000259384	GH1
ENSG00000259387	0	0.0218476	0	0.159955	ENSG00000259387	ADAMTS7P2
ENSG00000259388	0	0	0	0.0355942	ENSG00000259388	AC025040.2
ENSG00000259389	1.38775	1.48926	0.770456	0.605555	ENSG00000259389	H3F3AP1
ENSG00000259392	0.274879	0.784896	0.945492	4.89737	ENSG00000259392	AC090877.1
ENSG00000259393	0.272917	0.70238	0.325112	0.593297	ENSG00000259393	AC025918.2
ENSG00000259394	0	0.126157	0	0	ENSG00000259394	AC079328.1
ENSG00000259397	0.185063	0.176397	0.245624	0.397767	ENSG00000259397	AC021231.2
ENSG00000259399	1.36317	1.08233	0.336786	2.26149	ENSG00000259399	TGIF2-C20orf24
ENSG00000259400	0	0.184863	0.167039	0.211574	ENSG00000259400	ELMO2P1
ENSG00000259401	0	0.0313959	0.0287241	0.0357745	ENSG00000259401	RP11-566K19.8
ENSG00000259404	0.637517	1.32314	1.36646	0.627467	ENSG00000259404	EFTUD1P1
ENSG00000259405	0	0	1.5128	0	ENSG00000259405	AC020661.2
ENSG00000259411	0	0.426318	0.691529	0.49763	ENSG00000259411	HNRNPA1P45
ENSG00000259413	0.12236	0.118434	0.537089	0.953996	ENSG00000259413	AC011270.1
ENSG00000259414	0	2.59137	0.000892602	0	ENSG00000259414	AC242376.1
ENSG00000259419	0.0728228	0.0702573	0.133882	0	ENSG00000259419	HNRNPCP3
ENSG00000259421	0	0	0	0	ENSG00000259421	AL022318.2
ENSG00000259425	0.0181908	0	0	0.113833	ENSG00000259425	AC011767.1
ENSG00000259427	0	0	0.301653	0	ENSG00000259427	DPPA5P2
ENSG00000259428	0	0	0	0.265774	ENSG00000259428	HMGB3P26
ENSG00000259429	10.3822	29.8054	21.3093	18.7056	ENSG00000259429	UBE2Q2P2
ENSG00000259431	3.46571	3.35881	5.89127	2.74124	ENSG00000259431	THTPA
ENSG00000259433	0.494097	1.12673	1.02997	1.93969	ENSG00000259433	AC051619.3
ENSG00000259435	0	0	0	0	ENSG00000259435	OR4N3P
ENSG00000259440	0.496868	0.743452	1.3982	2.19809	ENSG00000259440	NPM1P43
ENSG00000259441	0.218669	0.347228	0.627465	0.549151	ENSG00000259441	AC079075.1
ENSG00000259449	0	0	0	0	ENSG00000259449	NIFKP8
ENSG00000259452	0.164396	0.980733	0.147418	1.7189	ENSG00000259452	AC009269.2
ENSG00000259454	0	0	0	0	ENSG00000259454	WBP1LP5
ENSG00000259455	0	0	0	0	ENSG00000259455	RP11-467N20.5
ENSG00000259458	0.130453	0.154488	0.340889	0.326954	ENSG00000259458	MGC15885
ENSG00000259461	0	0	0	0	ENSG00000259461	ANP32BP3
ENSG00000259464	0	0	0	0	ENSG00000259464	SNRPCP18
ENSG00000259465	0	0	0	0	ENSG00000259465	AHCYP7
ENSG00000259466	0	0	0	0	ENSG00000259466	NPM1P47
ENSG00000259467	0.720023	0.631938	0.58969	0.411803	ENSG00000259467	NDUFAF4P1
ENSG00000259470	0	0.349143	0.826767	0.22447	ENSG00000259470	KRT8P9
ENSG00000259471	0.586629	1.66119	0.890953	2.86967	ENSG00000259471	LINC01169
ENSG00000259472	5.74722	6.08673	4.93245	3.83736	ENSG00000259472	RP13-996F3.3
ENSG00000259477	0	0	0	0.14632	ENSG00000259477	AC012653.1
ENSG00000259479	3.18645	5.67053	2.24054	2.24881	ENSG00000259479	SORD2P
ENSG00000259480	0.708768	2.75619	1.08699	3.51265	ENSG00000259480	RP11-26F2.1
ENSG00000259489	0	0	0	0	ENSG00000259489	KRT18P47
ENSG00000259490	0.766267	2.14539	0.236321	8.62432	ENSG00000259490	IGHV3OR15-7
ENSG00000259493	0	0	0.0512499	0	ENSG00000259493	AC023968.2
ENSG00000259494	12.0186	12.0437	9.5639	5.2904	ENSG00000259494	MRPL46
ENSG00000259495	0	0	0	0	ENSG00000259495	AC016705.2
ENSG00000259496	0	0	0	0	ENSG00000259496	AC021818.2
ENSG00000259500	0.186457	0.296302	0.491758	0.302215	ENSG00000259500	KRT8P24
ENSG00000259501	0	0.184729	0	0	ENSG00000259501	RP11-467N20.1
ENSG00000259502	0.112799	0.216589	0.106578	0.364551	ENSG00000259502	AL132640.1
ENSG00000259505	0.0994406	0.526538	0.778751	1.69105	ENSG00000259505	AC009268.1
ENSG00000259507	0	0	0	0	ENSG00000259507	AC103968.1

ENSG00000259509	0	0	0	0	ENSG00000259509	AC073941.2
ENSG00000259511	3.1362	8.90341	8.52867	7.85424	ENSG00000259511	UBE2Q2L
ENSG00000259512	0.257374	0.24814	0.438027	0.61653	ENSG00000259512	HNRNPA1P5
ENSG00000259513	0.926792	0	0.529935	2.53957	ENSG00000259513	CYCSP38
ENSG00000259516	0.0908886	0.628886	0.891418	0.756805	ENSG00000259516	ANP32AP1
ENSG00000259517	0	0.203385	0	0	ENSG00000259517	LINC02169
ENSG00000259518	0.703969	1.70048	1.69718	3.38482	ENSG00000259518	LINC01583
ENSG00000259522	0.31298	0.422418	0.269222	0.582408	ENSG00000259522	AL136295.4
ENSG00000259525	0	0	0	0	ENSG00000259525	GCSHP2
ENSG00000259529	1.71179	4.19391	3.32803	5.17593	ENSG00000259529	AL136295.5
ENSG00000259531	0.0756619	0.108135	0.230469	0.286486	ENSG00000259531	AC022306.1
ENSG00000259533	0	0	0	0	ENSG00000259533	AC040958.1
ENSG00000259535	0.43678	0.423709	0.126077	0.311821	ENSG00000259535	RPL21P12
ENSG00000259538	2.03609	4.12492	9.26958	5.46494	ENSG00000259538	UBE2Q2P11
ENSG00000259545	0	1.24782	0.310846	0.899175	ENSG00000259545	AC013452.1
ENSG00000259547	1.39474	2.64629	1.78905	2.17108	ENSG00000259547	CYCSP2
ENSG00000259550	0	0	0	0.0834499	ENSG00000259550	HNRNPA1P74
ENSG00000259556	8.81575	7.89809	2.79966	6.8377	ENSG00000259556	AC090971.3
ENSG00000259557	0	0	0	0	ENSG00000259557	HMGN1P26
ENSG00000259558	0.143363	0.13825	0	0	ENSG00000259558	MESTP2
ENSG00000259562	3.84753	7.64884	8.74336	8.02896	ENSG00000259562	AC090607.2
ENSG00000259565	0.049536	0	0	0	ENSG00000259565	KRT8P23
ENSG00000259567	0	0.391775	0.870418	0.427291	ENSG00000259567	DNM1P38
ENSG00000259569	0	0	0	0	ENSG00000259569	AC013489.2
ENSG00000259570	0.318725	0	0.319374	0.349701	ENSG00000259570	AC243562.1
ENSG00000259571	0.664627	6.39138	1.15506	10.7767	ENSG00000259571	BLID
ENSG00000259573	0.152249	0.365984	0.0661332	0.413198	ENSG00000259573	NMNAT1P5
ENSG00000259581	0.656564	1.76334	1.48735	1.85021	ENSG00000259581	TYRO3P
ENSG00000259585	0.101828	0.389101	0.620697	0.833461	ENSG00000259585	RBM17P4
ENSG00000259586	2.45495	3.44602	0	1.21678	ENSG00000259586	AC015712.3
ENSG00000259592	0.14683	1.28302	0.565184	1.48471	ENSG00000259592	PRELID1P4
ENSG00000259593	0	0.416813	0	0	ENSG00000259593	MTND5P40
ENSG00000259600	0.0454651	0.191472	0.0683587	0.0859351	ENSG00000259600	AC066616.2
ENSG00000259601	0	0.0281868	0.0505229	0	ENSG00000259601	AC092079.1
ENSG00000259608	0	0	0	0	ENSG00000259608	AC104229.1
ENSG00000259609	0	0	0	0	ENSG00000259609	AC027807.1
ENSG00000259612	0.0853016	0	0.0371726	0.0493844	ENSG00000259612	EEF1A1P22
ENSG00000259613	0	0	0	0	ENSG00000259613	RP13-608F4.6
ENSG00000259614	0	0.0729924	0	0.164804	ENSG00000259614	AC087477.6
ENSG00000259619	0.135133	0.396781	0.737159	0.950144	ENSG00000259619	AC010867.1
ENSG00000259622	0	0	0	0	ENSG00000259622	AC026956.1
ENSG00000259626	0.298896	0.283962	0	1.25315	ENSG00000259626	MTND3P12
ENSG00000259630	1.71632	1.67575	2.74512	5.30711	ENSG00000259630	AC104046.1
ENSG00000259632	1.06366	1.90694	1.07509	1.71672	ENSG00000259632	AC090971.4
ENSG00000259633	0	0	0	0.703034	ENSG00000259633	UBE2Q2P8
ENSG00000259637	0.188638	0	0	0	ENSG00000259637	DNM1P38
ENSG00000259642	1.44758	2.53945	3.26015	2.31515	ENSG00000259642	ST20-AS1
ENSG00000259646	0	0	24.2417	0	ENSG00000259646	AC140725.2
ENSG00000259648	0.798279	0.827368	1.67512	2.67552	ENSG00000259648	AL132640.2
ENSG00000259649	0.628418	1.35742	0.870188	2.28103	ENSG00000259649	AC027808.2
ENSG00000259651	0.751252	0.711178	0.19778	1.12821	ENSG00000259651	MTCO3P23
ENSG00000259655	0	0	0	0	ENSG00000259655	AC090825.2
ENSG00000259657	1.08582	1.25983	1.41319	1.61043	ENSG00000259657	PIGHP1
ENSG00000259658	1.6566	1.81852	1.35666	3.94934	ENSG00000259658	AC027559.1

ENSG00000259660	2.77824	2.08325	2.1855	4.27476	ENSG00000259660	DNM1P47
ENSG00000259665	0	0.950391	0.839096	0.278804	ENSG00000259665	AC021231.3
ENSG00000259671	0.0550523	0.105972	0.0478882	0.343523	ENSG00000259671	MTCYBP23
ENSG00000259674	0	0.155234	0.0701397	0	ENSG00000259674	AC092868.1
ENSG00000259677	0.810242	1.80702	1.43859	2.8643	ENSG00000259677	AC027176.2
ENSG00000259680	0	0	0	0	ENSG00000259680	AC136428.1
ENSG00000259683	0.267575	0.894562	1.0526	0.719612	ENSG00000259683	AC243562.2
ENSG00000259686	0.20533	0.587153	0.114813	0.424873	ENSG00000259686	HNRNPA1P71
ENSG00000259688	0	2.30358	0.515716	0.620264	ENSG00000259688	AC019288.1
ENSG00000259689	0	0	0	0	ENSG00000259689	
ENSG00000259691	0	0.739411	0.998473	0.805663	ENSG00000259691	FKBP1AP2
ENSG00000259695	0	0	0	0	ENSG00000259695	AC090164.1
ENSG00000259696	0	0	0	0	ENSG00000259696	AC104759.1
ENSG00000259698	0.231979	1.96381	0.89719	3.14956	ENSG00000259698	FAM30C
ENSG00000259699	2.13967	3.88261	5.26511	6.27828	ENSG00000259699	HMGB1P8
ENSG00000259706	0.187224	0.563803	0.449132	0.750087	ENSG00000259706	HSP90B2P
ENSG00000259707	0	0.104472	0	0.234571	ENSG00000259707	AC105339.3
ENSG00000259710	0	0.217126	0.392207	0	ENSG00000259710	NUTF2P6
ENSG00000259722	0	1.45613	0.86678	3.65861	ENSG00000259722	AC087465.1
ENSG00000259726	2.29029	2.66401	3.93237	4.92248	ENSG00000259726	CSPG4P11
ENSG00000259728	2.59855	3.5513	4.23071	4.87477	ENSG00000259728	LINC00933
ENSG00000259738	0.355086	0.336599	0.317241	0	ENSG00000259738	ZNF444P1
ENSG00000259742	0.230322	0.148618	0.135281	0.807912	ENSG00000259742	AC090888.3
ENSG00000259743	0	0.0778583	0	0	ENSG00000259743	AC068714.1
ENSG00000259745	0.116006	0.167697	0.202662	0.190901	ENSG00000259745	RP11-809H16.3
ENSG00000259746	0	0.456296	0.39171	2.15675	ENSG00000259746	HSPE1P3
ENSG00000259749	0	0.253829	0	0.295284	ENSG00000259749	NCAPGP2
ENSG00000259750	0.0834995	0.371035	0.592201	0.447216	ENSG00000259750	AC092868.3
ENSG00000259751	0.0944461	0.408995	0.493076	0.670636	ENSG00000259751	AC018868.2
ENSG00000259752	28.0031	36.9624	40.2922	51.8808	ENSG00000259752	FKSG62
ENSG00000259753	0	0	0	0	ENSG00000259753	AC068234.1
ENSG00000259769	0	0	0	0	ENSG00000259769	AC127381.2
ENSG00000259770	0	0	0	0	ENSG00000259770	AC015871.1
ENSG00000259777	0.0306942	0	0	0	ENSG00000259777	SLC39A12
ENSG00000259781	17.9219	18.123	11.5691	24.7988	ENSG00000259781	HMGB1P6
ENSG00000259784	1.34694	1.1408	0.567483	0	ENSG00000259784	AC093525.1
ENSG00000259785	0.564089	0.536312	0.953675	0.616867	ENSG00000259785	ADAMTS7P1
ENSG00000259790	0.0509782	0.050321	0.244622	0.635071	ENSG00000259790	ANP32BP1
ENSG00000259795	0.970359	0.0926605	1.08559	0.41617	ENSG00000259795	TBC1D3
ENSG00000259800	0	0	0	0	ENSG00000259800	AC145350.1
ENSG00000259801	0	0	0	0	ENSG00000259801	AC126327.5
ENSG00000259803	0.356317	5.16285	0.68765	1.36227	ENSG00000259803	SLC22A31
ENSG00000259808	0.0493108	0.215285	0.169466	0.477668	ENSG00000259808	FRG2
ENSG00000259809	0.212401	0.136814	0.316843	0.098387	ENSG00000259809	RP11-163O19.8
ENSG00000259822	0	0	0	0	ENSG00000259822	AC140878.1
ENSG00000259823	0.584827	0.300909	0.353738	0.774048	ENSG00000259823	LYPD8
ENSG00000259824	0	0	0	0.884011	ENSG00000259824	TRBV12-4
ENSG00000259825	0	0	0	0	ENSG00000259825	TRBV4-3
ENSG00000259829	0	0	0	0	ENSG00000259829	TRBV4-2
ENSG00000259832	0	0	0	0	ENSG00000259832	CYP4A26P
ENSG00000259836	0.12711	0.0611376	0.449514	0.34591	ENSG00000259836	AGGF1P6
ENSG00000259838	0	0	0	0	ENSG00000259838	ELOCP2
ENSG00000259842	0	0	0	0	ENSG00000259842	IGHV3OR16-16
ENSG00000259844	0.0884478	0.0926896	0.225718	0.361481	ENSG00000259844	AC018555.1

ENSG00000259845	0	0.345262	0.115395	0.454155	ENSG00000259845	HERC2P10
ENSG00000259848	1.55059	2.43938	1.83034	0.229187	ENSG00000259848	AC097374.1
ENSG00000259851	0	0	0	0	ENSG00000259851	TRBV28
ENSG00000259852	0	0	0	0	ENSG00000259852	IGHV1OR16-2
ENSG00000259853	0	0	0	0	ENSG00000259853	OR4A19P
ENSG00000259856	2.12028	0	0	0	ENSG00000259856	RAB43P1
ENSG00000259857	2.50039	4.19064	6.75079	10.5737	ENSG00000259857	C17orf51
ENSG00000259858	2.00461	3.67088	2.75863	5.94588	ENSG00000259858	MGAM
ENSG00000259864	0	0	0	0	ENSG00000259864	AC018846.1
ENSG00000259866	0.306855	0.978511	0.670171	0.824938	ENSG00000259866	AC007599.1
ENSG00000259873	0	0	0	0	ENSG00000259873	AC009117.1
ENSG00000259874	0	0	0	0	ENSG00000259874	AC034105.2
ENSG00000259879	0	0	0	0	ENSG00000259879	RP11-244N20.7
ENSG00000259880	42.7462	61.0704	21.1734	20.422	ENSG00000259880	MANF
ENSG00000259882	0	0.0395764	0	0	ENSG00000259882	AC142384.1
ENSG00000259885	0.483232	0.312446	0.772204	0.447846	ENSG00000259885	SH2B2
ENSG00000259890	0	0	0	0	ENSG00000259890	DNM1P50
ENSG00000259892	0.131128	0.315287	0.346982	0.856042	ENSG00000259892	AC027139.1
ENSG00000259893	0.0804205	0.0475118	0.0516648	0.0639076	ENSG00000259893	AC073464.6
ENSG00000259896	4.10769	3.5345	4.04916	2.29361	ENSG00000259896	AC073464.6
ENSG00000259897	0	0	0	0	ENSG00000259897	FRG2JP
ENSG00000259898	0.604099	0.0249342	0	0	ENSG00000259898	CYP4F33P
ENSG00000259900	0	0	0	0.209824	ENSG00000259900	AC026464.1
ENSG00000259903	0	0	0	0.154764	ENSG00000259903	TRBV7-5
ENSG00000259904	0	0.17277	0.164342	0.135674	ENSG00000259904	ACTG1P15
ENSG00000259909	0	0	0	0	ENSG00000259909	AC100827.1
ENSG00000259913	0	0	0	0	ENSG00000259913	TRBV7-4
ENSG00000259916	0	0	0	0.145103	ENSG00000259916	AL845331.2
ENSG00000259917	0	0.0389123	0.0430298	0.391742	ENSG00000259917	HNRNPLP2
ENSG00000259918	1.49197	0.958844	0.508478	1.29874	ENSG00000259918	NDUFA5P11
ENSG00000259919	0.222817	0.343072	0.222921	0.778003	ENSG00000259919	GALNT9
ENSG00000259922	0	0.286796	0.103676	0.467092	ENSG00000259922	AC023825.1
ENSG00000259924	0.865113	2.14309	1.59525	4.96061	ENSG00000259924	AC011939.1
ENSG00000259927	0.0467661	0	0	0.0505773	ENSG00000259927	RPL7P3
ENSG00000259930	0	0	0.0276327	0	ENSG00000259930	HLA-P
ENSG00000259931	0.424149	1.20142	1.80082	2.61403	ENSG00000259931	AC105036.1
ENSG00000259934	0	0	0	0	ENSG00000259934	AC142086.2
ENSG00000259938	4.4325	8.05648	14.6884	9.8104	ENSG00000259938	CUX1
ENSG00000259948	0.822893	1.32057	0.48281	0	ENSG00000259948	AC124068.1
ENSG00000259950	2.43877	2.97291	2.22538	3.49692	ENSG00000259950	AC034105.3
ENSG00000259951	0	0	0	0	ENSG00000259951	TRBV5-2
ENSG00000259956	1.26463	2.4411	4.4148	2.79295	ENSG00000259956	RBM15B
ENSG00000259958	5.09826	8.61194	9.3467	7.53261	ENSG00000259958	KAT2A
ENSG00000259960	0	0	0	0	ENSG00000259960	TRBJ2-2P
ENSG00000259962	0	0	0	0	ENSG00000259962	AC007342.2
ENSG00000259963	0	0	0	0	ENSG00000259963	AC007012.1
ENSG00000259965	0.216734	0.405185	0.796981	0.717673	ENSG00000259965	CTA-313A17.3
ENSG00000259966	0	0	0	0	ENSG00000259966	AC137800.1
ENSG00000259973	0	0	0.0589215	0.0984172	ENSG00000259973	IL9RP2
ENSG00000259978	0	0	0	0.564443	ENSG00000259978	MRPS21P8
ENSG00000259979	0	0	0.0804654	0	ENSG00000259979	VN1R68P
ENSG00000259980	5.93699	6.44374	7.03219	3.03978	ENSG00000259980	MRPL45
ENSG00000259982	0.0649073	0	0	0	ENSG00000259982	AC145285.3

ENSG00000259983	0	0	0	0	ENSG00000259983	AC018845.2
ENSG00000259984	0	1.05963	0	0.373479	ENSG00000259984	AL928711.1
ENSG00000259987	0.100755	0	0	0.222297	ENSG00000259987	DUX4L46
ENSG00000259990	0	0	0	0	ENSG00000259990	AC133561.3
ENSG00000259991	0	0.0291324	0	0.0650243	ENSG00000259991	OR4C13
ENSG00000259993	0	0.0254683	0	0.0544966	ENSG00000259993	AC135731.1
ENSG00000259996	0	0	0	0	ENSG00000259996	RARRES2P8
ENSG00000259997	0	0	0	0	ENSG00000259997	IGHV1OR16-4
ENSG00000260001	3.87022	2.30378	2.17477	2.34168	ENSG00000260001	TGFBR3L
ENSG00000260007	0	0.296196	0	0	ENSG00000260007	AC107871.1
ENSG00000260010	0.0293329	0	0	0.101802	ENSG00000260010	ZNF720P1
ENSG00000260012	0.432589	1.33169	2.56558	1.32224	ENSG00000260012	AC007494.1
ENSG00000260013	0	0	0.110444	0	ENSG00000260013	APOOP5
ENSG00000260014	0	0	0	0.351646	ENSG00000260014	LSM3P5
ENSG00000260020	0	0	0	0	ENSG00000260020	U85056.3
ENSG00000260024	0	0	0	0	ENSG00000260024	MRPS21P7
ENSG00000260027	2.83429	3.83626	6.93784	8.87523	ENSG00000260027	HOXB7
ENSG00000260028	0	0	0	0	ENSG00000260028	TRBV16
ENSG00000260031	0	0.336812	0	0.736691	ENSG00000260031	RPL10P14
ENSG00000260033	2.62615	8.86691	7.01424	7.02201	ENSG00000260033	AC023813.2
ENSG00000260036	0	0.0914087	0.0818259	0.103521	ENSG00000260036	AC013355.1
ENSG00000260039	0	0	0	0.0121887	ENSG00000260039	TNRC18P3
ENSG00000260040	0.204096	0.41543	0.0945523	0.38295	ENSG00000260040	KEL
ENSG00000260045	12.2461	15.5108	13.9892	11.3511	ENSG00000260045	STAM
ENSG00000260047	0.261052	0	0.225756	0	ENSG00000260047	BCAP31P2
ENSG00000260048	0	0	0	0	ENSG00000260048	IGHV1OR16-3
ENSG00000260050	0	0	0	0	ENSG00000260050	TRBV20-1
ENSG00000260053	0	0	0	0	ENSG00000260053	ABCB10P4
ENSG00000260055	0	0	0	0	ENSG00000260055	HLA-P
ENSG00000260061	0	0	0	0	ENSG00000260061	RP11-163O19.3
ENSG00000260062	0.156168	0.0341947	0	0.0777648	ENSG00000260062	GOLGA2P11
ENSG00000260067	0	0	0	1.23332	ENSG00000260067	MTND4LP25
ENSG00000260068	0	0	0	0	ENSG00000260068	AC009101.1
ENSG00000260069	0.0617077	0.125205	0.263861	0.652295	ENSG00000260069	TBC1D3B
ENSG00000260074	0	0	0	0.14404	ENSG00000260074	TRBV6-9
ENSG00000260075	2.52035	2.22561	5.32794	4.03011	ENSG00000260075	AC217777.1
ENSG00000260076	0	0	0	0	ENSG00000260076	TRBV23-1
ENSG00000260078	1.30969	2.72014	2.3784	4.68373	ENSG00000260078	AC007342.3
ENSG00000260079	0	0	0	0	ENSG00000260079	OR4C48P
ENSG00000260080	0	0.206683	0.0933234	0.114374	ENSG00000260080	TRBV7-3
ENSG00000260082	0.117663	0	0.203962	0	ENSG00000260082	AC106886.1
ENSG00000260087	0	0.264193	0.237453	0.951359	ENSG00000260087	PCMTD1P2
ENSG00000260089	0.0801471	0.595368	0.270216	0.172759	ENSG00000260089	ADAM3B
ENSG00000260092	0	0	0.0630195	0	ENSG00000260092	AC009163.2
ENSG00000260096	0	0	0	0	ENSG00000260096	DNM1P33
ENSG00000260097	0	0	0.471967	0	ENSG00000260097	SPDYE6
ENSG00000260099	0.150684	0.914943	2.26037	2.55258	ENSG00000260099	ADAMTS13
ENSG00000260103	12.1996	26.2195	25.6213	35.2876	ENSG00000260103	AC012435.1
ENSG00000260104	0	0	0.920786	0	ENSG00000260104	AC068338.1
ENSG00000260105	0.802431	1.9306	1.2561	1.71535	ENSG00000260105	AOC4P
ENSG00000260106	0	0	0	0.241055	ENSG00000260106	TRBV65-6
ENSG00000260109	0.156581	0.13634	0	0.445598	ENSG00000260109	AC135628.1
ENSG00000260112	1.85086	3.34516	2.48218	5.25835	ENSG00000260112	AC008567.1
ENSG00000260113	0	0	0	0	ENSG00000260113	AC093249.1

ENSG00000260116	0	0	0	0	ENSG00000260116	TRBV6-6
ENSG00000260117	4.55746	7.08079	6.25073	11.3664	ENSG00000260117	CHAMP1
ENSG00000260119	0.129349	0.0474305	0.0112155	0.12542	ENSG00000260119	TRPV6
ENSG00000260128	0.342667	4.2228	1.65563	1.45045	ENSG00000260128	ULK4P2
ENSG00000260129	0	0	0	0	ENSG00000260129	DUX4L3
ENSG00000260130	0.762268	0.277089	0.35636	0.94577	ENSG00000260130	MYOM2
ENSG00000260133	0	0	0	0	ENSG00000260133	CA5AP1
ENSG00000260134	0	0	0	0	ENSG00000260134	C1QL1P1
ENSG00000260138	0	0.142986	0.118771	0.0673651	ENSG00000260138	AC073464.7
ENSG00000260139	0.0249681	0.0563628	0.12227	0.0640606	ENSG00000260139	CSPG4P13
ENSG00000260143	0	0	0	0.239043	ENSG00000260143	TRBV13
ENSG00000260144	0.273921	0.346317	0.408974	0.538065	ENSG00000260144	AC100827.2
ENSG00000260146	0.261684	0	0.225439	0.824293	ENSG00000260146	AC132186.1
ENSG00000260147	0	0	0	0	ENSG00000260147	MTND5P34
ENSG00000260150	3.21312	6.31022	7.71251	5.62518	ENSG00000260150	ZMYND11
ENSG00000260152	0.115565	0	0.20037	0	ENSG00000260152	AC113208.2
ENSG00000260153	0	0	0	0	ENSG00000260153	RARRES2P10
ENSG00000260155	0	0	0	0.0452164	ENSG00000260155	DUX4L7
ENSG00000260157	0	0	0	0	ENSG00000260157	AC233702.2
ENSG00000260159	0	0	0	0	ENSG00000260159	AC091304.2
ENSG00000260161	0.224197	0.430182	0.278488	0.716304	ENSG00000260161	MTCYBP28
ENSG00000260164	17.8858	35.8018	21.4334	14.5664	ENSG00000260164	MYO19
ENSG00000260165	0	1.26328	0	0	ENSG00000260165	AC105036.2
ENSG00000260168	0	0	0	0	ENSG00000260168	TRBV1
ENSG00000260169	0	0	0	0	ENSG00000260169	RP11-163O19.11
ENSG00000260170	1.17792	1.0276	0	0.876469	ENSG00000260170	AC090527.2
ENSG00000260174	0	0	0	0	ENSG00000260174	AC111152.3
ENSG00000260178	1.33992	3.07746	2.05679	1.36198	ENSG00000260178	DHX58
ENSG00000260181	73.842	89.6307	36.7113	35.287	ENSG00000260181	SURF4
ENSG00000260184	0	0	0	0	ENSG00000260184	AC023827.1
ENSG00000260187	0.155116	0	0	0	ENSG00000260187	AC009101.2
ENSG00000260189	11.3871	5.30588	6.36341	4.23728	ENSG00000260189	EXOSC4
ENSG00000260191	0.0526371	0.0882314	0.0344652	0.151332	ENSG00000260191	AL672296.1
ENSG00000260195	0.11167	0.00453721	0.130625	0.799588	ENSG00000260195	EPHB6
ENSG00000260199	0	0	0	0	ENSG00000260199	CCL3L3
ENSG00000260204	0	0	0	0	ENSG00000260204	TRBV18
ENSG00000260207	0	0	0	0	ENSG00000260207	DUX4L47
ENSG00000260211	0	0	0	0.0261636	ENSG00000260211	AC139426.1
ENSG00000260212	1.47647	3.08986	1.59998	4.86129	ENSG00000260212	AL356432.3
ENSG00000260215	0	0	0	0	ENSG00000260215	TRBV12-1
ENSG00000260216	0	0	0	0	ENSG00000260216	TRBV7-6
ENSG00000260218	0	0	0	0	ENSG00000260218	AC034105.4
ENSG00000260220	0.106764	0.276229	0.295202	0.529603	ENSG00000260220	CCDC187
ENSG00000260221	0	0	0	0.0941761	ENSG00000260221	HLA-P
ENSG00000260222	0	0	0	0	ENSG00000260222	TRBV3-1
ENSG00000260224	0	0	0	0	ENSG00000260224	UBL5P4
ENSG00000260225	0.773595	0.227065	0.263211	0.489048	ENSG00000260225	PCDHB2
ENSG00000260226	29.7358	35.2927	21.4458	14.9443	ENSG00000260226	GPAA1
ENSG00000260227	0	0	0	0	ENSG00000260227	TRBV5-1
ENSG00000260229	3.8376	7.81273	7.84675	12.3799	ENSG00000260229	AC092139.1
ENSG00000260230	0.59056	1.66788	1.26555	2.36933	ENSG00000260230	FRRS1L
ENSG00000260234	0	0	0	0	ENSG00000260234	AC020636.2
ENSG00000260238	3.0035	1.12248	0.451643	1.64297	ENSG00000260238	PMF1-BGLAP
ENSG00000260240	0	0.132634	0.349055	0.433764	ENSG00000260240	APOOP5

ENSG00000260245	48.4774	42.1415	12.5752	39.2361	ENSG00000260245	ACLY
ENSG00000260247	0.282044	0.268156	0.486276	1.7711	ENSG00000260247	SUB1P4
ENSG00000260250	0	0	0	0	ENSG00000260250	U66061.39
ENSG00000260251	0	0.179595	0	0	ENSG00000260251	AC092368.1
ENSG00000260255	0	0.160317	0.0965943	0.302771	ENSG00000260255	AC093524.1
ENSG00000260258	0.864069	2.23129	3.08131	4.89801	ENSG00000260258	AC007346.1
ENSG00000260259	1.88726	3.70437	5.11578	3.39578	ENSG00000260259	LINC02166
ENSG00000260266	4.35593	8.11338	6.69465	10.3714	ENSG00000260266	AC090826.1
ENSG00000260272	0	0	0	0.199044	ENSG00000260272	AC093525.2
ENSG00000260275	0	0	0	0.344184	ENSG00000260275	AC013565.2
ENSG00000260282	0.581978	0.553035	1.49979	1.52147	ENSG00000260282	EIF4EBP2P2
ENSG00000260283	17.5723	14.2211	11.9874	13.7918	ENSG00000260283	CNP
ENSG00000260284	0.345156	0.110434	0	0	ENSG00000260284	TPSP2
ENSG00000260286	0	0	0	0	ENSG00000260286	C6orf229
ENSG00000260287	0	4.59E-08	1.03758	0	ENSG00000260287	TBC1D3G
ENSG00000260290	0	0	0	0	ENSG00000260290	AC092115.1
ENSG00000260291	0.11379	0	0	0	ENSG00000260291	FRG2GP
ENSG00000260295	0.0884616	0.0360169	0.172136	0.132047	ENSG00000260295	RP11-163O19.1
ENSG00000260297	26.7168	40.0466	46.0798	63.6991	ENSG00000260297	AC005086.5
ENSG00000260298	0	0	0.0489237	0	ENSG00000260298	ACTG1P16
ENSG00000260300	1.1792	1.97815	3.60815	3.38785	ENSG00000260300	AC009119.2
ENSG00000260307	0	0	0	0	ENSG00000260307	AC138915.1
ENSG00000260308	0	0	0	0.678971	ENSG00000260308	AC136428.2
ENSG00000260309	0	0	0	0	ENSG00000260309	TRBV2
ENSG00000260313	2.58102	5.07722	4.02333	3.85558	ENSG00000260313	VPS28
ENSG00000260314	0	1.62E-06	2.60E-06	1.57E-06	ENSG00000260314	MRC1
ENSG00000260315	0	0	0	0	ENSG00000260315	VN1R28P
ENSG00000260318	5.41083	5.67859	6.78134	14.874	ENSG00000260318	COX6CP1
ENSG00000260319	0.0158578	0.0696402	0.163712	0.0347734	ENSG00000260319	SPATC1
ENSG00000260320	0.258439	0.387662	0.482716	0.385073	ENSG00000260320	ZNF385C
ENSG00000260324	0.393264	5.78E-09	0.206234	1.54881	ENSG00000260324	TMEM236
ENSG00000260325	0.528737	0.783939	0.932534	0.992931	ENSG00000260325	HSPB9
ENSG00000260326	0.235976	0.303308	0.272891	0.763519	ENSG00000260326	PHBP21
ENSG00000260327	0	0	0	0	ENSG00000260327	ACTR3BP3
ENSG00000260332	0	0	0	0	ENSG00000260332	AC010546.1
ENSG00000260334	2.09776	0.478463	0.503932	0.177469	ENSG00000260334	GAST
ENSG00000260335	3.0644	2.41397	0	1.15115	ENSG00000260335	AC133555.4
ENSG00000260341	0.0538515	0	0.0468471	0.235009	ENSG00000260341	C2orf69P2
ENSG00000260342	0.563034	2.46596	0.384199	0	ENSG00000260342	AC138811.2
ENSG00000260344	0	0	0	2.16188	ENSG00000260344	AC133485.1
ENSG00000260346	0	0	0	0	ENSG00000260346	TRBV26
ENSG00000260347	0	0.0688126	0	0.0396783	ENSG00000260347	MOCS1P1
ENSG00000260353	0	0	0	0	ENSG00000260353	PGBD4P1
ENSG00000260354	0	0	0	0	ENSG00000260354	RP11-163O19.10
ENSG00000260355	0.407924	0.842651	0.932962	1.81875	ENSG00000260355	ZNF716
ENSG00000260357	0.272944	0.604424	0.547056	1.15401	ENSG00000260357	DNM1P34
ENSG00000260362	0	0.284951	0.24041	0.313084	ENSG00000260362	AC007218.1
ENSG00000260363	0.0330326	0	0.086119	0.132953	ENSG00000260363	OR9A1P
ENSG00000260371	0	0	0	0	ENSG00000260371	AC026464.3
ENSG00000260373	0	0	0	0	ENSG00000260373	TRBJ2-5
ENSG00000260374	24.2017	28.943	23.7473	30.4119	ENSG00000260374	ARHGAP23
ENSG00000260375	0	0	0	0	ENSG00000260375	AC126323.4
ENSG00000260376	0	0	0	0	ENSG00000260376	DUX4L5
ENSG00000260379	0	0.333823	0	0.185463	ENSG00000260379	AC074052.1

ENSG00000260380	12.1828	23.3165	17.3609	15.2594	ENSG00000260380	FRG1
ENSG00000260382	0	0.194465	0.115125	0.286659	ENSG00000260382	AC087481.1
ENSG00000260383	13.3998	16.3315	14.1725	15.3959	ENSG00000260383	MROH1
ENSG00000260384	56.6306	70.4576	51.9718	28.0874	ENSG00000260384	SERINC2
ENSG00000260386	0.103167	0.07381	0.21953	0.324072	ENSG00000260386	LINC01225
ENSG00000260389	0.259508	0.271163	0.370524	0.574791	ENSG00000260389	WBP11P1
ENSG00000260395	0.268045	0.386627	0.349371	0.655925	ENSG00000260395	AC092119.1
ENSG00000260399	0	0	0	0	ENSG00000260399	AC100756.1
ENSG00000260405	0	0	0	0	ENSG00000260405	AC109446.1
ENSG00000260407	0	0	0	0	ENSG00000260407	TRBV7-1
ENSG00000260410	0.0606552	0.116725	0.210978	0.13215	ENSG00000260410	AC040169.2
ENSG00000260413	0.131033	0.230589	0	0	ENSG00000260413	AC025279.2
ENSG00000260414	0	0	0	0	ENSG00000260414	AC138869.1
ENSG00000260415	1.23135	1.7141	1.73762	2.61748	ENSG00000260415	AC068987.1
ENSG00000260424	0.197986	0	0.228655	0.424848	ENSG00000260424	TRBV19
ENSG00000260427	0.137733	0	0	0.224624	ENSG00000260427	AGGF1P9
ENSG00000260428	1.33576	0.962582	1.69852	1.73134	ENSG00000260428	SCX
ENSG00000260429	0	0	0	0	ENSG00000260429	TRBV6-7
ENSG00000260431	0	0	0	0	ENSG00000260431	AC074051.2
ENSG00000260435	0	0	0	0	ENSG00000260435	TRIM51DP
ENSG00000260437	0	0	0	0	ENSG00000260437	TRBV11-1
ENSG00000260438	0	0.0765482	0.138317	0.259113	ENSG00000260438	AC018552.1
ENSG00000260443	0	0	0	0	ENSG00000260443	AC127455.1
ENSG00000260444	0	0	0	0	ENSG00000260444	AC138749.2
ENSG00000260445	0	0	0	13.5594	ENSG00000260445	AC011904.1
ENSG00000260446	0	0.139238	0	0	ENSG00000260446	MOXD2P
ENSG00000260449	0.441741	1.69426	0.764833	0.787732	ENSG00000260449	RP11-244B22.14
ENSG00000260451	0	0.0921942	0	0	ENSG00000260451	GEMIN8P2
ENSG00000260452	0.983258	3.6114	2.97653	3.70744	ENSG00000260452	TPRKBP2
ENSG00000260456	2.10525	4.27652	3.38111	4.65883	ENSG00000260456	C16orf95
ENSG00000260458	0	0	0	0	ENSG00000260458	KCNJ18
ENSG00000260459	7.81565	6.04867	4.75532	3.06278	ENSG00000260459	FTLP14
ENSG00000260463	4.56931	11.5464	24.496	5.18596	ENSG00000260463	MAPK15
ENSG00000260471	0	0	0	0	ENSG00000260471	AC009120.3
ENSG00000260472	0	0	0	0	ENSG00000260472	AC074050.1
ENSG00000260474	0.0485927	0.140084	0.168732	0.26263	ENSG00000260474	PRSS3P3
ENSG00000260480	0.135765	0.136778	0	0	ENSG00000260480	C2orf69P4
ENSG00000260481	0	0	0	0	ENSG00000260481	TRBV12-5
ENSG00000260483	0.406903	0	0.74594	0	ENSG00000260483	AC015720.1
ENSG00000260485	39.2336	38.4673	38.9004	23.288	ENSG00000260485	PUF60
ENSG00000260486	0	0	0	0	ENSG00000260486	TRBV25-1
ENSG00000260489	3.93746	3.2165	3.6941	5.47602	ENSG00000260489	C9orf96
ENSG00000260490	0.303014	0	0.262933	0	ENSG00000260490	MYL12BP1
ENSG00000260491	0	0	0	0.0453801	ENSG00000260491	U66059.29
ENSG00000260494	0	0.269619	0.563048	0	ENSG00000260494	AC002310.3
ENSG00000260497	0	0	0	0	ENSG00000260497	AC141846.1
ENSG00000260501	298.863	267.165	158.144	158.139	ENSG00000260501	RPL7A
ENSG00000260502	4.98861	3.32897	3.54753	2.66502	ENSG00000260502	CACFD1
ENSG00000260508	13.4078	22.5328	13.0677	10.069	ENSG00000260508	GGNBP2
ENSG00000260513	0.0135725	0	0.0360173	0	ENSG00000260513	ZNF479
ENSG00000260514	0	0	0	0	ENSG00000260514	AC009086.1
ENSG00000260516	0	0	0	0	ENSG00000260516	AC133548.1
ENSG00000260518	1.40361	1.90578	4.0511	5.4325	ENSG00000260518	BMS1P8
ENSG00000260521	0	0.0808696	0.0753627	0.0468032	ENSG00000260521	CTD-2576F9.1

ENSG00000260522	0	0	0	0	ENSG00000260522	AC106785.1
ENSG00000260524	0	0	0	0	ENSG00000260524	CYP3A52P
ENSG00000260525	0	0	0	0	ENSG00000260525	AC140658.2
ENSG00000260533	18.0105	13.8419	24.9373	12.3168	ENSG00000260533	NRBP2
ENSG00000260535	0	0	0	0	ENSG00000260535	TRBJ2-3
ENSG00000260537	0	0.716599	0	0	ENSG00000260537	AC012184.2
ENSG00000260538	0	0	0	8.24E-08	ENSG00000260538	HLA-P
ENSG00000260540	0	0	0	0	ENSG00000260540	ABHD17AP8
ENSG00000260546	0.436152	0.521012	1.22317	0.230566	ENSG00000260546	TRBV10-2
ENSG00000260548	0.128408	0.741352	1.02249	2.60867	ENSG00000260548	AL035425.2
ENSG00000260549	0.452528	20.2263	0.707146	72.8152	ENSG00000260549	MT1L
ENSG00000260554	4.35E-09	0	0	0	ENSG00000260554	TRBV8-2
ENSG00000260557	0.0465144	0	0.121129	0.0503106	ENSG00000260557	C7orf34
ENSG00000260559	0.11261	0.409722	0.159338	0.540028	ENSG00000260559	OR4A49P
ENSG00000260562	2.1195	6.79414	7.62206	18.0788	ENSG00000260562	RP11-227P3.1
ENSG00000260571	1.33837	2.722	2.01095	4.15027	ENSG00000260571	BNIP3P5
ENSG00000260576	0.171961	0.698159	0.925685	1.52604	ENSG00000260576	EIF5A2P1
ENSG00000260582	0.165157	0.582849	0.526771	0.483076	ENSG00000260582	TPST2P1
ENSG00000260584	0	0	0	0	ENSG00000260584	AC142381.2
ENSG00000260587	1.71E-05	0	0	0	ENSG00000260587	DOCK3
ENSG00000260590	0	0	0	0.226105	ENSG00000260590	AC023824.2
ENSG00000260595	0.0700764	0.269552	0.243556	0.152339	ENSG00000260595	OR4C49P
ENSG00000260596	2.20148	5.95261	5.66126	6.18859	ENSG00000260596	DUX4
ENSG00000260598	0.0839359	0	0	0	ENSG00000260598	FRG2IP
ENSG00000260602	0	0.428392	0.194581	0.235002	ENSG00000260602	HMGN2P40
ENSG00000260610	0.403739	1.00902	1.19209	0.875599	ENSG00000260610	AC142086.3
ENSG00000260615	0	0.68058	0.196522	0.206896	ENSG00000260615	RPL23AP97
ENSG00000260622	0.613188	1.18709	0.803466	0.982952	ENSG00000260622	AC073476.2
ENSG00000260623	8.21136	8.40953	7.56901	7.4863	ENSG00000260623	VPRBP
ENSG00000260628	4.13364	3.56266	5.60382	4.79217	ENSG00000260628	AC142381.3
ENSG00000260631	0	0.0852905	0	0	ENSG00000260631	RBM22P12
ENSG00000260632	0	0	0	0.142031	ENSG00000260632	OR6W1P
ENSG00000260638	0	0	0	0.0982049	ENSG00000260638	HLA-P
ENSG00000260639	1.13423	0.836577	2.43493	2.79621	ENSG00000260639	AC025678.1
ENSG00000260644	7.96372	22.797	18.4539	35.2245	ENSG00000260644	HERC2P5
ENSG00000260649	1.74482	1.90722	1.08852	1.0461	ENSG00000260649	AC133485.4
ENSG00000260662	0	3.81867	0	0	ENSG00000260662	AC138915.2
ENSG00000260665	0	0	0	0	ENSG00000260665	DUX4L4
ENSG00000260667	0	0.054854	0.049544	0.125412	ENSG00000260667	AC097374.4
ENSG00000260668	0	0	0.123875	0	ENSG00000260668	AC093536.1
ENSG00000260674	0	3.74091	1.10187	3.34441	ENSG00000260674	AC026826.3
ENSG00000260675	0	0	0.132679	0.165934	ENSG00000260675	AC109446.2
ENSG00000260678	0.389691	0.187887	0.673429	1.03403	ENSG00000260678	AC093249.3
ENSG00000260680	0	0.131414	0	0.149912	ENSG00000260680	AGGF1P5
ENSG00000260685	0.0994116	1.16599	0.776512	0.651438	ENSG00000260685	AC027104.1
ENSG00000260688	0.972365	0.913087	1.60794	1.93884	ENSG00000260688	AC026470.2
ENSG00000260689	0.603039	0.650127	0.586828	1.09545	ENSG00000260689	HNRNPA3P11
ENSG00000260690	0	0	0	0	ENSG00000260690	CYCSP39
ENSG00000260691	0.0384406	0.130339	0.132506	0	ENSG00000260691	ANKRD20A1
ENSG00000260692	6.14564	7.11074	5.3643	5.0752	ENSG00000260692	SURF1
ENSG00000260696	0.0527557	0.0507817	0	0.0575707	ENSG00000260696	TAS2R38
ENSG00000260702	0	0	0.0896812	0.111582	ENSG00000260702	AL031713.1
ENSG00000260703	0.169949	1.14982	1.60089	0.853199	ENSG00000260703	TTC25
ENSG00000260705	0	0.210999	0	0	ENSG00000260705	TRBV11-3

ENSG00000260709	0	0	0	0.0850661	ENSG00000260709	RARRES2P4
ENSG00000260712	0	0	0	0	ENSG00000260712	TRBJ2-6
ENSG00000260713	0	0	0	0	ENSG00000260713	AC073464.11
ENSG00000260714	0.400806	0.757015	0.800848	0.996399	ENSG00000260714	AC133552.1
ENSG00000260716	1.83816	4.00262	1.99422	3.47603	ENSG00000260716	TONSL
ENSG00000260717	0	0.065814	0	0.196629	ENSG00000260717	CCL4L1
ENSG00000260722	0	0.794744	0.179527	0.823621	ENSG00000260722	VN1R67P
ENSG00000260724	0	0	0.11151	0	ENSG00000260724	AC023824.3
ENSG00000260726	0	0	0.0500603	0	ENSG00000260726	AC023827.2
ENSG00000260727	2.32915	19.4394	14.2895	7.82181	ENSG00000260727	SLC7A5P1
ENSG00000260731	0	0.119529	0.0364698	0.0452078	ENSG00000260731	KRT8P22
ENSG00000260732	0	0	0	0	ENSG00000260732	TRBV5-5
ENSG00000260734	0	0	0	0	ENSG00000260734	AC010547.4
ENSG00000260736	0	0.0662287	0.0299851	0.224624	ENSG00000260736	PRSS58
ENSG00000260745	0	0	0	0	ENSG00000260745	TRBV4-1
ENSG00000260746	0	0.0194317	0	0.0658983	ENSG00000260746	KIF18BP1
ENSG00000260747	0	0.4477	0	0	ENSG00000260747	AC022968.1
ENSG00000260749	0	0	0	0	ENSG00000260749	RP11-114G11.2
ENSG00000260753	8.98467	8.19939	8.37833	5.75185	ENSG00000260753	NT5C3B
ENSG00000260762	0.0819909	0.0892329	0.136742	0.266658	ENSG00000260762	ACSM5P1
ENSG00000260764	0	0	0	3.19119	ENSG00000260764	AC007224.1
ENSG00000260765	0	0	0.0834174	0.0523586	ENSG00000260765	CES1P2
ENSG00000260767	0	0	0	0	ENSG00000260767	TRBV24-1
ENSG00000260768	0	0	0	0	ENSG00000260768	TRBV21-1
ENSG00000260770	7.59693	3.50101	5.87586	6.72762	ENSG00000260770	NKIRAS2
ENSG00000260776	0.667655	0.0862462	0.364854	0.112239	ENSG00000260776	AC104758.3
ENSG00000260781	1.17478	1.81024	1.27406	1.60678	ENSG00000260781	ARHGAP23P1
ENSG00000260782	0.0309397	0.148731	0.215619	0.212681	ENSG00000260782	AC007225.1
ENSG00000260783	0	0	0	0	ENSG00000260783	TRBJ2-7
ENSG00000260784	0.052067	0.0505766	0.0452995	0.0568799	ENSG00000260784	AC026150.2
ENSG00000260789	11.2596	5.05604	9.98854	8.87584	ENSG00000260789	GPSM1
ENSG00000260791	0.0361047	0.173614	0.0313733	0.247134	ENSG00000260791	OR9A3P
ENSG00000260794	0.159659	0	0	0	ENSG00000260794	TRBVA
ENSG00000260795	0	0	0	0	ENSG00000260795	AC093519.1
ENSG00000260797	0.102965	0	0.0893272	0.11116	ENSG00000260797	AC106734.1
ENSG00000260799	0.275898	1.32993	0.812515	1.55914	ENSG00000260799	KRT8P50
ENSG00000260801	0	0.0735194	0.0332089	0	ENSG00000260801	OR4R3P
ENSG00000260809	0.0405871	0.117646	0	0	ENSG00000260809	VPS35P1
ENSG00000260811	0	0	0	0.0740994	ENSG00000260811	OR4C45
ENSG00000260812	0	0	0	0.178021	ENSG00000260812	RARRES2P7
ENSG00000260813	0.0467046	0.0061497	0.0409076	0.330916	ENSG00000260813	AC073464.4
ENSG00000260815	0	0	0	0	ENSG00000260815	AC019294.3
ENSG00000260817	0	0	0	0	ENSG00000260817	AC074051.3
ENSG00000260818	0.507534	1.02346	1.83126	2.11243	ENSG00000260818	AC137527.1
ENSG00000260825	0.0364679	0.0735672	0.304897	0.224426	ENSG00000260825	GPR179
ENSG00000260828	0.129047	0	0	0.138546	ENSG00000260828	AC018552.3
ENSG00000260829	0	0	0	0	ENSG00000260829	OR9P1P
ENSG00000260836	0	0	0	0	ENSG00000260836	AC245033.1
ENSG00000260839	0	0	0	0.148171	ENSG00000260839	AC144838.3
ENSG00000260842	0.204012	0.221556	0.103616	0.0718192	ENSG00000260842	TEKT4
ENSG00000260843	0	0	0.233348	0.144446	ENSG00000260843	TRBV5-4
ENSG00000260844	0	0	0	0	ENSG00000260844	AC055876.4
ENSG00000260846	0	0.0741657	0.0729348	0.167455	ENSG00000260846	FRG2HP
ENSG00000260849	0	0	0	0	ENSG00000260849	TRBV3-2

ENSG00000260851	0	0.592595	0.150832	0.654278	ENSG00000260851	AC010542.3
ENSG00000260860	4.61003	12.7534	13.5246	14.0572	ENSG00000260860	AC126773.3
ENSG00000260861	0.78249	1.60314	0.658187	1.30446	ENSG00000260861	AL049634.2
ENSG00000260863	0	0	0	0	ENSG00000260863	CYP2C60P
ENSG00000260864	0	0	0	0	ENSG00000260864	ABHD17AP7
ENSG00000260865	1.12472	2.59452	3.45275	2.16822	ENSG00000260865	AC010287.1
ENSG00000260866	0	0	0	0	ENSG00000260866	AC138915.3
ENSG00000260869	0.609822	0	0	0	ENSG00000260869	AC002310.4
ENSG00000260870	0	0	0	0	ENSG00000260870	NDUFB10P1
ENSG00000260873	4.71786	8.00239	3.10004	6.77609	ENSG00000260873	SNTB2
ENSG00000260875	0	0	0	0	ENSG00000260875	RPS24P6
ENSG00000260881	0	0	0	0.0938673	ENSG00000260881	TRBC2
ENSG00000260882	1.47376	2.30566	4.37443	5.59187	ENSG00000260882	AC026458.1
ENSG00000260883	0	0	0	0	ENSG00000260883	VN1R65P
ENSG00000260885	0	0	0	0.116669	ENSG00000260885	TRBV6-2
ENSG00000260889	0.0560037	0.0538994	0.0487131	0	ENSG00000260889	CKBP1
ENSG00000260890	0	0	0	0.867444	ENSG00000260890	TRBV7-9
ENSG00000260897	0	0	0	0	ENSG00000260897	DNM1P30
ENSG00000260900	0	0	0	0	ENSG00000260900	AC145350.3
ENSG00000260903	0.0613375	0.389538	0.269227	0.376127	ENSG00000260903	XKR7
ENSG00000260904	0	0.199493	0	1.76802	ENSG00000260904	TRBV12-3
ENSG00000260908	4.72997	5.98657	6.11903	9.42362	ENSG00000260908	AC009093.3
ENSG00000260909	0	0	0.185899	0	ENSG00000260909	AC012186.1
ENSG00000260914	3.95033	5.04304	2.98628	4.6036	ENSG00000260914	AC026464.4
ENSG00000260915	0	0	0	0	ENSG00000260915	TRBV14
ENSG00000260916	32.3006	46.3628	46.0973	61.5262	ENSG00000260916	CCPG1
ENSG00000260925	0	0	0	0	ENSG00000260925	TRBV8-1
ENSG00000260928	0.105449	0	0	0	ENSG00000260928	SPCS2P1
ENSG00000260933	0	0	0	0.135723	ENSG00000260933	AC091489.2
ENSG00000260935	0.145495	0.414776	0.512561	0.813427	ENSG00000260935	RP11-707F14.3
ENSG00000260939	0.0710418	0.213107	0.246207	0.538868	ENSG00000260939	AC007346.2
ENSG00000260950	1.47512	0.125778	0.994189	0.300795	ENSG00000260950	C17orf97
ENSG00000260952	4.22426	2.6771	0	0.102104	ENSG00000260952	ZNHIT3
ENSG00000260965	0	0	0	0	ENSG00000260965	RPL23AP91
ENSG00000260967	0	0	0	0	ENSG00000260967	RARRES2P5
ENSG00000260968	28.5508	36.0346	47.128	19.253	ENSG00000260968	SCRIB
ENSG00000260970	0.238817	0.476496	0.424275	1.00778	ENSG00000260970	AC006288.1
ENSG00000260984	0	0	0	0.0775995	ENSG00000260984	FGFR3P5
ENSG00000260991	0	0	0	0	ENSG00000260991	AC120498.5
ENSG00000260993	0.392685	1.44698	1.01005	1.87658	ENSG00000260993	RP11-163E9.1
ENSG00000260994	0	0	0	0	ENSG00000260994	AGGF1P7
ENSG00000260998	0	0	0	0	ENSG00000260998	CNN2P8
ENSG00000261006	0	0	0.0459468	0.0560286	ENSG00000261006	RP11-439L8.2
ENSG00000261007	0.496177	0.34331	0.246577	0.462817	ENSG00000261007	AC074051.4
ENSG00000261010	0	0	0.157913	0.194274	ENSG00000261010	RARRES2P6
ENSG00000261011	1.66295	0.99754	0.209886	0.611847	ENSG00000261011	AL136982.4
ENSG00000261016	0	0.290453	0	0	ENSG00000261016	LCN1P2
ENSG00000261017	0	0	0	0	ENSG00000261017	AC096996.1
ENSG00000261021	0	0.0385649	0	0	ENSG00000261021	PRPF38AP2
ENSG00000261022	0	0	0	0	ENSG00000261022	TRBV7-7
ENSG00000261023	2.46452	7.27398	6.85437	8.58988	ENSG00000261023	TRRAP
ENSG00000261027	0.0270024	0	0	0	ENSG00000261027	TUBB7P
ENSG00000261031	0.111335	0.425329	0.200454	0	ENSG00000261031	TRBV9
ENSG00000261032	0	0	0	0	ENSG00000261032	CH17-235K9.4

ENSG00000261041	0	0	0	0	ENSG00000261041	AC138749.3
ENSG00000261042	29.0533	31.7051	20.5668	12.6979	ENSG00000261042	SLC52A2
ENSG00000261046	0	0	0	0	ENSG00000261046	C2orf69P1
ENSG00000261047	0	0	0	0	ENSG00000261047	AC137527.2
ENSG00000261048	0	0	0	0	ENSG00000261048	AC012414.6
ENSG00000261052	19.1724	28.4832	25.9736	24.8724	ENSG00000261052	SULT1A3
ENSG00000261053	0	0	0	0	ENSG00000261053	NAMPTP3
ENSG00000261056	1.95005	3.596	3.85505	5.79153	ENSG00000261056	AC079416.1
ENSG00000261059	0	0	0	0	ENSG00000261059	OBP2B
ENSG00000261072	0.622277	5.32437	3.54609	4.18283	ENSG00000261072	AC084783.1
ENSG00000261073	2.96246	3.28193	3.39168	2.8013	ENSG00000261073	RP11-163E9.2
ENSG00000261074	4.97649	8.38853	7.53761	5.25442	ENSG00000261074	QSOX2
ENSG00000261077	0	0	0	0	ENSG00000261077	AC016180.1
ENSG00000261081	0	0	0.551628	0	ENSG00000261081	AC025678.2
ENSG00000261084	0	0	0	0	ENSG00000261084	AC116553.1
ENSG00000261086	0.197028	0.565652	0.170223	0.418099	ENSG00000261086	RP11-379H8.1
ENSG00000261089	0	0	0	0	ENSG00000261089	CDC37P2
ENSG00000261102	0.879404	3.32003	1.85877	3.19138	ENSG00000261102	ATP5J2P6
ENSG00000261107	0	0	0	0	ENSG00000261107	PHKG1P4
ENSG00000261108	0	0	0	0	ENSG00000261108	AC138907.4
ENSG00000261109	337.051	465.615	256.821	380.529	ENSG00000261109	PLEC
ENSG00000261110	0	0	0	0	ENSG00000261110	TRBV27
ENSG00000261111	0	0	0.20654	0.25827	ENSG00000261111	AC133569.1
ENSG00000261112	0	0	0	0	ENSG00000261112	TRBV17
ENSG00000261115	0.107427	0.233399	0.232694	0.525939	ENSG00000261115	TMEM178B
ENSG00000261119	0	0	0	0	ENSG00000261119	TRBJ2-4
ENSG00000261125	3.04175	1.4761	2.29767	1.73578	ENSG00000261125	HAP1
ENSG00000261127	0.106191	0.165597	0.190163	0.669768	ENSG00000261127	AC133548.2
ENSG00000261130	0.631566	5.72325	2.79002	1.9385	ENSG00000261130	AC140504.1
ENSG00000261132	23.046	29.8794	28.3032	24.3428	ENSG00000261132	HSF1
ENSG00000261134	0	0	0.0276327	0	ENSG00000261134	HLA-P
ENSG00000261137	0	0.0646241	0	0	ENSG00000261137	RP11-220H4.2
ENSG00000261138	0	0	3.03E-06	1.70E-06	ENSG00000261138	AC016489.1
ENSG00000261142	0	0.0811478	0	0	ENSG00000261142	RPL21P120
ENSG00000261143	0.144299	0.74043	0.182439	0.755678	ENSG00000261143	ADAMTS7P3
ENSG00000261144	0	0	0.631816	0	ENSG00000261144	AC092121.1
ENSG00000261145	14.2655	41.763	27.9733	9.96874	ENSG00000261145	AC009060.2
ENSG00000261147	0.187466	0.326276	0.110096	0.0271612	ENSG00000261147	AC091167.3
ENSG00000261149	1.24748	2.23903	1.77415	2.82193	ENSG00000261149	TMEM130
ENSG00000261150	5.41318	16.3453	23.6112	4.81213	ENSG00000261150	EPPK1
ENSG00000261151	0	0.13569	0.122603	0.0766719	ENSG00000261151	AC012182.1
ENSG00000261152	0	0	0	0	ENSG00000261152	CTB-91J4.1
ENSG00000261153	0	0	0	0	ENSG00000261153	AC136428.3
ENSG00000261155	0.0354633	0	0	0.0384906	ENSG00000261155	FGF3
ENSG00000261157	0	0	0	0	ENSG00000261157	AF146191.7
ENSG00000261160	0	0.0984311	0.118587	0	ENSG00000261160	OR4A1P
ENSG00000261162	0.242314	0.248497	0.437108	0.169862	ENSG00000261162	U85056.1
ENSG00000261163	1.47988	3.99007	4.47041	6.4972	ENSG00000261163	LEPREL4
ENSG00000261165	0.0890375	0.079306	0	0	ENSG00000261165	CYP4F32P
ENSG00000261174	0.426359	0.963332	0.702474	1.85441	ENSG00000261174	HMGB1P33
ENSG00000261178	0.0455481	0.287411	0.153178	0.581233	ENSG00000261178	AC009169.1
ENSG00000261180	0.666052	1.07505	1.30724	2.726	ENSG00000261180	CLEC5A
ENSG00000261181	0.646766	0	0	0	ENSG00000261181	AC136619.1
ENSG00000261190	0.02953	0.349772	0.334932	0.699111	ENSG00000261190	C16orf97

ENSG00000261192	0	0.0651933	0.0390212	0	ENSG00000261192	RNF126P1
ENSG00000261196	0	0	0	0	ENSG00000261196	CYP4A43P
ENSG00000261197	0	0	0	0	ENSG00000261197	AC133561.4
ENSG00000261199	0.170828	0.654509	0.886175	2.18356	ENSG00000261199	UBE2FP2
ENSG00000261201	0	0	0	0.0452164	ENSG00000261201	DUX4L2
ENSG00000261203	0	0.00390104	0	0	ENSG00000261203	AC106782.3
ENSG00000261205	1.64829	3.91848	3.71764	4.39573	ENSG00000261205	NIFKP4
ENSG00000261208	0.203127	0.590081	0.227926	0.512305	ENSG00000261208	AL365475.1
ENSG00000261209	0	0	0.932903	1.50932	ENSG00000261209	SULT1C2P2
ENSG00000261210	1.45273	2.86596	2.33471	4.32405	ENSG00000261210	CLEC19A
ENSG00000261214	0	0	0	0	ENSG00000261214	TRBV12-2
ENSG00000261217	0	0	0	0	ENSG00000261217	BCAP31P1
ENSG00000261221	2.08081	3.01513	4.00211	3.78944	ENSG00000261221	ZNF865
ENSG00000261225	0	0	0	0	ENSG00000261225	PRSS3P1
ENSG00000261228	0	0	0	0	ENSG00000261228	AC078899.1
ENSG00000261230	12.8771	12.8066	13.4062	14.3145	ENSG00000261230	CPSF1
ENSG00000261232	0.167574	0	0	0.452761	ENSG00000261232	AC090751.1
ENSG00000261233	0	0	0	0	ENSG00000261233	ABCD1P3
ENSG00000261234	0	0	0	0	ENSG00000261234	AC025281.1
ENSG00000261236	9.15393	9.23584	13.0493	7.27516	ENSG00000261236	BOP1
ENSG00000261237	0	0	0	0	ENSG00000261237	TRBV5-3
ENSG00000261239	0.264727	0.0758038	0.145772	0.771397	ENSG00000261239	ANKRD26P1
ENSG00000261245	0	0	0	0	ENSG00000261245	AC093520.2
ENSG00000261246	0.0579115	0	0	0	ENSG00000261246	CCDC166
ENSG00000261247	0	0.112894	0.34478	0.0391222	ENSG00000261247	GOLGA8T
ENSG00000261256	1.93968	0	0.65825	0.7911	ENSG00000261256	AC126327.6
ENSG00000261258	3.08854	13.9065	17.6257	68.8991	ENSG00000261258	FKBP10
ENSG00000261259	0.741512	1.45823	1.05442	1.988	ENSG00000261259	AC142086.5
ENSG00000261262	0	0	0.0776102	0	ENSG00000261262	TRBV30
ENSG00000261263	0	0	0	0.745305	ENSG00000261263	AC138907.5
ENSG00000261264	0.013902	0.0133985	0.0115264	0.0435617	ENSG00000261264	TRBV5
ENSG00000261272	0.0442491	0.0256121	0.0231585	0.0975298	ENSG00000261272	MUC22
ENSG00000261274	1.15758	1.37513	1.07878	0.359018	ENSG00000261274	TP53TG3GP
ENSG00000261277	0	0	0	0	ENSG00000261277	OR4H6P
ENSG00000261278	0.584499	2.1809	1.31903	4.73032	ENSG00000261278	AC009094.1
ENSG00000261279	0.373569	1.38032	1.41417	2.03349	ENSG00000261279	ULK4P1
ENSG00000261281	1.91591	1.81823	4.92971	1.6645	ENSG00000261281	AC009712.1
ENSG00000261282	0	0	0	0	ENSG00000261282	SOD1P2
ENSG00000261283	8.49639	6.26754	10.876	6.86442	ENSG00000261283	PRKRIP1
ENSG00000261284	0.217752	0.0139337	0.243426	0.104526	ENSG00000261284	RBM22P13
ENSG00000261287	0	0	0	0	ENSG00000261287	TRBV6-4
ENSG00000261289	0	0	0	0	ENSG00000261289	AC034105.5
ENSG00000261290	0	0	0	0	ENSG00000261290	CYP4A44P
ENSG00000261297	4.58664	4.41956	8.55745	8.14043	ENSG00000261297	SLC39A4
ENSG00000261299	0.0552842	0	0	0.0589336	ENSG00000261299	C2orf69P3
ENSG00000261300	1.59449	4.60438	5.36929	3.3035	ENSG00000261300	PIGW
ENSG00000261301	0	0	0.0483487	0	ENSG00000261301	OR9A4
ENSG00000261303	6.11193	11.0431	10.0179	13.8302	ENSG00000261303	AC022748.2
ENSG00000261306	9.81703	7.60638	14.3416	8.87615	ENSG00000261306	SURF6
ENSG00000261308	0.0288562	0.0593932	0.403112	0.189951	ENSG00000261308	FIGNL2
ENSG00000261309	0.0604731	0.0646573	0.16689	0.195077	ENSG00000261309	KCNJ12
ENSG00000261315	0.312194	0.927523	0.94389	2.23012	ENSG00000261315	AC103988.1
ENSG00000261321	1.59474	1.85776	1.72509	3.78579	ENSG00000261321	FAM101B
ENSG00000261323	0	0	0	0.0325491	ENSG00000261323	OR6V1

ENSG00000261328	0	0	0	0	ENSG00000261328	AC097374.3
ENSG00000261330	0	0	0	0.170247	ENSG00000261330	AC010650.1
ENSG00000261331	0.533252	2.70825	0.918514	1.21768	ENSG00000261331	CTD-2144E22.7
ENSG00000261333	0	1.99695	1.63994	0	ENSG00000261333	CD24P2
ENSG00000261336	0.159044	0.741046	0.644011	1.13742	ENSG00000261336	EIF4BP5
ENSG00000261339	0	0	0	0	ENSG00000261339	TRBJ2-2
ENSG00000261345	0.0106475	0	0.00928064	0.0117013	ENSG00000261345	GATA5
ENSG00000261349	1.01381	1.34283	0.751621	0	ENSG00000261349	AL031432.2
ENSG00000261352	5.17927	14.0658	11.9108	17.8297	ENSG00000261352	ZNF90
ENSG00000261354	0	0	0	0	ENSG00000261354	OR4A18P
ENSG00000261356	0	0	0	0	ENSG00000261356	AC092368.2
ENSG00000261359	0.542166	0	0.461826	0.679425	ENSG00000261359	PYCARD-AS1
ENSG00000261361	8.57606	1.21924	11.6141	1.72498	ENSG00000261361	SURF2
ENSG00000261362	0	0.132413	0.114396	0.527768	ENSG00000261362	AC136619.2
ENSG00000261365	0	0	0	0	ENSG00000261365	AC138749.4
ENSG00000261370	0	0	0	0	ENSG00000261370	RPL14P5
ENSG00000261371	0.898721	0.895283	1.01288	2.05836	ENSG00000261371	PECAM1
ENSG00000261375	0	0	0	0	ENSG00000261375	AC135983.4
ENSG00000261377	1.52865	3.02805	0.584223	2.23948	ENSG00000261377	PDCD6IPP2
ENSG00000261378	20.2567	14.0627	14.7495	15.6756	ENSG00000261378	RAB5C
ENSG00000261380	30.9635	25.8261	33.1248	17.361	ENSG00000261380	FAM83H
ENSG00000261381	0	0.640782	0.404342	0.2315	ENSG00000261381	CNN2P11
ENSG00000261383	0	0	0	0.0626068	ENSG00000261383	OR4C12
ENSG00000261387	0.43656	1.23648	0.745297	0.671518	ENSG00000261387	AC138744.2
ENSG00000261391	0	0	0	0	ENSG00000261391	AC138907.6
ENSG00000261395	6.51623	25.2815	13.9692	20.0344	ENSG00000261395	HSPE1P5
ENSG00000261401	0	0	0	0	ENSG00000261401	AC091304.3
ENSG00000261405	1.79166	2.1135	1.37109	3.54528	ENSG00000261405	AC136944.3
ENSG00000261406	0	0	0	0	ENSG00000261406	OR11J1P
ENSG00000261412	0	0	0	0.14502	ENSG00000261412	TRBV6-5
ENSG00000261413	3.72961	4.87688	4.92106	3.66006	ENSG00000261413	SOCS7
ENSG00000261414	0	0	0	0	ENSG00000261414	TRBV15
ENSG00000261418	0	0.602259	0	0	ENSG00000261418	AC100756.2
ENSG00000261419	0.912205	1.62598	0.308734	0.629341	ENSG00000261419	AC145285.5
ENSG00000261424	0	0.41791	0.58606	0.564829	ENSG00000261424	ATP5F1P7
ENSG00000261427	1.42102	4.67494	2.51764	5.71081	ENSG00000261427	AC099518.3
ENSG00000261429	0.144419	0	0.0627465	0	ENSG00000261429	DPPA2P4
ENSG00000261440	0	0	0	0.0678984	ENSG00000261440	DUX4L45
ENSG00000261443	2.29506	1.57984	1.77105	2.56196	ENSG00000261443	RAD54L2
ENSG00000261444	0	0	0	0	ENSG00000261444	AC106782.4
ENSG00000261450	0.424055	0.23013	0.274422	0.88173	ENSG00000261450	TRBV29-1
ENSG00000261456	0	0.150075	0	0.0457319	ENSG00000261456	TUBB8
ENSG00000261457	0	0	0	0	ENSG00000261457	AC002519.2
ENSG00000261458	0	0	0	0	ENSG00000261458	AC009132.1
ENSG00000261459	0	0	0.240514	0	ENSG00000261459	AC002310.5
ENSG00000261461	0.155829	0	0	0	ENSG00000261461	UBE2MP1
ENSG00000261463	0.139575	0	0	0.146159	ENSG00000261463	TRBV6-8
ENSG00000261473	0.756819	0.237366	0.444456	0.759485	ENSG00000261473	PRSS1
ENSG00000261484	0	0.131396	0	0	ENSG00000261484	TRBV5-7
ENSG00000261486	0	0	0	0	ENSG00000261486	RARRES2P9
ENSG00000261491	0	0	0	0	ENSG00000261491	DNM1P31
ENSG00000261492	1.07255	0	0.288116	1.00639	ENSG00000261492	MLLT10P2
ENSG00000261493	3.08075	1.47551	11.9208	4.19633	ENSG00000261493	REXO4
ENSG00000261495	0	0	0	0	ENSG00000261495	AHCYP8

ENSG00000261497	0	0	0	0	ENSG00000261497	AC091304.4
ENSG00000261499	2.75554	1.48469	1.82745	3.91541	ENSG00000261499	AC233699.1
ENSG00000261503	0	0	0	0	ENSG00000261503	CTC-260E6.2
ENSG00000261506	0	0	0	0.112631	ENSG00000261506	TRBV6-1
ENSG00000261508	6.34363	4.01011	2.8537	5.13675	ENSG00000261508	DHRS11
ENSG00000261509	0	0.20012	0.216064	1.13463	ENSG00000261509	TP53TG3B
ENSG00000261510	0	0	0	0	ENSG00000261510	RP11-244B22.13
ENSG00000261511	0	0	0	0	ENSG00000261511	CYP3A137P
ENSG00000261514	0	0	0	0	ENSG00000261514	LINC01976
ENSG00000261515	0.150919	0.145318	0.0655649	0.740086	ENSG00000261515	AC106785.3
ENSG00000261516	6.44285	6.16879	10.1896	6.02043	ENSG00000261516	ZNF707
ENSG00000261518	0	0	0.782146	0	ENSG00000261518	CTA-313A17.2
ENSG00000261522	0.453382	0.756473	2.20286	1.62501	ENSG00000261522	AL845331.3
ENSG00000261524	0	0	0	0	ENSG00000261524	ABCB10P3
ENSG00000261527	0.376884	0.974633	0.560269	0.598469	ENSG00000261527	AC026464.5
ENSG00000261528	0.549357	1.84247	1.32021	1.67067	ENSG00000261528	AC002400.1
ENSG00000261530	1.0238	0.301353	0.456471	0.485207	ENSG00000261530	BTC
ENSG00000261531	0	0	0	0	ENSG00000261531	SNX18P14
ENSG00000261536	0	0	0	0	ENSG00000261536	ABHD17AP9
ENSG00000261539	5.54484	8.87917	6.72257	1.71515	ENSG00000261539	FBXL6
ENSG00000261545	0	0	0	0	ENSG00000261545	CH17-260O16.1
ENSG00000261548	0.176606	0	0	0	ENSG00000261548	HLA-P
ENSG00000261549	0	0	0	0	ENSG00000261549	AC107954.1
ENSG00000261554	0	0	0	0	ENSG00000261554	AC037471.2
ENSG00000261556	5.31693	17.6293	16.7298	16.1861	ENSG00000261556	SMG1P7
ENSG00000261557	0	0.0408837	0.0368263	0.0462748	ENSG00000261557	AC092725.2
ENSG00000261559	0	0	0	0.175499	ENSG00000261559	FSCN1P1
ENSG00000261561	0	0	0	0	ENSG00000261561	AC091304.5
ENSG00000261563	0	0	0	0.519627	ENSG00000261563	TRBV5-8
ENSG00000261564	0	0	0	0	ENSG00000261564	AC120498.7
ENSG00000261567	3.59616	4.61962	4.16198	13.4886	ENSG00000261567	RP11-680G10.1
ENSG00000261571	0	0.756736	0.195316	1.78328	ENSG00000261571	TRBV7-8
ENSG00000261575	0.159835	0.306405	0.41499	0.511985	ENSG00000261575	AC005829.1
ENSG00000261577	319.103	156.831	164.012	86.004	ENSG00000261577	JUP
ENSG00000261579	5.9344	3.41803	7.10977	2.25832	ENSG00000261579	MED22
ENSG00000261580	0	0	0	0	ENSG00000261580	ENPP7P13
ENSG00000261581	0.341828	0	0.406368	0	ENSG00000261581	HERC2P11
ENSG00000261585	0	0	0	0	ENSG00000261585	LCN1P1
ENSG00000261587	0.927356	1.41146	2.71121	1.28388	ENSG00000261587	TMEM249
ENSG00000261588	0	0.822934	0.922265	1.43538	ENSG00000261588	AC093249.4
ENSG00000261590	0	0	0	0	ENSG00000261590	AC018554.2
ENSG00000261591	0.0944227	0.0439963	0.209861	0.0718973	ENSG00000261591	U85056.2
ENSG00000261593	0	0	0	0	ENSG00000261593	CYP4A27P
ENSG00000261594	0.0394586	0.0379759	0.0858352	0.0436753	ENSG00000261594	TPBGL
ENSG00000261599	7.96372	22.8372	18.9448	36.6058	ENSG00000261599	HERC2P8
ENSG00000261601	0	0	0	0	ENSG00000261601	TRBV10-3
ENSG00000261603	0	0.0606927	0	0	ENSG00000261603	PRSS46
ENSG00000261605	2.02392	4.79055	3.1705	2.69189	ENSG00000261605	ABC7-42389800N19.1
ENSG00000261607	0.848298	0.829604	1.08049	0.463477	ENSG00000261607	AC140658.3
ENSG00000261608	0	0	0.0728318	0	ENSG00000261608	SLC25A1P4
ENSG00000261609	9.81829	6.29969	9.50896	7.85885	ENSG00000261609	GAN
ENSG00000261611	0.185989	0.171286	0.377821	0.253819	ENSG00000261611	AC010547.5
ENSG00000261612	0	0	0	0	ENSG00000261612	SUB1P3
ENSG00000261614	0.0562804	0	0	0.123069	ENSG00000261614	AC106730.1

ENSG00000261619	0.28503	0	0.244685	0	ENSG00000261619	TRBV22-1
ENSG00000261620	0.20473	0	0.560033	0.239182	ENSG00000261620	AC106785.4
ENSG00000261624	0.162337	0.466659	0.14042	0.173209	ENSG00000261624	NDUFB10P2
ENSG00000261626	0	0	0	0.116669	ENSG00000261626	TRBV6-3
ENSG00000261628	0.295639	0	0.253865	0.541343	ENSG00000261628	AC087481.2
ENSG00000261631	0.213319	0.210827	0.180629	0.104999	ENSG00000261631	KLHL10
ENSG00000261635	0.64358	1.33291	0.730343	3.62055	ENSG00000261635	AC103988.2
ENSG00000261647	0	0	0	0.129325	ENSG00000261647	IMPDH1P11
ENSG00000261649	0.331895	0.640601	0.775058	1.44016	ENSG00000261649	GOLGA6L7P
ENSG00000261652	1.22072	1.01242	0.885921	0.699372	ENSG00000261652	C15orf65
ENSG00000261657	1.20381	1.98204	1.73062	1.42423	ENSG00000261657	SLC25A26
ENSG00000261660	7.04337	13.4035	10.368	11.0559	ENSG00000261660	PARP10
ENSG00000261665	0	0	0	0	ENSG00000261665	TUBAP4
ENSG00000261667	0.0626335	0.0609609	0	0	ENSG00000261667	LY6L
ENSG00000261674	4.71554	6.97962	7.62795	7.17838	ENSG00000261674	RP11-1407O15.2
ENSG00000261676	0.306046	1.07958	0.691332	0.566853	ENSG00000261676	RP13-580B18.1
ENSG00000261677	7.95785	15.2405	8.0792	6.90456	ENSG00000261677	PTPLA
ENSG00000261678	0	0	0	0	ENSG00000261678	SCRT1
ENSG00000261679	0	0	0	0	ENSG00000261679	AC009852.2
ENSG00000261680	0	0	0	0	ENSG00000261680	AC093249.5
ENSG00000261686	0	0.0852569	0	0.0321832	ENSG00000261686	OR9A2
ENSG00000261688	1.10632	1.34862	1.55465	1.78077	ENSG00000261688	CTB-75G16.1
ENSG00000261689	0	0.0777374	0.0727293	0.175388	ENSG00000261689	AGGF1P4
ENSG00000261694	12.9939	8.68724	12.5489	1.67949	ENSG00000261694	ADCK5
ENSG00000261698	20.5315	36.2442	12.8716	8.74953	ENSG00000261698	DGAT1
ENSG00000261700	0	0	0	0	ENSG00000261700	TRBV10-1
ENSG00000261701	0.282173	0.561143	0.498109	1.05223	ENSG00000261701	HPR
ENSG00000261702	0	0	0	0	ENSG00000261702	AC022254.1
ENSG00000261704	0	0	0	0	ENSG00000261704	IGHV1OR16-1
ENSG00000261708	0	0	0.128814	0.144446	ENSG00000261708	DNM1P32
ENSG00000261711	0.0735546	0.583178	0.325466	0.961839	ENSG00000261711	FRG2DP
ENSG00000261714	0.273096	1.15433	1.6775	1.62914	ENSG00000261714	AC105137.2
ENSG00000261717	1.83189	0.879363	0	1.71555	ENSG00000261717	AC009163.4
ENSG00000261719	0	0.580906	0	0	ENSG00000261719	AC137761.2
ENSG00000261721	35.2012	38.5713	33.1734	17.5721	ENSG00000261721	GRINA
ENSG00000261725	0	0.891792	0	0.482287	ENSG00000261725	AC007225.2
ENSG00000261727	0.115626	0.278091	0.201934	0.252995	ENSG00000261727	AC142381.4
ENSG00000261732	2.1649	2.8538	3.38176	3.47776	ENSG00000261732	AL031708.1
ENSG00000261733	0	0	0	0	ENSG00000261733	RP11-80F22.8
ENSG00000261735	0.207032	0.39587	0.446982	0.767737	ENSG00000261735	TRBVB
ENSG00000261739	0.354973	0.610647	0.509932	0.42809	ENSG00000261739	GOLGA8S
ENSG00000261740	29.22	23.1705	17.0347	11.4965	ENSG00000261740	BOLA2-SMG1P6
ENSG00000261741	0.238775	0.166107	0.184639	0.365117	ENSG00000261741	FRG2KP
ENSG00000261747	0	0	0	0	ENSG00000261747	AC120045.2
ENSG00000261748	0.0642638	0	0	0.139885	ENSG00000261748	AC098965.1
ENSG00000261752	0.640617	0.579782	0.703352	1.57642	ENSG00000261752	AGGF1P8
ENSG00000261753	0.0883029	0	0	0	ENSG00000261753	RP11-631M21.6
ENSG00000261755	0	0	0	0	ENSG00000261755	DUX4L6
ENSG00000261756	0	0	0	0	ENSG00000261756	SLC29A4P1
ENSG00000261764	0.0463923	0.184813	0	0.101909	ENSG00000261764	KRT18P18
ENSG00000261768	13.9034	13.9507	11.0847	10.3344	ENSG00000261768	SLC2A6
ENSG00000261772	0.172798	0.250039	0.156796	0.203823	ENSG00000261772	IQSEC3
ENSG00000261774	0.749983	1.04771	0.924015	1.93345	ENSG00000261774	AC009075.2
ENSG00000261776	0.796589	1.47904	1.16319	2.41525	ENSG00000261776	AC079414.2

ENSG00000261778	0	0	0	0	ENSG00000261778	AC006362.1
ENSG00000261782	1.48281	1.62201	2.59723	2.18477	ENSG00000261782	AC116553.2
ENSG00000261784	0	0	0	0	ENSG00000261784	DUX4L7
ENSG00000261785	0	0	0	0	ENSG00000261785	TRBV7-2
ENSG00000261787	0.353444	0.444649	0.508051	0.949678	ENSG00000261787	TCF24
ENSG00000261791	0.0429106	0	0.00764255	0.0940131	ENSG00000261791	RP11-1220K2.2
ENSG00000261792	0	0.157512	0.160634	0	ENSG00000261792	DNM1P28
ENSG00000261794	0	0.559762	0.367524	0.143423	ENSG00000261794	GOLGA8H
ENSG00000261796	1.98047	0.451818	0.00115085	0.000215633	ENSG00000261796	ISY1-RAB43
ENSG00000261806	0.141079	0.293042	0.192289	0	ENSG00000261806	Hsa-mir-8078
ENSG00000261808	0	0	0	0.0382885	ENSG00000261808	WBP1LP1
ENSG00000261809	0	0	0	0	ENSG00000261809	CYP3A54P
ENSG00000261812	0	0.129984	0	0	ENSG00000261812	TUBB8P7
ENSG00000261813	0	0.275026	0.248827	1.21111	ENSG00000261813	AC015720.2
ENSG00000261814	0	0	0.0276327	0	ENSG00000261814	HLA-P
ENSG00000261819	0.846302	0.981598	0.892057	1.39394	ENSG00000261819	AC138932.3
ENSG00000261820	0	0.157512	0	0	ENSG00000261820	DNM1P49
ENSG00000261830	0	0	0	0	ENSG00000261830	TRBJ2-1
ENSG00000261832	0.092925	0.597028	0.814056	0.389791	ENSG00000261832	AC138894.1
ENSG00000261833	0	0	2.01186	0	ENSG00000261833	AC104151.1
ENSG00000261834	0	0	0	0	ENSG00000261834	IGHV3OR16-15
ENSG00000261835	0.0672805	0	0	0.075658	ENSG00000261835	AC007610.3
ENSG00000261836	0.698396	0.34758	1.14831	0.737679	ENSG00000261836	RP11-244B22.12
ENSG00000261843	81.9118	94.2923	75.7421	92.2729	ENSG00000261843	SEPT9
ENSG00000261844	0.779077	0.225917	0.654055	0.898658	ENSG00000261844	ST13P11
ENSG00000261846	0.239008	0.343284	0.287434	0.603154	ENSG00000261846	AADACL2
ENSG00000261847	0	0.127103	0	0	ENSG00000261847	AP000705.3
ENSG00000261849	0	0	0	0	ENSG00000261849	KIR3DP1
ENSG00000261851	0.288226	0.588339	0.898864	1.4043	ENSG00000261851	AC005077.8
ENSG00000261852	0.084147	0.325688	0.0803379	0.105987	ENSG00000261852	KRTAP2-1
ENSG00000261853	0.230473	1.51745	0.560753	1.61834	ENSG00000261853	AC134349.3
ENSG00000261855	2.8669	2.96807	1.99521	0.835417	ENSG00000261855	HYAL3
ENSG00000261857	5.56079	7.07211	5.0696	6.39422	ENSG00000261857	MIA
ENSG00000261858	12.9107	11.2233	14.1902	6.42151	ENSG00000261858	RP11-110I1.5
ENSG00000261859	0	0	0	0	ENSG00000261859	AC134873.1
ENSG00000261860	0	0	0	0	ENSG00000261860	KIR3DL1
ENSG00000261862	0	0	0.0221834	0.501008	ENSG00000261862	KRTAP1-5
ENSG00000261866	0	0	0	0	ENSG00000261866	AC243312.1
ENSG00000261868	1.37197	3.78593	2.63724	4.27539	ENSG00000261868	MFSD1P1
ENSG00000261869	0.4043	0.774892	0.897828	0.75131	ENSG00000261869	LSMEM2
ENSG00000261870	0	0.0620178	0	0.0343753	ENSG00000261870	KIR2DS5
ENSG00000261871	5.09283	8.84713	5.47484	3.15624	ENSG00000261871	NAT6
ENSG00000261874	0	0	0	0	ENSG00000261874	RP11-735A19.2
ENSG00000261875	2.13544	2.15736	4.59954	4.64232	ENSG00000261875	AC006014.8
ENSG00000261876	4.81165	4.74532	7.25702	6.25663	ENSG00000261876	PMS2P3
ENSG00000261878	0.113977	0.138751	0.176977	0.096243	ENSG00000261878	ANKRD30BP3
ENSG00000261880	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000261880	NCR1
ENSG00000261882	0	0	0	0	ENSG00000261882	AC006600.1
ENSG00000261883	3.2642	5.05223	4.40826	4.68916	ENSG00000261883	HMBS
ENSG00000261884	0.875703	2.16789	2.49633	2.97047	ENSG00000261884	AC040162.1
ENSG00000261885	0.230473	1.51745	0.560753	1.61834	ENSG00000261885	TAS2R18
ENSG00000261887	2.29942	1.66902	1.76019	1.5768	ENSG00000261887	C5orf30
ENSG00000261890	0	0	0	0	ENSG00000261890	AC010492.5
ENSG00000261893	9.62731	8.46593	10.2535	12.8901	ENSG00000261893	CLK2

ENSG00000261894	0.0770734	0.12531	0.0903788	0.19504	ENSG00000261894	SPDYE7P
ENSG00000261896	0	0.00205894	0.0116618	0	ENSG00000261896	RP11-498B4.4
ENSG00000261897	0	0.0867347	0.0522571	0.0982057	ENSG00000261897	OR5T3
ENSG00000261899	56.6742	49.786	41.2562	76.3929	ENSG00000261899	CRIM1
ENSG00000261900	14.8436	29.1334	28.7014	28.3196	ENSG00000261900	ZNF518A
ENSG00000261904	0	0	0	0.043991	ENSG00000261904	MTND5P33
ENSG00000261905	2.6795	0.449254	1.86295	1.59642	ENSG00000261905	AC217785.1
ENSG00000261906	1.05696	1.31648	0.914794	1.33797	ENSG00000261906	LENG9
ENSG00000261910	0.601676	0.661183	0.811951	0.832111	ENSG00000261910	MYO7A
ENSG00000261911	3.92664	7.13318	4.01465	4.82383	ENSG00000261911	RFC2
ENSG00000261912	0	0	0.0124249	0.0198593	ENSG00000261912	KIR2DL3
ENSG00000261913	8950.6	8523.33	8870.7	2636.74	ENSG00000261913	MTRNR2L6
ENSG00000261914	0	0	0	0	ENSG00000261914	RPL23AP84
ENSG00000261915	0.153361	0.180246	0.215702	0	ENSG00000261915	AC026954.2
ENSG00000261917	3.53108	2.18181	2.5967	7.94617	ENSG00000261917	MBOAT7
ENSG00000261919	2.34104	2.69335	4.12137	3.77211	ENSG00000261919	NCF1
ENSG00000261920	6.98881	5.35987	7.35165	6.59465	ENSG00000261920	GTF2IRD1
ENSG00000261921	24.5025	22.147	12.4125	8.03161	ENSG00000261921	HYAL2
ENSG00000261923	0.624617	1.52522	1.26264	2.20742	ENSG00000261923	PDE3B
ENSG00000261927	0.0265978	0.360617	0.208855	0.207012	ENSG00000261927	CTD-2542C24.4
ENSG00000261928	0.0947697	0.227373	0.267167	0.310296	ENSG00000261928	RP11-641C17.4
ENSG00000261929	0.0332516	0.0790378	0.102802	0	ENSG00000261929	LILRA4
ENSG00000261930	0.0131325	0.00949554	0.0125962	0.044165	ENSG00000261930	KIR3DL2
ENSG00000261931	6.90641	6.48352	5.20337	7.25698	ENSG00000261931	CDC42EP5
ENSG00000261932	10.7937	13.668	13.0347	20.7309	ENSG00000261932	BDP1
ENSG00000261934	1.24029	0.833019	1.35063	1.94441	ENSG00000261934	PCDHGA9
ENSG00000261935	0.0111762	0.0215246	0	0	ENSG00000261935	LILRA3
ENSG00000261936	0.26941	0.53746	0.87515	2.0428	ENSG00000261936	TAS2R45
ENSG00000261937	0.0111762	0.0215246	0	0	ENSG00000261937	LILRA3
ENSG00000261939	5.11475	0	0	0	ENSG00000261939	LARP7P2
ENSG00000261940	0.702783	0.801356	1.2141	1.0776	ENSG00000261940	DNAJC30
ENSG00000261941	6.19E-05	0.297333	0	0.165722	ENSG00000261941	OMP
ENSG00000261946	0.480083	0.607065	0	0.735559	ENSG00000261946	KDM4D
ENSG00000261948	3.27025	2.75588	2.69683	3.74564	ENSG00000261948	RP11-396K3.1
ENSG00000261949	0.0302184	0.0873615	0	0.0662859	ENSG00000261949	GFY
ENSG00000261950	0.0174955	0	0	0.0380342	ENSG00000261950	AC010492.2
ENSG00000261951	0	0	0	0	ENSG00000261951	RP11-536P116.3
ENSG00000261952	0.192187	0.275651	0.481038	0.38938	ENSG00000261952	POM121B
ENSG00000261957	0	0	0	0	ENSG00000261957	RP11-578F21.4
ENSG00000261958	0	0	0	0	ENSG00000261958	OR9G1
ENSG00000261961	0.133284	0.247489	0.256662	0.413123	ENSG00000261961	GP6
ENSG00000261963	0.247206	0.157679	0.144082	0.622438	ENSG00000261963	CCDC92B
ENSG00000261964	0.454371	0.902088	0.94909	5.30541	ENSG00000261964	ADAMTS10
ENSG00000261965	0	0	0	0	ENSG00000261965	ISCA1P3
ENSG00000261967	0	0	0	0.0814559	ENSG00000261967	GOLGA8F
ENSG00000261968	0	0	0	0	ENSG00000261968	KRTAP4-8
ENSG00000261970	0.246201	1.87765	3.18271	3.11018	ENSG00000261970	AL391840.1
ENSG00000261972	0.0819234	0.541567	0.231913	0.322142	ENSG00000261972	CES5A
ENSG00000261974	24.5191	18.487	18.5159	17.2078	ENSG00000261974	CWC15
ENSG00000261975	3.73612	2.69337	3.04044	3.60671	ENSG00000261975	RDH13
ENSG00000261979	0	0	0.107761	0.129749	ENSG00000261979	AC010492.4
ENSG00000261981	0.0281512	0.080285	0.0730803	0.184337	ENSG00000261981	ENPP7
ENSG00000261984	0.18156	0.913382	0.610468	0.768707	ENSG00000261984	TAS2R14
ENSG00000261986	0.211251	0.0590885	0.133061	0.0571692	ENSG00000261986	KRT33A

ENSG00000261987	0	0	0	0	ENSG00000261987	KYNUP1
ENSG00000261988	0	0	0.0248651	0	ENSG00000261988	AC008984.6
ENSG00000261991	0	0	0	0	ENSG00000261991	RP11-100N3.2
ENSG00000261992	1.8829	2.51489	3.91181	3.89848	ENSG00000261992	GATAD2B
ENSG00000261998	0	0	0	0	ENSG00000261998	AC011515.2
ENSG00000262000	0	0	0	0	ENSG00000262000	AC120024.2
ENSG00000262003	2.13461	4.2192	5.2156	9.58728	ENSG00000262003	AC087392.1
ENSG00000262004	0.541289	0.571145	0.330792	1.93053	ENSG00000262004	LILRA2
ENSG00000262007	0.0131325	0.00949554	0.0125962	0.044165	ENSG00000262007	KIR3DL2
ENSG00000262008	0	0	1.38925	0	ENSG00000262008	AC010547.6
ENSG00000262009	0.00591224	0.0414758	0	0	ENSG00000262009	NLRP7
ENSG00000262015	2.41881	12.9502	3.9126	5.02083	ENSG00000262015	SEMA3B
ENSG00000262018	0.366135	0.409532	0.494426	0.423368	ENSG00000262018	VPS37D
ENSG00000262022	0.44244	9.27E-06	1.13396	3.86232	ENSG00000262022	ZNF100
ENSG00000262023	3.75544	5.11365	6.237	6.79099	ENSG00000262023	JH8
ENSG00000262024	9.89564	12.164	13.5351	9.07179	ENSG00000262024	TCF20
ENSG00000262025	0.24823	0.614718	0.808002	1.24343	ENSG00000262025	AL513523.5
ENSG00000262027	0	0.0254943	0.0230419	0.0578032	ENSG00000262027	CUBNP2
ENSG00000262028	1.44115	1.34663	0.940187	1.12964	ENSG00000262028	FDXACB1
ENSG00000262029	0	0.0677545	0.06117	0.0756507	ENSG00000262029	CCL26
ENSG00000262030	17.9022	14.6602	13.3499	18.0763	ENSG00000262030	WBSCR22
ENSG00000262034	0	0.825128	0.657912	2.28787	ENSG00000262034	RP11-124L9.4
ENSG00000262035	0	0	0	0	ENSG00000262035	AC098789.1
ENSG00000262036	0	0.0249062	0.109997	0.0552529	ENSG00000262036	AC068305.4
ENSG00000262037	1.07103	2.70719	1.68139	2.55665	ENSG00000262037	CTD-2626G11.1
ENSG00000262039	3.84032	7.75848	5.7579	12.7548	ENSG00000262039	AC091180.5
ENSG00000262040	0.838257	0.17339	0.0401656	0.450229	ENSG00000262040	AC003958.3
ENSG00000262041	1.66385	5.89225	0	4.66288	ENSG00000262041	RP11-974F13.1
ENSG00000262044	0.263198	0.435275	0.36488	0.257131	ENSG00000262044	LILRB3
ENSG00000262045	0.596279	0.339179	0	0	ENSG00000262045	KRT34
ENSG00000262046	4.89421	7.94985	3.06178	7.80549	ENSG00000262046	TMEM97
ENSG00000262048	0	0	0	0	ENSG00000262048	AL078601.3
ENSG00000262053	3.53108	2.18181	2.5967	7.94617	ENSG00000262053	MBOAT7
ENSG00000262055	0.316627	0.991074	1.93025	1.04916	ENSG00000262055	CYP2D8P
ENSG00000262057	9.13335	10.5105	11.5313	8.6433	ENSG00000262057	MCCC2
ENSG00000262059	0	0.0725253	0	0.0820089	ENSG00000262059	KRT18P40
ENSG00000262060	0.905796	4.86266	7.57799	1.82638	ENSG00000262060	RP11-313P13.4
ENSG00000262062	0.502542	0.190995	0.919889	0.420723	ENSG00000262062	VTN
ENSG00000262063	8.75641	8.71624	8.0739	8.46538	ENSG00000262063	LIMK1
ENSG00000262065	0	0	0	0	ENSG00000262065	AC010492.5
ENSG00000262067	0	0	0	0	ENSG00000262067	AC120057.2
ENSG00000262068	0.511816	0.29042	0	0.209109	ENSG00000262068	KRTAP3-1
ENSG00000262069	0.133284	0.247489	0.256662	0.413123	ENSG00000262069	GP6
ENSG00000262072	0	0.0320128	0.0876673	0.0362098	ENSG00000262072	OR6D1P
ENSG00000262073	1.43451	4.02834	4.37184	6.14772	ENSG00000262073	CLDN3
ENSG00000262076	0	0	0.207445	0	ENSG00000262076	RP11-66N11.6
ENSG00000262077	1.25665	1.36967	2.06257	3.08772	ENSG00000262077	MLXIPL
ENSG00000262080	6.8536	10.0732	12.2427	11.6916	ENSG00000262080	RP11-578F21.1
ENSG00000262081	0	0	0	0	ENSG00000262081	AP001005.1
ENSG00000262082	0	0	0.0292392	0	ENSG00000262082	AC084033.4
ENSG00000262085	0	0	0	0.135432	ENSG00000262085	OR1P1
ENSG00000262087	0.533813	1.70996	0.32249	0.581936	ENSG00000262087	LILRB3
ENSG00000262088	180.678	163.499	111.06	86.8003	ENSG00000262088	RPS25
ENSG00000262090	0	0	0	0	ENSG00000262090	AC136944.5

ENSG00000262092	13.9514	3.86813	5.63883	3.16433	ENSG00000262092	EPS8L1
ENSG00000262093	0	0.0933894	0	0	ENSG00000262093	AL512324.1
ENSG00000262095	0	0	0	0	ENSG00000262095	MTATP6P25
ENSG00000262096	0.106695	0.0458805	0.0312506	0.143234	ENSG00000262096	PCDHB19P
ENSG00000262100	0.103648	0.148175	0	0.0544578	ENSG00000262100	AC008984.5
ENSG00000262102	1.56681	1.46335	1.53373	4.4437	ENSG00000262102	DSEL
ENSG00000262103	0.522561	0.907946	1.46669	2.18859	ENSG00000262103	TAS2R14
ENSG00000262105	0	0	0	0	ENSG00000262105	AC008746.10
ENSG00000262106	0	0	0	0	ENSG00000262106	AC090282.2
ENSG00000262107	0	0	0	0	ENSG00000262107	MTND6P33
ENSG00000262110	3.73612	2.69337	3.04044	3.60671	ENSG00000262110	RDH13
ENSG00000262111	0.197502	1.38946	1.02511	4.09197	ENSG00000262111	TAS2R30
ENSG00000262113	0	0.174126	0.175893	0.461654	ENSG00000262113	AC010614.1
ENSG00000262118	0.303253	0.680329	0.658055	0.867815	ENSG00000262118	MTCO1P28
ENSG00000262120	0	0	0	0	ENSG00000262120	AC010547.7
ENSG00000262121	0	0	0	0	ENSG00000262121	KRTAP4-9
ENSG00000262122	3.20988	3.07539	4.19023	6.50765	ENSG00000262122	POM121
ENSG00000262124	4.54199	8.96003	9.94673	5.2134	ENSG00000262124	ZNF558
ENSG00000262128	1.83485	1.91684	2.3194	5.19722	ENSG00000262128	LAT2
ENSG00000262129	0.725057	0	0	1.23623	ENSG00000262129	RP11-708L7.7
ENSG00000262131	0.133284	0.247489	0.256662	0.413123	ENSG00000262131	GP6
ENSG00000262134	0	0.166051	0	0	ENSG00000262134	TRBC1
ENSG00000262135	0.185411	0.384044	0.403042	0.401801	ENSG00000262135	GARSP1
ENSG00000262138	0.105369	0	0.0887192	0.271426	ENSG00000262138	AC012314.1
ENSG00000262139	0.655703	6.8536	0	0.547076	ENSG00000262139	ANO4
ENSG00000262140	0.287636	0.0691576	0.437406	0.625031	ENSG00000262140	AC010653.1
ENSG00000262141	8.18411	3.7948	5.6176	1.33876	ENSG00000262141	AC040162.2
ENSG00000262143	0.23394	0.38731	0.32465	0.694744	ENSG00000262143	AC009892.10
ENSG00000262145	1.22707	3.09275	1.09202	2.38732	ENSG00000262145	ATP23
ENSG00000262148	0.11354	0.0545193	0.0492386	0.0870349	ENSG00000262148	RPS5P3
ENSG00000262149	0	0	0	0	ENSG00000262149	MYO1F
ENSG00000262150	12.0845	0.397334	0.329241	0.71898	ENSG00000262150	PSCA
ENSG00000262153	0	0	0.0384919	0	ENSG00000262153	CTC-550B14.1
ENSG00000262154	0.575927	0	0.247259	1.20498	ENSG00000262154	EIF1P4
ENSG00000262156	0	0	0	0	ENSG00000262156	APOBEC3A
ENSG00000262158	0	0.160203	0	0.72258	ENSG00000262158	MTCO3P24
ENSG00000262159	0	0.0439899	0.0909581	0	ENSG00000262159	AC068305.5
ENSG00000262161	0	0	0	0	ENSG00000262161	KIR2DS4
ENSG00000262162	0	0	0	0	ENSG00000262162	FAM8A2P
ENSG00000262163	3.73612	2.69337	3.04044	3.60671	ENSG00000262163	RDH13
ENSG00000262164	0.0420095	0.040374	0.0364746	0.0455203	ENSG00000262164	KRT39
ENSG00000262168	0.418188	0.39575	0.408938	0.372155	ENSG00000262168	LENG1
ENSG00000262169	3.16735	5.77418	5.17439	5.9992	ENSG00000262169	GTF2H2
ENSG00000262170	18.6997	14.8698	23.797	23.2842	ENSG00000262170	SMN2
ENSG00000262174	0.418188	0.39575	0.408938	0.372155	ENSG00000262174	LENG1
ENSG00000262175	1.7071	3.4412	2.66344	2.44994	ENSG00000262175	NLRP2
ENSG00000262176	3.7885	2.08947	1.98774	3.20154	ENSG00000262176	C11orf1
ENSG00000262178	0	0	0.0248651	0	ENSG00000262178	AC008984.6
ENSG00000262180	0.644563	1.44934	1.3068	2.95679	ENSG00000262180	OCLM
ENSG00000262181	0	0	0.129293	0.159728	ENSG00000262181	AP001005.2
ENSG00000262182	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000262182	NCR1
ENSG00000262184	4.24356	25.1053	11.0417	19.7796	ENSG00000262184	ELN
ENSG00000262186	4.07557	6.42465	3.91809	5.69496	ENSG00000262186	SLC46A1
ENSG00000262187	0	0	0	0	ENSG00000262187	AC137800.2

ENSG00000262189	0.308418	0.376853	0.203159	0.362216	ENSG00000262189	RP11-641C17.2
ENSG00000262191	0	0	0	0	ENSG00000262191	OR9G9
ENSG00000262192	0.103648	0.148175	0	0.0544578	ENSG00000262192	AC008984.5
ENSG00000262196	0	0	0	0	ENSG00000262196	CALCP
ENSG00000262197	0	0.276359	0.298685	0.592058	ENSG00000262197	RP11-1305N21.2
ENSG00000262199	0.609831	1.0646	1.33026	1.02998	ENSG00000262199	SRCIN1
ENSG00000262206	3.34707	21.6619	20.5821	24.2045	ENSG00000262206	LINC00674
ENSG00000262207	3.73612	2.69337	3.04044	3.60671	ENSG00000262207	RDH13
ENSG00000262208	11.6361	4.01475	1.56871	2.61249	ENSG00000262208	HYAL1
ENSG00000262209	0.873292	0.514299	0.988026	0.880677	ENSG00000262209	PCDHGB3
ENSG00000262210	0	0	0	0	ENSG00000262210	PEBP1P3
ENSG00000262214	0	0	0	0	ENSG00000262214	KRTAP9-12P
ENSG00000262216	0	0	0	0.0366664	ENSG00000262216	LAIR2
ENSG00000262217	0.532308	0.645057	0.779783	1.06654	ENSG00000262217	SLC5A8
ENSG00000262218	0	0.0192078	0	0.0217489	ENSG00000262218	KRTAP29-1
ENSG00000262219	0	0	0	0	ENSG00000262219	AC010492.5
ENSG00000262220	0	0	0	0	ENSG00000262220	VN1R105P
ENSG00000262221	0	0	0	0	ENSG00000262221	KRTAP9-7
ENSG00000262225	13.9514	3.86813	5.63883	3.16433	ENSG00000262225	EPS8L1
ENSG00000262233	0.26941	0.53746	0.87515	2.0428	ENSG00000262233	CH17-93H22.2
ENSG00000262234	11.1224	14.5492	11.8029	13.5213	ENSG00000262234	PPIP5K2
ENSG00000262235	0	0	0	0.252503	ENSG00000262235	TMF1P1
ENSG00000262236	1.74684	1.72409	2.55213	2.53781	ENSG00000262236	TTYH1
ENSG00000262238	0	0	0	0	ENSG00000262238	VN1R105P
ENSG00000262239	0.133284	0.247489	0.256662	0.413123	ENSG00000262239	GP6
ENSG00000262241	0.0400002	0.0769011	0.0694771	0.0867638	ENSG00000262241	RP11-748L13.2
ENSG00000262243	0.104533	0.156072	0.135057	0.617126	ENSG00000262243	CES1
ENSG00000262244	3.73612	2.69337	3.04044	3.60671	ENSG00000262244	RDH13
ENSG00000262245	0.0300533	0.197155	0.0505073	0.0949485	ENSG00000262245	FOXR1
ENSG00000262246	27.3138	36.9915	34.8164	37.0822	ENSG00000262246	CORO7
ENSG00000262248	1.42495	1.33744	1.98868	3.7989	ENSG00000262248	AC027796.2
ENSG00000262249	3.99141	5.32188	7.6393	4.90605	ENSG00000262249	ZNF626
ENSG00000262250	0	0	0	0	ENSG00000262250	ABCB10P4
ENSG00000262255	0	0	0	0	ENSG00000262255	FAM210CP
ENSG00000262258	0.059501	0.172055	0.176291	0.313666	ENSG00000262258	KDM4E
ENSG00000262259	0	0	0	0	ENSG00000262259	MTND4LP24
ENSG00000262260	1.7071	3.4412	2.66344	2.44994	ENSG00000262260	NLRP2
ENSG00000262261	6.45371	4.21776	6.77651	9.78193	ENSG00000262261	GTF2H2D
ENSG00000262262	0.561513	0.377408	1.89766	2.18715	ENSG00000262262	AC026271.3
ENSG00000262263	11.7219	8.96171	10.1312	9.13424	ENSG00000262263	STYXL1
ENSG00000262264	0	0	0	0	ENSG00000262264	B3GNT6
ENSG00000262266	0.428706	0	0	0	ENSG00000262266	AC010518.3
ENSG00000262268	0	0	0.0298422	0.112019	ENSG00000262268	OR9G3P
ENSG00000262270	0	0	0.858347	0	ENSG00000262270	AC005077.9
ENSG00000262271	0	0.0488007	0.0441073	0.0553447	ENSG00000262271	AC090079.1
ENSG00000262273	1.41499	4.06549	3.71493	6.15602	ENSG00000262273	PNLIPRP1
ENSG00000262274	0.589806	5.40704	4.61503	3.66828	ENSG00000262274	HMGN1P12
ENSG00000262275	0.736239	1.42104	0.775694	1.97886	ENSG00000262275	SLC16A6
ENSG00000262277	3.96091	2.5958	7.37889	9.80839	ENSG00000262277	DIXDC1
ENSG00000262279	0.189045	0.303202	0.298068	4.25479	ENSG00000262279	NCAM1
ENSG00000262281	0	0.308396	0.20206	0.556437	ENSG00000262281	RP11-641C17.1
ENSG00000262282	0	0	0	0	ENSG00000262282	AC003958.4
ENSG00000262284	0.0332516	0.0790378	0.102802	0	ENSG00000262284	LILRA4

ENSG00000262285	0.0355219	0.0341541	0	0.0385293	ENSG00000262285	RPL5P29
ENSG00000262286	0	0	0.123439	0	ENSG00000262286	RP1-232L24.4
ENSG00000262287	13.9514	3.86813	5.63883	3.16433	ENSG00000262287	EPS8L1
ENSG00000262289	0	0	0	0	ENSG00000262289	KIR3DL3
ENSG00000262293	4.05648	15.0618	10.8265	8.25606	ENSG00000262293	AC242308.1
ENSG00000262295	0	0	2.39865	5.62569	ENSG00000262295	SBDSP1
ENSG00000262297	0.428706	0	0	0	ENSG00000262297	AC010518.3
ENSG00000262299	0.110549	0.279204	0.385815	0.487801	ENSG00000262299	AL513523.6
ENSG00000262300	0	0.0118584	0	0.0133071	ENSG00000262300	VN1R104P
ENSG00000262301	0	0	0	0	ENSG00000262301	CTD-2557P19.1
ENSG00000262302	5.78114	5.06651	1.43847	0.561219	ENSG00000262302	AC003688.1
ENSG00000262304	0.389945	1.57807	2.33319	1.8747	ENSG00000262304	AC027796.3
ENSG00000262305	15.6747	9.74625	10.5785	15.1214	ENSG00000262305	SERF1B
ENSG00000262306	0	0	0	0	ENSG00000262306	CCL24
ENSG00000262309	10.8458	8.47816	6.12062	5.88644	ENSG00000262309	TMEM120A
ENSG00000262315	0.0673525	0.0323857	0	0.0366268	ENSG00000262315	OR8U8
ENSG00000262316	0.54461	0.173519	0.314679	0.294435	ENSG00000262316	AC025283.1
ENSG00000262317	0	0	0	0.0366664	ENSG00000262317	LAIR2
ENSG00000262318	0	0	0	0	ENSG00000262318	CTB-96E2.2
ENSG00000262320	0.60342	3.00762	2.21399	1.04E-09	ENSG00000262320	LILRA6
ENSG00000262321	3.36204	0.828816	1.42784	1.79429	ENSG00000262321	SRRM3
ENSG00000262322	0.274161	0.179306	0.276743	0.432826	ENSG00000262322	MTND4P34
ENSG00000262324	0.942934	1.10111	0.695241	0.739533	ENSG00000262324	CH17-93H22.3
ENSG00000262325	0.130213	0.219386	0.135032	0.384115	ENSG00000262325	MMP13
ENSG00000262327	8.06733	10.9772	10.652	9.3074	ENSG00000262327	AGK
ENSG00000262329	1.7071	3.4412	2.66344	2.44994	ENSG00000262329	NLRP2
ENSG00000262330	0.0816378	0.235406	0	0.442537	ENSG00000262330	AC012616.1
ENSG00000262331	0	0	0	0.354648	ENSG00000262331	RP11-1151M9.3
ENSG00000262333	1.28336	0.497	1.36763	0.999338	ENSG00000262333	HNRNPA1P16
ENSG00000262334	1.39758	2.36404	2.29808	3.74647	ENSG00000262334	RPH3AL
ENSG00000262335	0	0	0	0	ENSG00000262335	KIR3DL3
ENSG00000262341	2.17109	3.04378	2.97301	2.82107	ENSG00000262341	U73169.2
ENSG00000262347	0	0	0	0	ENSG00000262347	KRTAP1-3
ENSG00000262348	3.73612	2.69337	3.04044	3.60671	ENSG00000262348	RDH13
ENSG00000262351	0	0.024544	0	0	ENSG00000262351	OR13A1
ENSG00000262353	0	0	0	0	ENSG00000262353	RP11-147B8.1
ENSG00000262363	0	0	0.0384919	0	ENSG00000262363	CTC-550B14.1
ENSG00000262364	0.341828	0	0.406368	0	ENSG00000262364	RP11-665A22.1
ENSG00000262366	0.495018	0	0	0	ENSG00000262366	NDUFA3P6
ENSG00000262369	0.24196	1.44158	1.4946	3.86882	ENSG00000262369	CNOT3
ENSG00000262373	0	0	0	0	ENSG00000262373	RP11-444K7.8
ENSG00000262374	0.462329	0.801689	0.971503	1.40246	ENSG00000262374	RP11-483G21.3
ENSG00000262376	0	0	0	0	ENSG00000262376	KRTAP2-5P
ENSG00000262377	9.82809	18.5335	20.6267	9.32684	ENSG00000262377	TTC12
ENSG00000262378	8.93193	24.0858	1.71051	3.48756	ENSG00000262378	LY6K
ENSG00000262379	0.271046	1.75477	1.57694	0.268997	ENSG00000262379	TAS2R31
ENSG00000262381	0.20036	0.0962443	0	0.742	ENSG00000262381	MTATP6P24
ENSG00000262382	0	0	0.0384919	0	ENSG00000262382	CTC-550B14.1
ENSG00000262383	0.0111762	0.0215246	0	0	ENSG00000262383	LILRA3
ENSG00000262384	0	0	0	0	ENSG00000262384	AC034268.2
ENSG00000262386	0	0	0.0384919	0	ENSG00000262386	CTC-550B14.1
ENSG00000262388	0	0	0	0	ENSG00000262388	AC138783.13
ENSG00000262390	0	0	0	0	ENSG00000262390	AC098784.1
ENSG00000262393	0	1.60601	0.604398	0.952046	ENSG00000262393	TAS2R19

ENSG00000262396	6.91909	10.7667	7.35604	8.33192	ENSG00000262396	RP11-785H5.1
ENSG00000262397	0.745233	1.657	1.50797	2.75599	ENSG00000262397	LILRB4
ENSG00000262398	7.91381	8.66338	10.3284	19.7138	ENSG00000262398	AC005086.6
ENSG00000262399	0	0	0	0	ENSG00000262399	RP11-42L13.2
ENSG00000262400	0.570061	0.270729	0.244685	0.298228	ENSG00000262400	AL590084.3
ENSG00000262401	0	0.0443425	0	0	ENSG00000262401	XAGE1B
ENSG00000262402	0	1.99279	1.97237	1.4907	ENSG00000262402	AC090617.3
ENSG00000262406	0.121015	0.291544	0.105423	0.464539	ENSG00000262406	MMP12
ENSG00000262407	5.57535	14.8135	13.4245	21.3827	ENSG00000262407	CCDC125
ENSG00000262408	0	0	2.71951	0	ENSG00000262408	AC015912.2
ENSG00000262414	0	0	0.107761	0.129749	ENSG00000262414	AC010492.4
ENSG00000262416	0	0	0.0384919	0	ENSG00000262416	CTC-550B14.1
ENSG00000262418	3.28267	6.26293	5.04529	8.55509	ENSG00000262418	PTPRC
ENSG00000262421	0	0.114076	0.420376	0.216958	ENSG00000262421	TRIM74
ENSG00000262422	0	0	0	0	ENSG00000262422	AC009892.2
ENSG00000262423	0	0	0	0	ENSG00000262423	AC008746.10
ENSG00000262424	0	0	0.032812	0	ENSG00000262424	KRT18P48
ENSG00000262426	0	0.0570873	0.328356	0.0814314	ENSG00000262426	AC012314.19
ENSG00000262430	13.9514	3.86813	5.63883	3.16433	ENSG00000262430	EPS8L1
ENSG00000262431	0.135586	0.693678	0.612637	0.44682	ENSG00000262431	TAS2R63P
ENSG00000262435	2.02392	4.79055	3.1705	2.69189	ENSG00000262435	AC215219.2
ENSG00000262436	0	0	0.0384919	0	ENSG00000262436	CTC-550B14.1
ENSG00000262437	0	0	0	0	ENSG00000262437	AC098784.1
ENSG00000262438	0	0	0	0	ENSG00000262438	OR5G1P
ENSG00000262439	0	0	0	0	ENSG00000262439	KIR3DL3
ENSG00000262446	5.25346	6.0967	6.95089	7.2626	ENSG00000262446	GBA
ENSG00000262447	23.842	16.2692	18.5598	9.49109	ENSG00000262447	TNFAIP1
ENSG00000262448	3.08297	4.51726	4.54065	3.36711	ENSG00000262448	MARCH8
ENSG00000262452	0.0862014	0.0425588	0.195627	0.153447	ENSG00000262452	SPC25
ENSG00000262455	0	0	0	0	ENSG00000262455	RP1-232L24.4
ENSG00000262457	0.00591224	0.0414758	0	0	ENSG00000262457	NLRP7
ENSG00000262459	0.103582	0.23349	0.21	0.409097	ENSG00000262459	WBSCR28
ENSG00000262460	0	0	0	0	ENSG00000262460	AC008746.9
ENSG00000262461	1.31166	3.63058	3.61302	5.48428	ENSG00000262461	SPDYE9P
ENSG00000262462	0.059703	0.108637	0.0554507	0.139663	ENSG00000262462	LILRA1
ENSG00000262463	0	0	0	0	ENSG00000262463	KIR2DP1
ENSG00000262467	13.9514	3.86813	5.63883	3.16433	ENSG00000262467	EPS8L1
ENSG00000262470	0.455149	0.655415	0.496255	2.07424	ENSG00000262470	TVP23CP2
ENSG00000262471	0.549708	1.46204	0.393085	0	ENSG00000262471	AC009171.1
ENSG00000262472	25.1017	53.1423	15.1033	27.331	ENSG00000262472	KPNA2
ENSG00000262473	32.446	44.8678	52.0171	36.0542	ENSG00000262473	GART
ENSG00000262474	6.7033	3.28059	1.74779	0	ENSG00000262474	RP11-1275J23.3
ENSG00000262480	1.13713	2.58154	2.57449	2.23144	ENSG00000262480	SAMD11P1
ENSG00000262481	1.74042	0.382013	1.41357	1.24614	ENSG00000262481	TMEM256-PLSCR3
ENSG00000262484	0.757317	0.832116	0.986061	0.555391	ENSG00000262484	CCER2
ENSG00000262485	5.99091	3.76077	4.78971	1.98391	ENSG00000262485	TUSC2
ENSG00000262486	0.00527241	0.0101636	0.00924141	0.017363	ENSG00000262486	LILRP2
ENSG00000262488	0	0	0.0458247	0.114944	ENSG00000262488	AC133065.3
ENSG00000262489	16.3902	22.3716	19.3776	26.3149	ENSG00000262489	RRAS2
ENSG00000262492	0	0	0	0.20292	ENSG00000262492	AC104581.2
ENSG00000262494	0	0	0	0.135112	ENSG00000262494	CU467816.1
ENSG00000262495	0.403904	0.654726	0.189957	0.463769	ENSG00000262495	AC012146.2
ENSG00000262497	0.0937013	0	0	0	ENSG00000262497	FAM187B2P
ENSG00000262499	3.42521	2.46109	1.20825	0.890006	ENSG00000262499	WBSCR27

ENSG00000262500	0	0	0	0	ENSG00000262500	MAPK8IP1P1
ENSG00000262501	0	0	1.45543	0	ENSG00000262501	PPIHP1
ENSG00000262502	0.24079	0.1733	0.417329	0.517893	ENSG00000262502	RP11-641C17.3
ENSG00000262503	0.74032	1.68944	3.52839	1.90178	ENSG00000262503	AC027763.1
ENSG00000262504	0	0	0	0	ENSG00000262504	RP11-536P16.2
ENSG00000262505	0	0.0652249	0.0442213	0.0556408	ENSG00000262505	ASIC5
ENSG00000262506	5.69504	7.00381	9.18764	8.24352	ENSG00000262506	C11orf57
ENSG00000262508	0	0	0	0	ENSG00000262508	RP1-232L24.2
ENSG00000262509	3.06042	2.56584	5.62592	5.39221	ENSG00000262509	BLNK
ENSG00000262511	13.1758	12.1372	13.6374	10.9152	ENSG00000262511	RAD17
ENSG00000262512	0	0	0.0716621	0.171839	ENSG00000262512	KRTAP9-4
ENSG00000262515	2.57627	0.0629744	0.360315	0.391909	ENSG00000262515	LPHN3
ENSG00000262516	0.959009	1.76354	1.13067	3.04462	ENSG00000262516	AC007151.1
ENSG00000262518	0	0	0.148046	0.36945	ENSG00000262518	AC090079.2
ENSG00000262519	0	0	0	0	ENSG00000262519	TXNP4
ENSG00000262520	0.0947525	0.27943	0.523282	0.788594	ENSG00000262520	KRTAP4-16
ENSG00000262523	32.9709	18.5281	17.9815	9.23128	ENSG00000262523	ENDOD1
ENSG00000262525	0.094057	0.748871	0.222503	0.556636	ENSG00000262525	TAS2R46
ENSG00000262526	0	0	0	0	ENSG00000262526	AC120057.3
ENSG00000262532	0.268074	0.259554	0.289958	1.25766	ENSG00000262532	FKBP6
ENSG00000262535	0.0470206	0.0963031	0.0997123	0.0508468	ENSG00000262535	OR5G5P
ENSG00000262536	0	0	0	0	ENSG00000262536	AC192820.1
ENSG00000262539	0	0	0	0.238922	ENSG00000262539	AC005829.2
ENSG00000262540	0	0	0.226499	1.10436	ENSG00000262540	RP11-725K16.5
ENSG00000262542	0	0.0192078	0	0.0217489	ENSG00000262542	KRTAP29-1
ENSG00000262543	0.298819	0.287473	0.195449	0.243008	ENSG00000262543	SMIM28
ENSG00000262544	0	0	0	0	ENSG00000262544	OR8I1P
ENSG00000262548	0.00527241	0.0101636	0.00924141	0.017363	ENSG00000262548	LILRP2
ENSG00000262550	0	0	0	0	ENSG00000262550	OR8L1P
ENSG00000262552	0.436208	0.175385	0	0.0121534	ENSG00000262552	ALOX5
ENSG00000262554	1.24607	0	0	0	ENSG00000262554	AC004232.1
ENSG00000262555	0	0	0	0	ENSG00000262555	AC011515.2
ENSG00000262556	0	0	0.0108934	0	ENSG00000262556	KIR2DL1
ENSG00000262560	0	0	0.0536753	0.0501382	ENSG00000262560	AC018512.1
ENSG00000262561	0	0.671282	0	0.718832	ENSG00000262561	AC136932.1
ENSG00000262562	2.52462	5.19836	3.53648	4.98295	ENSG00000262562	ZNF85
ENSG00000262563	0.172329	0.181488	0.279031	0.453639	ENSG00000262563	G6PC2
ENSG00000262564	0.751243	1.03305	0.415189	1.61818	ENSG00000262564	C10orf82
ENSG00000262565	0.188731	0.370128	0.290832	0.623178	ENSG00000262565	PCDHB11
ENSG00000262566	0	0	0	0	ENSG00000262566	AL355375.2
ENSG00000262569	28.5744	27.5319	20.5744	13.5033	ENSG00000262569	POR
ENSG00000262572	1.72239	0.923682	1.12912	0.819366	ENSG00000262572	CBX8
ENSG00000262573	0	0	0	0	ENSG00000262573	KRTAP9-2
ENSG00000262575	0.078525	0	0	0.163728	ENSG00000262575	AC009892.5
ENSG00000262576	1.15923	0.593925	1.25127	0.879582	ENSG00000262576	PCDHGA4
ENSG00000262577	26.8923	39.9798	29.3645	36.4712	ENSG00000262577	ALG9
ENSG00000262578	8.36814	11.8239	7.28214	8.6939	ENSG00000262578	ZNF737
ENSG00000262581	0	0	0.154443	0.422939	ENSG00000262581	RP11-536P16.2
ENSG00000262582	0	0	0	0	ENSG00000262582	CU234142.1
ENSG00000262583	2.16971	4.75652	3.49368	2.90891	ENSG00000262583	AC009163.5
ENSG00000262586	0	0	0	0	ENSG00000262586	AC009892.2
ENSG00000262587	0.375045	1.07969	2.06927	0.918543	ENSG00000262587	AC133552.2
ENSG00000262589	0	0	0	0.434001	ENSG00000262589	NSUN5
ENSG00000262591	0	0	0	0	ENSG00000262591	TBC1D3P7

ENSG00000262594	0	0.0303879	0.0274648	0.068774	ENSG00000262594	KRTAP9-9
ENSG00000262595	1.34178	2.67563	2.01916	2.03304	ENSG00000262595	MRM1
ENSG00000262596	0.025291	0	0.0248213	0	ENSG00000262596	KIR2DS1
ENSG00000262599	3.40166	2.84355	3.68908	2.89477	ENSG00000262599	KIAA1147
ENSG00000262600	1.62572	0.621015	0.407007	0.446628	ENSG00000262600	C11orf52
ENSG00000262601	2.67129	4.51821	3.49763	9.14567	ENSG00000262601	CTC-786C10.1
ENSG00000262602	11.7622	24.2333	22.5489	29.8783	ENSG00000262602	LENG8
ENSG00000262604	0	0	0	0	ENSG00000262604	LILRP1
ENSG00000262605	0	0	0.369892	0.958661	ENSG00000262605	MRPS36
ENSG00000262607	0.172798	0.250039	0.156796	0.203823	ENSG00000262607	IQSEC3
ENSG00000262609	0.16336	0.156526	0.282594	0.348492	ENSG00000262609	AC005668.1
ENSG00000262610	0	0	0	0	ENSG00000262610	LILRA5
ENSG00000262611	0	0	0	0	ENSG00000262611	OR8H1
ENSG00000262612	0.606779	0	0.677157	2.99638	ENSG00000262612	TAS2R43
ENSG00000262615	1.7071	3.4412	2.66344	2.44994	ENSG00000262615	NLRP2
ENSG00000262616	0	0	0	0	ENSG00000262616	KRTAP3-4P
ENSG00000262617	0	0.185691	0	0	ENSG00000262617	AC020766.1
ENSG00000262618	0	0	0	0	ENSG00000262618	RP11-420K14.1
ENSG00000262621	0.38363	1.82731	0.8587	0.962463	ENSG00000262621	AC025283.2
ENSG00000262623	0	1.17829	0.422306	1.00779	ENSG00000262623	AC004584.2
ENSG00000262625	0	0	0	0	ENSG00000262625	KIR3DP1
ENSG00000262627	0.0263291	0.0255814	0.0684583	0.0296561	ENSG00000262627	RP11-536P16.5
ENSG00000262628	0	0	0	0	ENSG00000262628	OR1D5
ENSG00000262630	0.392579	0	0.2036	5.51E-10	ENSG00000262630	AC012314.2
ENSG00000262631	0	0.0118584	0	0.0133071	ENSG00000262631	VN1R104P
ENSG00000262633	0.258811	0.208658	0.408715	0.378296	ENSG00000262633	AC005670.2
ENSG00000262634	1.5668	6.11148	2.68942	4.67025	ENSG00000262634	SKA1
ENSG00000262635	0.354038	0.77446	0.59702	1.85683	ENSG00000262635	TDO2
ENSG00000262636	0	0	0.387588	0.46906	ENSG00000262636	AC099489.2
ENSG00000262641	1.28042	6.45425	3.14219	0	ENSG00000262641	RP11-124L9.6
ENSG00000262642	0.634137	0.692372	1.34471	1.24815	ENSG00000262642	LILRA6
ENSG00000262645	0	0	0	0	ENSG00000262645	AC009892.9
ENSG00000262646	0.0174955	0	0.0914926	0.0380342	ENSG00000262646	AC010492.2
ENSG00000262647	0	0	0	0	ENSG00000262647	OR9G4
ENSG00000262648	0	0.509709	0.390715	1.00457	ENSG00000262648	PHBP15
ENSG00000262650	0.146865	0.566458	0.29747	0.106417	ENSG00000262650	RPL7L1P3
ENSG00000262651	0	0	0	0	ENSG00000262651	AL513043.2
ENSG00000262654	0	0.10803	0.0719334	0.060245	ENSG00000262654	SLC13A2
ENSG00000262655	1.53694	3.0099	4.44003	10.7427	ENSG00000262655	SPON1
ENSG00000262658	0	0	0	0	ENSG00000262658	AC092566.1
ENSG00000262660	0	0.00224841	0	0	ENSG00000262660	AC139530.2
ENSG00000262661	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000262661	NCR1
ENSG00000262664	22.5792	5.84901	11.4893	4.32131	ENSG00000262664	OVCA2
ENSG00000262666	4.93126	8.1277	6.27232	9.6089	ENSG00000262666	FAM189B
ENSG00000262667	3.94693	5.22492	1.56778	1.84527	ENSG00000262667	OCLN
ENSG00000262672	0.0362719	0.088256	0.0617732	0.087484	ENSG00000262672	PTCHD3
ENSG00000262673	0.044376	0.0780537	0.0681454	0.154546	ENSG00000262673	MAPK4
ENSG00000262675	0.0360044	0	0	0	ENSG00000262675	OR9G2P
ENSG00000262676	6.04835	15.0995	6.19388	4.74295	ENSG00000262676	SLC37A4
ENSG00000262680	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000262680	NCR1
ENSG00000262683	1.48062	3.06612	4.88805	4.86193	ENSG00000262683	FHIT
ENSG00000262684	7.85428	11.9814	9.1372	7.75387	ENSG00000262684	DNAJC7
ENSG00000262689	0	0	0	0.546936	ENSG00000262689	AC097374.2

ENSG00000262690	0.00591224	0.0414758	0	0	ENSG00000262690	NLRP7
ENSG00000262694	9.0146	14.2028	14.6036	15.1899	ENSG00000262694	BAZ1B
ENSG00000262696	4.32792	7.11417	6.40977	2.27802	ENSG00000262696	NSUN5P2
ENSG00000262700	0.303422	0.151062	0.211462	0.266703	ENSG00000262700	AC133552.3
ENSG00000262705	0.0485563	0	0	0	ENSG00000262705	CR392000.1
ENSG00000262706	0	0	0.0384919	0	ENSG00000262706	CTC-550B14.1
ENSG00000262708	2.26646	4.23683	2.89461	5.77407	ENSG00000262708	AC027455.1
ENSG00000262711	0.0710347	0.549948	0.160148	0.877621	ENSG00000262711	AC005077.7
ENSG00000262713	0.150042	0.523627	0.42231	1.15985	ENSG00000262713	RP11-1305N21.3
ENSG00000262715	0	0	0	0	ENSG00000262715	AC008984.7
ENSG00000262716	3.5612	7.20078	5.77662	4.32221	ENSG00000262716	TSEN34
ENSG00000262717	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000262717	NCR1
ENSG00000262722	2.41686	1.09672	0.945521	0.595574	ENSG00000262722	GPRIN2
ENSG00000262724	0.103648	0.148175	0	0.0544578	ENSG00000262724	AC008984.5
ENSG00000262726	0.066712	0.585986	0.859493	0.644447	ENSG00000262726	RP11-1174L13.2
ENSG00000262727	0.284177	0.431107	0.0259567	0.338158	ENSG00000262727	LILRB1
ENSG00000262729	0.133284	0.247489	0.256662	0.413123	ENSG00000262729	GP6
ENSG00000262730	0	0	0	0	ENSG00000262730	AC104581.3
ENSG00000262731	0	0	0	0	ENSG00000262731	AC037482.2
ENSG00000262733	0	0	0	0	ENSG00000262733	RP11-147B8.2
ENSG00000262734	0	0.313142	0.196532	0	ENSG00000262734	AC217785.2
ENSG00000262736	0.00591224	0.0414758	0	0	ENSG00000262736	NLRP7
ENSG00000262739	0	0	0	0	ENSG00000262739	PRSS2
ENSG00000262740	0.542582	0.775236	1.18151	1.9682	ENSG00000262740	PIH1D2
ENSG00000262742	1.53475	2.60892	2.38122	2.75842	ENSG00000262742	MCTP1
ENSG00000262743	0.397008	0	0	0.605267	ENSG00000262743	CICP10
ENSG00000262744	15.3129	9.60571	16.0252	5.48187	ENSG00000262744	RHBDD2
ENSG00000262747	12.0258	15.8879	14.0958	9.68859	ENSG00000262747	AMZ2
ENSG00000262748	3.48553	0	0	1.85994	ENSG00000262748	AC207056.1
ENSG00000262749	0	0.00555827	0.0022856	0.0160341	ENSG00000262749	KRTAP9-3
ENSG00000262750	0	0	0	0	ENSG00000262750	AC009892.9
ENSG00000262751	0.350864	0.319754	0	0.556616	ENSG00000262751	AC005077.5
ENSG00000262752	1.03722	2.78169	3.02404	3.78457	ENSG00000262752	AP000705.5
ENSG00000262754	0.728781	0.351035	0	0.0577029	ENSG00000262754	LILRA2
ENSG00000262755	0	0.0640255	0	0.0362098	ENSG00000262755	OR8K3
ENSG00000262759	3.25376	3.98404	3.64586	2.39459	ENSG00000262759	MRPS21P9
ENSG00000262760	0	0.903329	0.19355	1.80078	ENSG00000262760	AC006014.7
ENSG00000262762	0.635402	0.898348	1.10603	0.813901	ENSG00000262762	CBX2
ENSG00000262763	0	0	0	0	ENSG00000262763	KIR3DL3
ENSG00000262764	14.4831	21.5564	10.718	14.0354	ENSG00000262764	PPP2R1B
ENSG00000262767	0	0	0	0	ENSG00000262767	GEMIN2P1
ENSG00000262771	41.5505	36.7423	33.1949	26.796	ENSG00000262771	SSBP1
ENSG00000262773	1.0924	3.06089	1.56331	3.78326	ENSG00000262773	NOSTRIN
ENSG00000262774	0.509812	0.189804	0	0.200187	ENSG00000262774	ZNF92P2
ENSG00000262782	0.109072	0	0	0	ENSG00000262782	ATP9B
ENSG00000262784	0	0	0.034396	0.101493	ENSG00000262784	OR5T1
ENSG00000262785	0.0616161	0.0862252	0.160192	0.0772759	ENSG00000262785	PKLR
ENSG00000262788	0.788805	0	0.871163	0.312935	ENSG00000262788	UTP4
ENSG00000262795	29.6483	49.8648	19.4929	15.5602	ENSG00000262795	IFNGR2
ENSG00000262796	0.0283695	0.0546426	0.0249353	0	ENSG00000262796	OR8J1
ENSG00000262797	0.133284	0.247489	0.256662	0.413123	ENSG00000262797	GP6
ENSG00000262799	0.0321967	0.092864	0.0836896	0	ENSG00000262799	RP11-735A19.3
ENSG00000262800	0.243694	0.525942	0.442282	0.881757	ENSG00000262800	LILRA5
ENSG00000262803	0.41739	1.6046	0.874295	2.17117	ENSG00000262803	AL354943.1

ENSG00000262806	0.508036	0.828791	1.10703	2.11598	ENSG00000262806	FCAR
ENSG00000262808	0.0348967	0	0	0.0379334	ENSG00000262808	KRTAP1-1
ENSG00000262809	1.0633	1.90773	1.81877	2.49982	ENSG00000262809	WTAPP1
ENSG00000262811	1.7071	3.4412	2.66344	2.44994	ENSG00000262811	NLRP2
ENSG00000262812	15.4315	35.218	25.9952	17.3693	ENSG00000262812	HYOU1
ENSG00000262814	4.89922	5.89303	11.0448	7.68159	ENSG00000262814	MRPL12
ENSG00000262818	0	0	0.35428	0	ENSG00000262818	AC055872.1
ENSG00000262819	0.219637	0.434342	0.391014	0.315767	ENSG00000262819	AC084033.6
ENSG00000262821	0	0	0	0	ENSG00000262821	RP11-536P16.4
ENSG00000262824	0	0	0	0	ENSG00000262824	RP11-483E23.7
ENSG00000262826	10.7193	19.5307	16.9445	18.852	ENSG00000262826	INTS3
ENSG00000262827	0.508036	0.828791	1.10703	2.11598	ENSG00000262827	FCAR
ENSG00000262828	0	0	0.396373	0	ENSG00000262828	RP11-325M4.2
ENSG00000262829	0	0	0.540102	2.93002	ENSG00000262829	AC242308.2
ENSG00000262830	0	0	0	0	ENSG00000262830	AC098784.1
ENSG00000262832	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000262832	NCR1
ENSG00000262834	0.470491	1.10518	1.3926	3.59585	ENSG00000262834	AC018720.10
ENSG00000262835	13.9514	3.86813	5.63883	3.16433	ENSG00000262835	EPS8L1
ENSG00000262840	1.68065	3.25693	3.08007	6.80721	ENSG00000262840	DNAH12
ENSG00000262841	7.39716	14.3162	10.7106	9.48697	ENSG00000262841	CDK7
ENSG00000262843	0	0	0	0	ENSG00000262843	LILRA5
ENSG00000262844	0.0302363	0.0291002	0.156591	0	ENSG00000262844	RP11-7O20.4
ENSG00000262845	0.157619	0.306264	0.270826	0.323529	ENSG00000262845	KRT40
ENSG00000262847	22.8288	25.6887	21.8568	19.9699	ENSG00000262847	MDH2
ENSG00000262849	0	0	0	0	ENSG00000262849	AC098789.1
ENSG00000262851	0	0.137675	0.11488	0.0677138	ENSG00000262851	OR5T2
ENSG00000262852	0.0621472	0	0.111457	0.0899456	ENSG00000262852	HSPB2
ENSG00000262854	0	0	0	0	ENSG00000262854	AC011515.2
ENSG00000262855	0	0.400474	0	0	ENSG00000262855	AC012146.4
ENSG00000262856	0	0	0	0.0415339	ENSG00000262856	PCGF7P
ENSG00000262858	39.5292	28.9872	29.8021	86.0617	ENSG00000262858	BPTF
ENSG00000262860	21.9097	19.958	20.2689	18.4107	ENSG00000262860	LSM14A
ENSG00000262862	0.486669	0	0	1.73518	ENSG00000262862	KRTAP2-3
ENSG00000262863	0.294268	0	0	0	ENSG00000262863	AC005488.11
ENSG00000262864	0	0	0	0	ENSG00000262864	RPS27P14
ENSG00000262866	8.01135	9.43237	11.6274	16.8596	ENSG00000262866	IFT20
ENSG00000262867	0.133284	0.247489	0.256662	0.413123	ENSG00000262867	GP6
ENSG00000262868	3.5612	7.20078	5.77662	4.32221	ENSG00000262868	TSEN34
ENSG00000262870	1.45667	3.10399	0.932903	2.64131	ENSG00000262870	CYCSP40
ENSG00000262872	0.479768	0.518223	0.685918	0.0989326	ENSG00000262872	GOLGA8G
ENSG00000262874	0.642461	0.168082	0.160795	0.611445	ENSG00000262874	C19orf84
ENSG00000262875	0.938653	1.79867	1.6146	2.21182	ENSG00000262875	CAPN5
ENSG00000262876	2.14392	5.05644	4.39013	7.51087	ENSG00000262876	AC005077.12
ENSG00000262878	13.9514	3.86813	5.63883	3.16433	ENSG00000262878	EPS8L1
ENSG00000262885	0	0	0	0	ENSG00000262885	AC135776.3
ENSG00000262886	1.7071	3.4412	2.66344	2.44994	ENSG00000262886	NLRP2
ENSG00000262887	1.77909	1.62404	2.26344	0.869953	ENSG00000262887	CU467002.1
ENSG00000262889	0.094057	0.299548	0.445005	0	ENSG00000262889	TAS2R46
ENSG00000262892	0	0	0	0	ENSG00000262892	AC013759.1
ENSG00000262895	4.75931	2.19855	8.34984	4.162	ENSG00000262895	TRIM73
ENSG00000262896	0	0	0	0	ENSG00000262896	KRTAP9-4
ENSG00000262897	0.0131325	0.00949554	0.0125962	0.044165	ENSG00000262897	KIR3DL2
ENSG00000262900	0.059703	0.108637	0.0554507	0.139663	ENSG00000262900	LILRA1
ENSG00000262902	0	0.242027	0	0.120257	ENSG00000262902	MTCO1P40

ENSG00000262904	0	0.143877	0	0.326409	ENSG00000262904	TMPOP2
ENSG00000262906	0	0	0	0	ENSG00000262906	RP11-536P16.4
ENSG00000262907	0.0279804	0.0980381	0.0830385	0.184153	ENSG00000262907	KIF5C
ENSG00000262908	0.812112	2.82215	1.35997	0.41823	ENSG00000262908	TAS2R30
ENSG00000262909	38.4465	50.3841	17.1627	92.1013	ENSG00000262909	SMURF2
ENSG00000262911	0.538707	0.284838	0.330181	0.16623	ENSG00000262911	DNAJC28
ENSG00000262913	0	0	0	0	ENSG00000262913	AC098789.1
ENSG00000262915	0	1.4569	0.890269	1.04686	ENSG00000262915	RP11-1280N14.3
ENSG00000262917	2.55608	17.0266	10.3794	12.0682	ENSG00000262917	POLG2
ENSG00000262918	0	0.00734616	0.00674381	0.0166242	ENSG00000262918	ZNF729
ENSG00000262919	7.81164	4.77901	2.891	0.761578	ENSG00000262919	FAM58A
ENSG00000262923	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000262923	NCR1
ENSG00000262924	5.34796	8.35321	7.52766	12.8133	ENSG00000262924	KIAA0355
ENSG00000262928	7.60967	13.6939	9.04973	15.6242	ENSG00000262928	ZNF43
ENSG00000262929	1.7071	3.4412	2.66344	2.44994	ENSG00000262929	NLRP2
ENSG00000262932	0	0.978575	0.883324	2.73172	ENSG00000262932	RP11-124L9.3
ENSG00000262933	1.35559	2.51769	0.822785	5.40316	ENSG00000262933	CALCA
ENSG00000262935	3.74555	7.23554	10.579	12.8347	ENSG00000262935	AC005086.7
ENSG00000262936	0.233848	0.244949	0.286938	0.32704	ENSG00000262936	LAIR1
ENSG00000262938	0	0.0285179	0.025876	0.0299501	ENSG00000262938	C21orf62
ENSG00000262939	0	0	0	0	ENSG00000262939	OR5G4P
ENSG00000262941	0.428706	0	0	0	ENSG00000262941	AC010518.3
ENSG00000262942	0	0	0	0	ENSG00000262942	ZNF676
ENSG00000262943	17.451	24.8031	38.8836	21.9762	ENSG00000262943	ALOX12P2
ENSG00000262946	0	0	0	0	ENSG00000262946	KRTAP9-11P
ENSG00000262947	5.9857	6.44069	3.76178	6.84619	ENSG00000262947	ABHD11
ENSG00000262948	6.51878	5.35984	5.1432	5.49502	ENSG00000262948	RPL23AP64
ENSG00000262953	0	0	0.0431024	0.108264	ENSG00000262953	EIF4A1P9
ENSG00000262958	0	0.791479	0	0	ENSG00000262958	RPL37AP8
ENSG00000262959	1.14484	3.08645	2.66925	2.39266	ENSG00000262959	RPL23AP86
ENSG00000262960	0	0.184204	0.132615	0	ENSG00000262960	NCF1C
ENSG00000262961	0	0.23467	0	0.176469	ENSG00000262961	AC006236.1
ENSG00000262962	0.197018	0.0763174	0.240706	0.271455	ENSG00000262962	KARSP3
ENSG00000262964	0.0149215	0.0177657	0.0279366	0	ENSG00000262964	TRIM50
ENSG00000262968	5.35415	9.17873	11.8382	3.63456	ENSG00000262968	CYP2R1
ENSG00000262970	13.2635	29.1118	13.1541	15.9256	ENSG00000262970	ACER3
ENSG00000262974	0.213754	0.537595	1.3978	1.40107	ENSG00000262974	AC136618.2
ENSG00000262978	0	0	0	0	ENSG00000262978	HSPB2-C11orf52
ENSG00000262980	0.0648262	0	0	0	ENSG00000262980	OR52L2P
ENSG00000262982	3.73612	2.69337	3.04044	3.60671	ENSG00000262982	RDH13
ENSG00000262984	0.0618943	0.0873047	0.0457377	0	ENSG00000262984	NCF1B
ENSG00000262985	0.284177	0.431107	0.759044	0.338158	ENSG00000262985	LILRB1
ENSG00000262986	6.91909	10.7667	7.35604	8.33192	ENSG00000262986	SMIM10L1
ENSG00000262987	0	0	0	0	ENSG00000262987	RP11-520H11.1
ENSG00000262988	116.578	14.7248	6.20021	13.0608	ENSG00000262988	CLDN4
ENSG00000262990	0	0	0	0	ENSG00000262990	AC004706.2
ENSG00000262991	0	0	0	0	ENSG00000262991	CU457734.1
ENSG00000262993	33.3889	2.59849	0	2.66407	ENSG00000262993	KRT31
ENSG00000262994	0	0.0900378	0	0	ENSG00000262994	AC217323.1
ENSG00000263000	0	0	0	0	ENSG00000263000	ACTL9
ENSG00000263001	0	0	3.43871	10.9637	ENSG00000263001	GTF2I
ENSG00000263002	7.34951	7.32305	10.6437	12.5961	ENSG00000263002	ZNF234
ENSG00000263003	1.50484	2.99661	3.53356	2.83855	ENSG00000263003	AC008746.5
ENSG00000263005	6.14637	7.01161	5.912	6.24327	ENSG00000263005	RASSF1

ENSG00000263006	2.10774	1.51606	1.54764	0.885105	ENSG00000263006	ROCK1P1
ENSG00000263007	18.4616	3.01475	5.31211	6.6403	ENSG00000263007	CRYAB
ENSG00000263008	7.91905	2.31723	5.38656	1.13455	ENSG00000263008	WBSCR16
ENSG00000263012	0.0763793	0.160854	0.033048	0.0218248	ENSG00000263012	KRT33B
ENSG00000263014	0	0	0.0770968	0.432101	ENSG00000263014	ATP6V1G3
ENSG00000263017	0.880452	3.07251	4.74934	11.0134	ENSG00000263017	AC036164.1
ENSG00000263020	0	0	0	0	ENSG00000263020	AL662899.3
ENSG00000263021	0.107233	0.270673	0.190263	0.319057	ENSG00000263021	LILRB5
ENSG00000263022	0.414538	0.151937	0.120172	0.402665	ENSG00000263022	KRT37
ENSG00000263024	12.1127	15.5984	7.06571	13.8636	ENSG00000263024	STX1A
ENSG00000263025	0	0	0	0	ENSG00000263025	AC009892.9
ENSG00000263026	0.00591224	0.0414758	0	0	ENSG00000263026	NLRP7
ENSG00000263027	0	0	0.0124249	0.0198593	ENSG00000263027	KIR2DL3
ENSG00000263028	0.193295	0.560465	0.363731	1.00266	ENSG00000263028	TAS2R19
ENSG00000263029	0	0	0.246991	0.876617	ENSG00000263029	AC136624.4
ENSG00000263030	6.90641	6.48352	5.20337	7.25698	ENSG00000263030	CDC42EP5
ENSG00000263031	2.67156	4.96934	3.79857	3.37823	ENSG00000263031	GIN1
ENSG00000263032	10.4274	8.13448	5.83689	7.07035	ENSG00000263032	DLAT
ENSG00000263035	3.61381	7.67941	6.34101	13.3488	ENSG00000263035	RP11-124L9.1
ENSG00000263037	0.0566686	0.0141613	0.0404738	0.0282926	ENSG00000263037	MTX1P1
ENSG00000263040	5.30205	10.8804	11.1669	10.4783	ENSG00000263040	PRR4
ENSG00000263042	0.0178741	0.331303	0.241532	0.247742	ENSG00000263042	WEE2
ENSG00000263043	22.9953	12.5783	22.4479	5.47889	ENSG00000263043	MARVELD2
ENSG00000263044	12.133	14.8199	14.9051	14.6171	ENSG00000263044	NSUN5P1
ENSG00000263045	7.2164	18.466	28.3459	10.8307	ENSG00000263045	AC090286.3
ENSG00000263046	10.8971	12.8452	14.0433	15.6554	ENSG00000263046	CEP95
ENSG00000263049	20.9602	17.935	15.7131	11.79	ENSG00000263049	TBL2
ENSG00000263052	1.42137	1.26386	0.685427	8.52053	ENSG00000263052	HSPA12A
ENSG00000263053	0.965289	0.821624	0.515174	1.72313	ENSG00000263053	RP11-1055B8.6
ENSG00000263054	6.72781	10.1063	9.9895	15.292	ENSG00000263054	CU467002.2
ENSG00000263055	0	0	0	0	ENSG00000263055	TRIAP1P1
ENSG00000263057	0.0822056	0	0.0143206	0.0181861	ENSG00000263057	KRT20
ENSG00000263061	0.745233	1.657	1.89996	2.75599	ENSG00000263061	LILRB4
ENSG00000263062	3.92312	5.48427	7.72174	10.2318	ENSG00000263062	NAIP
ENSG00000263064	0	0	0.244694	0.205226	ENSG00000263064	AC118758.1
ENSG00000263066	0.00527241	0.0101636	0.00924141	0.017363	ENSG00000263066	LILRP2
ENSG00000263067	16.4054	23.3751	31.5995	32.7688	ENSG00000263067	STAG3L3
ENSG00000263068	0.00591224	0.0414758	0	0	ENSG00000263068	NLRP7
ENSG00000263070	0	0	0	0	ENSG00000263070	AC019322.1
ENSG00000263071	0.151135	0.469027	0.481014	0.242542	ENSG00000263071	CFL1P5
ENSG00000263074	3.44938	5.30755	6.10137	10.7123	ENSG00000263074	ARSG
ENSG00000263076	0.265647	4.94039	6.01461	6.13855	ENSG00000263076	RPS9
ENSG00000263077	121.651	115.295	66.8261	92.6959	ENSG00000263077	DDX5
ENSG00000263083	0.505397	1.88944	0.933925	2.38092	ENSG00000263083	AC018630.4
ENSG00000263085	1.32275	1.51197	1.23361	1.55384	ENSG00000263085	C17orf58
ENSG00000263090	0	0	0	0	ENSG00000263090	KRTAP9-2
ENSG00000263091	0.00255968	0.00842366	0.00773467	0.00704228	ENSG00000263091	KRTAP2-4
ENSG00000263092	0	0	0	0	ENSG00000263092	VN1R105P
ENSG00000263093	14.4311	18.4772	23.365	9.71196	ENSG00000263093	IFRD2
ENSG00000263097	0.406569	0.794118	0.450554	1.72035	ENSG00000263097	TAS2R31
ENSG00000263100	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000263100	NCR1
ENSG00000263101	0	0	1.32E-09	0	ENSG00000263101	KRTAP3-3
ENSG00000263102	0	0	1.75576	1.76128	ENSG00000263102	CTC-352P4.1

ENSG00000263103	0	0	0	0	ENSG00000263103	KRTAP9-10P
ENSG00000263104	0	0	0	0	ENSG00000263104	AC005102.1
ENSG00000263107	0	0	0	0	ENSG00000263107	AC025627.2
ENSG00000263108	0.406169	0.744798	0.815275	1.20563	ENSG00000263108	LILRB4
ENSG00000263109	2.75272	3.61728	6.02456	5.43789	ENSG00000263109	TTYH1
ENSG00000263112	0	0	0	0	ENSG00000263112	AC008984.7
ENSG00000263113	11.891	35.2323	32.5973	49.3308	ENSG00000263113	RP11-124L9.2
ENSG00000263114	0.0482857	0.233135	0.142609	0.324907	ENSG00000263114	AC079953.2
ENSG00000263115	0	0	0	0	ENSG00000263115	KRTAP9-10P
ENSG00000263118	0	0	0	0	ENSG00000263118	RP1-232L24.1
ENSG00000263125	0	0	0.274978	0	ENSG00000263125	AC005951.1
ENSG00000263127	0.0520901	0.0251961	0	0	ENSG00000263127	RPL4P5
ENSG00000263129	0	0	0.0508766	0.03667	ENSG00000263129	OR5G3
ENSG00000263136	5.0345	6.74515	6.2617	7.60979	ENSG00000263136	PAGR1
ENSG00000263138	5.21042	5.44894	7.23279	2.02796	ENSG00000263138	MEGF11
ENSG00000263140	1.19986	1.99328	2.09467	2.74547	ENSG00000263140	C21orf62-AS1
ENSG00000263141	10.7618	17.9052	16.894	16.479	ENSG00000263141	PAXBP1
ENSG00000263142	1.9554	3.16711	3.26933	2.87297	ENSG00000263142	LRRC37A17P
ENSG00000263145	0	0	0	0	ENSG00000263145	KIR2DP1
ENSG00000263148	0.254553	0.470077	0.436185	0.673166	ENSG00000263148	ATP2B3
ENSG00000263149	0.078525	0	0	0.163728	ENSG00000263149	AC009892.5
ENSG00000263150	0	0	0	0	ENSG00000263150	OR8J2
ENSG00000263151	8.73537	6.30907	8.51349	6.10502	ENSG00000263151	BCL7B
ENSG00000263153	0	0	0	0	ENSG00000263153	AC008984.7
ENSG00000263155	3.58E-06	1.2866	1.14124	0	ENSG00000263155	MYZAP
ENSG00000263156	30.3288	25.9207	19.1129	25.0813	ENSG00000263156	GNAI2
ENSG00000263157	1.50484	2.99661	3.53356	2.83855	ENSG00000263157	AC008746.5
ENSG00000263158	0	0.578065	0.0765797	0.111705	ENSG00000263158	AC018630.5
ENSG00000263160	15.5369	20.0521	6.1952	11.7352	ENSG00000263160	TMEM50B
ENSG00000263162	13.9859	20.4525	28.0022	38.2527	ENSG00000263162	HERC2
ENSG00000263163	0.874339	3.67626	1.66539	2.15725	ENSG00000263163	SLC27A3
ENSG00000263166	0.520113	5.31468	0	0.611376	ENSG00000263166	CU457734.2
ENSG00000263168	0.00591224	0.0414758	0	0	ENSG00000263168	NLRP7
ENSG00000263169	0	0	0	0	ENSG00000263169	RP11-1E11.1
ENSG00000263173	0	0	0.0384919	0	ENSG00000263173	CTC-550B14.1
ENSG00000263175	0	0	0	0	ENSG00000263175	KIR2DL2
ENSG00000263177	0.196941	0.441959	0.547634	0.238379	ENSG00000263177	MTND1P8
ENSG00000263179	0.0710393	0	0	0	ENSG00000263179	HNRNPCP4
ENSG00000263180	0	0.0118584	0	0.0133071	ENSG00000263180	VN1R104P
ENSG00000263181	1.40113	2.56899	3.10374	2.44341	ENSG00000263181	CYP2D7
ENSG00000263183	0.029892	0.0866965	0.148272	0.0748208	ENSG00000263183	ARMC4P1
ENSG00000263184	0.0131325	0.00949554	0.0125962	0.044165	ENSG00000263184	KIR3DL2
ENSG00000263185	17.8315	13.8003	10.3096	9.71797	ENSG00000263185	TEX2
ENSG00000263186	0.0375269	0.197095	0.0809831	0.122208	ENSG00000263186	KRTAP16-1
ENSG00000263188	0	0	0.845031	0	ENSG00000263188	CDH12P4
ENSG00000263189	0.394143	0.561214	0.17161	0.508928	ENSG00000263189	AC023934.1
ENSG00000263192	17.5497	22.0935	22.2968	28.065	ENSG00000263192	CCDC84
ENSG00000263194	2.3006	4.08715	1.71402	1.12511	ENSG00000263194	THEM6
ENSG00000263196	0	0	0	0	ENSG00000263196	MTND3P13
ENSG00000263197	0.157858	0	0	0	ENSG00000263197	CHCHD2P2
ENSG00000263199	0	0	0	0	ENSG00000263199	AC005951.2
ENSG00000263202	0.901703	0.0570873	0	1.46576	ENSG00000263202	AC012314.19
ENSG00000263203	3.71565	2.93638	3.30327	0.985677	ENSG00000263203	CHTF8
ENSG00000263204	0	0	0	0	ENSG00000263204	RP11-1437A8.7

ENSG00000263206	0	0	0	0	ENSG00000263206	KYNUP3
ENSG00000263208	0	0	0.0108934	0	ENSG00000263208	KIR2DL1
ENSG00000263209	2.65595	4.12034	7.53407	12.6733	ENSG00000263209	OR2K2P
ENSG00000263211	0	0	0	0.0630897	ENSG00000263211	OR2Z1
ENSG00000263213	0	0	0	0	ENSG00000263213	PHBP5
ENSG00000263216	0.23394	0.38731	0.32465	0.694744	ENSG00000263216	AC009892.10
ENSG00000263219	0.634969	1.57096	1.12065	1.74445	ENSG00000263219	AC087742.1
ENSG00000263221	0	0	0.0193088	0	ENSG00000263221	LILRP1
ENSG00000263222	0	0	0	0	ENSG00000263222	CU457734.3
ENSG00000263224	0	0	0.107761	0.129749	ENSG00000263224	AC010492.4
ENSG00000263225	0.205115	0.445277	0.578343	0.445468	ENSG00000263225	SEBOX
ENSG00000263226	5.97855	7.87627	7.0929	16.7336	ENSG00000263226	CLIP2
ENSG00000263227	0.101061	0.151841	0.205075	0.422355	ENSG00000263227	AC005077.14
ENSG00000263228	0	0	0	0	ENSG00000263228	RP11-44D15.6
ENSG00000263229	0	3.50E-08	0	1.49E-08	ENSG00000263229	KRTAP4-11
ENSG00000263231	0	0	0	0	ENSG00000263231	AC217785.3
ENSG00000263232	0.0385164	0	0	0	ENSG00000263232	ATP5A1P3
ENSG00000263233	0.025291	0	0.0248213	0	ENSG00000263233	KIR2DS2
ENSG00000263236	0	0.0276239	0.0245948	0	ENSG00000263236	KRTAP4-12
ENSG00000263238	1.40907	1.84426	2.00618	1.97625	ENSG00000263238	CTSO
ENSG00000263239	0.133284	0.247489	0.256662	0.413123	ENSG00000263239	GP6
ENSG00000263240	0.229322	0.43567	0.493198	0.141489	ENSG00000263240	AC009414.1
ENSG00000263241	0.0794082	0.128535	0.330558	0.119509	ENSG00000263241	MTCYBP33
ENSG00000263242	0	0	0	0	ENSG00000263242	KRTAP1-4
ENSG00000263243	0	0	0.013232	0.0166583	ENSG00000263243	KRT12
ENSG00000263247	2.12411	7.68001	4.81855	6.35914	ENSG00000263247	PRR4
ENSG00000263249	0	0	0	0	ENSG00000263249	ZNF430
ENSG00000263251	0	0	0.0193088	0	ENSG00000263251	LILRP1
ENSG00000263252	0.0945557	0	0.0824195	0	ENSG00000263252	AC005341.1
ENSG00000263254	0.11898	0.0572962	0.113959	0.159035	ENSG00000263254	FZD9
ENSG00000263255	4.33032	8.16227	7.08387	9.18678	ENSG00000263255	ZNF486
ENSG00000263258	3.73612	2.69337	3.04044	3.60671	ENSG00000263258	RDH13
ENSG00000263260	0	0	0	0	ENSG00000263260	KIR2DP1
ENSG00000263262	0	0	0	0	ENSG00000263262	AC008746.9
ENSG00000263263	0.418453	0.740686	0.882134	1.06989	ENSG00000263263	KRTAP9-6
ENSG00000263264	0.408023	0.417889	0.43164	0.398475	ENSG00000263264	AC119396.1
ENSG00000263266	0.583448	0.113339	0.111145	0	ENSG00000263266	RPS7P1
ENSG00000263274	0	0	0.625175	0.726007	ENSG00000263274	GNG5P3
ENSG00000263277	0	0	0	0	ENSG00000263277	RP11-293B20.3
ENSG00000263282	9.41013	22.8345	24.9895	36.5359	ENSG00000263282	AC005086.8
ENSG00000263283	0.0134337	0.0388434	0.0351159	0.0443134	ENSG00000263283	RP11-1E11.2
ENSG00000263290	16.3168	10.1038	11.5246	8.22023	ENSG00000263290	SCAMP3
ENSG00000263291	0	0	0	0	ENSG00000263291	RP11-735A19.5
ENSG00000263295	13.9514	3.86813	5.63883	3.16433	ENSG00000263295	EPS8L1
ENSG00000263296	0	0	0	0	ENSG00000263296	KRTAP3-2
ENSG00000263298	0.0975044	0.0433499	0.039196	0.0642469	ENSG00000263298	ABCB11
ENSG00000263302	26.2952	27.6357	32.2329	22.2768	ENSG00000263302	TAF9
ENSG00000263303	0	0.543763	3.01E-08	0.879733	ENSG00000263303	LAIR1
ENSG00000263304	0.139422	0.309608	0.12357	0.968001	ENSG00000263304	MILR1
ENSG00000263309	22.7456	3.26158	5.62023	2.91007	ENSG00000263309	KRT23
ENSG00000263310	0.114693	0.0735194	0.132836	0.0228752	ENSG00000263310	SALL3
ENSG00000263311	0	0	0.182248	0	ENSG00000263311	AC009127.3
ENSG00000263313	0.0140023	0.340584	0.614199	9.84528	ENSG00000263313	MMP3

ENSG00000263324	0.966423	0.82364	0.64468	0.938463	ENSG00000263324	HCN3
ENSG00000263326	0.768588	0.821626	0.609706	1.19278	ENSG00000263326	AC133552.4
ENSG00000263328	0	0	0	0	ENSG00000263328	OR8K1
ENSG00000263330	1.48437	4.05368	3.24675	9.19059	ENSG00000263330	RP11-1264N5.1
ENSG00000263332	27.059	18.6102	11.6334	16.6401	ENSG00000263332	RPS9
ENSG00000263334	4.34465	4.235	3.65037	7.06945	ENSG00000263334	HIP1
ENSG00000263337	0	0.988359	0	0	ENSG00000263337	RP11-1277H1.3
ENSG00000263340	1.81231	1.09761	0.845892	2.0398	ENSG00000263340	RPL41P2
ENSG00000263341	0	0	0	0	ENSG00000263341	KRTAP17-1
ENSG00000263343	0	0	0	0	ENSG00000263343	AC009088.4
ENSG00000263344	59.0382	44.9789	48.8949	34.2798	ENSG00000263344	EIF4H
ENSG00000263346	0	0	0.0436344	0	ENSG00000263346	RP11-60C6.9
ENSG00000263349	0.0383436	0.451551	1.15089	1.99142	ENSG00000263349	AC145141.1
ENSG00000263353	0.42727	0	0.950324	0.16126	ENSG00000263353	PPIAL4A
ENSG00000263355	0.356226	1.0793	0.703433	1.24738	ENSG00000263355	AKR1B10P2
ENSG00000263366	0.00320998	0.0154325	0.0250474	0.00837705	ENSG00000263366	ABHD17AP5
ENSG00000263368	0.23184	0.300719	0.137024	0.669957	ENSG00000263368	AC069366.1
ENSG00000263369	0	0	0	0	ENSG00000263369	AC090616.1
ENSG00000263375	0	0	0	0	ENSG00000263375	AC233702.3
ENSG00000263376	18.579	35.4706	15.0314	11.594	ENSG00000263376	HIST2H2BF
ENSG00000263396	0	1.04748	0.318786	0.381896	ENSG00000263396	AP005119.1
ENSG00000263405	0	0	0.232167	0.120797	ENSG00000263405	AC068408.1
ENSG00000263417	0	0	0.353573	0	ENSG00000263417	GTSCR1
ENSG00000263428	0	0.0556668	0.254598	0	ENSG00000263428	AKR1C5P
ENSG00000263433	0	0	0	0	ENSG00000263433	AC069061.1
ENSG00000263440	0.15422	0.247701	0.289553	0.190906	ENSG00000263440	TUBAL3
ENSG00000263460	0	0	0	0	ENSG00000263460	BOD1P1
ENSG00000263461	16.4362	18.8437	17.8641	22.2089	ENSG00000263461	PIAS3
ENSG00000263464	0	0	0	0	ENSG00000263464	PPIAL4C
ENSG00000263465	9.38543	3.89334	6.6665	3.34775	ENSG00000263465	SRSF8
ENSG00000263469	0.385406	1.45957	11.0369	0.397773	ENSG00000263469	RP11-495P10.9
ENSG00000263471	0	0	0.020275	0	ENSG00000263471	AHCYP1
ENSG00000263480	2.55573	4.60078	7.39189	9.74629	ENSG00000263480	SYT15
ENSG00000263482	0	0	0	0	ENSG00000263482	ANTXRLP1
ENSG00000263483	0	0	0	0	ENSG00000263483	MTATP6P3
ENSG00000263498	0	0	0	0	ENSG00000263498	RP11-38J22.2
ENSG00000263503	0	0	0	0	ENSG00000263503	MAPK8IP1P2
ENSG00000263505	0	0.140057	0.127116	0.158201	ENSG00000263505	AP005265.1
ENSG00000263513	0.118109	0.817651	0.39766	0.380127	ENSG00000263513	FAM72C
ENSG00000263521	22.1752	39.7228	22.8871	12.7402	ENSG00000263521	RP11-38J22.2
ENSG00000263528	4.30891	7.43463	4.01265	5.26843	ENSG00000263528	IKBKE
ENSG00000263534	0.0218555	0.0349822	0.0376105	0.107764	ENSG00000263534	RP11-744H18.1
ENSG00000263535	0.291421	0.898096	2.51677	1.99842	ENSG00000263535	AC134669.1
ENSG00000263536	0.041823	0.239945	0.0728865	0.337773	ENSG00000263536	RP11-534L20.4
ENSG00000263560	0.411225	0.389893	0.880988	0.266431	ENSG00000263560	AC241377.1
ENSG00000263563	0	0	0.0370126	0	ENSG00000263563	UBBP4
ENSG00000263588	5.89802	9.75163	10.0563	11.5101	ENSG00000263588	AC091043.1
ENSG00000263604	0	0	0	0	ENSG00000263604	AC015688.1
ENSG00000263605	0	0	0	0	ENSG00000263605	BMS1P6
ENSG00000263606	0.0506368	0.430037	0.640735	1.61199	ENSG00000263606	AP000919.1
ENSG00000263620	0	0	0	0	ENSG00000263620	AC129492.3
ENSG00000263639	3.66718	3.60987	4.02814	7.2244	ENSG00000263639	MSMB

ENSG00000263647	19.969	16.0854	21.7142	8.35207	ENSG00000263647	BPTFP1
ENSG00000263648	0.846133	1.37588	1.95756	1.90591	ENSG00000263648	AC005244.1
ENSG00000263665	0.139546	0.373593	0.54686	0.193537	ENSG00000263665	CCT8P1
ENSG00000263668	0	0	0	0	ENSG00000263668	RPL7AP7
ENSG00000263682	0	0	0	0	ENSG00000263682	AP005139.1
ENSG00000263687	0	3.40706	0	1.201	ENSG00000263687	FAM72A
ENSG00000263699	1.73971	2.399	2.65276	58.3128	ENSG00000263699	LAMA4
ENSG00000263711	2.55292	6.47759	4.32719	8.44958	ENSG00000263711	AC079062.1
ENSG00000263716	0	0	0	0	ENSG00000263716	SLC25A51P2
ENSG00000263725	0	0	0	0	ENSG00000263725	AC138761.1
ENSG00000263729	2.1214	0	4.7911	0	ENSG00000263729	AC087393.1
ENSG00000263733	0	0	0	0	ENSG00000263733	AC091691.1
ENSG00000263748	0.0619599	0.119228	0.161624	0	ENSG00000263748	EXOGP1
ENSG00000263749	0.265599	0	0	0.55733	ENSG00000263749	OOSP1P2
ENSG00000263758	0	0	0.762338	0.17147	ENSG00000263758	AKR1C7P
ENSG00000263761	0	0	0.0127186	0.0160152	ENSG00000263761	GDF2
ENSG00000263771	0	0	0	0	ENSG00000263771	NKAIN1P1
ENSG00000263772	0	0	0	0	ENSG00000263772	AC017100.2
ENSG00000263773	0	0.140633	0	0.21142	ENSG00000263773	ANKRD35
ENSG00000263781	0	0	0	0	ENSG00000263781	AC024619.4
ENSG00000263788	0	0	0	0	ENSG00000263788	AC061975.2
ENSG00000263801	0	0	0	0	ENSG00000263801	AL591684.2
ENSG00000263809	0.248936	0.419144	0.344598	0.453985	ENSG00000263809	AC135178.2
ENSG00000263812	22.6203	57.3006	68.96	91.5131	ENSG00000263812	LINC00908
ENSG00000263818	1.73676	5.81256	6.56453	8.20468	ENSG00000263818	AC091178.1
ENSG00000263829	0.10783	0.306252	0.228262	0.594205	ENSG00000263829	FAM60BP
ENSG00000263846	0	0	0	0.0804405	ENSG00000263846	CIAPIN1P
ENSG00000263850	0.64138	0.23046	0.167124	0.0376837	ENSG00000263850	FCGR1B
ENSG00000263865	5.88679	2.2143	0	3.36143	ENSG00000263865	RP13-766D20.1
ENSG00000263867	0	0	0	0	ENSG00000263867	RP11-822E23.3
ENSG00000263870	0	0	0.319581	0.398966	ENSG00000263870	AC015917.1
ENSG00000263883	0.879214	1.4041	0.633917	1.54537	ENSG00000263883	EEF1DP7
ENSG00000263887	0.0538819	0.118829	0.0453886	0.216496	ENSG00000263887	AC053481.2
ENSG00000263914	0	0.227094	0.153927	0.192882	ENSG00000263914	MTND2P13
ENSG00000263915	0.0725412	0.255329	0.293455	0.421834	ENSG00000263915	RP11-325P15.2
ENSG00000263935	0	0.213529	0	0	ENSG00000263935	TOMM20P3
ENSG00000263946	0	0.591184	0.508155	0.530379	ENSG00000263946	AC015818.3
ENSG00000263956	0	0.194216	0.581264	0.316516	ENSG00000263956	NBPF11
ENSG00000263961	3.71815	8.38075	8.71633	8.84039	ENSG00000263961	C1orf186
ENSG00000263962	2.77314	9.77099	5.80132	2.38545	ENSG00000263962	AC245100.1
ENSG00000263965	5.57135	15.0148	3.41812	4.30573	ENSG00000263965	HIST2H2AB
ENSG00000263976	12.6115	66.7863	35.2804	91.1104	ENSG00000263976	YWHAEP3
ENSG00000263977	9.84457	6.18921	7.51618	6.34517	ENSG00000263977	SF3B4
ENSG00000263992	0	0	0	0.062455	ENSG00000263992	HLA-W
ENSG00000264006	0	0	0.067041	0	ENSG00000264006	AKR1C8P
ENSG00000264011	0	0	0.0182327	0	ENSG00000264011	RP11-314N2.2
ENSG00000264029	0	0	0	0.5269	ENSG00000264029	AC061975.3
ENSG00000264033	2.22184	5.91584	1.51992	5.10103	ENSG00000264033	PFN1P7
ENSG00000264040	3.06749	6.32681	9.28032	8.92449	ENSG00000264040	AC022662.1
ENSG00000264050	0.186728	0.0897467	0.243126	0.201952	ENSG00000264050	AC005412.3
ENSG00000264054	0	0	0	0	ENSG00000264054	AC113195.1
ENSG00000264057	26.7318	33.8954	37.8102	58.2193	ENSG00000264057	AC103810.1
ENSG00000264058	1.50603	1.59612	1.15247	0.704101	ENSG00000264058	AC073508.2
ENSG00000264061	0	0.357781	0	0.390809	ENSG00000264061	FGF7P1

ENSG00000264064	0	0	0	0	ENSG00000264064	AC226154.1
ENSG00000264070	0.18399	1.33451	0.455034	0.910441	ENSG00000264070	AC126544.1
ENSG00000264082	5.7606	6.74815	5.01556	2.12056	ENSG00000264082	VPS45
ENSG00000264093	0	0	0	0	ENSG00000264093	AC007448.1
ENSG00000264096	0	0	0	0	ENSG00000264096	PDLIM1P2
ENSG00000264100	0	0	0.117234	0	ENSG00000264100	HLA-T
ENSG00000264104	0.0457064	0.0226785	0.100912	0.255864	ENSG00000264104	AC114689.1
ENSG00000264116	0	0	0	0	ENSG00000264116	AC116003.1
ENSG00000264117	0.0408189	0.470813	0.141784	0.486791	ENSG00000264117	RP11-337V18.7
ENSG00000264127	0	0	0.0479898	0.0601724	ENSG00000264127	SCML2P1
ENSG00000264138	0.200008	0	0	0.636379	ENSG00000264138	AC024267.2
ENSG00000264145	0	0	0.118807	0.0426336	ENSG00000264145	AC239859.4
ENSG00000264148	0	0	0.982073	2.95243	ENSG00000264148	AC138207.3
ENSG00000264150	0.191366	0.549263	0.330631	0	ENSG00000264150	AP005136.1
ENSG00000264154	0.0769148	0.628546	0.134782	0.251845	ENSG00000264154	OR13Z1P
ENSG00000264162	1.12177	4.00438	2.84822	6.5169	ENSG00000264162	ITGA10
ENSG00000264164	0	0	0.904474	0.554914	ENSG00000264164	AC090616.2
ENSG00000264168	0.197432	0.189881	0.459575	0.468065	ENSG00000264168	MTND1P15
ENSG00000264172	0.117931	0	0.204423	0.127576	ENSG00000264172	PDLIM1P3
ENSG00000264176	0.574098	1.29046	1.32042	1.71018	ENSG00000264176	MAGOH2P
ENSG00000264179	0.861635	0.414369	0.248689	0.154614	ENSG00000264179	AP000894.1
ENSG00000264186	0	0.669413	0.335132	1.43226	ENSG00000264186	SNRPCP4
ENSG00000264187	0.340284	0.126051	0.541516	0.253968	ENSG00000264187	AC055811.2
ENSG00000264189	0.0619599	0	0.216362	0.0677512	ENSG00000264189	AP005262.1
ENSG00000264193	0.484348	0.912179	0.408176	2.46488	ENSG00000264193	AC027229.1
ENSG00000264194	0.624484	1.70304	2.35227	3.8205	ENSG00000264194	AC000003.2
ENSG00000264199	18.0404	15.4356	36.2667	26.7466	ENSG00000264199	FAM25C
ENSG00000264204	0.0316254	1.2165	0.473063	0.0876141	ENSG00000264204	AGAP7P
ENSG00000264216	0	0	0	0	ENSG00000264216	NOS2P1
ENSG00000264217	0	0	0	1.6129	ENSG00000264217	RPL35AP25
ENSG00000264230	52.1517	71.9368	74.184	10.0854	ENSG00000264230	ANXA8L1
ENSG00000264236	0	0	0.0959212	0.357455	ENSG00000264236	AC096708.1
ENSG00000264240	0	0	0	0	ENSG00000264240	CPDP1
ENSG00000264242	0.11087	0	0	0	ENSG00000264242	AC011840.4
ENSG00000264245	0	0.324658	0	0.177791	ENSG00000264245	AC233702.4
ENSG00000264246	0	0	0	0	ENSG00000264246	AP005208.1
ENSG00000264253	0.208322	1.07805	1.83054	0.594803	ENSG00000264253	FOXN1
ENSG00000264257	0	0	0	0	ENSG00000264257	KIR3DP1
ENSG00000264278	1.0478	2.00738	1.51975	2.62079	ENSG00000264278	AC027575.2
ENSG00000264281	1.20056	1.53507	2.6726	5.09262	ENSG00000264281	AC016596.1
ENSG00000264282	0.184828	0.118284	0.27768	0.26131	ENSG00000264282	FAM25E
ENSG00000264289	0	0	0	0	ENSG00000264289	AC103987.3
ENSG00000264296	0.361778	1.49501	2.06773	1.1539	ENSG00000264296	AC090666.1
ENSG00000264300	5.65537	2.1155	2.60355	2.90312	ENSG00000264300	AC090616.3
ENSG00000264307	0.0331768	0.048211	0.0577945	0.0545453	ENSG00000264307	AC016731.6
ENSG00000264311	0	1.06922	0	0.242568	ENSG00000264311	CCDC58P1
ENSG00000264315	0	0	0	0	ENSG00000264315	HNRNPA1P11
ENSG00000264316	0	0	0	0	ENSG00000264316	MTCO3P13
ENSG00000264324	0.105535	0.338825	0.294494	0.220034	ENSG00000264324	AC006030.1
ENSG00000264325	0	0	0	0	ENSG00000264325	CR925767.1
ENSG00000264335	0	0	0	0	ENSG00000264335	RP11-439A17.5
ENSG00000264337	12.9821	16.5172	12.4663	11.7393	ENSG00000264337	GPR89A
ENSG00000264343	6.49425	8.5816	10.7589	21.6099	ENSG00000264343	NOTCH2NL
ENSG00000264350	0	0	0	0	ENSG00000264350	AC090897.1

ENSG00000264359	0	0	0	0	ENSG00000264359	NEK4P2
ENSG00000264363	0.804794	0.350305	2.37237	1.32152	ENSG00000264363	HIST2H2BB
ENSG00000264364	6.43754	7.08386	8.3473	7.9221	ENSG00000264364	DYNLL2
ENSG00000264369	5.08841	10.5369	10.7664	11.9229	ENSG00000264369	TAMM41
ENSG00000264373	4.5915	0	0	4.58228	ENSG00000264373	AC005899.2
ENSG00000264388	0	0	0	0	ENSG00000264388	AC090312.1
ENSG00000264416	0.125451	1.72278	0.0821945	0.45449	ENSG00000264416	FAM72D
ENSG00000264424	0.0177087	0.0256253	0.0155514	0.225032	ENSG00000264424	MYH4
ENSG00000264431	0	0	0.0167605	0.0842905	ENSG00000264431	AC131274.2
ENSG00000264435	0	0	0	0.156256	ENSG00000264435	AC104982.3
ENSG00000264436	0	0	0	0	ENSG00000264436	DUSP8P2
ENSG00000264440	1.182	2.45831	1.65693	2.22552	ENSG00000264440	FAM229B
ENSG00000264444	0	0	0.127127	0	ENSG00000264444	AC096708.2
ENSG00000264472	0	0.137355	0	0.835317	ENSG00000264472	AC096708.3
ENSG00000264481	0	0.0311751	0	0	ENSG00000264481	RP11-337C18.4
ENSG00000264487	15.3181	8.48971	0.293017	0	ENSG00000264487	HLA-U
ENSG00000264497	0	2.5495	0	0	ENSG00000264497	AC090616.4
ENSG00000264499	0	0	0	0	ENSG00000264499	GJA8
ENSG00000264503	0	0	0	0	ENSG00000264503	AP001180.3
ENSG00000264509	0.199681	0.167395	0.09764	0.192722	ENSG00000264509	CPA1
ENSG00000264522	2.51265	1.59622	2.77427	0.603514	ENSG00000264522	OTUD7B
ENSG00000264524	2.89657	8.98324	4.89979	5.32756	ENSG00000264524	MTMR11
ENSG00000264528	5.18	24.9352	20.0874	12.2883	ENSG00000264528	TUBE1
ENSG00000264529	1.05264	2.24955	3.28683	2.72579	ENSG00000264529	AC006270.2
ENSG00000264533	0.284643	1.09089	2.06495	1.01267	ENSG00000264533	RP11-343H5.4
ENSG00000264538	17.8547	35.0563	34.0959	43.6034	ENSG00000264538	SUZ12P1
ENSG00000264543	0.658476	0	0	1.98109	ENSG00000264543	RP11-744K17.7
ENSG00000264545	1.2082	1.55011	1.62654	2.51658	ENSG00000264545	AL359922.1
ENSG00000264547	5.36874	12.9858	9.05529	14.0995	ENSG00000264547	RP11-192H23.4
ENSG00000264561	0.657966	1.39318	0.993169	1.29319	ENSG00000264561	AGAP9
ENSG00000264562	1.89067	2.21637	5.97569	2.72516	ENSG00000264562	AC138761.2
ENSG00000264564	0	0	0	0	ENSG00000264564	AC090897.2
ENSG00000264570	0.0280161	0.198116	0.198827	0.0981702	ENSG00000264570	AP005058.1
ENSG00000264586	0	0	0.0747919	0	ENSG00000264586	RP11-109G10.2
ENSG00000264606	0.196419	0.475046	0.286472	0.459274	ENSG00000264606	CTSE
ENSG00000264617	0	0.153705	0.118496	0.147807	ENSG00000264617	AC233702.5
ENSG00000264619	0.679767	1.82221	0.626018	0.33876	ENSG00000264619	MSH5-SAPCD1
ENSG00000264639	0.609855	0.951099	1.30964	2.65631	ENSG00000264639	NBPF13P
ENSG00000264644	0.0957093	0.147444	0.0416361	0.0540199	ENSG00000264644	KRT18P8
ENSG00000264651	0.148183	0.275315	0.165642	0.169526	ENSG00000264651	FAM35BP
ENSG00000264654	0.397867	0.176631	0.417903	0.138963	ENSG00000264654	CA14
ENSG00000264655	0	0	0.137055	0	ENSG00000264655	AC080112.1
ENSG00000264662	0.251638	0.9808	0.221176	1.64047	ENSG00000264662	AC126365.2
ENSG00000264663	0	0	0.0510198	0	ENSG00000264663	KRT8P34
ENSG00000264668	0.339212	0	0.573596	0.0998898	ENSG00000264668	AC138696.1
ENSG00000264683	0	0	0	0	ENSG00000264683	SSX39BP1
ENSG00000264685	0	0	0	0	ENSG00000264685	PRPF19P1
ENSG00000264689	0	0	0	0	ENSG00000264689	AC015688.2
ENSG00000264697	0	0	0	0	ENSG00000264697	AC067819.1
ENSG00000264708	1.6337	2.34456	3.84135	12.1197	ENSG00000264708	PDE4DIP
ENSG00000264714	0.187547	0.327148	0.291769	0.384881	ENSG00000264714	AP005117.1
ENSG00000264717	0.212814	0.166967	0.219576	0	ENSG00000264717	NPY4R2
ENSG00000264719	8.40735	9.33412	4.15687	3.50123	ENSG00000264719	HIST2H2BE
ENSG00000264736	0.0568188	0.0273513	0	0	ENSG00000264736	BDP1P

ENSG00000264738	0.268595	0.461995	0.498962	0.52463	ENSG00000264738	RP11-458I7.1
ENSG00000264743	0.634186	2.337	2.83699	2.33752	ENSG00000264743	DPRXP4
ENSG00000264751	2.51948	0.776379	0.164841	0.37292	ENSG00000264751	HLA-G
ENSG00000264775	0	0	0.136063	0.166737	ENSG00000264775	PPIAP14
ENSG00000264776	8.69339	12.4114	8.02934	3.83062	ENSG00000264776	GPR89B
ENSG00000264795	0	0	0	0	ENSG00000264795	AC14483.2
ENSG00000264801	0.42709	0.689629	0.655773	1.03254	ENSG00000264801	ERVFRD-3
ENSG00000264805	0	0	0	0	ENSG00000264805	RP11-666A1.4
ENSG00000264806	6.7719	11.8752	14.1248	13.8126	ENSG00000264806	POLR3C
ENSG00000264811	0.386073	2.50426	4.19147	6.62531	ENSG00000264811	AC138761.3
ENSG00000264813	0.00349342	0.0237706	0.0207014	0.026685	ENSG00000264813	AC113554.2
ENSG00000264820	0.461336	2.22864	0.622228	0.928109	ENSG00000264820	FAM72B
ENSG00000264832	2.29677	2.99096	4.10869	6.78928	ENSG00000264832	PTPN20B
ENSG00000264837	0	0	0.0754277	0.169671	ENSG00000264837	AC069061.3
ENSG00000264842	4.18593	3.67363	3.86587	5.65133	ENSG00000264842	AGAP4
ENSG00000264845	0	0	0	1.16751	ENSG00000264845	AC119868.1
ENSG00000264852	0	0	0	0	ENSG00000264852	RP11-481A12.2
ENSG00000264863	6.0374	6.91644	11.2294	3.83177	ENSG00000264863	AC241585.1
ENSG00000264872	6.36149	5.62721	2.41403	2.59757	ENSG00000264872	MEST
ENSG00000264874	0	0	0	0	ENSG00000264874	AC087499.7
ENSG00000264883	0.948937	0	2.16135	2.47667	ENSG00000264883	FAM25G
ENSG00000264889	2.89494	4.97372	5.09086	6.13934	ENSG00000264889	RP11-175I17.2
ENSG00000264892	0	0	0	0	ENSG00000264892	NOS2P4
ENSG00000264907	0.134358	0.128915	0.232772	1.00857	ENSG00000264907	PRELID3BP3
ENSG00000264911	0	0.199769	0.451088	0.448954	ENSG00000264911	AC022069.1
ENSG00000264917	0.0829873	0	0.0870113	0.0884692	ENSG00000264917	LOC732538
ENSG00000264930	0	0	0.273873	0.332899	ENSG00000264930	AC131055.1
ENSG00000264938	0.0190617	0.202388	0.0825047	0.04219	ENSG00000264938	RP11-344P13.3
ENSG00000264939	2.05667	4.19296	6.10437	7.24386	ENSG00000264939	RP11-1109M24.9
ENSG00000264943	0.446564	1.10034	1.22688	1.63273	ENSG00000264943	SH3GL1P2
ENSG00000264945	0	0	0	0	ENSG00000264945	KIR3DP1
ENSG00000264958	0.0970216	0.280233	0.0422145	0.0529885	ENSG00000264958	ALOX12P1
ENSG00000264970	0	0	0	0	ENSG00000264970	AC131274.3
ENSG00000264971	0	0.192516	0	0.423304	ENSG00000264971	PRR13P4
ENSG00000264980	7.22262	19.3411	24.7926	21.3857	ENSG00000264980	CHD1L
ENSG00000264981	3.59731	3.84022	4.46654	1.36144	ENSG00000264981	AC015818.5
ENSG00000264983	5.54635	5.39569	7.9049	10.3477	ENSG00000264983	NOTCH2NL
ENSG00000264992	0.14792	0.246026	1.57658	2.59501	ENSG00000264992	AC239802.1
ENSG00000265015	0	0	0	0.270544	ENSG00000265015	AP005901.3
ENSG00000265018	0.171062	0	0	0.279915	ENSG00000265018	AGAP12P
ENSG00000265019	0	0	0	0.37733	ENSG00000265019	ABBA01006766.1
ENSG00000265027	0	0.0972037	0.0439068	0.904603	ENSG00000265027	AVPR1B
ENSG00000265038	0	0.0888042	0.0793432	0.397883	ENSG00000265038	AP001180.5
ENSG00000265041	0	0	0	0	ENSG00000265041	AC015688.3
ENSG00000265060	0.104207	0.401646	0.457422	0.224918	ENSG00000265060	PPY2P
ENSG00000265066	0	0	0	0	ENSG00000265066	RP5-998N21.3
ENSG00000265088	0.0289227	0	0	0	ENSG00000265088	HCG4P5
ENSG00000265095	0	0.170786	0	0	ENSG00000265095	AC093484.3
ENSG00000265096	1.03297	0.660138	1.23473	2.02946	ENSG00000265096	C1QTNF1-AS1
ENSG00000265097	0.131034	0.0635026	0.128441	0.221688	ENSG00000265097	RBM22P1
ENSG00000265099	0	0	0.264967	0	ENSG00000265099	AC090774.2
ENSG00000265107	4.29697	0.328134	1.22959	1.00544	ENSG00000265107	GJA5
ENSG00000265111	1.12063	2.33757	1.52193	2.31764	ENSG00000265111	PDZK1
ENSG00000265118	0.317649	0.945036	1.45905	2.57907	ENSG00000265118	AC134669.2

ENSG00000265124	0.862567	1.6178	4.0092	3.70367	ENSG00000265124	BMS1P5
ENSG00000265133	7.49488	20.7567	4.23216	4.49128	ENSG00000265133	HIST2H3D
ENSG00000265136	0.348476	2.14647	2.27985	3.91508	ENSG00000265136	AC124283.4
ENSG00000265153	0	0	0	0	ENSG00000265153	RP11-822E23.5
ENSG00000265158	0.385212	0.61552	1.09405	1.34949	ENSG00000265158	LRRC37A7P
ENSG00000265182	0	0	0.0285688	0.0718674	ENSG00000265182	AC100778.3
ENSG00000265184	2.51423	4.11444	4.24146	4.29501	ENSG00000265184	DYRK3
ENSG00000265188	2.89239	6.42418	6.4683	4.81835	ENSG00000265188	AP001496.3
ENSG00000265190	154.903	107.459	112.874	67.3244	ENSG00000265190	ANXA8
ENSG00000265196	0.319163	0.768089	1.33424	0.932541	ENSG00000265196	PDIA3P1
ENSG00000265203	0.0190393	0.0689638	0.0227986	0.0912868	ENSG00000265203	RBP3
ENSG00000265228	20.1738	21.6789	23.5669	24.9901	ENSG00000265228	PRPF3
ENSG00000265231	0.309757	4.60926	3.08996	3.80162	ENSG00000265231	AKR1C2
ENSG00000265232	0.136214	1.0188	2.63203	0.820883	ENSG00000265232	HIST2H3PS2
ENSG00000265233	0	0	0	0	ENSG00000265233	ABBA01006766.2
ENSG00000265240	0	0	0	0	ENSG00000265240	AC114689.2
ENSG00000265241	5.30793	3.07706	5.7923	3.55574	ENSG00000265241	RBM8A
ENSG00000265243	0	0	0	0	ENSG00000265243	IGLJCOR18
ENSG00000265261	0.324136	0.8194	0.749731	0.816548	ENSG00000265261	AC027575.3
ENSG00000265262	0	0	0.663766	0.269886	ENSG00000265262	TRMT112P3
ENSG00000265264	0.711868	0.402386	0.428496	0	ENSG00000265264	TIMM10B
ENSG00000265273	0.040887	0.15701	0.0715072	0	ENSG00000265273	AC009831.2
ENSG00000265277	2.49197	1.61167	1.77802	0.467957	ENSG00000265277	ACP6
ENSG00000265279	0.542615	1.1667	1.12517	1.45725	ENSG00000265279	CLUHP6
ENSG00000265293	1.84964	3.64476	3.57885	3.63937	ENSG00000265293	ARGFXP2
ENSG00000265296	0	0	0	0	ENSG00000265296	AP005212.1
ENSG00000265298	13.1539	7.66861	12.7973	5.14694	ENSG00000265298	AC132812.1
ENSG00000265303	0	0	0.492548	0	ENSG00000265303	AC099850.2
ENSG00000265305	0.309225	0.981027	0.368848	0.514101	ENSG00000265305	EMBP1
ENSG00000265307	0.476957	3.77008	1.99066	3.34189	ENSG00000265307	SV2A
ENSG00000265340	0	0	0	0	ENSG00000265340	OR4K7P
ENSG00000265346	0	1.06712	0	0	ENSG00000265346	ANP32E
ENSG00000265348	0.0700634	0.201666	0.113753	0.145522	ENSG00000265348	HYDIN2
ENSG00000265352	0	0	1.167	0	ENSG00000265352	LINC01899
ENSG00000265354	5.89493	4.76004	10.7975	9.54215	ENSG00000265354	TIMM23
ENSG00000265366	2.94715	7.21358	6.10186	7.6172	ENSG00000265366	GLUD1P2
ENSG00000265385	6.69777	14.0557	12.0261	21.2531	ENSG00000265385	AL353608.2
ENSG00000265397	0	0	0	0	ENSG00000265397	FRMPD2P1
ENSG00000265402	0	0	0.145598	0	ENSG00000265402	AC011260.1
ENSG00000265417	0	0.386056	0.0968783	0.492271	ENSG00000265417	AP005119.2
ENSG00000265424	0	0.0960097	0.00943135	0.0837891	ENSG00000265424	DUSP8P1
ENSG00000265428	0	0.657101	0.592995	1.43888	ENSG00000265428	AC006441.2
ENSG00000265434	2.67894	2.19898	1.54474	2.60401	ENSG00000265434	HLA-ABC
ENSG00000265437	0	0	0	0	ENSG00000265437	AP005212.2
ENSG00000265447	0	0	0.319581	0.398966	ENSG00000265447	CTD-2350C19.5
ENSG00000265448	0	0	0	0	ENSG00000265448	RP11-421E17.4
ENSG00000265449	0	0	0	0	ENSG00000265449	RP11-301M17.2
ENSG00000265453	0	0	0	0.322353	ENSG00000265453	AC026254.3
ENSG00000265460	0.511079	1.16336	1.59097	2.68245	ENSG00000265460	AC015910.1
ENSG00000265464	0	0.224903	0.757779	0	ENSG00000265464	RP11-495P10.10
ENSG00000265469	0	0	0	0	ENSG00000265469	AC097641.2
ENSG00000265472	0	0	0	0	ENSG00000265472	AC022655.2
ENSG00000265475	0	2.19E-05	0	0	ENSG00000265475	RP11-403I13.6
ENSG00000265476	0.38548	0.535349	0.455218	0.830699	ENSG00000265476	C1orf147

ENSG00000265480	0.0749262	0.216342	0.0718847	0.246049	ENSG00000265480	KRT18P55
ENSG00000265491	2.7267	1.40643	3.1181	0	ENSG00000265491	RNF115
ENSG00000265531	0	0	0	0	ENSG00000265531	FCGR1CP
ENSG00000265540	0	0	0.674799	0	ENSG00000265540	HIST2H2BA
ENSG00000265541	0	0	0	0	ENSG00000265541	H3F3BP2
ENSG00000265545	0	0	0	0	ENSG00000265545	AP005403.1
ENSG00000265551	6.64161	6.40745	9.30862	8.36609	ENSG00000265551	FAM21C
ENSG00000265564	0	0	0	0	ENSG00000265564	PIGPP4
ENSG00000265567	2.76419	7.64505	4.26811	13.8886	ENSG00000265567	AC138761.5
ENSG00000265570	3.87037	4.83459	4.31827	3.17405	ENSG00000265570	BOLA1
ENSG00000265571	0	0	0	0.174874	ENSG00000265571	AC016831.3
ENSG00000265574	0	0.060862	0	0.200056	ENSG00000265574	WDR45BP1
ENSG00000265578	0.278217	0.114766	0.537589	0.136803	ENSG00000265578	FAM35DP
ENSG00000265581	0.35915	0.687164	0.629361	1.02678	ENSG00000265581	PFN1P12
ENSG00000265590	2.66502	1.38151	2.62159	0.287112	ENSG00000265590	AP000275.2
ENSG00000265593	0.129692	0.49771	0.224681	0.675098	ENSG00000265593	NPM1P45
ENSG00000265594	3.55047	6.05954	4.71852	6.09663	ENSG00000265594	CEP41
ENSG00000265608	0.299183	0.305225	0.593108	0.605739	ENSG00000265608	UCN3
ENSG00000265609	0.117285	0.127981	0.116941	0	ENSG00000265609	PDZK1P2
ENSG00000265614	0	0.234706	0	0	ENSG00000265614	AC011193.2
ENSG00000265620	0	0.324658	0	0.177791	ENSG00000265620	RP11-822E23.4
ENSG00000265626	0	0	0	0	ENSG00000265626	AC139085.1
ENSG00000265629	1.60372	3.13186	3.25929	3.43492	ENSG00000265629	AC011897.1
ENSG00000265630	0	0.501253	0	0	ENSG00000265630	GLUD1P8
ENSG00000265631	0.85949	2.21427	0	0.135915	ENSG00000265631	AP005901.4
ENSG00000265639	0	0	0	0	ENSG00000265639	AC090415.1
ENSG00000265646	0	0	0	0	ENSG00000265646	AC069061.4
ENSG00000265681	755.958	580.465	373.624	365.623	ENSG00000265681	RPL17
ENSG00000265683	1.00538	0.614778	0.317347	0.197767	ENSG00000265683	SYPL1P2
ENSG00000265685	0.775841	1.50263	4.04494	1.50836	ENSG00000265685	AKR1C3
ENSG00000265690	1.12582	1.83705	1.20706	2.20387	ENSG00000265690	AC074143.1
ENSG00000265693	7.91805	2.25219	6.61662	8.07956	ENSG00000265693	AC026271.5
ENSG00000265698	0	0	0.244685	0	ENSG00000265698	LARP7P3
ENSG00000265705	0.186658	0	0	0	ENSG00000265705	RP11-744K17.8
ENSG00000265712	0.19731	0.284386	0.599383	0.430428	ENSG00000265712	AC027216.1
ENSG00000265713	0.65234	1.58341	1.19068	2.62637	ENSG00000265713	AC023389.2
ENSG00000265723	0	0	1.15274	0	ENSG00000265723	HIST2H3DP1
ENSG00000265746	0.0443604	0.0427184	0.0772248	0.0485	ENSG00000265746	KYNUP2
ENSG00000265761	0	0	0	0	ENSG00000265761	RP11-445P17.6
ENSG00000265763	0.201048	0.729094	0.244868	0.393184	ENSG00000265763	ZNF488
ENSG00000265773	0	0	0	0	ENSG00000265773	NUP210P2
ENSG00000265790	0	0.18072	0.078495	0.0988212	ENSG00000265790	AC090774.3
ENSG00000265797	4.69017	8.73537	6.46576	9.53551	ENSG00000265797	SRGAP2B
ENSG00000265798	0.453913	1.7119	1.9182	2.65904	ENSG00000265798	AC138207.6
ENSG00000265808	26.8445	16.5968	21.6389	31.475	ENSG00000265808	SEC22B
ENSG00000265817	1.44565	2.8951	2.70013	2.61071	ENSG00000265817	FSBP
ENSG00000265818	0	0	0	0	ENSG00000265818	EEF1E1-BLOC1S5
ENSG00000265823	19.0297	23.7067	23.03	15.9911	ENSG00000265823	EIF2D
ENSG00000265832	5.49905	3.85052	5.19907	2.79975	ENSG00000265832	PEX11B
ENSG00000265833	0	0	0	0	ENSG00000265833	AC130289.1
ENSG00000265836	0	0.131628	0.118807	0	ENSG00000265836	CCND3P2
ENSG00000265853	0	0	0	0	ENSG00000265853	AL353996.1
ENSG00000265854	0	0	0.264752	0	ENSG00000265854	CTSLP3
ENSG00000265863	0.980458	1.95804	1.95074	3.26823	ENSG00000265863	RASSF5

ENSG00000265869	1.19462	0	0	1.18101	ENSG00000265869	RP11-76K13.2
ENSG00000265880	3.63738	6.98346	5.81331	6.89249	ENSG00000265880	CBWD3
ENSG00000265881	0	0	0	0	ENSG00000265881	PDLIM1P2
ENSG00000265883	0	0	0	0	ENSG00000265883	AC060771.1
ENSG00000265897	0	0.149859	0.270845	0.987716	ENSG00000265897	AC233263.1
ENSG00000265906	0	0	0	0	ENSG00000265906	RP11-163O19.15
ENSG00000265916	0	0.803445	0.473659	0.235536	ENSG00000265916	AC015818.6
ENSG00000265934	0	0	0	0	ENSG00000265934	AC110743.1
ENSG00000265936	1.13718	0	0	1.12867	ENSG00000265936	AC091042.1
ENSG00000265937	0	0	0	0	ENSG00000265937	RP11-289I10.2
ENSG00000265939	0.147666	0.283176	0	0	ENSG00000265939	AC091147.1
ENSG00000265944	0	0	0.202613	0.251552	ENSG00000265944	LINC01387
ENSG00000265946	0.243517	0	0.206542	0	ENSG00000265946	AC090312.2
ENSG00000265970	0.0687763	0.0764003	0.0690527	0.148367	ENSG00000265970	HFE2
ENSG00000265972	122.615	166.526	309.866	85.7048	ENSG00000265972	TXNIP
ENSG00000265973	0.310582	0.139335	0.180498	0.468338	ENSG00000265973	AP006587.6
ENSG00000265982	70.5755	104.385	75.7386	51.5176	ENSG00000265982	AC103810.3
ENSG00000266003	0	0.126216	0.0760567	0.286629	ENSG00000266003	AC109315.1
ENSG00000266009	0	0	0	0	ENSG00000266009	AC087393.3
ENSG00000266027	0.28937	0.426415	0.21442	0	ENSG00000266027	MSH5-SAPCD1
ENSG00000266028	41.3064	53.8447	34.1033	67.4027	ENSG00000266028	SRGAP2
ENSG00000266034	0.403672	0.597575	1.13449	0	ENSG00000266034	RHEBP2
ENSG00000266042	0	0	0	0.0311066	ENSG00000266042	AC015818.7
ENSG00000266048	0	0	0	0	ENSG00000266048	AC091178.2
ENSG00000266050	0.441462	1.64169	2.31387	2.29425	ENSG00000266050	AC233702.7
ENSG00000266054	2.26405	2.87964	2.43231	2.63373	ENSG00000266054	NUDT17
ENSG00000266066	0.0159812	0	0.230812	0.308072	ENSG00000266066	AC008158.1
ENSG00000266074	1.35048	4.86295	3.23155	5.87463	ENSG00000266074	BAHCC1
ENSG00000266076	0	0	0	0.13104	ENSG00000266076	AC004805.1
ENSG00000266080	0	0	0	0	ENSG00000266080	H3F3BP2
ENSG00000266086	8.57877	33.3207	27.9789	18.4048	ENSG00000266086	AC015813.2
ENSG00000266094	9.29841	1.3906	0.962085	0.793256	ENSG00000266094	RASSF5
ENSG00000266095	1.16529	3.18447	4.09268	2.90751	ENSG00000266095	BCL9
ENSG00000266105	0	0	0	0	ENSG00000266105	AC009831.3
ENSG00000266117	0.0829873	0	0.0870113	0.0884692	ENSG00000266117	FBXO36P1
ENSG00000266118	0.519375	1.12166	1.04329	1.89096	ENSG00000266118	RP11-507M3.1
ENSG00000266127	0.264411	0.793975	0.672758	1.88605	ENSG00000266127	ZNF415P1
ENSG00000266129	0	0	0	0	ENSG00000266129	SRP68P1
ENSG00000266134	0.209249	0.390646	3.39657	0.36313	ENSG00000266134	WISP3
ENSG00000266145	0	0	0	0	ENSG00000266145	AP001004.1
ENSG00000266155	0.470478	0.442671	0.396373	0	ENSG00000266155	AC103810.4
ENSG00000266157	0	0	0	0.0454167	ENSG00000266157	FOXD4L3
ENSG00000266159	0.268574	0.173545	0.605028	0.891263	ENSG00000266159	TSGA13
ENSG00000266161	0	0	0	0	ENSG00000266161	HLA-K
ENSG00000266162	0	0	0	9.85E-05	ENSG00000266162	YWHAEP2
ENSG00000266169	0	0	0.161818	0	ENSG00000266169	RP11-445P17.5
ENSG00000266170	0	0.111179	0.01767	0.200687	ENSG00000266170	AC244230.2
ENSG00000266172	0	0	0	0	ENSG00000266172	AC244230.2
ENSG00000266173	13.485	24.6116	25.31	31.3642	ENSG00000266173	STRADA
ENSG00000266177	1.01353	0.820569	1.31338	1.9679	ENSG00000266177	C1orf54
ENSG00000266179	461.714	353.51	342.239	348.511	ENSG00000266179	AC025627.3
ENSG00000266181	0	0	0	0.114712	ENSG00000266181	EIF4A3P1
ENSG00000266184	0	0	0	0	ENSG00000266184	AC018371.2
ENSG00000266190	0	0	0	0	ENSG00000266190	AC090287.1

ENSG00000266198	2.01883	4.98427	11.1253	2.72039	ENSG00000266198	PRKAB2
ENSG00000266200	0.00456344	0.0692227	0.0536505	0.00451189	ENSG00000266200	PNLIPRP2
ENSG00000266201	0	0	0	0	ENSG00000266201	SS18L2P2
ENSG00000266202	0	0	0	0	ENSG00000266202	AC005697.1
ENSG00000266208	2.37039	0.664507	2.43942	1.28219	ENSG00000266208	AC080112.2
ENSG00000266217	0	0	0	0	ENSG00000266217	CTSLP2
ENSG00000266225	57.6173	74.4969	39.4664	29.6576	ENSG00000266225	HIST2H2AA4
ENSG00000266227	0	0	0	0	ENSG00000266227	AC016839.1
ENSG00000266242	0.100841	0.441713	0.400354	0.337925	ENSG00000266242	GRAMD4P7
ENSG00000266249	0	0	0.161605	0.260087	ENSG00000266249	CD160
ENSG00000266251	0	0	0	1.31058	ENSG00000266251	COX6CP3
ENSG00000266258	7.65355	21.0077	18.0631	27.248	ENSG00000266258	LINC01909
ENSG00000266265	0.0387226	0.037552	0.0508453	0.0641269	ENSG00000266265	KLF14
ENSG00000266282	0	2.4145	1.07761	1.31202	ENSG00000266282	UBL5P2
ENSG00000266286	0	0	0	0	ENSG00000266286	AC037482.3
ENSG00000266292	0.12116	0.161207	0.0281975	0.317913	ENSG00000266292	CPA5
ENSG00000266296	0	0	0.0344882	0	ENSG00000266296	AC027141.1
ENSG00000266301	0.397549	0	0	0.571605	ENSG00000266301	CTGLF8P
ENSG00000266302	0.00056229	0.53368	0.303966	0.494689	ENSG00000266302	AC098850.4
ENSG00000266306	0	0	0.0352442	0.177189	ENSG00000266306	AC061975.5
ENSG00000266332	0.541904	0.133385	0.252688	0.0983392	ENSG00000266332	FCGR1A
ENSG00000266334	44.5299	39.9657	28.2028	12.453	ENSG00000266334	APH1A
ENSG00000266338	9.41989	18.5113	11.9112	29.8401	ENSG00000266338	NBPF15
ENSG00000266350	0.923842	1.28672	3.38026	7.98511	ENSG00000266350	WI2-18996O14.1
ENSG00000266356	0	0	1.18118	1.41967	ENSG00000266356	AC090615.1
ENSG00000266359	0.203242	1.21801	0.455063	1.15423	ENSG00000266359	AKR1C4
ENSG00000266364	0	0	0	0	ENSG00000266364	AC087499.8
ENSG00000266365	0	0	0	0	ENSG00000266365	AC053481.3
ENSG00000266373	0	0	0	0	ENSG00000266373	AP002472.1
ENSG00000266379	0	0	0.391508	0	ENSG00000266379	AC090616.5
ENSG00000266394	0	0	0.0887399	0.108843	ENSG00000266394	RP11-196G18.1
ENSG00000266405	0.504893	1.91616	1.60766	1.96735	ENSG00000266405	CBX3P2
ENSG00000266412	40.5095	21.2091	21.6568	16.0782	ENSG00000266412	NCOA4
ENSG00000266416	0	0	0	0	ENSG00000266416	AC130289.2
ENSG00000266433	0.27224	0.461139	0.270015	0.348293	ENSG00000266433	TBC1D3P5
ENSG00000266434	0	0	0	0	ENSG00000266434	RP5-998N21.8
ENSG00000266442	0.28937	0.426415	0.21442	0	ENSG00000266442	MSH5-SAPCD1
ENSG00000266448	0	0	0	0	ENSG00000266448	AC007923.3
ENSG00000266470	0	0	0	0	ENSG00000266470	AP001180.6
ENSG00000266472	22.2276	10.0572	21.9302	7.54949	ENSG00000266472	MRPS21
ENSG00000266479	3.11899	0	0	0.5269	ENSG00000266479	AC105245.1
ENSG00000266486	0.323928	0.595654	0.42811	0	ENSG00000266486	FAM106CP
ENSG00000266488	0	0	0.0593747	0	ENSG00000266488	AC226154.2
ENSG00000266497	0.457258	0.867425	2.31423	3.38127	ENSG00000266497	AC138645.1
ENSG00000266501	0	0	1.28581	1.20933	ENSG00000266501	AC025198.1
ENSG00000266504	0.457258	0.867425	2.31423	3.38127	ENSG00000266504	AC091132.3
ENSG00000266516	0	0	0.551017	0.701317	ENSG00000266516	RP11-303K3.1
ENSG00000266519	0	0	0.241007	0	ENSG00000266519	MCCD1P1
ENSG00000266520	0.246464	0.354792	0.320384	0.529875	ENSG00000266520	AC022884.2
ENSG00000266522	0	0.253513	0.137812	0	ENSG00000266522	AP005242.2
ENSG00000266524	0.014048	0.0479073	0.0295439	0	ENSG00000266524	GDF10
ENSG00000266529	0	0.0552444	0	0	ENSG00000266529	MTCYBP13
ENSG00000266537	0.0839529	0.576653	0.0724704	0.638178	ENSG00000266537	SPDYE22P

ENSG00000266549	0	0	0	0	ENSG00000266549	AC023575.1
ENSG00000266561	0	0	0	0	ENSG00000266561	AC011195.1
ENSG00000266562	3.86489	4.4237	4.61723	3.80644	ENSG00000266562	RPRD2
ENSG00000266563	0	0	0	0	ENSG00000266563	EIF1P5
ENSG00000266572	0.264299	0.755255	0.227546	0.693498	ENSG00000266572	AC016831.5
ENSG00000266575	0	0	0	0	ENSG00000266575	BOLA2P1
ENSG00000266576	0	0	0.0479684	0.0596198	ENSG00000266576	MARK2P14
ENSG00000266592	5.4914	12.9289	7.95818	5.46488	ENSG00000266592	AKR1C1
ENSG00000266605	0.232527	0	0	0	ENSG00000266605	AP006261.1
ENSG00000266607	0.271674	0.484493	0.547002	0.644025	ENSG00000266607	PGM5
ENSG00000266613	0.0257945	0.074524	0.0224399	0.198054	ENSG00000266613	AP001094.4
ENSG00000266614	0	0	0	0	ENSG00000266614	AC103808.5
ENSG00000266639	0	0.231626	0.697308	0.313895	ENSG00000266639	RP11-666A1.3
ENSG00000266641	16.0838	22.2564	17.0109	26.4772	ENSG00000266641	MAPKAPK2
ENSG00000266647	0.872126	0	0	0	ENSG00000266647	AC053481.4
ENSG00000266648	0	0	0.138471	0.17419	ENSG00000266648	SETP3
ENSG00000266659	3.48712	4.27964	3.41445	4.17598	ENSG00000266659	SRGAP2C
ENSG00000266662	0.480562	0.252654	0.33535	0.386047	ENSG00000266662	FSCN2
ENSG00000266673	0	0	0	0	ENSG00000266673	AC233702.9
ENSG00000266681	0.0724045	0.431293	0.125378	0.160749	ENSG00000266681	RP11-301M17.1
ENSG00000266691	0	0	0.0357453	0.134769	ENSG00000266691	AC138761.6
ENSG00000266693	0.0584007	0	0.0507908	0	ENSG00000266693	OR4K8P
ENSG00000266695	1.1952	0.505946	0.914505	0.278665	ENSG00000266695	AC090958.2
ENSG00000266707	0	0	0.117874	0.145267	ENSG00000266707	AC006120.1
ENSG00000266714	16.0125	26.3562	25.2361	31.6844	ENSG00000266714	MYO15B
ENSG00000266728	0	0	0	0	ENSG00000266728	AC015688.5
ENSG00000266733	1.74705	1.48976	2.17534	1.02879	ENSG00000266733	TBC1D29
ENSG00000266736	0	0	0	0	ENSG00000266736	GTF2IP6
ENSG00000266741	2.50637	2.52174	1.73697	1.82222	ENSG00000266741	POLR3GL
ENSG00000266746	2.91404	5.89336	3.33907	6.70384	ENSG00000266746	AC209154.1
ENSG00000266748	0.0683522	0.271385	0.124455	0.0790965	ENSG00000266748	FMO5
ENSG00000266764	9.60865	3.42906	4.04588	3.77476	ENSG00000266764	C1orf51
ENSG00000266766	5.68467	7.38497	4.72243	5.14544	ENSG00000266766	AL512503.1
ENSG00000266771	17.2717	55.0568	44.8299	28.9286	ENSG00000266771	AC015688.6
ENSG00000266777	3.41138	6.30895	10.2566	7.05824	ENSG00000266777	AC090616.6
ENSG00000266779	8.84977	10.7468	9.02676	8.19705	ENSG00000266779	COPG2
ENSG00000266786	0.295731	0.249838	0	0.192598	ENSG00000266786	LGALS9DP
ENSG00000266796	0.425162	0.487594	1.25175	0.538301	ENSG00000266796	CT009496.1
ENSG00000266797	0.078099	0.149422	0	0.0145338	ENSG00000266797	NBPF23
ENSG00000266806	0	0	0	0	ENSG00000266806	AC087575.1
ENSG00000266809	0	0	0	0	ENSG00000266809	AC022884.3
ENSG00000266810	0	0	0	0	ENSG00000266810	MICG
ENSG00000266815	0	0	0.870044	1.06268	ENSG00000266815	RP11-400O7.4
ENSG00000266818	0.164951	0.568934	0.0669636	0.0822892	ENSG00000266818	AP005901.5
ENSG00000266820	18.9893	11.6014	21.5006	8.55268	ENSG00000266820	KPNA2P3
ENSG00000266826	0.0605419	0	0	0	ENSG00000266826	AC011195.2
ENSG00000266836	0.505989	1.65981	1.39159	3.54971	ENSG00000266836	RP11-1109M24.8
ENSG00000266842	0	0.139689	0	0	ENSG00000266842	RP11-495P10.4
ENSG00000266845	0	0.0338616	0	0.0392417	ENSG00000266845	RP11-325P15.1
ENSG00000266853	0.102761	0	0	0.563015	ENSG00000266853	AC015688.7
ENSG00000266858	0.0754898	0.150742	0	0.163665	ENSG00000266858	RPSAP67
ENSG00000266865	10.7566	16.6354	16.1704	20.528	ENSG00000266865	AC138207.8
ENSG00000266876	0	0.0630666	0	0	ENSG00000266876	AC104996.2
ENSG00000266880	0	1.2274	1.3864	0.568922	ENSG00000266880	RHEBP1

ENSG00000266891	1.30797	2.91565	2.31018	4.92068	ENSG00000266891	AP000902.1
ENSG00000266899	0	0	0	0	ENSG00000266899	AKR1B1P7
ENSG00000266906	0	1.38632	0	0.723694	ENSG00000266906	AC005357.1
ENSG00000266907	0.0259298	0.0752357	0.0227898	0	ENSG00000266907	AC006116.1
ENSG00000266909	0.394966	0.126312	0.342118	0.423842	ENSG00000266909	SLC25A6P4
ENSG00000266910	0.45452	1.24936	1.57242	2.84103	ENSG00000266910	AC008507.1
ENSG00000266915	0	0	0	0	ENSG00000266915	MRPS5P4
ENSG00000266920	0	0.0531635	0	0	ENSG00000266920	ACTBP9
ENSG00000266931	0	0	0	0	ENSG00000266931	AC125232.2
ENSG00000266932	0	0.0602602	0.0544583	0.1364	ENSG00000266932	AC006116.2
ENSG00000266938	0.118199	0	0	0	ENSG00000266938	AC119403.2
ENSG00000266943	0	0.334253	0	0	ENSG00000266943	RPSAP66
ENSG00000266944	2.7739	3.09983	1.98263	4.88593	ENSG00000266944	AC005262.1
ENSG00000266945	9.16395	21.3819	22.9071	26.9876	ENSG00000266945	OR4G3P
ENSG00000266946	0.396902	0.848574	1.0027	0.96347	ENSG00000266946	MRPL37P1
ENSG00000266949	0	0	0	0	ENSG00000266949	LYPD8
ENSG00000266953	0	0	0.727772	0	ENSG00000266953	AC092073.1
ENSG00000266956	0.600861	2.26281	1.79173	2.50834	ENSG00000266956	CTB-186H2.3
ENSG00000266958	1.11439	2.63646	3.31631	1.80078	ENSG00000266958	AC005779.1
ENSG00000266959	0	0	0	2.88341	ENSG00000266959	AC005786.1
ENSG00000266960	0.15152	0.32017	1.01019	0.323975	ENSG00000266960	FAM106DP
ENSG00000266964	0.475158	0.607274	1.10018	1.0149	ENSG00000266964	FXYD1
ENSG00000266967	16.6361	21.5292	34.5954	31.9364	ENSG00000266967	AARSD1
ENSG00000266971	0	0	0	0	ENSG00000266971	OR4F8P
ENSG00000266972	0.0578262	0.153975	0.162496	0.255638	ENSG00000266972	LRRC37A9P
ENSG00000266984	0.21008	0.71052	0.893283	0.355491	ENSG00000266984	POLR3GP2
ENSG00000266986	0	0.956142	0.639242	0.32723	ENSG00000266986	RP11-428O23.1
ENSG00000266989	0	0	0	0	ENSG00000266989	FTLP5
ENSG00000266992	0	0.394536	0.0689607	0	ENSG00000266992	DHX40P1
ENSG00000266995	0.0684346	5.29151	6.33829	10.3087	ENSG00000266995	AP001542.1
ENSG00000266996	0	0.161453	0.334872	1.11388	ENSG00000266996	TCEB3CL2
ENSG00000266997	0	0	0	0	ENSG00000266997	AC090227.1
ENSG00000267001	0	0	0	0	ENSG00000267001	AC006538.2
ENSG00000267005	0	0.171353	0.309411	0.571192	ENSG00000267005	AC002984.1
ENSG00000267019	0	0	0	0.0694409	ENSG00000267019	NTF6A
ENSG00000267022	0	0.20903	0.0996414	0.0342373	ENSG00000267022	AC067968.1
ENSG00000267023	5.11071	5.35751	6.71605	4.10851	ENSG00000267023	LRRC37A16P
ENSG00000267029	0	0	4.14035	20.1133	ENSG00000267029	AC092299.7
ENSG00000267032	0	0	0.0505073	0	ENSG00000267032	AP001357.1
ENSG00000267036	0.0888729	0.53259	0.165366	0.309452	ENSG00000267036	AC005559.1
ENSG00000267041	3.24888	4.38801	6.48834	9.09939	ENSG00000267041	ZNF850
ENSG00000267043	3.41965	3.1416	2.62433	0.970545	ENSG00000267043	CTB-91J4.3
ENSG00000267046	0	0	0	0	ENSG00000267046	E2F3P1
ENSG00000267056	4.46582	3.58599	0.25993	3.59243	ENSG00000267056	AC005336.1
ENSG00000267059	1.16199	0	0.72643	0	ENSG00000267059	AC005943.1
ENSG00000267060	3.72143	6.90558	6.04842	13.7326	ENSG00000267060	PTGES3L
ENSG00000267066	0	0	0	0	ENSG00000267066	AC107990.1
ENSG00000267071	0	0.0659104	0.125741	0.212513	ENSG00000267071	RP11-147L13.7
ENSG00000267076	0.990634	0.542961	0.82367	0.509099	ENSG00000267076	CCDC58P3
ENSG00000267083	0.0950748	0.570436	0.158811	0.547887	ENSG00000267083	KRT18P61
ENSG00000267084	0.880569	2.49172	1.6309	2.82445	ENSG00000267084	AC015802.2
ENSG00000267085	2.44187	2.82865	2.43608	4.86318	ENSG00000267085	AL512605.2
ENSG00000267086	0	0	0	0	ENSG00000267086	YWHAEP6
ENSG00000267088	0	0.17549	1.26773	0.77974	ENSG00000267088	AC087683.1

ENSG00000267091	0	0	0.044292	0.105544	ENSG00000267091	CTBP2P7
ENSG00000267099	0	0	0	0	ENSG00000267099	NTF6G
ENSG00000267102	3.01479	1.8888	2.71113	4.00907	ENSG00000267102	AC060766.1
ENSG00000267106	8.98478	16.8204	16.2875	23.3111	ENSG00000267106	ZNF561-AS1
ENSG00000267110	0	0	0	0.16596	ENSG00000267110	AC010327.1
ENSG00000267113	0	0	0	0	ENSG00000267113	AF038458.1
ENSG00000267114	3.80689	5.63458	6.88633	6.69988	ENSG00000267114	AC011481.1
ENSG00000267116	0.181813	0.0873648	0.0790659	0	ENSG00000267116	AP005264.2
ENSG00000267119	0.645331	0	0	0	ENSG00000267119	RPL10P15
ENSG00000267120	0	0.437588	0.603768	0.199687	ENSG00000267120	AD000671.2
ENSG00000267127	1.3966	2.74806	3.93245	4.03996	ENSG00000267127	AC090360.1
ENSG00000267129	0	0	0	0	ENSG00000267129	AC087498.2
ENSG00000267132	0	0	0	0	ENSG00000267132	AC067852.3
ENSG00000267135	11.2916	17.7475	10.1554	6.09045	ENSG00000267135	AD000091.1
ENSG00000267140	0.700512	2.22	1.9382	1.54798	ENSG00000267140	AC007998.2
ENSG00000267142	0	0.0594731	0.0537497	0.29236	ENSG00000267142	AC092296.2
ENSG00000267145	0	0	0	0	ENSG00000267145	AC006116.3
ENSG00000267148	0.90205	0.850251	0	0	ENSG00000267148	AC005777.1
ENSG00000267153	0	0	0.0412149	0	ENSG00000267153	CTBP2P3
ENSG00000267154	0	0	0	0	ENSG00000267154	OR1M4P
ENSG00000267156	0	0	0	0	ENSG00000267156	TPMTP1
ENSG00000267157	0.514827	0.297005	0.622608	0	ENSG00000267157	AC011499.1
ENSG00000267162	0	0	0	0	ENSG00000267162	SDHDP1
ENSG00000267168	0	0.390929	0	0	ENSG00000267168	AC005837.2
ENSG00000267170	0.185342	0	0.160338	0	ENSG00000267170	AC005242.1
ENSG00000267173	0	0	0	0	ENSG00000267173	AC245748.1
ENSG00000267178	0.61979	0.596905	1.1305	1.84265	ENSG00000267178	PHF5CP
ENSG00000267179	2.42112	3.20606	3.26284	4.95207	ENSG00000267179	AC008770.3
ENSG00000267180	0.843339	0.822325	0	0.920146	ENSG00000267180	AC007136.1
ENSG00000267181	0	0.956142	0.639242	0.32723	ENSG00000267181	RP11-428O23.1
ENSG00000267182	0	0	0	0	ENSG00000267182	SNRPCP20
ENSG00000267184	0	0	0	0	ENSG00000267184	AC002545.1
ENSG00000267185	0.541003	0.164155	0	0	ENSG00000267185	AC067852.4
ENSG00000267187	0	0	0.109112	0	ENSG00000267187	AC026898.1
ENSG00000267189	0	0	0	0	ENSG00000267189	AC067852.5
ENSG00000267190	0.194846	0	0	0	ENSG00000267190	TYMSP2
ENSG00000267203	1.78224	6.73969	10.3419	13.2129	ENSG00000267203	AC115085.1
ENSG00000267206	0.405174	0	0	0.150903	ENSG00000267206	LCN6
ENSG00000267208	0	0	0	0	ENSG00000267208	AC209539.1
ENSG00000267216	5.74466	5.97147	7.61339	4.87431	ENSG00000267216	AC020915.2
ENSG00000267218	0.409997	0.0647729	0.141375	0.0743719	ENSG00000267218	AC005336.2
ENSG00000267220	0	0.422099	0.181461	0.423602	ENSG00000267220	AC011447.2
ENSG00000267227	0	0	0	0	ENSG00000267227	AC005324.6
ENSG00000267228	0.716929	0.620108	0.232363	1.79794	ENSG00000267228	AC012254.2
ENSG00000267229	0	0	0	0	ENSG00000267229	ALG9
ENSG00000267233	0	0	0	0	ENSG00000267233	HNRNPA3P16
ENSG00000267235	0	0.415288	0	0	ENSG00000267235	ZNF861P
ENSG00000267237	0	0.534496	0.393882	0.591773	ENSG00000267237	AC073135.2
ENSG00000267241	0.175115	0	0	0	ENSG00000267241	CYP4F10P
ENSG00000267245	0.49911	0.237934	0.235493	0.270313	ENSG00000267245	AC008805.1
ENSG00000267253	0.0983662	0.655404	0.389404	0.430968	ENSG00000267253	AC055813.1
ENSG00000267256	0.41632	0.993143	0.734006	0.991243	ENSG00000267256	CTC-260E6.8
ENSG00000267258	0.182727	0	0.144254	0	ENSG00000267258	AC008507.3
ENSG00000267260	1.39068	2.98697	2.82076	3.11979	ENSG00000267260	AC020928.1

ENSG00000267261	1.13525	0	0.322051	0	ENSG00000267261	AC099811.2
ENSG00000267264	1.13949	2.59576	1.60342	1.83013	ENSG00000267264	AC006504.3
ENSG00000267270	4.71558	7.27599	9.19939	7.5732	ENSG00000267270	PARD6G-AS1
ENSG00000267271	0	0	0	0	ENSG00000267271	AC060766.2
ENSG00000267281	2.15173	3.63227	2.21874	2.44207	ENSG00000267281	AC023509.3
ENSG00000267292	0	0	0.215077	0.26267	ENSG00000267292	AP001542.2
ENSG00000267293	0.305433	0.592934	0.532204	1.06057	ENSG00000267293	AC012569.1
ENSG00000267294	0.491916	1.05388	0.825006	0.92121	ENSG00000267294	SH3GL1P3
ENSG00000267295	0.759166	2.2792	1.20605	1.84971	ENSG00000267295	AC025048.3
ENSG00000267297	5.11071	5.35751	6.71605	4.10851	ENSG00000267297	LRRC37A16P
ENSG00000267301	0.194108	0.498753	0	0	ENSG00000267301	RPL23AP77
ENSG00000267303	0	0	0	0.163632	ENSG00000267303	AC011511.4
ENSG00000267305	31.4516	50.857	40.4672	44.3183	ENSG00000267305	AL592148.2
ENSG00000267310	0	0	0	0	ENSG00000267310	OR4G1P
ENSG00000267312	0	0.0559235	0.0523065	0.0646953	ENSG00000267312	AC015911.4
ENSG00000267314	0	0.149898	0	0	ENSG00000267314	AC104532.1
ENSG00000267315	0	0	0	0	ENSG00000267315	AC060766.3
ENSG00000267318	2.59014	5.34474	5.7637	7.79221	ENSG00000267318	AC005702.2
ENSG00000267319	0	0.770326	0.60082	0.419879	ENSG00000267319	AC093227.2
ENSG00000267323	3.57432	3.54395	4.80689	1.57379	ENSG00000267323	SLC25A1P5
ENSG00000267324	0	0.0924618	0.125357	0	ENSG00000267324	AC006557.2
ENSG00000267326	0	0.0807274	0.220588	0.178339	ENSG00000267326	AC015849.14
ENSG00000267332	0	0	0	0	ENSG00000267332	BOLA3P2
ENSG00000267333	0.0355664	0.207121	0.247793	0.157197	ENSG00000267333	ASNSP6
ENSG00000267335	0.0889358	0.439607	1.14215	0.704406	ENSG00000267335	AC008687.1
ENSG00000267336	0.115201	0.332125	0.100043	0.125385	ENSG00000267336	EIF4A2P1
ENSG00000267340	1.59475	3.75914	1.97766	1.59105	ENSG00000267340	AC060780.2
ENSG00000267343	0.442779	1.71056	1.1965	0.93989	ENSG00000267343	ZNF833P
ENSG00000267346	0.341656	1.30902	1.18157	1.27611	ENSG00000267346	EIF5AP3
ENSG00000267352	0.491916	1.05388	0.825006	0.92121	ENSG00000267352	AC005332.2
ENSG00000267355	0.119562	0.344217	0.942252	0.385802	ENSG00000267355	AC022966.1
ENSG00000267360	4.51164	3.3339	6.40858	10.7842	ENSG00000267360	AC012309.1
ENSG00000267361	0.0986836	0.142511	0.216178	0.862179	ENSG00000267361	AC005495.1
ENSG00000267368	64.0636	50.3343	28.0767	36.3346	ENSG00000267368	UPK3BL1
ENSG00000267369	0	0	0	0	ENSG00000267369	AC015911.7
ENSG00000267370	2.87866	5.99603	5.30039	6.11099	ENSG00000267370	AC008752.3
ENSG00000267371	0	0.287201	0	0.171172	ENSG00000267371	AP001017.1
ENSG00000267376	0	0	0	1.41251	ENSG00000267376	AC015801.1
ENSG00000267382	0.0402926	0	0.0701605	0	ENSG00000267382	AC010928.1
ENSG00000267384	0	0	0	0	ENSG00000267384	SMCO4P1
ENSG00000267385	0.768391	1.38719	1.39849	3.0592	ENSG00000267385	AC011498.4
ENSG00000267389	0	0.0756228	0.0683232	0.0853412	ENSG00000267389	AC006504.4
ENSG00000267392	0.0439841	0.0875289	0.0765715	0.144278	ENSG00000267392	CYP4F9P
ENSG00000267398	0	0	0	0	ENSG00000267398	AC006130.2
ENSG00000267400	0	0	0	0	ENSG00000267400	AC010928.2
ENSG00000267404	0.0598846	0.230493	1.14569	0.19574	ENSG00000267404	AC023043.2
ENSG00000267408	0	0.151808	0.137073	0	ENSG00000267408	AC011498.5
ENSG00000267415	0	0.39855	0	2.16662	ENSG00000267415	AC011471.1
ENSG00000267418	0	0	0	0	ENSG00000267418	ELOCP29
ENSG00000267422	1.39038	0.670348	1.70989	1.19801	ENSG00000267422	AC016582.2
ENSG00000267426	0.698251	1.28315	1.0565	1.3552	ENSG00000267426	AC087289.3
ENSG00000267428	0	0	0	0	ENSG00000267428	AC091135.1
ENSG00000267430	1.35868	1.97469	1.97645	2.86573	ENSG00000267430	AC036176.2
ENSG00000267433	0	0	0	0	ENSG00000267433	AC008798.1

ENSG00000267441	0	0	0	0	ENSG00000267441	AL353997.3
ENSG00000267444	0	0	0.0691585	0.172742	ENSG00000267444	SMUG1P1
ENSG00000267447	0.200748	0.0964297	0	0	ENSG00000267447	VN2R11P
ENSG00000267450	0.165079	0.88819	0.970369	3.97258	ENSG00000267450	OR1AB1P
ENSG00000267451	0.621565	0.584332	0.733716	0.674924	ENSG00000267451	LOC440461
ENSG00000267456	0.227325	0.651379	1.76493	0	ENSG00000267456	AC023043.3
ENSG00000267459	5.90778	0	1.88324	0	ENSG00000267459	AC006116.7
ENSG00000267460	0	0	0	0	ENSG00000267460	CTB-186H2.1
ENSG00000267463	0.494566	1.21497	1.92734	2.32131	ENSG00000267463	UBE2V2P2
ENSG00000267464	2.44101	1.53037	0	0	ENSG00000267464	CTC-260E6.7
ENSG00000267467	0.776324	1.01012	2.66028	3.93634	ENSG00000267467	APOC4
ENSG00000267471	0.536259	0	0.230843	0.844042	ENSG00000267471	AC005771.1
ENSG00000267472	0.621565	0.584332	0.733716	0.674924	ENSG00000267472	AC005332.3
ENSG00000267477	0	0.540881	0.277776	0	ENSG00000267477	AC008481.3
ENSG00000267478	0.0407598	0.0433305	0.103555	0.0867842	ENSG00000267478	AP002414.3
ENSG00000267482	33.5453	56.1891	61.2035	133.43	ENSG00000267482	AC104996.3
ENSG00000267483	0.737882	1.71663	2.19856	2.791	ENSG00000267483	RBFOX3
ENSG00000267486	0	0.190591	0.172149	0	ENSG00000267486	GLUD1P4
ENSG00000267487	0	0	0	0	ENSG00000267487	AC100843.3
ENSG00000267490	0	0	0.054788	0	ENSG00000267490	AC008759.1
ENSG00000267492	2.38924	17.1222	7.20771	34.1609	ENSG00000267492	AL353997.4
ENSG00000267496	1.75082	2.43193	5.95307	1.93527	ENSG00000267496	FAM215A
ENSG00000267497	0.119669	0.311579	0.341622	0.480017	ENSG00000267497	NFE2L3P1
ENSG00000267500	0.457438	1.78143	0.544198	1.23394	ENSG00000267500	ZNF887P
ENSG00000267507	0	0.15365	0.412419	0.170942	ENSG00000267507	AC010327.2
ENSG00000267508	1.57762	2.07137	2.7331	2.88458	ENSG00000267508	ZNF285
ENSG00000267511	0.532759	0.409343	0.0924103	0.229885	ENSG00000267511	ADAD1P2
ENSG00000267513	0	0	0.292932	0	ENSG00000267513	HMGN1P31
ENSG00000267515	0.252744	0.808057	1.15194	1.42727	ENSG00000267515	AP001029.3
ENSG00000267518	0	0.884536	0.266392	0.651494	ENSG00000267518	AC090699.1
ENSG00000267524	0	0.0741657	0	0	ENSG00000267524	RPSAP57
ENSG00000267526	0.346107	1.27276	0.90928	1.41936	ENSG00000267526	AC005702.3
ENSG00000267531	0.923982	1.07328	1.58623	1.04727	ENSG00000267531	AC020922.1
ENSG00000267533	0	0.0524193	0	0	ENSG00000267533	AP002414.4
ENSG00000267534	3.72856	2.98276	2.51052	3.76368	ENSG00000267534	S1PR2
ENSG00000267541	0	0	2.40074	2.95983	ENSG00000267541	MTCO2P2
ENSG00000267544	0	0	0.239874	0.249762	ENSG00000267544	AC007229.1
ENSG00000267545	1.2178	1.02214	0.585231	1.64938	ENSG00000267545	AC005779.2
ENSG00000267552	0.178677	0.660107	0.199862	2.39027	ENSG00000267552	AC093227.3
ENSG00000267554	0	0	0.112062	0.277763	ENSG00000267554	AC015911.8
ENSG00000267556	0.281667	0.149372	0.213419	0.666901	ENSG00000267556	SARM1
ENSG00000267558	1.8096	3.36869	0	0	ENSG00000267558	AC087685.1
ENSG00000267561	0.195636	0.230802	0.381027	0.675376	ENSG00000267561	AC093155.3
ENSG00000267562	0.728494	1.27136	0.944183	2.01385	ENSG00000267562	CTC-421K24.1
ENSG00000267570	0	0	0.0664178	0.248997	ENSG00000267570	STK25P1
ENSG00000267573	0	0	0	0	ENSG00000267573	KRT8P5
ENSG00000267584	0	0.422099	0.181461	0.423602	ENSG00000267584	CTC-260E6.9
ENSG00000267585	0.274405	0	0.118807	0	ENSG00000267585	AC013290.1
ENSG00000267587	1.12577	3.8247	3.11248	6.46496	ENSG00000267587	AC090241.1
ENSG00000267589	0	1.12089	0.341751	0.588704	ENSG00000267589	AC011444.4
ENSG00000267590	0.487741	8.4073	2.49282	6.55435	ENSG00000267590	NDUFA3P1
ENSG00000267591	1.18217	0.188551	0.51067	0.627149	ENSG00000267591	AC105224.1
ENSG00000267592	3.04708	2.41439	2.55715	5.44925	ENSG00000267592	AC004134.1
ENSG00000267594	0.237856	0.122504	0	0.039996	ENSG00000267594	CYP4F24P

ENSG00000267595	9.58861	9.73065	38.6682	5.14502	ENSG00000267595	AC060780.3
ENSG00000267596	0.6838	2.03151	2.21757	2.93134	ENSG00000267596	CCL15
ENSG00000267597	0	0	0.0773114	0.0963959	ENSG00000267597	RPIAP1
ENSG00000267600	16.5145	60.1144	82.9805	62.3408	ENSG00000267600	AC098474.1
ENSG00000267609	0	0	0	0.106454	ENSG00000267609	SNX33P1
ENSG00000267611	0	0.850251	0.745945	0	ENSG00000267611	AC008521.1
ENSG00000267618	0.471113	0	0	0	ENSG00000267618	AC004223.3
ENSG00000267619	17.7891	20.9984	17.1669	20.8237	ENSG00000267619	TRAPPC4
ENSG00000267620	0.178588	0	0.124997	0.117513	ENSG00000267620	AC090771.1
ENSG00000267623	0.0576219	0.263175	0	0.634577	ENSG00000267623	AC005357.2
ENSG00000267624	0	0	0	0.383906	ENSG00000267624	AC087645.1
ENSG00000267630	0	0	0	0	ENSG00000267630	AC005758.1
ENSG00000267631	0.0889358	0	0	0	ENSG00000267631	CGB1
ENSG00000267634	0	0	0	0	ENSG00000267634	RPL7L1P5
ENSG00000267635	0	0	0	0	ENSG00000267635	AC209539.2
ENSG00000267639	0	0.178442	0	0	ENSG00000267639	AC073135.3
ENSG00000267641	0.41632	0.993143	0.734006	0.991243	ENSG00000267641	BNIP3P16
ENSG00000267645	0	7.13986	0.69266	1.48416	ENSG00000267645	POLR2J2
ENSG00000267647	0.591278	0	0.253865	0.927486	ENSG00000267647	AC098848.2
ENSG00000267648	1.23402	1.08609	1.4693	1.7373	ENSG00000267648	AC060766.5
ENSG00000267652	4.0216	4.8474	1.62857	0.579112	ENSG00000267652	AC011712.1
ENSG00000267656	0.188424	0.0905264	0	0	ENSG00000267656	AP001357.2
ENSG00000267657	0	0	0	0	ENSG00000267657	CTB-186H2.2
ENSG00000267661	0	0	0	0	ENSG00000267661	AP001269.3
ENSG00000267663	0.336119	1.12708	0	0.716539	ENSG00000267663	AP005264.5
ENSG00000267664	0.444265	0	0.256389	0.158402	ENSG00000267664	RPL17P45
ENSG00000267669	0	0.13893	0.718811	0.369388	ENSG00000267669	AC098847.2
ENSG00000267671	0.161298	2.52755	0.345889	0.68074	ENSG00000267671	YWHAEP7
ENSG00000267673	14.5484	9.14441	11.8209	7.74288	ENSG00000267673	FDX2
ENSG00000267676	0	0	0.183216	0	ENSG00000267676	THA1P
ENSG00000267678	0	0	0	0	ENSG00000267678	AC011921.2
ENSG00000267679	0.12857	0.756143	0.159016	1.05988	ENSG00000267679	EIF5AP2
ENSG00000267680	19.8931	29.7493	30.2405	34.2908	ENSG00000267680	ZNF224
ENSG00000267681	1.2464	8.71164	19.3971	6.09058	ENSG00000267681	AC135721.2
ENSG00000267685	0	0	0	0.0694409	ENSG00000267685	NTF6B
ENSG00000267687	0	0	0	0.145547	ENSG00000267687	AC010928.3
ENSG00000267689	1.58986	2.4793	0.679415	4.29918	ENSG00000267689	AC010525.2
ENSG00000267691	0.23233	0.486744	0.967372	1.58144	ENSG00000267691	AC003102.2
ENSG00000267692	2.15449	3.51742	5.19912	17.9411	ENSG00000267692	AC008507.4
ENSG00000267693	0	0.436607	0.39047	0	ENSG00000267693	AC011477.5
ENSG00000267697	1.41919	0	1.77337	0	ENSG00000267697	LUZP6
ENSG00000267699	0.373674	0	0	0	ENSG00000267699	AC091551.1
ENSG00000267704	0.0369608	0.0356059	0.0643717	0.0809535	ENSG00000267704	FRG2LP
ENSG00000267706	0.682287	1.76417	2.74258	1.95573	ENSG00000267706	AC020922.1
ENSG00000267708	0	0.0659104	0.125741	0.212513	ENSG00000267708	AC005332.4
ENSG00000267710	8.08234	13.6107	22.9956	22.4488	ENSG00000267710	EDDM13
ENSG00000267713	0	0	0	0	ENSG00000267713	AC012433.1
ENSG00000267716	0	0.0975577	0	0	ENSG00000267716	AC083760.1
ENSG00000267717	0.257455	0.247434	0.447064	0.185924	ENSG00000267717	AC090330.1
ENSG00000267721	7.33239	7.21259	8.6673	4.61694	ENSG00000267721	TMEM199
ENSG00000267725	0	0	0.39047	0	ENSG00000267725	AC008521.2
ENSG00000267728	0	9.10E-09	3.88E-09	0	ENSG00000267728	KRTAP9-9
ENSG00000267733	2.46616	3.2127	2.88999	4.85657	ENSG00000267733	AP005264.6
ENSG00000267736	0.114291	0	0	0	ENSG00000267736	HMGB2P1

ENSG00000267740	1.76566	1.07313	0.895255	0.405463	ENSG00000267740	AC024592.3
ENSG00000267741	0.181794	0.175414	0.784305	0.766591	ENSG00000267741	UBE2L4
ENSG00000267742	0	0	0.292191	0	ENSG00000267742	FAM60CP
ENSG00000267744	0	0	0	0	ENSG00000267744	AC022916.3
ENSG00000267748	0.340539	0.714144	0.610283	0.330013	ENSG00000267748	AC011479.1
ENSG00000267752	0	0	0	0	ENSG00000267752	AC067796.1
ENSG00000267756	3.31617	8.22211	5.79734	10.4975	ENSG00000267756	AC006557.4
ENSG00000267757	1.24274	2.60266	2.7636	4.02033	ENSG00000267757	EML2-AS1
ENSG00000267768	0	0	0	0	ENSG00000267768	AC006504.6
ENSG00000267770	0	0	0	0	ENSG00000267770	AC016182.1
ENSG00000267771	2.44101	1.53037	0	0	ENSG00000267771	AC011447.4
ENSG00000267772	0	0.271492	0.355442	0.295525	ENSG00000267772	LINC01999
ENSG00000267773	0	0	0	0	ENSG00000267773	AP001120.3
ENSG00000267775	0	0	0	0	ENSG00000267775	OR7E16P
ENSG00000267781	1.13791	0.972227	0.731318	1.46277	ENSG00000267781	SLC25A36P1
ENSG00000267792	0	0.68594	0	0	ENSG00000267792	WBP1LP11
ENSG00000267793	1.13598	2.97951	3.82093	1.35593	ENSG00000267793	AC009977.1
ENSG00000267794	2.61565	7.0916	0.802026	5.16799	ENSG00000267794	AP001120.4
ENSG00000267795	50.9773	4.77876	6.47999	9.03305	ENSG00000267795	SMIM22
ENSG00000267796	12.887	10.3163	11.4696	10.6589	ENSG00000267796	LIN37
ENSG00000267797	0	0	0.0644444	0.163092	ENSG00000267797	NRBF2P1
ENSG00000267799	0	0	0.036793	0.188653	ENSG00000267799	MAN1A2P1
ENSG00000267800	1.47324	5.33757	9.30534	4.83866	ENSG00000267800	AC012254.4
ENSG00000267802	0.0831831	0.188324	0	2.51754	ENSG00000267802	AL358333.1
ENSG00000267803	0	0	0	0	ENSG00000267803	AC244161.1
ENSG00000267806	0.292789	0.477686	0.446509	0.701287	ENSG00000267806	AL360004.2
ENSG00000267807	529.234	308.17	190.092	284.031	ENSG00000267807	ACTG1
ENSG00000267809	1.47777	1.53595	1.03298	0.559465	ENSG00000267809	NDUFV2P1
ENSG00000267812	5.47209	11.356	12.8725	13.645	ENSG00000267812	FKSG68
ENSG00000267816	28.9765	18.6552	13.9395	19.1933	ENSG00000267816	IDS
ENSG00000267817	0	0.206683	0.0933234	0	ENSG00000267817	RP11-164F3.8
ENSG00000267819	0.456485	0.582773	0.679101	0.874219	ENSG00000267819	AC092850.1
ENSG00000267820	0.153752	0	0	0.438685	ENSG00000267820	LL0XNC01-240C2.1
ENSG00000267821	0	0.0576584	0	0	ENSG00000267821	RPL19P21
ENSG00000267822	0.580351	0.647853	0.685244	0.205342	ENSG00000267822	VN1R85P
ENSG00000267823	18.8039	21.2709	4.87202	9.90011	ENSG00000267823	TIMM17B
ENSG00000267824	0.60245	1.83144	1.68318	2.54689	ENSG00000267824	AC137056.1
ENSG00000267825	75.1165	26.4508	17.5909	12.9591	ENSG00000267825	ZNF185
ENSG00000267829	0.239584	0.258303	0.0328562	0.770267	ENSG00000267829	KCND1
ENSG00000267832	0.856315	1.1707	1.43805	1.53423	ENSG00000267832	NANOGNBP3
ENSG00000267833	0.228319	0.0313706	0	0.216676	ENSG00000267833	SSX8
ENSG00000267836	0	0	0	0.0363477	ENSG00000267836	RP11-104D21.1
ENSG00000267840	19.8305	32.8583	17.6783	25.286	ENSG00000267840	BX005439.2
ENSG00000267841	0.0265127	0.123725	0.084428	0.212289	ENSG00000267841	GATA1
ENSG00000267843	17.5144	19.6427	12.5292	14.6763	ENSG00000267843	WDR13
ENSG00000267845	0	0.126632	0	0	ENSG00000267845	DKFZP434A062
ENSG00000267846	0.267607	0.15111	0.903012	0.886981	ENSG00000267846	AC239803.1
ENSG00000267848	1.67288	2.79798	3.84357	6.98069	ENSG00000267848	AL118506.1
ENSG00000267849	1.4969	6.11675	2.52206	10.6587	ENSG00000267849	AL133262.1
ENSG00000267854	0	0	0	0	ENSG00000267854	KIR2DL4
ENSG00000267855	49.8707	46.7271	41.9713	37.2403	ENSG00000267855	NDUFA7
ENSG00000267856	0	0	0	0	ENSG00000267856	RP3-507I15.1
ENSG00000267857	1.08163	4.33047	6.3235	6.92573	ENSG00000267857	AL133499.1
ENSG00000267860	0.133248	0.0256517	0	0	ENSG00000267860	EEF1A1P31

ENSG00000267862	0	0.0276648	0.0250025	0.0313377	ENSG00000267862	RP1-279N11.1
ENSG00000267864	0	0	0	0	ENSG00000267864	SSX2
ENSG00000267866	0	0	0	0	ENSG00000267866	RP3-481A17.1
ENSG00000267867	0.339087	0.675691	0.45483	3.9813	ENSG00000267867	PHLDB1
ENSG00000267873	0	0	0	0	ENSG00000267873	AC121757.1
ENSG00000267876	0	0	0	0	ENSG00000267876	GSC2
ENSG00000267877	2.31131	3.21756	3.52154	7.00564	ENSG00000267877	RPL13P5
ENSG00000267878	2.75668	3.01002	2.75719	2.912	ENSG00000267878	PIM2
ENSG00000267880	0	0	0	0	ENSG00000267880	AC037199.1
ENSG00000267881	0	0	0	0.0665423	ENSG00000267881	AC243967.1
ENSG00000267882	1.83498	4.23688	2.289	4.58199	ENSG00000267882	AL031666.2
ENSG00000267883	0.523368	0.498638	1.12719	2.74764	ENSG00000267883	PRED60
ENSG00000267884	0.293922	0.954101	1.11374	1.91329	ENSG00000267884	AL626787.1
ENSG00000267885	0.955789	0	2.58275	0.892102	ENSG00000267885	FKSG48
ENSG00000267887	0.0221909	0.042682	0.0196878	0.169939	ENSG00000267887	AF196972.4
ENSG00000267889	0	0	0	0	ENSG00000267889	AC079354.2
ENSG00000267891	0.0491389	0.18201	0.223186	0.0929349	ENSG00000267891	PABPC1L2B
ENSG00000267893	0.761546	1.99519	1.44595	2.67482	ENSG00000267893	AC007461.1
ENSG00000267894	5.45037	5.7627	6.80589	7.88436	ENSG00000267894	ZNF322
ENSG00000267895	0.241636	0	0	0	ENSG00000267895	AC063977.1
ENSG00000267899	0.0360882	0.074055	0.114847	0.134785	ENSG00000267899	CROCCP1
ENSG00000267900	0	0	0.0156153	0	ENSG00000267900	LUZP4
ENSG00000267901	0.189327	1.26808	0.993932	0.87576	ENSG00000267901	AC004817.1
ENSG00000267902	0	0	0.060841	0.232082	ENSG00000267902	FTH1P19
ENSG00000267906	33.48	79.2922	90.7869	125.782	ENSG00000267906	AC073333.1
ENSG00000267908	0.0974252	0.116529	0.27775	0.183655	ENSG00000267908	ZSCAN5DP
ENSG00000267909	0.106036	0.0313926	0	0.108148	ENSG00000267909	CCDC177
ENSG00000267910	11.0642	21.0045	17.85	27.5622	ENSG00000267910	KMT2A
ENSG00000267912	0.214931	0.519037	0.593166	0.333921	ENSG00000267912	WAS
ENSG00000267913	0.673864	0.323483	0.681674	1.21004	ENSG00000267913	AP001055.1
ENSG00000267915	0.262064	0.243797	0.268805	0.279114	ENSG00000267915	PDZD4
ENSG00000267918	76.3225	38.0662	6.43384	98.5697	ENSG00000267918	AL117190.2
ENSG00000267920	0	0.281547	0.212436	0.573046	ENSG00000267920	SNX6P1
ENSG00000267921	0	0	0.0557551	0.138211	ENSG00000267921	RRM2P4
ENSG00000267923	0.364241	1.69395	0.862591	2.73488	ENSG00000267923	LAIR1
ENSG00000267928	0	0.0652987	0.0589391	0.072959	ENSG00000267928	HMGB1P16
ENSG00000267929	17.1747	10.8125	8.47211	5.21022	ENSG00000267929	SLC35A2
ENSG00000267930	0	0	0	0	ENSG00000267930	RPS26P8
ENSG00000267935	0	3.42979	3.52977	3.73149	ENSG00000267935	AC016752.1
ENSG00000267937	0	0	1.02555	0	ENSG00000267937	AP001421.1
ENSG00000267938	0.578789	0.275849	0.249964	0	ENSG00000267938	EIF1P6
ENSG00000267941	3.44794	4.0473	5.15729	6.66899	ENSG00000267941	AC008267.1
ENSG00000267942	46.978	104.372	64.3862	142.845	ENSG00000267942	AC090673.2
ENSG00000267944	1.73178	4.28707	2.6825	5.81931	ENSG00000267944	RP11-258C19.4
ENSG00000267945	0	0	0.669702	2.20236	ENSG00000267945	AC139677.8
ENSG00000267946	2.93119	4.73217	4.50395	4.39313	ENSG00000267946	TMLHE
ENSG00000267947	0.0296109	0.0333849	0.0543341	0.032034	ENSG00000267947	AC078899.3
ENSG00000267949	0	0	0	0.067987	ENSG00000267949	LA16c-4G1.5
ENSG00000267950	0	0	1.62821	0	ENSG00000267950	AC136297.1
ENSG00000267951	13.6504	22.3638	20.7924	19.0336	ENSG00000267951	L1CAM
ENSG00000267952	2.60681	0	0	0.174006	ENSG00000267952	AC008878.1
ENSG00000267954	0	0.0419016	0.233671	0.148697	ENSG00000267954	AP000349.1
ENSG00000267955	1.20598	1.78072	1.68939	2.75395	ENSG00000267955	RP11-770J1.4
ENSG00000267956	0	0	0.0554816	0	ENSG00000267956	VN1R78P

ENSG00000267958	0	0	0	2.80413	ENSG00000267958	CATX-2
ENSG00000267960	0	0.0489826	0.0737983	0.148568	ENSG00000267960	RHOXF2B
ENSG00000267961	0.0694197	0	0.180963	0.301867	ENSG00000267961	OR10B1P
ENSG00000267963	0	0	0	0	ENSG00000267963	AC013469.1
ENSG00000267964	0.982153	0.38134	1.13216	0.447152	ENSG00000267964	AC022400.2
ENSG00000267966	6.94119	10.5268	12.0528	16.2516	ENSG00000267966	RPL23AP82
ENSG00000267967	0	0	0	0	ENSG00000267967	MTND1P33
ENSG00000267970	0	0.0275626	0.0497132	0.092838	ENSG00000267970	AC004899.1
ENSG00000267972	0	0	0	0.0151809	ENSG00000267972	DGKK
ENSG00000267975	0	0.0804462	0	0.163662	ENSG00000267975	BTF3P8
ENSG00000267976	0.768142	0.431156	1.24127	1.69837	ENSG00000267976	AP000695.1
ENSG00000267977	87.2938	86.0176	45.3177	30.1692	ENSG00000267977	BCAP31
ENSG00000267978	0.0264856	0	0.0460838	0.0643849	ENSG00000267978	MAGEA9B
ENSG00000267979	18.6592	36.5339	40.248	47.3134	ENSG00000267979	AC092964.2
ENSG00000267981	19.4648	34.5349	30.8276	57.7008	ENSG00000267981	AP003041.2
ENSG00000267983	11.1845	9.14965	10.0762	8.41283	ENSG00000267983	OTUD5
ENSG00000267985	21.6355	34.0864	33.6731	49.6725	ENSG00000267985	AC005488.1
ENSG00000267987	0	0	0	0	ENSG00000267987	AL161784.1
ENSG00000267988	1.43556	2.83987	5.84306	1.03636	ENSG00000267988	AC096582.1
ENSG00000267989	13.2432	10.9375	11.4417	9.30879	ENSG00000267989	IDH3G
ENSG00000267990	0.197028	0	0.170223	0.836198	ENSG00000267990	AC063977.2
ENSG00000267993	27.5114	21.1569	9.6522	12.4696	ENSG00000267993	DNASE1L1
ENSG00000267995	0.298157	0.733311	0.374392	1.27785	ENSG00000267995	SSX7
ENSG00000267997	0.134389	0	0	0.0721368	ENSG00000267997	HSPB1P2
ENSG00000267999	0	0	0	0	ENSG00000267999	RP11-552E4.2
ENSG00000268000	0.0769148	0	0.20043	0	ENSG00000268000	Hsa-mir-150
ENSG00000268004	0	0	0	0	ENSG00000268004	VDAC1P2
ENSG00000268005	0	0	0.054688	0.0677963	ENSG00000268005	BX682235.1
ENSG00000268008	0	0	0.111642	0	ENSG00000268008	RP1-203P18.1
ENSG00000268009	0	0	0	0	ENSG00000268009	SSX4
ENSG00000268010	0	0	0	0	ENSG00000268010	TMEM185AP1
ENSG00000268011	0	0	0	0.0513945	ENSG00000268011	RP11-104D21.2
ENSG00000268012	0	7.46821	11.171	2.38657	ENSG00000268012	AC016559.1
ENSG00000268013	0.0638874	0	0.00939236	0.0355251	ENSG00000268013	TKTL1
ENSG00000268014	0	0	0	0	ENSG00000268014	RPL36P18
ENSG00000268016	0	0	0	0	ENSG00000268016	GAGE12E
ENSG00000268017	0	0	0.154525	0	ENSG00000268017	HMGN1P37
ENSG00000268018	21.5974	19.8542	11.9194	33.7149	ENSG00000268018	MAGED1
ENSG00000268019	0	0.0295675	0.0267153	0.0670593	ENSG00000268019	LDHBP2
ENSG00000268020	9.54513	21.4552	23.0395	27.4014	ENSG00000268020	AL627309.6
ENSG00000268021	0	0.278169	0.362838	1.02125	ENSG00000268021	TREH
ENSG00000268022	0	0	0	0	ENSG00000268022	RP11-344N17.6
ENSG00000268023	0.0967251	0.0937466	0.0862406	0.205342	ENSG00000268023	CBX1P1
ENSG00000268024	0	0	0	0	ENSG00000268024	AC005549.3
ENSG00000268025	0	0	0.0940372	0.713601	ENSG00000268025	AC118758.3
ENSG00000268028	0	6.84291	20.1512	13.2029	ENSG00000268028	AC025262.1
ENSG00000268029	0	0	0	0.0089544	ENSG00000268029	TCP11X2
ENSG00000268032	0.0385828	0.109553	0.102455	0.0456406	ENSG00000268032	CTB-52I2.4
ENSG00000268034	0.0485048	0	0	0	ENSG00000268034	AC243960.2
ENSG00000268035	0.365066	0.469878	0.554332	1.04492	ENSG00000268035	NAP1L6
ENSG00000268036	3.39983	7.47282	8.75488	0.326657	ENSG00000268036	AC007228.1
ENSG00000268037	0	0	0	0	ENSG00000268037	CU151838.1
ENSG00000268040	0.265599	1.77081	0.914505	4.15283	ENSG00000268040	PRED62
ENSG00000268041	0.298672	0.768449	0.499456	1.08207	ENSG00000268041	AC010616.1

ENSG00000268043	0.375699	0.411972	1.53894	0.476947	ENSG00000268043	NBPF12
ENSG00000268045	0.0381208	0.071319	0.0660104	0.0402735	ENSG00000268045	RP6-204F4.2
ENSG00000268046	33.012	57.7293	49.864	91.5396	ENSG00000268046	AP001094.1
ENSG00000268048	0	0.351246	0.158257	0	ENSG00000268048	RP3-461F17.1
ENSG00000268053	0.504143	0.827704	0.936491	1.06897	ENSG00000268053	AC007785.2
ENSG00000268054	0	0	0	0	ENSG00000268054	RP13-34L8.7
ENSG00000268058	0.91462	2.02424	1.93179	1.26218	ENSG00000268058	BNIP3P40
ENSG00000268059	3.4392	2.43652	3.59122	4.3167	ENSG00000268059	AL441883.1
ENSG00000268060	0.0890643	0.059008	0.110826	0.184549	ENSG00000268060	PCDHB10
ENSG00000268062	0	0	0	0	ENSG00000268062	AL031274.2
ENSG00000268064	0	0	0	0	ENSG00000268064	KIR3DX1
ENSG00000268067	0	0	0	0	ENSG00000268067	OR5AH1P
ENSG00000268069	1.55469	2.38116	1.91404	3.90644	ENSG00000268069	AC004466.1
ENSG00000268070	0.879344	3.49575	3.8526	0.809802	ENSG00000268070	AC006539.2
ENSG00000268071	0	0	0	0	ENSG00000268071	RBM22P6
ENSG00000268074	0	0	0	0	ENSG00000268074	AC246680.2
ENSG00000268076	5.96215	35.5346	12.7879	32.8412	ENSG00000268076	AC087239.1
ENSG00000268077	0	0	0	0	ENSG00000268077	CENPVP1
ENSG00000268079	0.166686	0	0.0552128	0	ENSG00000268079	BNIP3P30
ENSG00000268080	0	0	0	0	ENSG00000268080	AC016885.3
ENSG00000268082	0	0.2823	0	0.598348	ENSG00000268082	RP11-38O23.3
ENSG00000268083	1.74034	0	0	0	ENSG00000268083	AC008982.1
ENSG00000268084	0.179343	0.559581	0.807398	0.873788	ENSG00000268084	SMIM9
ENSG00000268085	0	1.08785	0	4.9787	ENSG00000268085	AC051642.1
ENSG00000268086	0	0.233448	0	0	ENSG00000268086	RP1-172N19.3
ENSG00000268088	0.250762	0.477947	0	0	ENSG00000268088	AC093063.1
ENSG00000268089	0.110032	0.00624371	0	0.0855338	ENSG00000268089	GABRQ
ENSG00000268090	0	0.0187221	0	0.463658	ENSG00000268090	PAGE4
ENSG00000268091	0	0	0	0	ENSG00000268091	AC078925.1
ENSG00000268092	0	0	0	0	ENSG00000268092	RP11-38O23.7
ENSG00000268094	2.12114	3.34031	3.13171	3.29138	ENSG00000268094	PFN1P8
ENSG00000268096	0.0331593	0.0956711	0	0.0721459	ENSG00000268096	MAGEA7P
ENSG00000268098	2.77111	9.16155	14.0933	2.62575	ENSG00000268098	AP000688.1
ENSG00000268100	0	0.034725	0	0.0388254	ENSG00000268100	AC011493.1
ENSG00000268101	0	0	0	0.209967	ENSG00000268101	CYP2G2P
ENSG00000268103	7.09604	8.59752	8.924	9.85995	ENSG00000268103	FMR1
ENSG00000268104	48.8381	0.903329	0.223109	1.50389	ENSG00000268104	SLC6A14
ENSG00000268105	0.0704801	0.40671	0.122437	0.253556	ENSG00000268105	AC124856.1
ENSG00000268107	0	0	0	0	ENSG00000268107	AC003005.1
ENSG00000268109	7.9392	8.26102	7.12869	9.54089	ENSG00000268109	FUNDC2
ENSG00000268110	13.5031	12.8116	9.88327	7.05416	ENSG00000268110	UBE4A
ENSG00000268111	25.7404	39.3961	33.2362	68.212	ENSG00000268111	AL031663.1
ENSG00000268113	0.164181	0.310268	0.284169	0.267981	ENSG00000268113	RP11-114H20.1
ENSG00000268114	0	0	0	0	ENSG00000268114	RP11-552J9.15
ENSG00000268115	0	0	0	0	ENSG00000268115	RP5-101O16.9
ENSG00000268116	0	0	0	0	ENSG00000268116	AC073539.2
ENSG00000268117	0.34111	0.29134	0.528145	1.85368	ENSG00000268117	VN1R84P
ENSG00000268118	0	0	0	0	ENSG00000268118	RP11-552E4.5
ENSG00000268122	0.255542	0	0	0	ENSG00000268122	HSFX1
ENSG00000268123	8.07904	17.7375	12.5828	12.0531	ENSG00000268123	C12orf57
ENSG00000268124	0	0	0	0	ENSG00000268124	RP11-344N17.3
ENSG00000268126	25.9086	62.6148	54.6599	111.647	ENSG00000268126	AC091948.1
ENSG00000268130	0	21.3737	21.7628	20.5113	ENSG00000268130	AL137002.1
ENSG00000268132	0.180101	0.319413	0.312253	0.203153	ENSG00000268132	CSAG4

ENSG00000268133	0.0295835	0	0	0	ENSG00000268133	AC003002.2
ENSG00000268134	2.96514	0.450255	0.910265	0.0847205	ENSG00000268134	FAM156A
ENSG00000268135	1.62672	0.60047	1.61305	1.82063	ENSG00000268135	LRRC23
ENSG00000268136	3.3447	13.6975	3.83343	7.31988	ENSG00000268136	CDCA3
ENSG00000268138	25.9162	21.6114	13.2204	11.7089	ENSG00000268138	PORCN
ENSG00000268139	0	0	0	0	ENSG00000268139	PRICKLE3
ENSG00000268140	0	0	0	0.0415339	ENSG00000268140	PCGF7P
ENSG00000268141	0	0	0	0	ENSG00000268141	AL606500.1
ENSG00000268142	9.92911	6.53928	12.2944	8.3372	ENSG00000268142	PQBP1
ENSG00000268144	0.0756799	0	0	0.164992	ENSG00000268144	NIFKP6
ENSG00000268146	0.0168373	0.110611	0.207276	0.224435	ENSG00000268146	AL590483.1
ENSG00000268148	0	0	0	1.13146	ENSG00000268148	VN1R91P
ENSG00000268151	12.5766	17.1711	16.007	16.5884	ENSG00000268151	ARMCX2
ENSG00000268152	0	0	0	0	ENSG00000268152	RP1-73A14.1
ENSG00000268153	0.636251	1.63782	1.6675	3.02009	ENSG00000268153	AC005176.1
ENSG00000268154	61.1831	97.1344	122.079	181.525	ENSG00000268154	AL591806.1
ENSG00000268155	0	11.9796	9.91575	6.92094	ENSG00000268155	AL161450.1
ENSG00000268156	29.1116	66.943	56.2167	66.5184	ENSG00000268156	FKSG61
ENSG00000268158	1.97912	4.47037	4.03457	5.64554	ENSG00000268158	FAM120C
ENSG00000268159	0.0571456	0.3968	0.297264	0.184608	ENSG00000268159	DMRTC1B
ENSG00000268160	0	3.72917	0	0	ENSG00000268160	FAM3A
ENSG00000268162	0.480465	0.230535	0.312277	0.258362	ENSG00000268162	HBCBP
ENSG00000268163	0.814181	0.993962	0.853245	0	ENSG00000268163	AC004076.1
ENSG00000268169	0	0	0	0	ENSG00000268169	RP11-357K9.2
ENSG00000268170	0	0	0.544981	1.45012	ENSG00000268170	AC073342.2
ENSG00000268171	0.650489	2.42016	1.46553	2.88131	ENSG00000268171	AC068620.1
ENSG00000268172	0.615399	1.8205	1.48044	3.76742	ENSG00000268172	AL590452.1
ENSG00000268173	0.31189	0	0.491388	1.0746	ENSG00000268173	AC007192.1
ENSG00000268174	0.371745	1.35637	0.786146	0.322253	ENSG00000268174	BNIP3P22
ENSG00000268175	0.791702	0.648193	1.55096	0.90983	ENSG00000268175	AC117395.1
ENSG00000268176	2.06697	1.99963	2.11543	4.0214	ENSG00000268176	ZCCHC18
ENSG00000268179	0	0	0	0	ENSG00000268179	AL645608.1
ENSG00000268181	0	0	0	0	ENSG00000268181	AC073188.6
ENSG00000268182	0.751902	1.20253	0.651531	1.0772	ENSG00000268182	SMIM17
ENSG00000268183	0.0583023	0.167874	0.15162	0.1255	ENSG00000268183	ABCD1P4
ENSG00000268185	0.0172629	0.0339526	0	0	ENSG00000268185	SALL1P1
ENSG00000268187	0	0	1.58E-08	0	ENSG00000268187	AC118758.4
ENSG00000268188	15.2836	9.89143	11.5168	7.04157	ENSG00000268188	HSD17B10
ENSG00000268190	4.2073	4.89946	4.82358	2.79618	ENSG00000268190	SP2B2
ENSG00000268192	1.05815	0	0	0	ENSG00000268192	AP002956.1
ENSG00000268193	0.765704	0.198869	1.24174	1.12354	ENSG00000268193	AC002985.1
ENSG00000268194	0.286845	0.339937	0.388676	0.384375	ENSG00000268194	LINC01101
ENSG00000268195	0.4579	1.02511	1.5768	2.27283	ENSG00000268195	GNB3
ENSG00000268196	0	0	0	0	ENSG00000268196	MAGEA3
ENSG00000268197	4.40421	9.33662	7.59653	11.5752	ENSG00000268197	AF196972.3
ENSG00000268198	0.0507767	0	0	0	ENSG00000268198	Ghc-602D8.2
ENSG00000268200	0.128456	0.165057	0.0882369	0.068308	ENSG00000268200	RP11-420K14.3
ENSG00000268206	50.8116	116.235	95.5427	216.348	ENSG00000268206	AC061975.10
ENSG00000268208	0	0	0	0	ENSG00000268208	AC008372.1
ENSG00000268209	0.0456186	0	0	0.298305	ENSG00000268209	AC114786.4
ENSG00000268210	0.238738	0.285045	0.247772	0.337296	ENSG00000268210	TMEM257
ENSG00000268211	1.84358	3.79439	3.36893	7.05983	ENSG00000268211	AL359091.2
ENSG00000268212	0.00976883	0.0394198	0.051094	0.133379	ENSG00000268212	CXorf30
ENSG00000268213	10.1879	6.91126	7.93171	5.2887	ENSG00000268213	ARMCX6

ENSG00000268214	0	0	0	0	ENSG00000268214	KIR2DL4
ENSG00000268217	0	1.08785	0	0	ENSG00000268217	AC008387.1
ENSG00000268218	3.22099	8.84015	8.68737	15.1198	ENSG00000268218	AC137932.3
ENSG00000268221	0	0	0	0	ENSG00000268221	OPN1MW
ENSG00000268222	0	0	0.0367634	0.0461789	ENSG00000268222	EEF1A1P7
ENSG00000268223	1.63843	2.5258	1.72117	3.57757	ENSG00000268223	ARL14EPL
ENSG00000268225	1.70334	2.19221	2.21798	0.87667	ENSG00000268225	AC010487.1
ENSG00000268226	11.7033	15.5968	23.8135	17.2248	ENSG00000268226	DKC1
ENSG00000268229	3.6298	4.38263	4.71545	5.63971	ENSG00000268229	ARHGEF9
ENSG00000268233	0	0	0	0	ENSG00000268233	RP13-36C9.5
ENSG00000268234	0	0	0	0.032491	ENSG00000268234	FKBP4P6
ENSG00000268235	0	0	0	0.0089544	ENSG00000268235	TCP11X1
ENSG00000268236	0.344292	0	0.579878	0	ENSG00000268236	AC078899.4
ENSG00000268238	0	0	0	0	ENSG00000268238	IGFL1P2
ENSG00000268239	0	0	0	0.0449071	ENSG00000268239	SPANXA2
ENSG00000268241	0	0	0	0	ENSG00000268241	AC018470.1
ENSG00000268242	7.71433	12.9223	8.90549	17.5799	ENSG00000268242	AC131935.1
ENSG00000268243	0	0	0	0	ENSG00000268243	RPS29P30
ENSG00000268245	0	0.113743	0.252468	0.121781	ENSG00000268245	RBMX2P2
ENSG00000268246	0	0.0301048	0	0.0340585	ENSG00000268246	RP13-228J13.6
ENSG00000268247	0	0	0	0	ENSG00000268247	RP13-77O11.11
ENSG00000268248	0	0	0	4.87E-05	ENSG00000268248	AC118758.5
ENSG00000268249	1.44516	1.73928	3.07756	1.7406	ENSG00000268249	TIMMA8
ENSG00000268256	0.13298	0.707185	0.510932	0.881636	ENSG00000268256	SSX5
ENSG00000268258	0	0	0	0	ENSG00000268258	RP11-492O8.1
ENSG00000268259	0.0194219	0.0935406	0	0.0212604	ENSG00000268259	ESX1
ENSG00000268260	10.1445	26.0479	21.435	6.52098	ENSG00000268260	SPACA5
ENSG00000268264	0.0602201	0.153425	0.264517	0.114834	ENSG00000268264	CCNB3
ENSG00000268265	0	0	0	0	ENSG00000268265	AP000304.1
ENSG00000268267	0	0.0523214	0	0	ENSG00000268267	SIGLEC29P
ENSG00000268269	3.75734	4.7853	7.24067	5.804	ENSG00000268269	TSPYL2
ENSG00000268270	0	0.17889	0	0.390809	ENSG00000268270	RP11-161N3.3
ENSG00000268272	0	0	0.0554816	0	ENSG00000268272	VN1R78P
ENSG00000268273	0.901168	0.8131	1.27164	1.04031	ENSG00000268273	GSPT2
ENSG00000268274	0.0479682	0.0460971	0.291477	0.15558	ENSG00000268274	U82695.9
ENSG00000268275	0	0	0	0	ENSG00000268275	AL035588.1
ENSG00000268276	6.63462	22.2606	10.6306	6.63619	ENSG00000268276	AL590523.
ENSG00000268278	0.0441251	0	0	0	ENSG00000268278	AC123912.3
ENSG00000268279	4.5819	4.81891	4.18229	6.32367	ENSG00000268279	AC090004.1
ENSG00000268280	369.594	772.355	683.473	1086.24	ENSG00000268280	AC008914.1
ENSG00000268281	20.7449	18.4157	21.8755	18.0883	ENSG00000268281	NAA10
ENSG00000268282	0.600867	0.559318	0.237619	0.716004	ENSG00000268282	AC010328.2
ENSG00000268284	0	0	0.125314	1.16765	ENSG00000268284	RP11-707O23.5
ENSG00000268291	0.169429	0.282272	0.18237	0.409683	ENSG00000268291	RP11-420K14.7
ENSG00000268293	0.277683	0	1.90958	0.872673	ENSG00000268293	AC008751.1
ENSG00000268294	0	0	0	0	ENSG00000268294	RP11-353J17.3
ENSG00000268295	0.456067	0.430217	0	0.530527	ENSG00000268295	POLR3GP1
ENSG00000268297	0	0	0	0.237959	ENSG00000268297	CLEC4GP1
ENSG00000268300	0	0	0	0	ENSG00000268300	CTD-2183H9.3
ENSG00000268301	4.23546	11.731	6.7839	16.4658	ENSG00000268301	AC018630.1
ENSG00000268302	10.252	16.3176	0.758385	3.45277	ENSG00000268302	AL035252.1
ENSG00000268310	0.456792	1.59759	0	0.969207	ENSG00000268310	AC087645.1
ENSG00000268312	5.67178	6.76896	6.7779	6.87685	ENSG00000268312	PHF8
ENSG00000268313	0	1.37185	0	2.3102	ENSG00000268313	AC119673.1

ENSG00000268314	5.81525	8.78074	7.46665	2.8011	ENSG00000268314	CXorf40A
ENSG00000268317	0	0	0	0	ENSG00000268317	AC026461.1
ENSG00000268319	0	0	0	0	ENSG00000268319	RP11-272G22.2
ENSG00000268320	0	0	0	0	ENSG00000268320	SCGB1C2
ENSG00000268322	1.86783	2.61298	2.10465	1.73534	ENSG00000268322	BNIP3P25
ENSG00000268324	0.295363	0.774617	0.875406	1.5748	ENSG00000268324	LRRC2-AS1
ENSG00000268327	5.04313	9.59052	2.87315	14.6529	ENSG00000268327	C15ORF31
ENSG00000268328	2.45075	3.20113	4.21453	1.7013	ENSG00000268328	AC019206.1
ENSG00000268329	8.57805	9.48245	8.82907	5.12085	ENSG00000268329	KATNB1
ENSG00000268330	21.6355	34.0864	33.6731	49.6725	ENSG00000268330	AC211486.1
ENSG00000268332	0	0	0	0.239229	ENSG00000268332	AL035406.1
ENSG00000268335	0.0755052	0	0	0.182798	ENSG00000268335	BNIP3P23
ENSG00000268336	0	0	0	0	ENSG00000268336	SIGLEC20P
ENSG00000268337	0	0	0	1.23E-08	ENSG00000268337	MAGEA9B
ENSG00000268341	0.819786	0	0	0	ENSG00000268341	L47234.1
ENSG00000268342	0	0	0	0.032491	ENSG00000268342	CTD-2340F8.1
ENSG00000268343	0	0.0477595	0.0431396	0	ENSG00000268343	AC012414.1
ENSG00000268344	28.0588	63.6934	59.1826	108.851	ENSG00000268344	AL138815.2
ENSG00000268345	0.061278	0.137914	0.0533573	0.0895414	ENSG00000268345	RP11-432N13.2
ENSG00000268347	0	0	0	0	ENSG00000268347	CTD-2267G17.2
ENSG00000268349	0	0.040902	0	0.0461068	ENSG00000268349	RHOXF1
ENSG00000268350	2.96514	0.450255	0.910265	0.0847205	ENSG00000268350	FAM156A
ENSG00000268351	0	0	0	0	ENSG00000268351	AP001888.1
ENSG00000268353	2.12384	1.15131	1.49498	2.38159	ENSG00000268353	SYP
ENSG00000268356	0	0	0	0	ENSG00000268356	RP1-172N19.4
ENSG00000268357	2.87427	6.14446	4.2638	4.76376	ENSG00000268357	VN1R81P
ENSG00000268358	2.87356	1.89352	0.685286	0.656035	ENSG00000268358	EPB41L4A-AS2
ENSG00000268359	0.0232902	0.172436	0.170452	0.222191	ENSG00000268359	RAB39B
ENSG00000268361	0	0	0	0	ENSG00000268361	L34079.1
ENSG00000268363	0.0325351	0.0645822	0	0	ENSG00000268363	RP11-232D9.2
ENSG00000268365	0	0	0	0	ENSG00000268365	AL646016.1
ENSG00000268367	4.48637	12.1099	8.64651	12.2594	ENSG00000268367	AC126614.1
ENSG00000268368	0	0	0	0.540433	ENSG00000268368	TMSB15A
ENSG00000268370	0	0	0	0	ENSG00000268370	RP11-45J1.1
ENSG00000268372	1.49144	1.48042	2.19863	2.02854	ENSG00000268372	IQSEC2
ENSG00000268374	0.34111	0.29134	0.528145	1.85368	ENSG00000268374	VN1R84P
ENSG00000268377	0	0.026875	0.0758672	0.154267	ENSG00000268377	TCEAL6
ENSG00000268379	0.35569	0.183923	0.237783	0.149647	ENSG00000268379	AC025588.1
ENSG00000268381	0.0353247	0.0829495	0.0959269	0.0500352	ENSG00000268381	H2BFWT
ENSG00000268384	3.1042	2.99353	2.24227	1.27141	ENSG00000268384	TMEM187
ENSG00000268386	0	0	0	0	ENSG00000268386	VN1R79P
ENSG00000268387	0.5775	0.542565	0.948115	0.902103	ENSG00000268387	AL590714.1
ENSG00000268389	0	0.0593743	0	0.0672591	ENSG00000268389	API5P1
ENSG00000268391	0	0	0	0.0772846	ENSG00000268391	MTCO3P42
ENSG00000268393	0	0	0	0	ENSG00000268393	SPACA5B
ENSG00000268394	86.7328	97.7141	13.3466	24.2009	ENSG00000268394	EBP
ENSG00000268396	10.3405	10.7789	17.955	5.56686	ENSG00000268396	AC012485.1
ENSG00000268397	1.50355	1.8988	1.40501	2.2379	ENSG00000268397	AC008443.1
ENSG00000268399	0.371745	1.35637	0.786146	0.322253	ENSG00000268399	CTC-513N18.5
ENSG00000268400	0.178898	0.17258	1.11571	0	ENSG00000268400	AC008763.2
ENSG00000268402	4.23261	24.5852	18.2522	20.8474	ENSG00000268402	AL031320.1
ENSG00000268403	7.91694	19.1849	11.5375	6.85091	ENSG00000268403	AC132192.2
ENSG00000268407	0	0	0	0	ENSG00000268407	AC006115.2
ENSG00000268412	0	0	0	0	ENSG00000268412	TRMT112P6

ENSG00000268413	0	0	0	0	ENSG00000268413	AC003043.1
ENSG00000268417	0.0434986	0.0686276	0.10947	0.310342	ENSG00000268417	LRCH2
ENSG00000268418	0.317552	0.992092	1.49826	1.29167	ENSG00000268418	AC233300.1
ENSG00000268420	0	0	0.0290007	0.0726033	ENSG00000268420	RP6-99M1.1
ENSG00000268421	0.107435	0.309539	0.465857	0.926984	ENSG00000268421	AL355531.2
ENSG00000268422	0.13544	0.477178	0.27434	0.390848	ENSG00000268422	MAGEA8
ENSG00000268423	2.68675	6.0377	6.1936	9.36028	ENSG00000268423	AC093503.1
ENSG00000268424	0	0	0	0	ENSG00000268424	AC008948.1
ENSG00000268425	0	0	0	0	ENSG00000268425	AF238380.8
ENSG00000268426	0.0468877	0.114703	0.0612091	0.204937	ENSG00000268426	ERAS
ENSG00000268427	0	0	0	0	ENSG00000268427	AL022328.1
ENSG00000268429	0.093871	0.225483	0.288268	0.46572	ENSG00000268429	DOC2B
ENSG00000268430	3.98309	3.37943	2.12406	1.2239	ENSG00000268430	SHANK2
ENSG00000268431	7.29543	6.21829	4.39632	5.13537	ENSG00000268431	PRRG1
ENSG00000268432	0.716248	3.39633	1.98791	0.487572	ENSG00000268432	AC026407.1
ENSG00000268433	0.25245	0	0.175536	0	ENSG00000268433	MTDHP3
ENSG00000268434	0	0	0.413942	0	ENSG00000268434	AC011530.1
ENSG00000268437	0	0	0	0.0227979	ENSG00000268437	FAM47DP
ENSG00000268438	2.65043	3.10671	1.55026	4.53735	ENSG00000268438	BNIP3P27
ENSG00000268439	17.8959	12.3655	8.20963	7.93167	ENSG00000268439	EMG1
ENSG00000268440	13.3019	11.2597	11.8591	6.09197	ENSG00000268440	VBP1
ENSG00000268442	0.289396	0.389894	0.823716	0.883256	ENSG00000268442	AC073534.1
ENSG00000268444	1.24042	1.22062	2.68037	1.22865	ENSG00000268444	SRPK3
ENSG00000268447	0	0	0	0	ENSG00000268447	SSX2B
ENSG00000268448	0	0	0	0	ENSG00000268448	RP11-552J9.9
ENSG00000268449	0	0	0	0	ENSG00000268449	RP13-36C9.4
ENSG00000268451	0	0	0	0	ENSG00000268451	FTH1P18
ENSG00000268455	0.10841	0.0351272	0.125878	0.158901	ENSG00000268455	AC073544.1
ENSG00000268456	0.931283	0.900284	0.298212	0.586977	ENSG00000268456	IL13RA2
ENSG00000268457	626.083	871.685	290.9	713.302	ENSG00000268457	AL160175.1
ENSG00000268459	0	0	0	0	ENSG00000268459	RP13-150K15.1
ENSG00000268461	0.550262	0.516946	0	1.6689	ENSG00000268461	AC078899.2
ENSG00000268462	21.5686	18.03	17.7095	15.3011	ENSG00000268462	USP5
ENSG00000268465	0.327463	0.628531	0.966517	0.494517	ENSG00000268465	AC008403.1
ENSG00000268466	4.60255	9.66562	9.01924	14.0898	ENSG00000268466	AL132989.1
ENSG00000268467	0	0	0	0	ENSG00000268467	AP000889.3
ENSG00000268469	0	0.516993	0.584024	0.622327	ENSG00000268469	BNIP3P38
ENSG00000268470	0.299831	0.557693	0.424357	0.708695	ENSG00000268470	DNAH17-AS1
ENSG00000268472	0.733066	0.902154	1.14788	1.42297	ENSG00000268472	AP002884.5
ENSG00000268473	0	0	0	0	ENSG00000268473	AC092327.1
ENSG00000268476	0.698747	1.35193	1.5594	4.06705	ENSG00000268476	GPR173
ENSG00000268481	0	0	0	0	ENSG00000268481	PYY3
ENSG00000268482	0	1.35718	1.20342	1.45201	ENSG00000268482	AL160274.1
ENSG00000268483	0.24156	0.646148	0.46406	2.6268	ENSG00000268483	RPL7AP69
ENSG00000268484	0.202309	0.323287	0.699023	0.428891	ENSG00000268484	AC087477.1
ENSG00000268485	0	0	0	0.318141	ENSG00000268485	AC104841.2
ENSG00000268486	0	0	0	0	ENSG00000268486	FO681491.1
ENSG00000268487	0	0.0615134	0.0277951	0.0696936	ENSG00000268487	VN1R110P
ENSG00000268488	1.16009	4.75865	7.95947	6.12516	ENSG00000268488	AC018512.1
ENSG00000268489	101.362	40.7798	46.8926	28.8715	ENSG00000268489	RBM3
ENSG00000268490	0	0	0	0	ENSG00000268490	SPANXN3
ENSG00000268494	0	0	0	0	ENSG00000268494	RP13-77O11.8
ENSG00000268498	7.24052	9.78437	8.7016	11.2435	ENSG00000268498	HDAC8
ENSG00000268500	0	0	0	0	ENSG00000268500	AC018755.2

ENSG00000268501	6.1684	0.453566	0.124068	0	ENSG00000268501	CCDC22
ENSG00000268502	0	0	0	0	ENSG00000268502	BX842568.4
ENSG00000268503	7.36486	9.18939	5.05484	1.21678	ENSG00000268503	AC007421.1
ENSG00000268507	0.0750534	0.252227	0	0.435298	ENSG00000268507	AC078899.2
ENSG00000268509	0	0	0.164222	0.167164	ENSG00000268509	AC026202.3
ENSG00000268510	0.362815	1.00159	2.01675	3.2859	ENSG00000268510	IFNL3P1
ENSG00000268511	0	0.0767257	0.034677	0.108973	ENSG00000268511	NCLP2
ENSG00000268512	6.95576	5.7747	3.64917	4.12646	ENSG00000268512	CETN2
ENSG00000268514	0	0	0	0.0603742	ENSG00000268514	RP11-85L21.5
ENSG00000268519	0	0	0	0	ENSG00000268519	AC073528.1
ENSG00000268521	2.71334	2.95524	4.16653	4.68919	ENSG00000268521	VN1R83P
ENSG00000268523	0.0667835	0.0952754	0.113969	0.0713369	ENSG00000268523	RP5-937E21.1
ENSG00000268524	0	0	0	0	ENSG00000268524	GAGE12B
ENSG00000268526	0.0246944	0.0237861	0.0214882	0.0269685	ENSG00000268526	HNRNPH1P2
ENSG00000268529	0.315619	0.234079	0.20559	0.0855964	ENSG00000268529	CYP2T3P
ENSG00000268531	0	0.0477595	0.0431396	0	ENSG00000268531	AC060814.4
ENSG00000268533	6.6746	19.1195	17.9768	24.6822	ENSG00000268533	AC003002.3
ENSG00000268534	0	0	0	0	ENSG00000268534	SSXP5
ENSG00000268535	0.128456	0.165057	0.0882369	0.068308	ENSG00000268535	MTDHP4
ENSG00000268537	0	0	0	0	ENSG00000268537	AC109583.1
ENSG00000268538	9.8059	11.4208	15.5249	10.0879	ENSG00000268538	KIAA1658
ENSG00000268539	0	0.0820738	0.148179	0.182544	ENSG00000268539	RP11-322A17.1
ENSG00000268541	0.368738	0.69832	0	0	ENSG00000268541	VN1R88P
ENSG00000268542	0.201334	0.0977487	0.13755	0.109889	ENSG00000268542	RP3-525N14.2
ENSG00000268545	2.14984	0	0	0.711317	ENSG00000268545	VN1R107P
ENSG00000268546	0.0530431	0.171548	0.0341501	0.455038	ENSG00000268546	SSX1
ENSG00000268547	0	0.140018	0	0	ENSG00000268547	RP11-183K14.1
ENSG00000268548	142.848	117.095	79.5247	75.1267	ENSG00000268548	TPI1
ENSG00000268550	0	0.364891	0.328445	0.397773	ENSG00000268550	AC090427.1
ENSG00000268551	47.2707	34.3399	25.8631	20.6222	ENSG00000268551	ATP5L
ENSG00000268552	4.34988	0	0	0	ENSG00000268552	AL109927.1
ENSG00000268553	0	0	0	0	ENSG00000268553	AC027309.1
ENSG00000268554	4.35522	12.8689	13.2163	12.8311	ENSG00000268554	RP11-353N4.7
ENSG00000268556	0	0	0	0	ENSG00000268556	AC012360.1
ENSG00000268557	9.13834	9.64404	9.55353	6.01932	ENSG00000268557	EMD
ENSG00000268558	0.0943192	0.180519	0.162983	0.30056	ENSG00000268558	RP11-370B6.1
ENSG00000268563	5.34683	5.94737	6.83639	8.21242	ENSG00000268563	MECP2
ENSG00000268569	4.50253	5.18039	6.79874	6.15029	ENSG00000268569	HIRA
ENSG00000268570	5.61269	5.68962	7.00043	4.92844	ENSG00000268570	FAM199X
ENSG00000268572	0	0	0	0	ENSG00000268572	RP11-204I15.1
ENSG00000268574	0.049494	0.178033	0.103193	0.419403	ENSG00000268574	PABPC1L2A
ENSG00000268576	7.0484	10.2463	16.7493	20.1751	ENSG00000268576	AC239811.1
ENSG00000268578	0	3.39731	2.80279	6.27339	ENSG00000268578	AL354718.1
ENSG00000268579	2.92766	3.5494	3.07844	1.69032	ENSG00000268579	PHKA1
ENSG00000268581	0	0	0	0	ENSG00000268581	SIGLEC18P
ENSG00000268582	0	0	0	0	ENSG00000268582	AC243960.4
ENSG00000268585	0	0	0	0	ENSG00000268585	PRP11-234P3.4
ENSG00000268589	0	0	0	0	ENSG00000268589	AC011467.2
ENSG00000268590	0	0	0	0	ENSG00000268590	BAGE5
ENSG00000268591	5.89402	5.61367	7.91293	5.73892	ENSG00000268591	PLXNB3
ENSG00000268593	0.832901	1.74009	2.82393	4.51538	ENSG00000268593	AC008749.1
ENSG00000268598	1.70135	2.42517	4.13938	2.67041	ENSG00000268598	VN1R80P
ENSG00000268600	0	0	0	0	ENSG00000268600	RP13-210D15.1

ENSG00000268602	0	0	0	0	ENSG00000268602	AP002353.1
ENSG00000268604	1.60013	14.5152	2.48551	0.741816	ENSG00000268604	SLC10A3
ENSG00000268606	7.54E-05	0	0	0	ENSG00000268606	MAGEA2
ENSG00000268607	0	0.014036	0.000353627	0.0478109	ENSG00000268607	HSPA8P7
ENSG00000268608	0.198633	1.86385	2.18357	0.803712	ENSG00000268608	IDSP1
ENSG00000268609	0	0	0	0	ENSG00000268609	AF277315.19
ENSG00000268611	0	0	0	0	ENSG00000268611	AF196972.10
ENSG00000268612	4.2123	2.95422	3.10517	2.43695	ENSG00000268612	ABT1
ENSG00000268614	0	0.0919358	0	0.0785977	ENSG00000268614	AC008878.2
ENSG00000268620	0.344292	0	0.579878	0	ENSG00000268620	AC078899.3
ENSG00000268623	0	0	0.0790675	0	ENSG00000268623	AC020904.1
ENSG00000268624	0	0	0	0	ENSG00000268624	AC243428.1
ENSG00000268625	0	0	0	0	ENSG00000268625	WASF4P
ENSG00000268626	0	0	0	0	ENSG00000268626	AC103809.2
ENSG00000268628	1.59796	1.74423	0.984586	0.964222	ENSG00000268628	AL121761.2
ENSG00000268629	0.051447	0	0	0	ENSG00000268629	TEX13A
ENSG00000268630	1.33849	4.36982	3.42431	2.80391	ENSG00000268630	DDX26B
ENSG00000268632	25.3586	52.8464	33.9966	59.3691	ENSG00000268632	AC073657.1
ENSG00000268633	0.0383857	0.0657918	0.0905063	0.0773425	ENSG00000268633	RP3-514P16.1
ENSG00000268635	4.65028	3.87091	4.7071	11.4297	ENSG00000268635	AP003680.1
ENSG00000268637	17.8635	53.2022	63.1733	20.5964	ENSG00000268637	CR753820.1
ENSG00000268638	0.256922	0.267588	0.777344	0.380334	ENSG00000268638	KRT18P62
ENSG00000268640	146.93	226.513	232.465	283.79	ENSG00000268640	AC026369.1
ENSG00000268641	0	0	0	0	ENSG00000268641	RP11-157B13.3
ENSG00000268642	17.0854	9.2679	11.0091	10.0779	ENSG00000268642	HNRNPH2
ENSG00000268643	0	0.645169	1.25829	1.31555	ENSG00000268643	AC006486.1
ENSG00000268644	0.0880032	0.119891	0.0906927	0.145303	ENSG00000268644	PNMA5
ENSG00000268645	0	0	0	0	ENSG00000268645	RP5-1014O16.10
ENSG00000268646	4.51251	2.5765	0.763609	1.01503	ENSG00000268646	PCSK1N
ENSG00000268648	0	0	0	0	ENSG00000268648	RP13-228J13.9
ENSG00000268651	0	0.833518	0	0	ENSG00000268651	CTAG1A
ENSG00000268652	0	0.0700286	0	0	ENSG00000268652	AC063977.4
ENSG00000268656	0	0	0	7.46298	ENSG00000268656	AC110084.1
ENSG00000268657	0.976456	1.23886	0.981849	2.1711	ENSG00000268657	AL133373.1
ENSG00000268660	0.103803	0.351827	0.249621	0.659216	ENSG00000268660	LETM1P2
ENSG00000268662	34.7978	94.5852	47.0485	86.771	ENSG00000268662	AL596220.1
ENSG00000268663	0	0.303096	0.309359	0	ENSG00000268663	WBP1LP6
ENSG00000268667	0.0913621	0.494067	0.285282	0.22121	ENSG00000268667	TMSB15B
ENSG00000268668	1.11058	2.8919	2.28357	3.31033	ENSG00000268668	SHROOM4
ENSG00000268669	0	0	0	0.139559	ENSG00000268669	AC008687.5
ENSG00000268671	2.9335	6.66979	6.95396	6.84704	ENSG00000268671	HAUS7
ENSG00000268674	0	0	0.255665	0	ENSG00000268674	FAM231D
ENSG00000268675	4.99587	3.68374	4.05098	3.36238	ENSG00000268675	GPKOW
ENSG00000268679	1.53115	0.465719	0	0.336722	ENSG00000268679	AC233294.1
ENSG00000268681	0.71676	0	0	0.718832	ENSG00000268681	COX6CP7
ENSG00000268682	0.795036	0.407631	1.39869	9.40493	ENSG00000268682	MAGED4B
ENSG00000268685	0	0	0	0.419685	ENSG00000268685	AC011494.1
ENSG00000268688	9.69207	13.2818	8.66541	14.9535	ENSG00000268688	AC007382.1
ENSG00000268690	15.6236	17.5823	16.7452	18.1408	ENSG00000268690	GDI1
ENSG00000268691	2.58633	3.07531	2.91372	4.17553	ENSG00000268691	LDOC1
ENSG00000268692	0	0	0	0	ENSG00000268692	RP11-272G22.3
ENSG00000268693	1.39758	2.36404	2.29808	3.74647	ENSG00000268693	RPH3AL
ENSG00000268694	0	0.157017	0.0708699	0	ENSG00000268694	DUTP4

ENSG00000268695	0.233588	0.123547	0.220798	0.259566	ENSG00000268695	CT55
ENSG00000268696	0.163758	0.303998	0.163053	0.26124	ENSG00000268696	ZNF723
ENSG00000268699	0.789852	2.82036	3.08563	4.03078	ENSG00000268699	GAB3
ENSG00000268700	1.87862	3.59487	3.46408	1.91412	ENSG00000268700	MTCP1
ENSG00000268702	55.7876	17.0942	7.38277	24.0328	ENSG00000268702	AL049829.1
ENSG00000268703	0.179783	0.495723	0.745437	0.180923	ENSG00000268703	RP11-232D9.4
ENSG00000268705	1.47738	1.6666	1.36503	1.29124	ENSG00000268705	BNIP3P26
ENSG00000268706	140.064	386.822	293.104	479.352	ENSG00000268706	AC009802.1
ENSG00000268708	0	0	0	1.24894	ENSG00000268708	BX088651.2
ENSG00000268709	0.0403835	0.00784444	0.0720191	0.0558687	ENSG00000268709	MAGEA11
ENSG00000268711	0	0	0	0	ENSG00000268711	AC008750.6
ENSG00000268712	0	0	0	0	ENSG00000268712	GLOD5
ENSG00000268714	0	0	0	0	ENSG00000268714	ARL14EPL
ENSG00000268715	0	0	0	0	ENSG00000268715	YAP1P2
ENSG00000268716	0	0	0	0	ENSG00000268716	AC055736.1
ENSG00000268717	0.126528	0	0	0.136835	ENSG00000268717	BNIP3P33
ENSG00000268718	0	0	0	0.257549	ENSG00000268718	RP1-169P22.2
ENSG00000268719	0	0	0	0	ENSG00000268719	AL671561.1
ENSG00000268721	0.0536842	0.0516731	0.0467021	0.175716	ENSG00000268721	RP11-588H23.5
ENSG00000268722	4.11793	6.84835	6.09008	9.8316	ENSG00000268722	ARMCX4
ENSG00000268723	0.308983	0	0	0.892923	ENSG00000268723	AC005261.5
ENSG00000268726	0	0	0	0	ENSG00000268726	RP13-444K19.1
ENSG00000268727	0	0	0	0.0264192	ENSG00000268727	ASS1P5
ENSG00000268728	19.8305	32.8583	17.6783	25.286	ENSG00000268728	BX001040.1
ENSG00000268730	4.84319	4.87334	4.25152	13.3139	ENSG00000268730	AC022819.2
ENSG00000268731	0.495405	0.710388	0.209042	0.768321	ENSG00000268731	AC010615.3
ENSG00000268733	6.34865	4.67594	7.28136	6.32849	ENSG00000268733	NCS1
ENSG00000268735	4.91508	18.5761	0	11.4972	ENSG00000268735	AL139080.1
ENSG00000268736	0	0	0	0.0772846	ENSG00000268736	MTCO3P39
ENSG00000268737	0.115522	0.245276	0.265857	0.39995	ENSG00000268737	SLITRK2
ENSG00000268738	0	0	0.931522	0.747474	ENSG00000268738	HSFX2
ENSG00000268740	1.76024	4.18157	0.521621	0.438737	ENSG00000268740	SUV39H1
ENSG00000268742	0	0	0	0	ENSG00000268742	AC010503.3
ENSG00000268744	0.93528	1.73824	1.10574	1.80061	ENSG00000268744	AC008758.4
ENSG00000268747	1.33338	0	1.69839	0.688367	ENSG00000268747	AC022432.1
ENSG00000268750	5.53541	5.71409	7.76279	9.98414	ENSG00000268750	AC010522.1
ENSG00000268753	0	0	0	0	ENSG00000268753	LA16c-4G1.4
ENSG00000268757	1.80534	1.53359	1.31966	2.47447	ENSG00000268757	ABCD1
ENSG00000268758	0.111695	0.399935	0.349111	0.595623	ENSG00000268758	ADGRE4P
ENSG00000268759	0.142357	0.277229	0.263592	0.288321	ENSG00000268759	AC135983.2
ENSG00000268760	0.0774689	0.0930421	0.168105	0.493846	ENSG00000268760	TMEM255A
ENSG00000268762	1.3175	1.26968	1.01164	1.37033	ENSG00000268762	SPIN4
ENSG00000268763	4.23546	11.731	6.7839	16.4658	ENSG00000268763	AC018630.2
ENSG00000268765	0.0974455	0.213717	0.166217	0.162543	ENSG00000268765	CYBB
ENSG00000268766	0	0.0810189	0.0731318	0.139085	ENSG00000268766	AP002954.6
ENSG00000268767	81.7602	45.9974	61.0274	20.0534	ENSG00000268767	PLS3
ENSG00000268768	7.87845	7.86789	6.28205	8.57649	ENSG00000268768	HCFC1
ENSG00000268771	0	0	0	0	ENSG00000268771	MRPL32P1
ENSG00000268775	0	0	0	0	ENSG00000268775	RP11-552J9.11
ENSG00000268776	0	0	0	0	ENSG00000268776	RP13-34L8.8
ENSG00000268779	0.308375	0.821533	0.638384	1.10022	ENSG00000268779	CD4
ENSG00000268780	0	0	0.0764747	0.0482504	ENSG00000268780	RP3-339A18.3

ENSG00000268781	0	0	0	0	ENSG00000268781	AL590235.1
ENSG00000268784	4.23345	5.31596	8.16121	13.0275	ENSG00000268784	AC016629.1
ENSG00000268785	0	0.176041	0	0	ENSG00000268785	RPL7P50
ENSG00000268786	1.83827	2.54679	2.01658	4.33132	ENSG00000268786	AC115618.2
ENSG00000268788	3.17041	5.88725	0.249935	0.493381	ENSG00000268788	AC110615.1
ENSG00000268789	0	0	0.136659	0	ENSG00000268789	VN1R87P
ENSG00000268790	0.517888	0	0.475075	0	ENSG00000268790	AC008764.4
ENSG00000268791	4.48567	9.99393	9.47166	15.2582	ENSG00000268791	AC093323.1
ENSG00000268792	0.71775	0.431978	0.35141	0.274858	ENSG00000268792	SPANXN5
ENSG00000268793	0	0	0	0	ENSG00000268793	SSXP9
ENSG00000268794	0	0	0.12804	0.0990545	ENSG00000268794	VN1R90P
ENSG00000268796	0	0	0	0	ENSG00000268796	SSU72P1
ENSG00000268797	0	0	0	0	ENSG00000268797	AC008537.1
ENSG00000268798	2.27255	3.99417	3.55574	2.24406	ENSG00000268798	AC027307.3
ENSG00000268799	0.414064	0	0	0	ENSG00000268799	AC106774.4
ENSG00000268800	1.28764	0	9.1239	0	ENSG00000268800	AC112205.1
ENSG00000268803	0.0456186	0	0	0	ENSG00000268803	AC114797.1
ENSG00000268805	0.546914	7.55093	13.7635	12.3254	ENSG00000268805	PRED57
ENSG00000268806	0	0.043007	0	0.0968853	ENSG00000268806	RPL7AP71
ENSG00000268807	0	0	0	0	ENSG00000268807	GAPDHP67
ENSG00000268809	0	0	0	0	ENSG00000268809	AC012360.2
ENSG00000268815	10.6154	13.8046	6.23248	5.17589	ENSG00000268815	GLA
ENSG00000268818	0.565222	0	3.16523	4.8415	ENSG00000268818	AL049747.1
ENSG00000268819	0	0	0	0	ENSG00000268819	AL590812.1
ENSG00000268820	0	0.17432	0.443495	0.363927	ENSG00000268820	RPL21P132
ENSG00000268821	0	20.4206	23.5556	69.2658	ENSG00000268821	AC068039.1
ENSG00000268822	0	0	0	0	ENSG00000268822	AC011298.1
ENSG00000268825	0.0131877	0.0762661	0.0344739	0.0434295	ENSG00000268825	RP11-432N13.4
ENSG00000268826	0	0	0.0376479	0.0190546	ENSG00000268826	LL0XNC01
ENSG00000268827	0.321816	0.371323	0.225015	1.04596	ENSG00000268827	FMR1NB
ENSG00000268828	3.08693	8.15854	4.57589	17.4918	ENSG00000268828	LEPREL2
ENSG00000268829	0	0	1.56038	3.94862	ENSG00000268829	LPCAT3
ENSG00000268830	0	0	0.113753	0	ENSG00000268830	BNIP3P32
ENSG00000268832	0	0	0	0	ENSG00000268832	OPN1LW
ENSG00000268834	0.207426	0.465449	0.240323	0.375847	ENSG00000268834	OR7A1P
ENSG00000268838	0.0937754	0.496611	0.244836	0.309219	ENSG00000268838	AC027288.1
ENSG00000268839	0	0	0	0	ENSG00000268839	AC020914.3
ENSG00000268843	0	0	0.0940372	4.87E-05	ENSG00000268843	AC118758.6
ENSG00000268846	5.70615	11.2351	5.03811	15.0974	ENSG00000268846	AC018867.2
ENSG00000268847	0.132327	0	0	0.141967	ENSG00000268847	SIGLEC31P
ENSG00000268848	0	0.0436827	0	0.0491869	ENSG00000268848	RP13-565O16.2
ENSG00000268849	0	0.129248	0	0	ENSG00000268849	SIGLEC22P
ENSG00000268851	0	0	0.00896809	0.0112895	ENSG00000268851	AL162851.1
ENSG00000268852	2.50768	6.26423	5.27885	11.1303	ENSG00000268852	AC132872.2
ENSG00000268853	0.0522752	0.0617862	0	0.0899141	ENSG00000268853	FGF16
ENSG00000268856	5.96395	9.24225	7.81274	7.57981	ENSG00000268856	AP001579.1
ENSG00000268857	0	0	0	0	ENSG00000268857	AC011308.1
ENSG00000268858	0	0	0.659837	0	ENSG00000268858	AL118506.1
ENSG00000268861	8.88E-08	0.183598	0.213178	0.0936188	ENSG00000268861	AC008878.3
ENSG00000268862	8.5582	24.8249	18.3485	13.0542	ENSG00000268862	PLXNA3
ENSG00000268863	0.289264	0.366562	0.342383	0.112141	ENSG00000268863	AC135048.1
ENSG00000268864	2.11462	3.37737	3.71582	6.2607	ENSG00000268864	AC011487.2
ENSG00000268865	0.644227	0.323281	0.4863	1.0386	ENSG00000268865	AC026310.1

ENSG00000268866	0	0.248164	0.112133	0	ENSG00000268866	AC020915.5
ENSG00000268867	0	0	0	0.0276344	ENSG00000268867	BX842568.2
ENSG00000268869	2.46678	2.2662	1.54796	1.55335	ENSG00000268869	ESPNP
ENSG00000268870	0	0.410219	0	0	ENSG00000268870	AC008758.5
ENSG00000268871	5.62304	0.116325	7.82064	5.10415	ENSG00000268871	CXorf40B
ENSG00000268872	3.3068	6.27533	6.05689	10.979	ENSG00000268872	ATN1
ENSG00000268876	0.885998	1.6818	0.986356	1.8138	ENSG00000268876	ARHGAP4
ENSG00000268879	6.3583	1.77606	5.22015	2.87673	ENSG00000268879	IGFL1P1
ENSG00000268882	0	12.6209	0	1.36394	ENSG00000268882	AL360181.1
ENSG00000268883	0	0.120955	0	0.276357	ENSG00000268883	PNMA6B
ENSG00000268884	0	0.282531	0.412028	0.443664	ENSG00000268884	AC010323.2
ENSG00000268885	2.98428	4.02918	5.47041	4.5154	ENSG00000268885	AC026740.1
ENSG00000268891	21.6355	34.0864	33.6731	49.6725	ENSG00000268891	AC006014.1
ENSG00000268892	0	0.109394	0	0.123774	ENSG00000268892	AC010620.1
ENSG00000268893	0	0.210026	0.189644	0.156256	ENSG00000268893	RP11-274K13.5
ENSG00000268897	0.389096	2.10936	2.53574	2.40177	ENSG00000268897	BTK
ENSG00000268898	0	0	0	31.0131	ENSG00000268898	AC007377.1
ENSG00000268903	0	0	0	0	ENSG00000268903	AL627309.7
ENSG00000268904	6.25081	13.8882	10.3122	3.78278	ENSG00000268904	TAZ
ENSG00000268905	0	0	0	0	ENSG00000268905	RBM22P10
ENSG00000268908	0.270112	0.779274	0.0815013	1.24838	ENSG00000268908	VN1R92P
ENSG00000268910	0.0828423	0.451818	0.552469	1.23483	ENSG00000268910	RP11-22B10.3
ENSG00000268914	0.035809	0	0.150633	0.0389052	ENSG00000268914	HNRNPCP10
ENSG00000268916	1.19062	2.86616	2.19939	3.21398	ENSG00000268916	CSAG3
ENSG00000268917	0	0	0	0	ENSG00000268917	RP11-344N17.9
ENSG00000268918	0	0	0	0	ENSG00000268918	RP5-1170D6.1
ENSG00000268919	0.0225664	0	0	0	ENSG00000268919	RHOXF2
ENSG00000268920	0.0301358	0.0576578	0.0315043	0.0669767	ENSG00000268920	CSAG1
ENSG00000268921	0.194746	0.467952	0.37258	1.69253	ENSG00000268921	RP3-393P12.1
ENSG00000268922	0	0	0	0	ENSG00000268922	AC012616.1
ENSG00000268923	6.56519	9.974	24.618	45.9789	ENSG00000268923	AL645922.1
ENSG00000268924	0	0	0.0286367	0.110864	ENSG00000268924	RP13-228J13.8
ENSG00000268925	0	0	0	0	ENSG00000268925	AL161645.2
ENSG00000268926	0.329822	0.761368	0.660088	0.956257	ENSG00000268926	AL354861.3
ENSG00000268927	0.340141	1.67834	1.87792	1.97583	ENSG00000268927	FLJ00418
ENSG00000268928	25.7868	22.6344	11.6134	15.2142	ENSG00000268928	SLC25A1
ENSG00000268933	0	0	0.0289661	0	ENSG00000268933	U82671.8
ENSG00000268934	0	0	0	0	ENSG00000268934	RBM22P7
ENSG00000268935	2.05572	0.895161	0.356389	1.31157	ENSG00000268935	RP4-545K15.3
ENSG00000268936	0.10188	0.239509	0.407822	0.276507	ENSG00000268936	AP003062.1
ENSG00000268937	0.0358342	0.0631107	0	0.146523	ENSG00000268937	AC115617.2
ENSG00000268940	0.0977046	0	0	0	ENSG00000268940	CT45A1
ENSG00000268941	0.135849	0.635378	0.977558	1.10526	ENSG00000268941	LINC01711
ENSG00000268942	0	1.04065	0	0	ENSG00000268942	CKS1BP3
ENSG00000268943	0.403696	1.70223	1.38133	0.452523	ENSG00000268943	CLIC2
ENSG00000268944	21.2747	19.0568	21.0137	15.7978	ENSG00000268944	IRAK1
ENSG00000268946	2.81158	6.54484	15.3634	25.4657	ENSG00000268946	ATRX
ENSG00000268948	10.7428	15.8185	14.4828	22.622	ENSG00000268948	AC004017.1
ENSG00000268949	1.56502	3.69593	3.72945	6.18739	ENSG00000268949	MRPS17P1
ENSG00000268950	0.434172	4.57498	2.79319	4.67888	ENSG00000268950	AC114494.1
ENSG00000268951	0	0.118826	0	0	ENSG00000268951	AL772155.3
ENSG00000268953	0.217206	0	0.374802	1.14821	ENSG00000268953	AC020952.1
ENSG00000268954	4.53221	6.3694	4.0226	2.96146	ENSG00000268954	PTPN6
ENSG00000268955	1.07014	14.018	8.84805	18.3263	ENSG00000268955	AC068020.1

ENSG00000268956	3.43755	9.2273	11.9369	10.8624	ENSG00000268956	RP11-313P13.3
ENSG00000268957	0	0	0	0	ENSG00000268957	AC020914.4
ENSG00000268960	0	0.154787	0.269006	0.305574	ENSG00000268960	AC091150.1
ENSG00000268962	0	0	0	0	ENSG00000268962	RP11-552E4.4
ENSG00000268963	645.152	571.843	455.107	305.689	ENSG00000268963	RPL10
ENSG00000268964	0	0.143353	0	0	ENSG00000268964	ERVV-2
ENSG00000268965	0.3869	1.85101	1.39689	1.84808	ENSG00000268965	AC061992.1
ENSG00000268967	0	0	0	0	ENSG00000268967	AC119751.7
ENSG00000268975	0.167591	0	0	0	ENSG00000268975	MIA-RAB4B
ENSG00000268977	0	4.11991	5.89564	8.66181	ENSG00000268977	PIH1
ENSG00000268980	2.11783	5.6798	3.73923	3.79513	ENSG00000268980	HUWE1
ENSG00000268982	33.0071	35.9382	22.9535	17.4518	ENSG00000268982	SLC6A8
ENSG00000268986	0	0	0	0	ENSG00000268986	AC225613.8
ENSG00000268988	0	0	0	0.00439554	ENSG00000268988	SPANXN2
ENSG00000268990	0	0.210343	0	0	ENSG00000268990	U82670.9
ENSG00000268991	0	0	0	0	ENSG00000268991	FAM231B
ENSG00000268992	0.778473	1.91117	1.34497	1.03714	ENSG00000268992	CDC42EP3P1
ENSG00000268993	0	0	0	0	ENSG00000268993	AC244453.4
ENSG00000268995	8.4932	4.71922	5.45926	3.38505	ENSG00000268995	VN1R82P
ENSG00000268996	2.2477	2.13243	2.20297	1.00392	ENSG00000268996	MAN1B1-AS1
ENSG00000268997	0	0	0	0	ENSG00000268997	DNAJC19P3
ENSG00000268998	0.0696583	0.0325235	0.0297489	0.07334	ENSG00000268998	VN1R14P
ENSG00000268999	0	0.0407909	0.0382286	0.0951634	ENSG00000268999	XRCC6P2
ENSG00000269000	0	0	0	0	ENSG00000269000	AC108868.1
ENSG00000269001	5.77501	5.975	3.20689	4.27753	ENSG00000269001	AC092070.2
ENSG00000269002	0.758167	0.749504	0.936844	0.618571	ENSG00000269002	FOXP3
ENSG00000269003	0.311287	0.541821	0.832236	0.666906	ENSG00000269003	NUDT10
ENSG00000269004	0	0	0	0	ENSG00000269004	RP11-272G22.1
ENSG00000269007	3.09533	1.9666	3.28881	3.26987	ENSG00000269007	LAGE3
ENSG00000269009	0.731728	0.465143	1.26126	0	ENSG00000269009	SLC6A21P
ENSG00000269010	0.333371	0.0643923	0	0	ENSG00000269010	CT83
ENSG00000269011	0	0	0.00896809	0.0112895	ENSG00000269011	AL050303.1
ENSG00000269012	0	0	0	0	ENSG00000269012	KRT18P40
ENSG00000269013	0	0	0	0	ENSG00000269013	RP11-157B13.1
ENSG00000269014	0	0	0	0	ENSG00000269014	AC008622.1
ENSG00000269016	0	0	0	0	ENSG00000269016	GAGE2A
ENSG00000269017	0.197109	0.230624	0.183093	0.253604	ENSG00000269017	RP11-97N5.2
ENSG00000269018	0.170341	0	0.72377	1.39157	ENSG00000269018	AP001362.1
ENSG00000269020	19.8305	32.8583	17.6783	25.286	ENSG00000269020	CR753864.1
ENSG00000269021	0.063711	0	0.0553915	0	ENSG00000269021	AC063977.5
ENSG00000269024	0	0	0	0	ENSG00000269024	RP6-29D12.3
ENSG00000269025	0	0	3.26426	5.20605	ENSG00000269025	AC011467.4
ENSG00000269026	0	0	0	0.439406	ENSG00000269026	AC003006.1
ENSG00000269027	0	0	0	0	ENSG00000269027	AC010368.2
ENSG00000269028	134811	139154	181243	160361	ENSG00000269028	MTRNR2L12
ENSG00000269029	0	0	0	0	ENSG00000269029	RP35-1158E12.2
ENSG00000269030	0	0	0	0	ENSG00000269030	GAGE10
ENSG00000269031	3.91683	3.64454	3.16323	2.66995	ENSG00000269031	MTM1
ENSG00000269032	0.0381712	3.76997	0	3.64341	ENSG00000269032	AC016629.2
ENSG00000269034	68.6859	88.462	40.5775	23.2975	ENSG00000269034	PLP2
ENSG00000269035	0	0	0	0	ENSG00000269035	AC010319.2
ENSG00000269036	6.89976	7.33748	4.42591	3.33141	ENSG00000269036	SLC9A6
ENSG00000269040	0.148773	1.00942	0.582471	0.851745	ENSG00000269040	BNIP3P24
ENSG00000269041	13.4488	8.33632	12.6558	6.79843	ENSG00000269041	IDS

ENSG00000269042	0	0	0	37.6565	ENSG00000269042	AP001925.1
ENSG00000269047	0	0	0	0	ENSG00000269047	AC009041.2
ENSG00000269048	0.468589	1.22577	1.77093	2.87747	ENSG00000269048	Z98049.1
ENSG00000269049	4.91057	8.64562	8.41575	20.8664	ENSG00000269049	AC092291.2
ENSG00000269052	0	0.303617	0	0.338298	ENSG00000269052	XAGE3
ENSG00000269055	0.0750534	0.252227	0	0.435298	ENSG00000269055	BNIP3P18
ENSG00000269056	3.6572	3.722	3.59119	2.47347	ENSG00000269056	PBDC1
ENSG00000269057	1.32459	3.1351	2.79181	3.05745	ENSG00000269057	CACNA1F
ENSG00000269058	0.196194	0.185769	0.0926215	0.0500692	ENSG00000269058	CALR3
ENSG00000269059	0	0	0	0	ENSG00000269059	CTD-2183H9.7
ENSG00000269062	0	0	0	0	ENSG00000269062	BX842568.1
ENSG00000269063	0	0	0	0.0449071	ENSG00000269063	SPANXA1
ENSG00000269064	106.27	1286.26	197.518	613.282	ENSG00000269064	AL160286.1
ENSG00000269065	0.137952	0.182932	0.109954	0.173159	ENSG00000269065	LL0XNC01-116E7.4
ENSG00000269067	0.791561	1.96263	0.881966	1.60225	ENSG00000269067	ZNF728
ENSG00000269069	0.502337	1.12384	1.7018	1.55435	ENSG00000269069	AC007842.1
ENSG00000269071	0.214618	0	0.555415	0.950567	ENSG00000269071	AC138517.1
ENSG00000269074	0	0	0	0	ENSG00000269074	AC099344.1
ENSG00000269075	0.0288577	0.100819	0.0858465	0.162255	ENSG00000269075	HTR2C
ENSG00000269076	0	0	0	0	ENSG00000269076	XAGE2B
ENSG00000269079	80.9921	89.3107	73.9614	37.5676	ENSG00000269079	PHB2
ENSG00000269080	0.144119	0.444797	0.496854	0.144856	ENSG00000269080	RP11-232D9.1
ENSG00000269081	7.54E-05	0	0	0	ENSG00000269081	MAGE2A
ENSG00000269083	26.3212	26.6972	17.6537	17.3382	ENSG00000269083	COX7B
ENSG00000269084	20.5238	89.8472	64.8983	139.137	ENSG00000269084	AC009977.1
ENSG00000269087	4.04283	23.2195	4.27067	5.81086	ENSG00000269087	G6PD
ENSG00000269088	0	0.405913	1.74095	0.595531	ENSG00000269088	RP11-234P3.2
ENSG00000269089	0.6846	0.675598	1.14654	0.850249	ENSG00000269089	AP003733.1
ENSG00000269092	0	0	0	0	ENSG00000269092	CTD-2230M5.1
ENSG00000269093	1.05592	3.0035	2.37402	0.991311	ENSG00000269093	AC007773.3
ENSG00000269094	4.33669	7.05771	7.9903	6.00294	ENSG00000269094	AC006449.1
ENSG00000269095	0.386563	0.378413	0.503404	0.615494	ENSG00000269095	AC010646.1
ENSG00000269096	0	0	0	0	ENSG00000269096	CT45A3
ENSG00000269097	0.431951	0	0.0811862	0.0935606	ENSG00000269097	TPRG1LP1
ENSG00000269099	0	1.75939	0	0	ENSG00000269099	LSP1P1
ENSG00000269100	0.434172	4.57498	2.79319	4.67888	ENSG00000269100	AC114494.2
ENSG00000269101	16.4253	25.8964	18.2922	25.3209	ENSG00000269101	HDAC6
ENSG00000269103	33.3801	90.6158	112.223	170.482	ENSG00000269103	AC002472.1
ENSG00000269104	0	0	0	0	ENSG00000269104	AL035681.1
ENSG00000269108	0	0	0	0.397773	ENSG00000269108	GS1-164F24.1
ENSG00000269109	0.0867049	0	0.16259	0	ENSG00000269109	PNMA6C
ENSG00000269111	0.148773	1.00942	0.582471	0.851745	ENSG00000269111	CTD-2626G11.3
ENSG00000269113	0.188252	0.404806	0.506785	0.744649	ENSG00000269113	TRABD2B
ENSG00000269114	0	0	0	0	ENSG00000269114	MAGEA6
ENSG00000269115	0.32439	0.530343	0.757616	0.5456	ENSG00000269115	TTC36
ENSG00000269117	2.14387	5.94518	3.11435	4.36332	ENSG00000269117	AL121901.1
ENSG00000269118	0	1.03E-05	2.94E-05	2.65E-05	ENSG00000269118	FAM90A28P
ENSG00000269119	0	0	0	0.0365034	ENSG00000269119	HNRNPA1P52
ENSG00000269120	0	1.72145	1.51103	0	ENSG00000269120	AL133318.1
ENSG00000269121	40.9585	65.121	61.2712	177.126	ENSG00000269121	AC007216.2
ENSG00000269122	1.63324	3.11634	2.38126	3.92602	ENSG00000269122	SSX3
ENSG00000269123	0.22754	0.798009	0.788226	0.864693	ENSG00000269123	RPL7P57
ENSG00000269126	0	0	0.113447	0.0471657	ENSG00000269126	RP11-143H17.1
ENSG00000269128	0	0	0	0	ENSG00000269128	RP13-77O11.12

ENSG00000269130	0	1.41209	0.510543	0.310777	ENSG00000269130	AC020914.5
ENSG00000269133	0	0	0	0	ENSG00000269133	OPN1MW2
ENSG00000269135	0.11222	0.0631192	0.109461	0.125562	ENSG00000269135	PGAM4
ENSG00000269136	0.169429	0.282272	0.18237	0.409683	ENSG00000269136	BRI3BPP1
ENSG00000269138	0.145645	0.117449	0.106327	0.135927	ENSG00000269138	ZNF209P
ENSG00000269142	0.0481153	0.0524747	0.197778	1.13452	ENSG00000269142	RPL7L1P11
ENSG00000269144	0	0	0	0	ENSG00000269144	RP11-344N17.13
ENSG00000269147	0	0	0	0	ENSG00000269147	CTD-2542C24.7
ENSG00000269149	0	0	0	0	ENSG00000269149	GAGE12J
ENSG00000269153	0	0	0	0	ENSG00000269153	LYPLA2P2
ENSG00000269154	0.61924	0.592953	0	0.614895	ENSG00000269154	BNIP3P13
ENSG00000269155	0.92955	1.4488	0.8543	0.731222	ENSG00000269155	AL009178.2
ENSG00000269156	0.0558027	0.368731	0.553969	0.323113	ENSG00000269156	AC234771.2
ENSG00000269158	0.00264751	0	0	0	ENSG00000269158	SLITRK4
ENSG00000269159	0	0	0.806021	0.311284	ENSG00000269159	CU151838.2
ENSG00000269162	1.76473	2.60636	2.77675	2.66002	ENSG00000269162	ZNF75D
ENSG00000269164	0	0	0	0	ENSG00000269164	RP6-29D12.4
ENSG00000269165	0.952502	1.78102	1.94466	1.55099	ENSG00000269165	AC069547.1
ENSG00000269167	6.56519	9.974	24.618	45.9789	ENSG00000269167	CR753845.2
ENSG00000269168	0.0263198	0.0946319	1.63545	13.297	ENSG00000269168	BGN
ENSG00000269169	33.3039	0	44.0288	115.125	ENSG00000269169	AC004528.1
ENSG00000269173	8.95329	5.7352	8.30177	10.4198	ENSG00000269173	ARMCX3
ENSG00000269175	2.7055	4.89894	4.69874	7.45703	ENSG00000269175	AC093157.1
ENSG00000269179	0	0	0	0	ENSG00000269179	AC011452.1
ENSG00000269180	59.2785	89.1668	89.6197	131.927	ENSG00000269180	KIFC3
ENSG00000269181	0	0	0	0	ENSG00000269181	AC020914.6
ENSG00000269182	0	0	0	0	ENSG00000269182	AC010760.1
ENSG00000269183	0	0	0	0	ENSG00000269183	AKR1B1P8
ENSG00000269184	0	0	1.29349	3.14232	ENSG00000269184	AC234771.3
ENSG00000269185	0.43656	0.412159	0.738867	4.47679	ENSG00000269185	FLJ00325
ENSG00000269187	0	0.0149304	0	0	ENSG00000269187	CTAG1A
ENSG00000269188	0.166994	0.479945	0.288851	0.356042	ENSG00000269188	AC011500.1
ENSG00000269190	7.35329	15.4305	15.1467	16.8232	ENSG00000269190	FBXO17
ENSG00000269197	0	0	0	0	ENSG00000269197	AC090574.1
ENSG00000269198	3.09509	5.39385	3.92005	8.76365	ENSG00000269198	RENBP
ENSG00000269203	0.933962	1.85294	2.52126	1.96102	ENSG00000269203	NUDT11
ENSG00000269205	0	0	0	0.214673	ENSG00000269205	AC005606.1
ENSG00000269210	0	0	0.0803226	0	ENSG00000269210	AC019171.1
ENSG00000269212	0.357311	0.338527	1.37348	0.741157	ENSG00000269212	AC000081.2
ENSG00000269215	0.247912	0.430648	0.334696	1.07906	ENSG00000269215	AC008964.1
ENSG00000269216	0.247394	2.06935	3.45775	0.675262	ENSG00000269216	CLTCL1
ENSG00000269219	0.717455	1.11944	1.19754	1.83659	ENSG00000269219	RP11-316K19.3
ENSG00000269223	0	0.443365	0.667308	1.15338	ENSG00000269223	AL158091.1
ENSG00000269225	0	0.0209455	1.70E-06	0.070422	ENSG00000269225	RP11-15E1.3
ENSG00000269226	0.0913621	0.494067	0.285282	0.22121	ENSG00000269226	TMSB15B
ENSG00000269227	1.53694	4.02652	3.19807	4.78593	ENSG00000269227	RP11-345P4.6
ENSG00000269228	0.381969	1.17709	0.529331	0.909216	ENSG00000269228	RPS27AP19
ENSG00000269230	0.00828579	0.031839	0.0217737	0.0226356	ENSG00000269230	FAM47C
ENSG00000269231	7.19034	6.51391	4.83398	4.4656	ENSG00000269231	MMGT1
ENSG00000269236	0.0632447	0.121681	0.0549877	0	ENSG00000269236	AC008751.2
ENSG00000269237	0.673269	3.76973	4.40759	3.76231	ENSG00000269237	AC010615.4
ENSG00000269239	0.720488	0.664007	0.198186	0.718376	ENSG00000269239	RP11-236P24.1
ENSG00000269240	1.77765	2.92047	1.13365	2.08937	ENSG00000269240	CLCN5
ENSG00000269242	1.02173	1.084	0	0	ENSG00000269242	AC010422.3

ENSG00000269244	0	0	0	0	ENSG00000269244	RPL23AP78
ENSG00000269249	0.351531	0.968412	0.370161	1.58335	ENSG00000269249	XAGE5
ENSG00000269251	0	0	0.007018	0	ENSG00000269251	RP11-432N13.3
ENSG00000269253	0	0	0	0	ENSG00000269253	SIGLEC21P
ENSG00000269257	3.9993	4.24855	3.38621	3.21723	ENSG00000269257	TAF9B
ENSG00000269259	0.0558228	0.0537258	0.0485563	0	ENSG00000269259	HUG1
ENSG00000269261	0.436768	0.288924	0.845589	0.453418	ENSG00000269261	F8
ENSG00000269265	0.532953	1.23863	1.01923	0.75651	ENSG00000269265	RIBC1
ENSG00000269266	0	0	0	0	ENSG00000269266	DNAJC19P2
ENSG00000269267	0	3.42744	5.45457	3.69073	ENSG00000269267	AC008498.1
ENSG00000269274	0.0296109	0.0333849	0.0543341	0.032034	ENSG00000269274	AC078899.4
ENSG00000269277	13.5228	15.2972	14.5026	13.4985	ENSG00000269277	PPP2R2D
ENSG00000269278	6.98574	9.29196	10.4838	9.08705	ENSG00000269278	IFT46
ENSG00000269279	0	0.495052	0.486319	0	ENSG00000269279	AL136376.1
ENSG00000269281	0	0	0	0	ENSG00000269281	AC244505.7
ENSG00000269282	1.22972	2.60443	2.9912	4.07824	ENSG00000269282	AC024257.1
ENSG00000269283	0.103849	0.0570515	0	0.753411	ENSG00000269283	AC036108.1
ENSG00000269284	0.0755052	0	0	0.182798	ENSG00000269284	CTC-513N18.3
ENSG00000269285	0.0340276	0.0311992	0.0582165	0.0532281	ENSG00000269285	AKAP4
ENSG00000269287	1.2472	7.97E-09	3.27459	6.28509	ENSG00000269287	RP11-38O23.4
ENSG00000269291	7.69206	19.2094	12.4246	19.5327	ENSG00000269291	AC010877.1
ENSG00000269295	1.39149	2.90854	6.10553	10.4361	ENSG00000269295	AL358113.1
ENSG00000269297	0	0	0	0	ENSG00000269297	LL0XNC01-37G1.2
ENSG00000269299	0	0	0	0	ENSG00000269299	PGBD4P6
ENSG00000269301	3.38984	4.43895	3.95221	5.39902	ENSG00000269301	C22orf39
ENSG00000269302	0.0935323	0.539256	0.405936	0.404618	ENSG00000269302	AC110771.1
ENSG00000269304	1.97352	3.65797	5.33009	4.1212	ENSG00000269304	FKBP1AP1
ENSG00000269305	3.46496	1.60077	13.6848	8.33655	ENSG00000269305	AL158147.2
ENSG00000269306	0	0	0	0	ENSG00000269306	SSX9
ENSG00000269307	0	0	0	0	ENSG00000269307	AC010463.1
ENSG00000269308	0	0	0	0	ENSG00000269308	AL645608.2
ENSG00000269309	0.112742	0	0	0	ENSG00000269309	SPANXC
ENSG00000269313	0.449913	0.146513	0	0.0699757	ENSG00000269313	MAGIX
ENSG00000269314	0	0.360048	0	2.0483	ENSG00000269314	AC139677.9
ENSG00000269315	212.546	195.307	162.08	113.35	ENSG00000269315	RPL36A
ENSG00000269316	0.124068	0.298426	0.269695	0.337781	ENSG00000269316	AC011467.5
ENSG00000269319	9.01531	9.46988	10.1335	7.41134	ENSG00000269319	TMEM25
ENSG00000269320	0.161282	0.843098	1.35401	2.28333	ENSG00000269320	AC073544.2
ENSG00000269322	0.079193	0.227713	0.0685364	0	ENSG00000269322	RP3-461F17.2
ENSG00000269324	0.364722	0.157515	0.232265	0.397507	ENSG00000269324	HMCN2
ENSG00000269326	1.3884	2.283	2.40909	5.50363	ENSG00000269326	MPP1
ENSG00000269327	2.56375	4.45487	4.70101	2.94232	ENSG00000269327	ZNF449
ENSG00000269328	0.139608	0	0.120746	0.0748266	ENSG00000269328	RPL18AP16
ENSG00000269329	185.134	352.86	244.884	293.602	ENSG00000269329	FLNA
ENSG00000269332	2.76766	1.79866	1.28464	1.35112	ENSG00000269332	GOLGA2P9
ENSG00000269334	0.765516	1.46781	1.7399	1.67938	ENSG00000269334	ZNF182
ENSG00000269335	0	4.19297	0	0.298363	ENSG00000269335	IKBKG
ENSG00000269336	13.0684	6.64504	3.71131	5.32819	ENSG00000269336	NSDHL
ENSG00000269337	3.19097	6.41408	8.90135	8.51982	ENSG00000269337	AL591479.1
ENSG00000269339	0	0	0	16.417	ENSG00000269339	AC139768.1
ENSG00000269342	0.838466	0.45599	0.923033	0.490633	ENSG00000269342	TREX2
ENSG00000269343	8.85274	14.7055	16.103	15.2991	ENSG00000269343	ZNF587B
ENSG00000269344	0	0	0	0.368346	ENSG00000269344	RP3-433G13.1
ENSG00000269345	0.580351	0.647853	0.685244	0.205342	ENSG00000269345	VN1R85P

ENSG00000269346	0	0	0	0	ENSG00000269346	FNDC3CP
ENSG00000269348	0	0	0	0	ENSG00000269348	MOB1AP2
ENSG00000269354	0	0	0	0	ENSG00000269354	AC243960.5
ENSG00000269358	53.1132	91.7101	75.1324	119.406	ENSG00000269358	AC138393.1
ENSG00000269360	1.79222	3.24566	2.93742	6.25758	ENSG00000269360	AC112693.2
ENSG00000269361	0.909515	1.3716	1.34944	2.09384	ENSG00000269361	DSTNP2
ENSG00000269362	0	0.0541034	0	0.0604979	ENSG00000269362	IPO7P1
ENSG00000269363	10.0196	12.6282	7.04498	0	ENSG00000269363	MGC4771
ENSG00000269367	51.2579	106.237	131.73	199.755	ENSG00000269367	AC020629.1
ENSG00000269372	0	0	6.34582	0	ENSG00000269372	CTC-513N18.4
ENSG00000269373	0	2.09379	1.98162	0.954892	ENSG00000269373	AC008739.2
ENSG00000269374	2.12063	2.4022	1.70315	1.3008	ENSG00000269374	AC011497.2
ENSG00000269375	1.55574	2.13236	1.62289	3.5933	ENSG00000269375	AL117190.3
ENSG00000269378	52.8787	55.6221	22.3581	25.1441	ENSG00000269378	AC022149.1
ENSG00000269380	0.150852	0.179428	0.16178	0.186865	ENSG00000269380	XK
ENSG00000269381	0.395641	0.563398	0.777601	0.638155	ENSG00000269381	RP11-770J1.5
ENSG00000269382	26.9447	17.2236	16.8587	21.5735	ENSG00000269382	ARCN1
ENSG00000269383	0	0	0	0	ENSG00000269383	AC012493.2
ENSG00000269384	5.27518	9.07358	4.89969	9.56779	ENSG00000269384	SMC1A
ENSG00000269385	0	0	0	0	ENSG00000269385	AC020895.1
ENSG00000269388	1.17421	0.867602	1.40952	0.443779	ENSG00000269388	AC018755.3
ENSG00000269389	0	0	0	0	ENSG00000269389	AF196779.12
ENSG00000269390	0.144057	0.0930406	0.57493	0.452386	ENSG00000269390	RP1-241P17.4
ENSG00000269393	0	3.42979	3.52977	3.73149	ENSG00000269393	AC007965.1
ENSG00000269394	1.06059	1.07953	4.33072	3.28719	ENSG00000269394	AC139677.10
ENSG00000269395	4.56006	4.25137	4.20449	4.41519	ENSG00000269395	ATP7A
ENSG00000269396	0.15152	1.7431	1.04923	5.1836	ENSG00000269396	AC187652.1
ENSG00000269398	0	0	0	0	ENSG00000269398	RP5-1014O16.1
ENSG00000269402	8.33217	13.7267	14.0178	23.4287	ENSG00000269402	AC116407.2
ENSG00000269403	0.191421	0	0.153157	0.186741	ENSG00000269403	AC008750.8
ENSG00000269404	1.37201	3.5466	3.71057	7.80659	ENSG00000269404	SPIB
ENSG00000269405	0.0221335	0	0.00659751	0	ENSG00000269405	NXF2
ENSG00000269406	21.6355	34.0864	33.6731	49.6725	ENSG00000269406	AC211476.1
ENSG00000269407	0	24.9436	2.99489	17.4044	ENSG00000269407	AL096677.1
ENSG00000269408	0	0	0	0	ENSG00000269408	AL390778.1
ENSG00000269411	26.4062	16.5759	8.69718	15.572	ENSG00000269411	HMGB3
ENSG00000269415	0	0	0.799175	0.648093	ENSG00000269415	NPCDR1
ENSG00000269417	0	0	11.4399	0	ENSG00000269417	AC022210.1
ENSG00000269419	2.553	0	0	0	ENSG00000269419	AC008737.2
ENSG00000269421	0.603655	0.72418	0.29487	0.21804	ENSG00000269421	ZNF92P3
ENSG00000269422	0	0	0	3.50541	ENSG00000269422	AC092384.1
ENSG00000269426	0.104457	0	0	0	ENSG00000269426	H3F3AP5
ENSG00000269430	2.46418	2.34501	1.35243	2.90644	ENSG00000269430	LRRC3DN
ENSG00000269431	0.517476	0.868832	1.68094	0.555527	ENSG00000269431	BNIP3P8
ENSG00000269433	0	0	0	0	ENSG00000269433	OPN1MW3
ENSG00000269436	0	0	0	0.0253899	ENSG00000269436	SPANXN1
ENSG00000269437	0.0221335	0	0.00659751	0	ENSG00000269437	NXF2B
ENSG00000269438	0.0602201	0.153425	0.264517	0.114834	ENSG00000269438	CCNB3
ENSG00000269446	1.45369	4.12318	3.08654	6.19379	ENSG00000269446	AC006967.3
ENSG00000269447	0	0	0	0	ENSG00000269447	ELL2P4
ENSG00000269448	0	0.0141887	0.0384803	0.0323015	ENSG00000269448	CXorf67
ENSG00000269449	1.05575	2.12823	1.59083	3.05586	ENSG00000269449	AC002451.1
ENSG00000269452	0.000184377	0.0786797	0.0377864	0.0984552	ENSG00000269452	MAGEA12

ENSG00000269453	0	0	0	0	ENSG00000269453	RPS15AP40
ENSG00000269455	0	0	0	0	ENSG00000269455	AF277315.13
ENSG00000269458	0	0	0	0	ENSG00000269458	AC022145.2
ENSG00000269459	0	0	0	0	ENSG00000269459	CU151839.1
ENSG00000269461	0	0	0	0	ENSG00000269461	RPL36AP53
ENSG00000269464	0	0	0	0	ENSG00000269464	AC012067.1
ENSG00000269466	0	0	0	0	ENSG00000269466	AC233724.13
ENSG00000269468	37.2818	85.8132	68.845	138.915	ENSG00000269468	AC004824.2
ENSG00000269469	0	0	0	0.708873	ENSG00000269469	AC010619.1
ENSG00000269471	0	0.256509	0	0.573499	ENSG00000269471	AC092329.2
ENSG00000269474	0	0	0	0.032491	ENSG00000269474	BX649597.4
ENSG00000269475	0.0263015	0.025284	0.0228434	0.0285321	ENSG00000269475	AC244102.2
ENSG00000269476	0	0.144823	0	0	ENSG00000269476	AC010326.2
ENSG00000269478	9.10348	9.52409	9.65398	15.641	ENSG00000269478	CD99L2
ENSG00000269479	0	0	0	0	ENSG00000269479	BMP15
ENSG00000269488	1.58232	0.925699	1.03643	0.532753	ENSG00000269488	HIST2H2BC
ENSG00000269490	0	0	0.386981	1.57669	ENSG00000269490	SBP1
ENSG00000269493	0	0.31894	0.0643639	0.319491	ENSG00000269493	U40455.1
ENSG00000269494	0	0	0	0.583785	ENSG00000269494	AL359693.1
ENSG00000269496	0.933895	0.878522	0.786881	1.42619	ENSG00000269496	AC007919.2
ENSG00000269498	0.166686	0	0.0552128	0	ENSG00000269498	RP11-157B13.6
ENSG00000269499	2.00044	1.95348	3.02317	3.37218	ENSG00000269499	TBC1D25
ENSG00000269500	0.0707543	0.236489	0.153672	0.217205	ENSG00000269500	EEF1A1P30
ENSG00000269501	49.5536	87.1507	94.0943	51.6927	ENSG00000269501	RP11-353N4.6
ENSG00000269502	0	0	0	0	ENSG00000269502	DMRTC1
ENSG00000269503	0.169452	0.427512	0.336407	0.978949	ENSG00000269503	BEX5
ENSG00000269505	0	0	0.194643	0	ENSG00000269505	ZNF92P2
ENSG00000269506	8.47693	11.3236	2.99065	4.78703	ENSG00000269506	AC110792.3
ENSG00000269509	0	0	0	0.15232	ENSG00000269509	BNIP3P34
ENSG00000269510	1.54824	1.87688	2.86204	2.27879	ENSG00000269510	FLJ00273
ENSG00000269511	0.310939	0.432468	0.447169	0.548703	ENSG00000269511	WNK3
ENSG00000269512	0.16961	0.0788705	0.0623436	0.0807399	ENSG00000269512	IL1RAPL2
ENSG00000269513	0	0.0259303	0.342164	3.70522	ENSG00000269513	AC0139677.11
ENSG00000269514	1.19812	2.46721	2.26447	3.32987	ENSG00000269514	AC024257.3
ENSG00000269515	0	0	0	0	ENSG00000269515	AL137026.1
ENSG00000269516	0	0	0	0.080048	ENSG00000269516	CYP4F23P
ENSG00000269518	0	0	0	0	ENSG00000269518	AC234783.1
ENSG00000269519	0	0	0	0	ENSG00000269519	AC005176.2
ENSG00000269520	73.5109	65.3757	34.0657	21.8015	ENSG00000269520	SSR4
ENSG00000269523	0.735405	0.388299	0.867092	0.596127	ENSG00000269523	ZFP92
ENSG00000269525	8.99827	15.9983	9.25339	8.77306	ENSG00000269525	AC244163.1
ENSG00000269526	0.20315	0.550422	0.465946	0.364146	ENSG00000269526	ERVV-1
ENSG00000269527	0	0	0	0	ENSG00000269527	TPMTP3
ENSG00000269528	1.53277	2.05405	1.22862	8.47759	ENSG00000269528	ENO2
ENSG00000269529	1.49743	6.06968	3.35791	9.36736	ENSG00000269529	AC140061.12
ENSG00000269530	0.20466	1.28459	0.39924	0.590279	ENSG00000269530	SSXP4
ENSG00000269531	0	0	0	0	ENSG00000269531	AC073569.1
ENSG00000269533	0.740965	0.618007	1.73003	0.366227	ENSG00000269533	AC003002.4
ENSG00000269540	0	0.0420701	0.15178	0.0954887	ENSG00000269540	AC010624.4
ENSG00000269544	0	0	0	0	ENSG00000269544	SSXP1
ENSG00000269545	0.223689	0.427522	0.779032	0.414889	ENSG00000269545	CTD-3138B18.4
ENSG00000269546	0.100636	0.505362	0.358584	0.570925	ENSG00000269546	CLIC4P2
ENSG00000269547	0	0.257149	0	0	ENSG00000269547	AC011455.3
ENSG00000269549	0.543466	0.736654	0.834456	1.60667	ENSG00000269549	AL031663.2

ENSG00000269550	0	0	0	0	ENSG00000269550	TM4SF2
ENSG00000269551	0	0	0	0	ENSG00000269551	RP11-434J24.2
ENSG00000269552	0	0	0	0	ENSG00000269552	OR7A8P
ENSG00000269554	0.934099	2.37801	2.47349	3.11099	ENSG00000269554	AL590822.2
ENSG00000269556	7.16885	7.44358	5.89304	3.86657	ENSG00000269556	TMEM185A
ENSG00000269557	0.0266239	0.0128407	0.166083	0.0441429	ENSG00000269557	RP11-49C9.2
ENSG00000269558	0.176976	0	0	0	ENSG00000269558	AC104057.1
ENSG00000269559	0.897675	3.46465	2.25523	1.84011	ENSG00000269559	AC093677.2
ENSG00000269561	0	0	0	0	ENSG00000269561	RP11-344N17.2
ENSG00000269562	12.3398	13.2991	12.142	18.7175	ENSG00000269562	DLGAP4
ENSG00000269563	2.77592	5.34955	5.75135	9.24341	ENSG00000269563	AC138655.1
ENSG00000269565	0.159263	0	0	0	ENSG00000269565	GPR32P1
ENSG00000269566	0	0	0	0	ENSG00000269566	AC005000.4
ENSG00000269567	0	0	0.096946	0	ENSG00000269567	RP11-552E4.3
ENSG00000269569	0	0	0.118771	0	ENSG00000269569	RP11-29O6.2
ENSG00000269570	4.47046	5.43079	1.84035	6.89713	ENSG00000269570	AP001350.1
ENSG00000269571	9.52417	9.17476	16.9612	6.65343	ENSG00000269571	RXRA
ENSG00000269572	0	0.00755585	0.00683153	0.0172428	ENSG00000269572	RBMXL3
ENSG00000269575	0	0	0	0	ENSG00000269575	MTDHP5
ENSG00000269576	0	0	0.204423	0.258068	ENSG00000269576	HNRNPMP2
ENSG00000269580	0	0	0	0	ENSG00000269580	AC020914.7
ENSG00000269581	0.0481952	0.0464024	0	0.0735551	ENSG00000269581	U82695.5
ENSG00000269584	0.306271	0	0	0	ENSG00000269584	TDGF1P7
ENSG00000269586	0	0	0	0	ENSG00000269586	CT45A10
ENSG00000269587	0	0	0	0.908154	ENSG00000269587	SLC38A5
ENSG00000269588	0	0	0	0	ENSG00000269588	AC011500.2
ENSG00000269590	0	0	0	0	ENSG00000269590	AC010422.5
ENSG00000269591	0.679025	3.83711	2.6364	7.18024	ENSG00000269591	AL354808.2
ENSG00000269592	0	0	0	0	ENSG00000269592	CTAG2
ENSG00000269594	4.06852	9.6573	6.95805	10.9026	ENSG00000269594	ZNF81
ENSG00000269601	0	4.08112	0	2.23873	ENSG00000269601	AP000758.1
ENSG00000269602	0.0190495	0.0459191	0.0332956	0.0418911	ENSG00000269602	AGTR2
ENSG00000269603	4.61046	3.7082	4.27974	2.73654	ENSG00000269603	ZBTB33
ENSG00000269605	67.973	149.865	121.824	266.427	ENSG00000269605	Z97053.1
ENSG00000269607	0	0	0	0	ENSG00000269607	CENPVP3
ENSG00000269608	0	0	0	0	ENSG00000269608	AC011487.3
ENSG00000269612	30.1833	26.2826	22.7935	31.8829	ENSG00000269612	DDX6
ENSG00000269615	0	0	0.00575446	0	ENSG00000269615	MTDHP2
ENSG00000269618	1.35063	1.63402	1.06592	1.47094	ENSG00000269618	CMC4
ENSG00000269620	0	0	0	0.843537	ENSG00000269620	AL590560.1
ENSG00000269622	0.247051	0.118544	0.107047	0	ENSG00000269622	TP53TG3HP
ENSG00000269623	0.0354691	0	0.0204954	0	ENSG00000269623	AVPR2
ENSG00000269624	0.841634	1.39982	1.171	3.84764	ENSG00000269624	AL138847.1
ENSG00000269625	0	0	0	0	ENSG00000269625	DPPA3P1
ENSG00000269627	0.390355	1.08478	1.2651	0.827158	ENSG00000269627	RPL5P30
ENSG00000269630	0	0	0	0	ENSG00000269630	AC015989.2
ENSG00000269632	0.157818	0.231327	0.0800459	0.606284	ENSG00000269632	SSXP3
ENSG00000269633	44.6124	67.8503	63.4633	103.684	ENSG00000269633	AC017081.1
ENSG00000269636	6.60331	9.57501	4.45804	5.53974	ENSG00000269636	AC010441.1
ENSG00000269637	0	1.29E-06	0	0.16485	ENSG00000269637	RPL12P41
ENSG00000269639	29.6359	32.8409	18.8215	18.2701	ENSG00000269639	MAGT1
ENSG00000269641	0.0855352	0	0	0	ENSG00000269641	CTB-167G5.6
ENSG00000269642	0	0	0	0	ENSG00000269642	KIR2DS4
ENSG00000269644	0	0	0	0	ENSG00000269644	RP13-346H10.2

ENSG00000269645	18.2638	11.8046	14.8055	18.9645	ENSG00000269645	FAM50A
ENSG00000269647	0.267607	0.15111	0.903012	0.886981	ENSG00000269647	BX842679.1
ENSG00000269649	1.6655	2.0556	2.25142	1.61404	ENSG00000269649	ZNF630
ENSG00000269650	0	0	0	0	ENSG00000269650	AL121895.1
ENSG00000269651	0.0754596	0	0.196695	0	ENSG00000269651	AC022146.1
ENSG00000269654	0.997661	0.982963	0.640176	1.00701	ENSG00000269654	MAGEE1
ENSG00000269655	1.05322	1.7626	1.82098	2.3989	ENSG00000269655	LCA10
ENSG00000269657	5.60362	12.4908	10.3279	16.6993	ENSG00000269657	AC079210.1
ENSG00000269659	0	0	0	0	ENSG00000269659	AC002523.1
ENSG00000269662	0.960041	0.512799	0.568763	0.887779	ENSG00000269662	BNIP3P39
ENSG00000269663	0.201861	0.401905	0.282222	0.520517	ENSG00000269663	GAGE1
ENSG00000269664	0	0	0	0	ENSG00000269664	RP11-31H15.2
ENSG00000269666	193.113	129.978	80.9352	86.7691	ENSG00000269666	PGK1
ENSG00000269668	60.7442	46.3393	37.1754	31.077	ENSG00000269668	ATP6AP1
ENSG00000269669	0	0.179226	0	0.0994901	ENSG00000269669	HMGB1P15
ENSG00000269670	0.387593	0.480455	0.263677	0.531088	ENSG00000269670	LANCL3
ENSG00000269671	7.97182	13.7807	14.0347	14.4073	ENSG00000269671	RABL2B
ENSG00000269672	0	0	0	0	ENSG00000269672	CYCSP45
ENSG00000269673	0	0.0772503	0.017522	0.0228706	ENSG00000269673	SSX6
ENSG00000269676	0.067616	0	0	0.220585	ENSG00000269676	MUC8
ENSG00000269678	0	0	0	0	ENSG00000269678	OR7A18P
ENSG00000269679	0	0.48182	1.72128	1.03842	ENSG00000269679	AC018445.1
ENSG00000269681	0	0	0	0	ENSG00000269681	AC063977.7
ENSG00000269683	0	0	0	0	ENSG00000269683	RP11-344N17.11
ENSG00000269685	0.284093	0.855498	0.668813	0.609563	ENSG00000269685	H2BFM
ENSG00000269686	0.843214	1.34293	2.36062	3.09695	ENSG00000269686	AC011755.1
ENSG00000269687	0.457258	0.867425	2.31423	3.38127	ENSG00000269687	RP11-995C19.2
ENSG00000269690	0.275338	0.26394	0.556333	11.8469	ENSG00000269690	AC096677.1
ENSG00000269692	0	0	0	0	ENSG00000269692	FKBP4P2
ENSG00000269693	1.22946	1.32401	1.32939	1.10314	ENSG00000269693	AC010422.6
ENSG00000269698	12.8226	9.03897	10.16	7.21002	ENSG00000269698	WDR45
ENSG00000269699	8.61135	13.2246	5.75922	10.6638	ENSG00000269699	ZIM2
ENSG00000269700	0.520047	2.0428	1.52197	2.35933	ENSG00000269700	AC069547.2
ENSG00000269703	0	0	0	0.35886	ENSG00000269703	AC244163.2
ENSG00000269704	0	0	0	0	ENSG00000269704	FTH1P27
ENSG00000269706	0	0	0	0	ENSG00000269706	AC008687.6
ENSG00000269709	0.82484	3.08147	2.5131	3.86209	ENSG00000269709	AL109659.1
ENSG00000269710	0	0	0	0	ENSG00000269710	AC245177.1
ENSG00000269711	0	0	0	0	ENSG00000269711	AC008763.3
ENSG00000269713	5.00689	5.3613	8.11051	5.98584	ENSG00000269713	NBPF9
ENSG00000269714	7.10682	8.47023	10.2682	8.82433	ENSG00000269714	TTC23
ENSG00000269715	0.613935	13.7309	0.755478	0	ENSG00000269715	UBL4A
ENSG00000269719	1.16942	1.1865	1.66521	1.59657	ENSG00000269719	RPL36A-HNRNPH2
ENSG00000269721	0.600437	0.591743	0.745185	0.660622	ENSG00000269721	RPL23AP51
ENSG00000269723	4.38934	3.6115	2.84304	3.46927	ENSG00000269723	AC244090.2
ENSG00000269725	0	0	0.00896809	0.0112895	ENSG00000269725	BX072566.2
ENSG00000269726	0	0	0	0	ENSG00000269726	RP11-552J9.1
ENSG00000269730	19.8305	32.8583	17.6783	25.286	ENSG00000269730	AL662847.1
ENSG00000269731	0.642251	2.08164	0.0801329	0.532618	ENSG00000269731	LA16c-13E4.3
ENSG00000269732	0	0	0	0	ENSG00000269732	WBP1LP7
ENSG00000269733	0.309834	0.355476	0.270657	0.618039	ENSG00000269733	PGPEP1L
ENSG00000269738	3.87816	41.1508	21.3771	43.197	ENSG00000269738	AL162424.1
ENSG00000269741	13.8262	5.63176	3.71514	5.30071	ENSG00000269741	AC011473.4
ENSG00000269742	0.943534	1.37438	0.436449	0.823215	ENSG00000269742	BNIP3P29

ENSG00000269743	0.526369	1.10502	1.05157	1.92068	ENSG00000269743	SLC25A53
ENSG00000269744	0.338206	0	1.14671	0.678971	ENSG00000269744	FABP5P15
ENSG00000269746	52.0792	129.046	115.504	158.758	ENSG00000269746	AC009060.1
ENSG00000269748	8.66349	8.20364	4.47273	3.06229	ENSG00000269748	TFE3
ENSG00000269753	0.170828	0.327255	0.603996	0.840624	ENSG00000269753	AL589739.1
ENSG00000269754	0.0727876	0.156562	0.352237	0.269915	ENSG00000269754	AFF2
ENSG00000269755	1.89019	6.02598	2.08517	8.43073	ENSG00000269755	AC008758.6
ENSG00000269759	16.2165	13.7313	9.93321	13.3898	ENSG00000269759	MTMR1
ENSG00000269761	0	0	0	0	ENSG00000269761	AC025278.2
ENSG00000269763	0.155137	0.14692	0	0	ENSG00000269763	EXOSC3P2
ENSG00000269764	0	0	0.0940372	4.87E-05	ENSG00000269764	AC118758.7
ENSG00000269765	0	0	0	0	ENSG00000269765	CTB-187L3.1
ENSG00000269766	0	0	0	0	ENSG00000269766	AL356215.1
ENSG00000269769	0.0353729	0	0.030734	0	ENSG00000269769	OR3B1P
ENSG00000269773	0.90601	0.911684	2.22776	2.47073	ENSG00000269773	PNCK
ENSG00000269774	18.4847	39.2907	36.6206	84.1532	ENSG00000269774	AC005399.1
ENSG00000269776	0	0.533616	0.241046	0.293728	ENSG00000269776	DPPA5P1
ENSG00000269777	0	0	0	0.0849338	ENSG00000269777	FTH1P8
ENSG00000269779	0.701306	1.10271	0.968366	2.25873	ENSG00000269779	AC010329.2
ENSG00000269780	0	0	0	0	ENSG00000269780	RP11-552J9.6
ENSG00000269781	1.89577	3.72824	3.10765	4.61297	ENSG00000269781	FLJ20306
ENSG00000269783	0.519307	0.483777	0.467426	0.820744	ENSG00000269783	GOLGA7B
ENSG00000269786	0	0	0	0	ENSG00000269786	AC044792.1
ENSG00000269787	0	0.472535	0	0.876565	ENSG00000269787	OR7A3P
ENSG00000269788	0.000315153	9.65E-08	0.0610172	0	ENSG00000269788	RP11-399F4.2
ENSG00000269790	0	0.0121047	0.00916318	0.0264408	ENSG00000269790	MAGEA1
ENSG00000269791	0	0	0	0	ENSG00000269791	SSX4B
ENSG00000269794	0.196992	0.237068	0.686191	0.32271	ENSG00000269794	AC010642.1
ENSG00000269795	11.9411	20.5787	20.3242	51.5263	ENSG00000269795	AC092782.1
ENSG00000269797	12.7083	12.0488	11.5203	13.8327	ENSG00000269797	GPR107
ENSG00000269798	0.133958	0.2479	0.31226	0.333971	ENSG00000269798	DUSP9
ENSG00000269800	0	0	0	0	ENSG00000269800	PLEKHA3P1
ENSG00000269801	2.473	3.13176	2.55607	3.3212	ENSG00000269801	ARMCX1
ENSG00000269803	1.46007	3.43435	3.67765	6.24842	ENSG00000269803	RP5-1000K24.2
ENSG00000269804	1.42748	3.78695	5.63151	5.28998	ENSG00000269804	AL353354.2
ENSG00000269805	0	0	0	0	ENSG00000269805	XAGE1A
ENSG00000269808	1.05318	0.830062	1.8492	2.15864	ENSG00000269808	AC010327.2
ENSG00000269810	0	0	0	0	ENSG00000269810	AC015660.1
ENSG00000269811	0.4125	0.591465	1.3333	1.91352	ENSG00000269811	SCGB2B3P
ENSG00000269816	23.7859	24.5446	31.5579	32.0976	ENSG00000269816	KDM5C
ENSG00000269817	0	0	0	0	ENSG00000269817	TCP11X3P
ENSG00000269819	0	0	0	0	ENSG00000269819	EIF4A2P4
ENSG00000269820	0.0089866	0.0346615	0.0705107	0.108718	ENSG00000269820	SAGE1
ENSG00000269822	0.0584007	0.140499	0.0761862	0.190953	ENSG00000269822	LL0XNC01-116E7.1
ENSG00000269823	0.775257	1.84264	1.83777	1.6142	ENSG00000269823	AL513523.9
ENSG00000269824	0.0761243	0	0.268194	0	ENSG00000269824	AL022578.1
ENSG00000269830	0.3066	0.381823	0.618756	1.20775	ENSG00000269830	GPR162
ENSG00000269831	52.1505	149.805	116.762	207.208	ENSG00000269831	AL669831.1
ENSG00000269832	2.52984	5.16635	4.52106	10.241	ENSG00000269832	AL627171.2
ENSG00000269833	0	0	0.0565918	0	ENSG00000269833	AC234771.5
ENSG00000269837	3.57285	3.39674	3.72181	5.20343	ENSG00000269837	IPO5P1
ENSG00000269838	0	0	0	0	ENSG00000269838	SPANXD
ENSG00000269839	0.325386	0	0.466949	0.875306	ENSG00000269839	AC010620.2

ENSG00000269840	0	0	0.0889759	0	ENSG00000269840	PAGE1
ENSG00000269844	0	0	0	0	ENSG00000269844	RP6-29D12.2
ENSG00000269845	0.677396	1.68946	0.91356	1.92027	ENSG00000269845	AC092364.2
ENSG00000269846	1.54296	3.88126	3.7412	5.95517	ENSG00000269846	AL136172.1
ENSG00000269848	0	0	0	0	ENSG00000269848	AC119751.8
ENSG00000269849	0.522104	0.70984	0.343491	0	ENSG00000269849	MAMLD1
ENSG00000269853	0	0	0	0	ENSG00000269853	SPANXB1
ENSG00000269855	5.08559	1.40988	0.989645	0.653692	ENSG00000269855	RNF225
ENSG00000269858	33.846	39.6883	41.0126	33.6359	ENSG00000269858	EGLN2
ENSG00000269860	0	0	0	0	ENSG00000269860	RP13-228J13.10
ENSG00000269861	0.532681	1.15916	1.00461	0.768747	ENSG00000269861	HIST2H2BD
ENSG00000269864	0	0	0	0	ENSG00000269864	RP5-1189K21.2
ENSG00000269866	0	6.41577	13.9465	7.84891	ENSG00000269866	FKSG63
ENSG00000269868	0	0	0	0	ENSG00000269868	RP11-552J9.14
ENSG00000269870	0.518269	1.00531	1.26986	1.23054	ENSG00000269870	PPP1R3F
ENSG00000269871	41.8425	20.5992	10.0603	14.1899	ENSG00000269871	AC040977.1
ENSG00000269875	28.2933	21.6229	22.2273	16.2441	ENSG00000269875	FTSJ1
ENSG00000269876	0	0	0	0	ENSG00000269876	CYCSP44
ENSG00000269879	1.27136	6.30041	8.5471	4.01208	ENSG00000269879	AL353583.1
ENSG00000269880	0	0	0	0	ENSG00000269880	CTD-2557P19.4
ENSG00000269881	0	0	0	0	ENSG00000269881	AC004754.1
ENSG00000269882	4.04478	8.26972	11.8516	32.3488	ENSG00000269882	C1S
ENSG00000269883	0.120366	0.254896	0.459888	0.713296	ENSG00000269883	AC007375.3
ENSG00000269884	4.43629	5.69423	5.16923	8.01641	ENSG00000269884	BRCC3
ENSG00000269885	0	0	0	0	ENSG00000269885	VN1R79P
ENSG00000269891	0.305548	0.755147	0.673618	1.30508	ENSG00000269891	ARHGAP19-SLIT1
ENSG00000269897	6.22064	4.28307	5.43619	1.07699	ENSG00000269897	COMMD3-BMI1
ENSG00000269904	0.490883	1.01835	1.69272	1.9917	ENSG00000269904	MAP2K4P1
ENSG00000269907	3.25753	3.95741	7.56207	10.4596	ENSG00000269907	AL158827.2
ENSG00000269920	0.0383573	0.127347	0.0854015	0.15871	ENSG00000269920	RP11-690P14.4
ENSG00000269948	1.39443	2.79593	1.67907	2.99688	ENSG00000269948	RP11-248J23.6
ENSG00000269955	1.58163	0	0	0	ENSG00000269955	C7orf55-LUC7L2
ENSG00000269964	0.14536	0.204879	0.126701	0.321044	ENSG00000269964	MEI4
ENSG00000269981	0	0	0	0	ENSG00000269981	AL627309.8
ENSG00000270011	3.04937	7.40994	9.69864	14.9621	ENSG00000270011	ZNF559-ZNF177
ENSG00000270024	0.418109	0	0.362621	0.691319	ENSG00000270024	C8orf44-SGK3
ENSG00000270025	0	0	0	0	ENSG00000270025	BMS1P7
ENSG00000270033	0	0	0	0	ENSG00000270033	AC053481.5
ENSG00000270063	0	0	0	0	ENSG00000270063	HCG4B
ENSG00000270073	0	0	0	0	ENSG00000270073	TSPY6P
ENSG00000270092	2.60313	6.87705	8.11392	6.58029	ENSG00000270092	RP11-318K12.3
ENSG00000270098	0	0	0	0	ENSG00000270098	AC079230.1
ENSG00000270099	0	0	0	0	ENSG00000270099	AL365273.2
ENSG00000270106	0.257977	0.256303	0.201265	0.321306	ENSG00000270106	TSNAX-DISC1
ENSG00000270136	0.265065	0.249839	0.207119	0.593519	ENSG00000270136	MINOS1-NBL1
ENSG00000270149	32.5067	26.8368	17.8543	4.3928	ENSG00000270149	AL591806.3
ENSG00000270166	0	0	0.358155	0.431548	ENSG00000270166	AL390838.2
ENSG00000270181	8.38019	6.34699	5.31462	2.55109	ENSG00000270181	BIVM-ERCC5
ENSG00000270185	0	0	0	0	ENSG00000270185	IGHD1OR15-1B
ENSG00000270186	0	0	0.0108934	0	ENSG00000270186	KIR2DL1
ENSG00000270187	0	0	0	0	ENSG00000270187	IGKV1OR2-11
ENSG00000270188	69.3429	64.9133	96.8815	101.376	ENSG00000270188	MTRNR2L11
ENSG00000270191	0.130271	0	0	0	ENSG00000270191	BNIP3P31
ENSG00000270192	0.0943836	0.181381	0.0819222	0	ENSG00000270192	MRPS35P3

ENSG00000270193	0.0890613	0.171145	0.154623	0.0963959	ENSG00000270193	AC009237.12
ENSG00000270196	0.219859	0.33169	0.190661	0.118499	ENSG00000270196	AC007255.2
ENSG00000270197	0	0	0	0	ENSG00000270197	IGHVIII-44
ENSG00000270200	0	0	0	0	ENSG00000270200	AC005229.3
ENSG00000270201	0	0	0	0	ENSG00000270201	IGHVIII-67-3
ENSG00000270202	0	0	0	0	ENSG00000270202	AP003973.1
ENSG00000270204	0	0.142394	0.128559	0	ENSG00000270204	AC020549.2
ENSG00000270206	0	0	0	0.997561	ENSG00000270206	RP3-365I19.2
ENSG00000270208	0	0	0	0	ENSG00000270208	IGHVIII-51-1
ENSG00000270209	0	0.188551	0.171306	0	ENSG00000270209	AL035411.2
ENSG00000270213	0	0	0	0	ENSG00000270213	RP11-452D24.1
ENSG00000270214	0	0	0.167733	0	ENSG00000270214	IGHV3-16
ENSG00000270215	0	0	0	0	ENSG00000270215	IGHV3-75
ENSG00000270216	0.0317508	0.072743	1.51278	3.34031	ENSG00000270216	LILRB3
ENSG00000270217	0.078525	0	0	0.163728	ENSG00000270217	AC009892.5
ENSG00000270218	0.362026	1.15801	1.35945	0.519067	ENSG00000270218	AC013553.2
ENSG00000270220	0	0	0	0	ENSG00000270220	KIR3DX1
ENSG00000270222	0.141272	0.294178	0.359009	0.333104	ENSG00000270222	DUXAP11
ENSG00000270224	0.171238	0.0549481	0.0998003	0.191448	ENSG00000270224	AB019441.29
ENSG00000270225	0.0994303	0.286616	0	0.214895	ENSG00000270225	MTCO2P22
ENSG00000270226	0	0	0.121356	0	ENSG00000270226	AC006548.2
ENSG00000270227	0	0	0	0.112631	ENSG00000270227	IGHV3-36
ENSG00000270228	4.01147	5.65218	4.71782	2.34082	ENSG00000270228	AC079880.1
ENSG00000270230	0.560778	0	0.340358	0	ENSG00000270230	MTND6P22
ENSG00000270231	11.5266	18.1025	14.2577	8.77213	ENSG00000270231	NBPF8
ENSG00000270232	0	0	0	0.191033	ENSG00000270232	MTCYBP22
ENSG00000270234	0	0	0	0	ENSG00000270234	AL355333.1
ENSG00000270236	0.737475	0.734039	0.319813	0.763792	ENSG00000270236	AL162730.1
ENSG00000270238	1.50484	2.99661	3.53356	2.83855	ENSG00000270238	AC008746.5
ENSG00000270239	0	0	0	0	ENSG00000270239	RP11-763B22.10
ENSG00000270241	0	0	0	0	ENSG00000270241	AC115286.1
ENSG00000270242	0	0	0	0	ENSG00000270242	ACTR3BP1
ENSG00000270243	0	0	0	0	ENSG00000270243	AC022217.4
ENSG00000270244	0.555366	0.266924	0	0.290891	ENSG00000270244	AC104687.2
ENSG00000270247	0	0	0	0	ENSG00000270247	AC098784.1
ENSG00000270248	0.825001	0.199723	0.568528	0.451026	ENSG00000270248	AC011468.4
ENSG00000270249	0	0.28389	0	0	ENSG00000270249	AC093668.1
ENSG00000270250	0	0	0	13.8969	ENSG00000270250	IGHVIII-38-1
ENSG00000270251	0	0	0	0	ENSG00000270251	AL670379.1
ENSG00000270252	0	0	0	0	ENSG00000270252	IGKV3OR2-5
ENSG00000270254	0	0	0	0.75018	ENSG00000270254	IGHV5-78
ENSG00000270255	1.22204	3.19118	2.09776	4.14518	ENSG00000270255	AC009884.2
ENSG00000270256	0	0	0.380271	0.77023	ENSG00000270256	RP11-175I17.6
ENSG00000270257	13.3331	24.9319	9.45943	40.7652	ENSG00000270257	AC096720.1
ENSG00000270258	0	0	0.45982	0.221334	ENSG00000270258	DUXAP4
ENSG00000270259	0.737475	0	0	0	ENSG00000270259	BX255925.2
ENSG00000270262	3.36334	3.59335	3.89904	5.43854	ENSG00000270262	CNOT3
ENSG00000270263	1.83986	7.54592	2.14069	2.30046	ENSG00000270263	HIST2H3A
ENSG00000270264	0.96576	0.526373	0.481026	0.300678	ENSG00000270264	AC004686.1
ENSG00000270267	0	0.0570873	0.328356	0.0814314	ENSG00000270267	AC012314.19
ENSG00000270268	0.0807479	0.0776168	0	0.35024	ENSG00000270268	AL009028.1
ENSG00000270269	0.658872	3.03776	1.34014	2.40837	ENSG00000270269	IMMP1LP1
ENSG00000270270	0.755354	1.97587	2.49552	1.47202	ENSG00000270270	BNIP3P10
ENSG00000270272	19.2887	8.73425	5.36901	6.15278	ENSG00000270272	NDUFB11

ENSG00000270273	0	0	0	0	ENSG00000270273	AC121334.2
ENSG00000270275	0	0	0	0	ENSG00000270275	TRMT112P7
ENSG00000270276	22.4704	99.2338	23.9434	24.1079	ENSG00000270276	HIST2H4B
ENSG00000270278	0.230627	0.147353	0.269027	0.821477	ENSG00000270278	RP1-290F12.3
ENSG00000270280	0	0.580906	0	1.87799	ENSG00000270280	AL451086.1
ENSG00000270281	0.115052	0.220869	0	0.123871	ENSG00000270281	AC020910.2
ENSG00000270282	0.243909	0.232571	1.26126	3.59671	ENSG00000270282	AL096855.2
ENSG00000270284	0	0	0	0	ENSG00000270284	IGHV3-62
ENSG00000270285	4.30862	11.5179	9.7375	19.2171	ENSG00000270285	AC124916.2
ENSG00000270287	0	0.137355	0.124004	0.459982	ENSG00000270287	AL359704.2
ENSG00000270288	2.92782	9.95851	3.45064	3.85475	ENSG00000270288	C14orf80
ENSG00000270289	0.390644	0	0	0	ENSG00000270289	AC012669.1
ENSG00000270290	0	0	0	0	ENSG00000270290	GAGE12C
ENSG00000270291	0	0	0	0	ENSG00000270291	IGHVII-65-1
ENSG00000270292	0.0984961	0.948272	0.51425	0.914345	ENSG00000270292	AC079880.2
ENSG00000270293	0.168606	0	0.728962	0.217133	ENSG00000270293	AC025588.2
ENSG00000270294	0	0	0	0	ENSG00000270294	XIAPP1
ENSG00000270295	0	0	0	0	ENSG00000270295	IGHV4-31
ENSG00000270296	0	1.5532	0	2.28212	ENSG00000270296	STX8P1
ENSG00000270298	0	0	0	0	ENSG00000270298	IGHV2-26
ENSG00000270299	0.216922	1.45668	0.955649	1.40375	ENSG00000270299	AL121758.1
ENSG00000270300	0.454884	1.19658	1.18874	1.95433	ENSG00000270300	PHACTR2P1
ENSG00000270301	0	0	0	0	ENSG00000270301	AC174071.1
ENSG00000270303	0.2215	0.283176	0.639161	0.315962	ENSG00000270303	RP11-1113N2.4
ENSG00000270304	0.705248	1.33631	1.68508	2.53863	ENSG00000270304	AC087283.1
ENSG00000270305	0.0606138	0	0	0	ENSG00000270305	IGHV3-74
ENSG00000270306	0.126837	0	0.109907	0	ENSG00000270306	AL158050.2
ENSG00000270307	0	0	0	0	ENSG00000270307	MTATP6P2
ENSG00000270308	0	0	0	0	ENSG00000270308	AL137843.1
ENSG00000270309	0	0	0	0	ENSG00000270309	IGHVII-46-1
ENSG00000270311	0	0	0	0	ENSG00000270311	IGHD5-5
ENSG00000270313	0.667166	0.621358	0.553552	3.5022	ENSG00000270313	COX6CP16
ENSG00000270314	0.218584	0.587665	0.285217	0.83452	ENSG00000270314	AC007161.2
ENSG00000270315	0	0	0	0	ENSG00000270315	IGHV3-43
ENSG00000270316	0	0	0	0	ENSG00000270316	BORCS7-ASMT
ENSG00000270317	0	0	0	0	ENSG00000270317	AC004004.1
ENSG00000270318	0	0	0	0	ENSG00000270318	IGHV3OR16-11
ENSG00000270319	0	0	0	0	ENSG00000270319	LILRP1
ENSG00000270322	0	0.881011	0.773805	0	ENSG00000270322	AC091167.4
ENSG00000270323	0	0	0	0	ENSG00000270323	AP000860.1
ENSG00000270324	1.34734	3.85028	7.18843	8.76395	ENSG00000270324	AC005972.2
ENSG00000270325	0.131655	0	0	0	ENSG00000270325	BNIP3P9
ENSG00000270326	0	0	0	2.52161	ENSG00000270326	AL021997.1
ENSG00000270328	0.240596	0.924937	0.645841	0.902232	ENSG00000270328	AC009597.2
ENSG00000270330	0	0	0	0.27348	ENSG00000270330	AL009183.1
ENSG00000270333	0	0	0	0	ENSG00000270333	AL390123.1
ENSG00000270335	0	0.313417	0.0947844	0.117285	ENSG00000270335	AC093159.2
ENSG00000270336	0	0	0	0	ENSG00000270336	AC105148.1
ENSG00000270338	0	0.0118584	0	0.0133071	ENSG00000270338	VN1R104P
ENSG00000270339	0	0.243112	0.118486	0.198619	ENSG00000270339	AC243756.1
ENSG00000270340	0	0.019946	0.496555	0.113285	ENSG00000270340	IGHE
ENSG00000270341	0	0	0	0	ENSG00000270341	IGHV3-37
ENSG00000270342	0	0	0	0	ENSG00000270342	AL499605.1
ENSG00000270343	2.21575	2.83404	7.74696	3.86969	ENSG00000270343	UNGP3

ENSG00000270345	0	6.67216	2.87171	4.46442	ENSG00000270345	IGHJ2P
ENSG00000270347	0	0	0	0	ENSG00000270347	AC011453.2
ENSG00000270349	0.254865	0.292622	0.387346	0.748491	ENSG00000270349	RGN
ENSG00000270350	0	0	0	0	ENSG00000270350	MTND4LP5
ENSG00000270352	0	0	0	0.190397	ENSG00000270352	AC022387.2
ENSG00000270353	0.550262	1.29237	0.2307	0	ENSG00000270353	RP11-708L7.9
ENSG00000270354	0	0.603626	0	0.648746	ENSG00000270354	AC012368.3
ENSG00000270355	0	0	0	0	ENSG00000270355	IGHG3
ENSG00000270356	0	0.256685	0.231885	0	ENSG00000270356	IGHV1OR15-4
ENSG00000270357	0.854407	1.37126	1.32965	1.58212	ENSG00000270357	RPS20P33
ENSG00000270358	0	0	0	0	ENSG00000270358	IGHV4-61
ENSG00000270359	0	0	0	0	ENSG00000270359	AL358335.3
ENSG00000270363	0	0	0	0	ENSG00000270363	RP11-289I10.3
ENSG00000270365	6.90641	6.48352	5.20337	7.25698	ENSG00000270365	CDC42EP5
ENSG00000270366	0.0332516	0.0790378	0.102802	0	ENSG00000270366	LILRA4
ENSG00000270367	0.365851	0.811192	0.573062	1.71253	ENSG00000270367	AC092053.1
ENSG00000270369	0.381423	0.396027	0.785925	1.54049	ENSG00000270369	AL591684.3
ENSG00000270370	1.7071	3.4412	2.66344	2.44994	ENSG00000270370	NLRP2
ENSG00000270371	0	0	0	0	ENSG00000270371	AL122127.1
ENSG00000270373	0	0	0	0	ENSG00000270373	IGHV1-17
ENSG00000270375	0	0	0	0	ENSG00000270375	REXO1L2P
ENSG00000270376	0.0943192	0	0	0	ENSG00000270376	IGHV2-70
ENSG00000270377	3.29692	7.20247	4.90456	3.26862	ENSG00000270377	AC097639.2
ENSG00000270378	0	0	0	0	ENSG00000270378	AC020891.4
ENSG00000270379	0.0219817	0.117319	0.150472	0.202654	ENSG00000270379	HEATR9
ENSG00000270381	3.63431	3.46611	3.04154	8.47462	ENSG00000270381	AL138963.2
ENSG00000270382	0	0	0	0	ENSG00000270382	AL109918.2
ENSG00000270385	0	0	0	0	ENSG00000270385	AC133539.2
ENSG00000270386	0	0	0	0	ENSG00000270386	UGT2A1
ENSG00000270387	0.519894	2.0712	1.35225	2.98444	ENSG00000270387	AC115621.1
ENSG00000270388	0	0	0.0721369	0	ENSG00000270388	MTCO3P22
ENSG00000270390	0.0826793	0.0794656	0.358959	0.448078	ENSG00000270390	AC013444.2
ENSG00000270392	11.1747	21.9445	17.6634	36.9322	ENSG00000270392	PFN1P2
ENSG00000270393	0.145213	0	0.315482	0.0788824	ENSG00000270393	AC000095.1
ENSG00000270394	45.5439	35.496	39.6871	26.6974	ENSG00000270394	MTRNR2L13
ENSG00000270395	0	0	0	0	ENSG00000270395	MREGP1
ENSG00000270396	0	0	0	0	ENSG00000270396	IGHJ3
ENSG00000270397	0	0	0	0	ENSG00000270397	AL670379.2
ENSG00000270398	0	0	0	0	ENSG00000270398	IGHV3-7
ENSG00000270399	10.2921	3.12768	2.35588	0	ENSG00000270399	RP11-1407O15.3
ENSG00000270400	0	0	0	0	ENSG00000270400	AL512782.1
ENSG00000270401	0	0	0.682638	0	ENSG00000270401	AC140658.4
ENSG00000270402	0.226585	0.773499	1.12557	0.610176	ENSG00000270402	AC011458.1
ENSG00000270405	3.09191	3.70344	2.85723	0.985952	ENSG00000270405	AC104692.2
ENSG00000270407	0.442603	1.45097	0.227368	0.329992	ENSG00000270407	CTC-260E6.10
ENSG00000270409	5.05727	9.08539	10.2258	26.8127	ENSG00000270409	AC090950.1
ENSG00000270410	25.3951	35.6953	43.1827	34.9721	ENSG00000270410	MTA1
ENSG00000270411	0.303875	1.15421	4.17347	1.90372	ENSG00000270411	AL354984.3
ENSG00000270413	0	0	0	0	ENSG00000270413	AL355812.1
ENSG00000270415	0.571987	2.91872	0	1.82212	ENSG00000270415	DPPA3P3
ENSG00000270416	0.0352121	0	0	0	ENSG00000270416	REXO1L4P
ENSG00000270417	0	0	0	0	ENSG00000270417	IGHVIII-11-1
ENSG00000270418	0	0	0	0	ENSG00000270418	IGHD4-11
ENSG00000270420	0	0	0	0	ENSG00000270420	AC245884.1

ENSG00000270421	2.54273	4.16246	4.38313	7.7567	ENSG00000270421	AC022022.2
ENSG00000270422	0	0	0.27748	0	ENSG00000270422	AL133247.2
ENSG00000270423	0	0.190591	0.172149	0	ENSG00000270423	AP001981.2
ENSG00000270424	5.42E-08	1.66807	1.13284	1.2875	ENSG00000270424	AC145285.6
ENSG00000270425	0.0621828	0	0	0	ENSG00000270425	AC002487.1
ENSG00000270427	1.15567	1.86147	3.3054	3.61344	ENSG00000270427	NRBF2P5
ENSG00000270428	0	0	0	0	ENSG00000270428	IGHVII-22-1
ENSG00000270429	0.493026	0.992693	0.858261	1.86192	ENSG00000270429	KNOP1P2
ENSG00000270430	0.0917625	0.0886634	0.0801124	0.0506041	ENSG00000270430	AC024589.2
ENSG00000270431	0.165299	0	0	0	ENSG00000270431	AC005000.2
ENSG00000270432	0	0	0.160954	0	ENSG00000270432	OR7E108P
ENSG00000270433	1.56835	2.98517	2.78331	7.02465	ENSG00000270433	AL049829.3
ENSG00000270434	0	0	0.380271	0.77023	ENSG00000270434	AC012044.1
ENSG00000270435	0.213544	0.901931	1.36438	1.4504	ENSG00000270435	AC068733.2
ENSG00000270436	0	0	0	0	ENSG00000270436	IGHV3-63
ENSG00000270437	0.0435044	0.0837917	0.113608	0.0951462	ENSG00000270437	AC009501.3
ENSG00000270439	0	0	0	0	ENSG00000270439	IGHV3-22
ENSG00000270440	0	0	0	0	ENSG00000270440	AC012175.1
ENSG00000270441	0.0949148	0.548758	0.496591	0.41627	ENSG00000270441	AC135506.1
ENSG00000270442	4.40407	1.13341	0.970716	11.8995	ENSG00000270442	AC008725.1
ENSG00000270443	10.4847	12.6585	14.8534	17.6845	ENSG00000270443	AL139344.1
ENSG00000270444	0	0	0	0	ENSG00000270444	AZU1P1
ENSG00000270445	0.286547	0.272201	0.24594	0.299759	ENSG00000270445	AC145423.1
ENSG00000270446	0	2.59658	1.5776	4.53321	ENSG00000270446	AL136363.1
ENSG00000270447	0	0	0	0	ENSG00000270447	AC007179.3
ENSG00000270449	0.785599	0.737941	0	2.36201	ENSG00000270449	AP001485.1
ENSG00000270450	0	0	0	0	ENSG00000270450	IGKV2OR2-7
ENSG00000270451	0	0	0	0	ENSG00000270451	IGHD4OR15-4B
ENSG00000270452	0	0	0	0	ENSG00000270452	IGHV1-2
ENSG00000270453	0	0	0.5263	0.215252	ENSG00000270453	AC007566.2
ENSG00000270454	0	0	0	0	ENSG00000270454	IGHD1-26
ENSG00000270455	0.0413524	0	0	0.110685	ENSG00000270455	AC134882.1
ENSG00000270456	0	0	0	0	ENSG00000270456	AL670379.3
ENSG00000270458	0	0	0	0	ENSG00000270458	AC009779.6
ENSG00000270459	0.466149	0.613771	0.636461	0.692479	ENSG00000270459	CXorf31
ENSG00000270463	0	0.436607	0.196053	0.47213	ENSG00000270463	IGHVII-51-2
ENSG00000270464	0	0	0	0	ENSG00000270464	IGHA2
ENSG00000270465	0	0	0	0	ENSG00000270465	IGHVII-40-1
ENSG00000270466	0	0	0	0	ENSG00000270466	SEPT1
ENSG00000270467	0	0	0	0	ENSG00000270467	IGHV3OR16-12
ENSG00000270468	0	0	0	0	ENSG00000270468	IGHVII-31-1
ENSG00000270469	0	0.535838	0.276634	0.431856	ENSG00000270469	AC006557.5
ENSG00000270470	0	0.0547246	0.0494644	0.0619967	ENSG00000270470	AC064872.1
ENSG00000270471	0	0	0.107761	0.129749	ENSG00000270471	AC010492.4
ENSG00000270472	0	0	0	0	ENSG00000270472	IGHV3OR16-9
ENSG00000270473	0	0	0	0	ENSG00000270473	IGHD1-20
ENSG00000270474	0	0	0	0	ENSG00000270474	IGHV3-29
ENSG00000270475	0	0.154147	0	0	ENSG00000270475	AC024563.2
ENSG00000270476	0	0.139689	0.252577	0	ENSG00000270476	IGHVIII-47-1
ENSG00000270477	0	0	0	1.41251	ENSG00000270477	AL033523.1
ENSG00000270478	17.0859	36.1953	20.0672	29.0564	ENSG00000270478	AP2B1
ENSG00000270479	3.19512	6.67459	4.63938	11.6275	ENSG00000270479	BNIP3P37
ENSG00000270480	1.63079	1.30592	2.281	1.37252	ENSG00000270480	AC073413.1

ENSG00000270481	0	0	0	0	ENSG00000270481	KIR3DP1
ENSG00000270484	0.519603	1.90329	1.45369	2.81942	ENSG00000270484	AL078595.2
ENSG00000270488	0	0	0	0	ENSG00000270488	AC079587.1
ENSG00000270489	0	0	0	0	ENSG00000270489	IGHV3-65
ENSG00000270490	0.051932	0.125139	0.0226263	0.0855256	ENSG00000270490	AC110048.1
ENSG00000270491	0	0	0	0	ENSG00000270491	AL359999.1
ENSG00000270492	1.93516	1.09321	1.69795	2.94293	ENSG00000270492	AC137695.1
ENSG00000270493	1.08E-08	0	0	0	ENSG00000270493	AL670379.4
ENSG00000270494	0	0	0	0	ENSG00000270494	AL513534.2
ENSG00000270495	0	0	0	0	ENSG00000270495	AC008825.2
ENSG00000270496	0	0	0	0	ENSG00000270496	BNIP3P7
ENSG00000270497	0.230627	0.147353	0.269027	0.821477	ENSG00000270497	BX322635.1
ENSG00000270498	0	0.0262706	0	0	ENSG00000270498	IGHG4
ENSG00000270499	0.0398897	0.0775401	0.138921	0.268658	ENSG00000270499	MKI67P1
ENSG00000270500	0	0	0.497019	0	ENSG00000270500	COX6CP4
ENSG00000270501	0.541289	0.571145	0.330792	1.93053	ENSG00000270501	LILRA2
ENSG00000270502	3.49584	7.18013	5.77662	4.32221	ENSG00000270502	TSEN34
ENSG00000270503	0.099082	0.146747	0	0.164436	ENSG00000270503	YTHDF2P1
ENSG00000270505	0	0	0	0	ENSG00000270505	IGHV1OR15-1
ENSG00000270506	0	0	0	0	ENSG00000270506	AC021646.1
ENSG00000270507	1.50045	2.78235	1.21435	1.45548	ENSG00000270507	AL049861.1
ENSG00000270509	0	0	0	0	ENSG00000270509	AL713998.2
ENSG00000270510	0.210957	1.75136	0.827617	1.11553	ENSG00000270510	AP000811.1
ENSG00000270512	0.348476	0	0	0	ENSG00000270512	AC005377.1
ENSG00000270513	0	0	0	0	ENSG00000270513	AC113368.1
ENSG00000270516	0	0.187089	0.223847	0.447895	ENSG00000270516	AC079791.1
ENSG00000270517	0.278876	1.20186	0.775469	1.1073	ENSG00000270517	RDM1
ENSG00000270518	12.5551	16.7524	16.2388	33.3343	ENSG00000270518	AC008626.1
ENSG00000270521	0	0.368312	0.247362	1.27403	ENSG00000270521	AL450336.1
ENSG00000270524	0	0.13592	0.0491362	0.123193	ENSG00000270524	QTRT1P1
ENSG00000270526	0	0	0	0	ENSG00000270526	SNRPGP19
ENSG00000270528	0	0.846205	0.267802	1.49166	ENSG00000270528	AC021171.1
ENSG00000270529	0	0	0.149087	0.180923	ENSG00000270529	IGHV3-42
ENSG00000270530	0	0	0	0	ENSG00000270530	IGHV1-68
ENSG00000270531	0.867024	1.63673	2.56865	3.15077	ENSG00000270531	AC022001.1
ENSG00000270532	0.265091	0.898476	0.459903	0.14078	ENSG00000270532	PEBP1P2
ENSG00000270533	0.172019	0	0	0.171286	ENSG00000270533	CR382285.1
ENSG00000270534	0	0	0	0	ENSG00000270534	AC011515.2
ENSG00000270535	0	0	0	0.157046	ENSG00000270535	ELOCP34
ENSG00000270536	0.124117	0.304113	0.107556	0	ENSG00000270536	CTC-575C13.2
ENSG00000270537	0.371723	0.463414	8.13E-07	3.89375	ENSG00000270537	AC242842.1
ENSG00000270538	0	0	0	0	ENSG00000270538	AC121247.2
ENSG00000270541	0	0	0.442511	0	ENSG00000270541	AC069545.1
ENSG00000270542	0	0	0	0	ENSG00000270542	AL356218.2
ENSG00000270545	0	0	0	0	ENSG00000270545	ATP5G1P1
ENSG00000270549	1.63673	6.15222	1.83045	2.75804	ENSG00000270549	AL451044.1
ENSG00000270550	0	0	0.0410332	0	ENSG00000270550	IGHV3-30
ENSG00000270551	0.180945	0	0	0	ENSG00000270551	IGHV3-76
ENSG00000270552	0	0	0	0	ENSG00000270552	DUXAP3
ENSG00000270553	0.508561	1.92944	1.31409	1.62705	ENSG00000270553	AC011921.3
ENSG00000270554	0.497054	1.64781	1.58775	2.16848	ENSG00000270554	AC069431.2
ENSG00000270555	0	0.627766	0.197367	1.15749	ENSG00000270555	AC211469.1
ENSG00000270558	1.72812	3.62681	2.96891	4.29358	ENSG00000270558	AC025449.1
ENSG00000270559	0	0	0	0	ENSG00000270559	HOMER2P1

ENSG00000270560	0	0	0	0	ENSG00000270560	APOOP1
ENSG00000270564	0	0	0	0	ENSG00000270564	IGHJ4
ENSG00000270565	0	0	0.0410332	0	ENSG00000270565	IGHV3-33
ENSG00000270566	0	0	0	0	ENSG00000270566	IGHV3-19
ENSG00000270568	0	0	3.58E-08	3.89E-08	ENSG00000270568	RP11-592B15.8
ENSG00000270569	0.466456	0.737562	1.51464	0.319419	ENSG00000270569	AC068276.1
ENSG00000270570	0	4.29173	2.25832	0	ENSG00000270570	AC140113.1
ENSG00000270572	0	0	0.247259	0.451868	ENSG00000270572	IGHV3-47
ENSG00000270575	5.26257	10.1914	3.38113	16.805	ENSG00000270575	AL160281.1
ENSG00000270576	0	0	3.76758	0	ENSG00000270576	AC005520.4
ENSG00000270577	0	1.74643	2.26192	0.953954	ENSG00000270577	AC006023.1
ENSG00000270578	0.88786	0.852011	1.75852	0.544952	ENSG00000270578	AP000787.2
ENSG00000270583	0.419413	0.615368	0.303628	0.153332	ENSG00000270583	AL365400.2
ENSG00000270584	0	0	0.399135	0	ENSG00000270584	AC093813.1
ENSG00000270585	1.33325	3.2511	3.16893	5.93934	ENSG00000270585	AL445435.1
ENSG00000270587	0.616837	0.194232	0.611179	0.873002	ENSG00000270587	AC046185.2
ENSG00000270588	0	0	0.100407	0	ENSG00000270588	AC021749.1
ENSG00000270591	1.20398	3.03521	3.01291	4.51539	ENSG00000270591	AL049840.6
ENSG00000270592	0.0174955	0	0.0914926	0.0380342	ENSG00000270592	AC010492.2
ENSG00000270593	0	0	0	0	ENSG00000270593	AC073333.2
ENSG00000270596	0	0	0	0	ENSG00000270596	IGHV3-25
ENSG00000270597	0	0	0	0	ENSG00000270597	IGHV3-48
ENSG00000270598	0	0	0	0	ENSG00000270598	AL512343.1
ENSG00000270600	0	0	0	0	ENSG00000270600	IGHVIII-5-1
ENSG00000270601	0.163839	0.254736	0.133972	0.268899	ENSG00000270601	PRAMEF5
ENSG00000270603	0.212075	0	0.180082	0.217836	ENSG00000270603	RP11-344N17.15
ENSG00000270606	0.156104	1.04688	1.62091	3.33516	ENSG00000270606	AC025518.2
ENSG00000270608	0	0	0	0	ENSG00000270608	IGHD1-7
ENSG00000270609	0	0	0	0	ENSG00000270609	IGHV3-6
ENSG00000270610	0	0	0.101752	0.126331	ENSG00000270610	AL160191.2
ENSG00000270611	0	0	0	0	ENSG00000270611	AC006363.1
ENSG00000270612	0	0	0	0	ENSG00000270612	AC112191.3
ENSG00000270613	0	0	0	0	ENSG00000270613	IGHVII-44-2
ENSG00000270614	0.236399	0.917907	1.46197	1.3989	ENSG00000270614	AC011451.2
ENSG00000270615	0.120878	0.354111	0.771765	0.440926	ENSG00000270615	SGO1P1
ENSG00000270616	1.38616	1.0988	1.77314	0.224528	ENSG00000270616	TEX22
ENSG00000270617	1.09745	0	0	0	ENSG00000270617	URGCP-MRPS24
ENSG00000270618	0.0607975	0.175497	0.158603	0.0662278	ENSG00000270618	AL160237.3
ENSG00000270619	0	0	0	0.87125	ENSG00000270619	AL391358.1
ENSG00000270620	2.77856	3.50194	6.90294	2.78809	ENSG00000270620	AL034555.1
ENSG00000270622	0	0	0	0	ENSG00000270622	IGHD6-19
ENSG00000270623	0	0	0.20037	0	ENSG00000270623	SPCS2P2
ENSG00000270624	0	0	0	0	ENSG00000270624	AC008555.4
ENSG00000270625	0	0	0	0.109243	ENSG00000270625	AC004835.2
ENSG00000270627	0	1.31914	0	0.729234	ENSG00000270627	AL592221.1
ENSG00000270628	0	0	0	0	ENSG00000270628	RP11-26F2.2
ENSG00000270629	14.0231	27.1346	26.515	49.5815	ENSG00000270629	NBPF14
ENSG00000270631	0	0	0	0	ENSG00000270631	AL592436.1
ENSG00000270632	0.390644	1.47882	0.332824	1.61133	ENSG00000270632	AL356575.1
ENSG00000270633	24.3252	16.722	21.0775	15.8767	ENSG00000270633	CDK16
ENSG00000270634	0.786309	0.744444	0.334973	0.810781	ENSG00000270634	AC005518.2
ENSG00000270635	0	0	0	0	ENSG00000270635	IGHV3-35
ENSG00000270636	0	0	0	0	ENSG00000270636	IGHVIII-2-1
ENSG00000270639	0	0	0.0403332	0	ENSG00000270639	ECM1P1

ENSG00000270642	0	0	0	0	ENSG00000270642	IGHV3-21
ENSG00000270643	0	0	0	0	ENSG00000270643	IGHD4-17
ENSG00000270644	0	0	0.0890803	0	ENSG00000270644	IGHV1-45
ENSG00000270645	0	0	0	0	ENSG00000270645	KIR2DP1
ENSG00000270646	0	0	0	0	ENSG00000270646	AL670379.5
ENSG00000270647	12.5504	24.5826	29.0635	22.5314	ENSG00000270647	TAF15
ENSG00000270648	0	0	0	0	ENSG00000270648	CYP2C61P
ENSG00000270649	0	0.233448	0	0	ENSG00000270649	IGHVIII-26-1
ENSG00000270650	1.28616	1.12793	0	9.51E-05	ENSG00000270650	AC245389.1
ENSG00000270652	0.13648	0.916574	0.354558	1.17033	ENSG00000270652	DPRXP5
ENSG00000270654	0	0	0	0	ENSG00000270654	NUTF2P8
ENSG00000270655	0	0.737461	0.226176	0.813082	ENSG00000270655	AL031320.1
ENSG00000270656	0	0	0	0	ENSG00000270656	RP3-328E19.5
ENSG00000270662	0	0	0	0	ENSG00000270662	IGHJ5
ENSG00000270664	0	0	0	0.70405	ENSG00000270664	AC010900.2
ENSG00000270665	0	0	0	0	ENSG00000270665	HNRNPA1P67
ENSG00000270666	0	0	0	0	ENSG00000270666	AL021918.1
ENSG00000270668	0.249975	0.437288	0.679821	0.841474	ENSG00000270668	IGHV4-59
ENSG00000270669	0	0.326188	0.300385	0.544215	ENSG00000270669	AC008638.3
ENSG00000270670	0.72989	0.735469	0.57018	0.61818	ENSG00000270670	MARK2P16
ENSG00000270671	0.324504	0	0.773569	1.20644	ENSG00000270671	AC245884.2
ENSG00000270672	0	0	0	0	ENSG00000270672	MTRNR2L6
ENSG00000270675	0	0	0	0	ENSG00000270675	AC092118.1
ENSG00000270676	0	0	0	0	ENSG00000270676	IGHV3-13
ENSG00000270677	0	0.10806	0.100498	0	ENSG00000270677	AC007363.1
ENSG00000270678	0	0	0	0	ENSG00000270678	AL670379.6
ENSG00000270679	0.744705	1.09308	0.161208	1.44566	ENSG00000270679	AC138473.1
ENSG00000270680	0	0	0	0	ENSG00000270680	AL596092.1
ENSG00000270682	1.547	1.43205	1.23877	11.9768	ENSG00000270682	AP003357.1
ENSG00000270683	0	0	0	0.457532	ENSG00000270683	FAM71BP1
ENSG00000270684	0	0	0	0	ENSG00000270684	IGHV3-60
ENSG00000270685	0.552519	0	0	0	ENSG00000270685	IGHV1OR15-6
ENSG00000270686	0	0	0	0	ENSG00000270686	IGHD1-14
ENSG00000270687	0	0	0	0	ENSG00000270687	AC009892.2
ENSG00000270688	0	0	0	1.13146	ENSG00000270688	AL137849.1
ENSG00000270689	0.507248	0.187924	0.815377	0.469823	ENSG00000270689	BUD13P1
ENSG00000270690	0.635486	1.54476	0.274978	1.44726	ENSG00000270690	AC105129.3
ENSG00000270691	0.110633	0.854202	0.288631	1.82077	ENSG00000270691	AL161912.3
ENSG00000270692	0.804084	1.22188	0.697751	1.70155	ENSG00000270692	RP11-89F17.5
ENSG00000270693	0	0	0	0	ENSG00000270693	IGHVIII-76-1
ENSG00000270694	0.368711	0	0.306166	0.369796	ENSG00000270694	AC211469.2
ENSG00000270695	0	0	0	0	ENSG00000270695	AL133393.1
ENSG00000270698	0	0	0	0	ENSG00000270698	AC018695.5
ENSG00000270699	0	0	0	0	ENSG00000270699	AC012493.3
ENSG00000270701	0	0	0	0	ENSG00000270701	AP002802.2
ENSG00000270702	1.8062	1.30878	0.589989	3.93463	ENSG00000270702	AC073657.2
ENSG00000270703	0	0	0	0.106823	ENSG00000270703	IGHV6-1
ENSG00000270705	0	0	0	0	ENSG00000270705	AL161669.2
ENSG00000270706	0.671204	1.92075	1.39804	2.85666	ENSG00000270706	PRMT1P1
ENSG00000270707	0	0	0.0424124	0	ENSG00000270707	ELK2BP
ENSG00000270708	0.344587	2.28626	1.83636	1.83639	ENSG00000270708	KF455155.1
ENSG00000270709	0	0	0	0	ENSG00000270709	AL109653.1
ENSG00000270710	0	0	0	0	ENSG00000270710	FO393422.1
ENSG00000270711	1.63731	4.49956	3.71251	4.12036	ENSG00000270711	AL162431.4

ENSG00000270712	0	0	0.151516	0.188974	ENSG00000270712	AL591222.2
ENSG00000270713	0	1.13325	0.511871	2.9742	ENSG00000270713	AL132994.2
ENSG00000270714	0	1.655	0	1.84118	ENSG00000270714	AC132812.2
ENSG00000270715	0	0	0	0	ENSG00000270715	IGHEP1
ENSG00000270716	0.174343	0	0	0	ENSG00000270716	BNIP3P15
ENSG00000270717	0	0	0	0	ENSG00000270717	IGHVII-74-1
ENSG00000270718	0	0	0	0	ENSG00000270718	AC084373.1
ENSG00000270719	0	0	0	0	ENSG00000270719	AL390877.1
ENSG00000270723	0	1.3484	0	0.485812	ENSG00000270723	RPL23AP92
ENSG00000270724	0.185988	0.266953	0	0.197626	ENSG00000270724	IGHV3-73
ENSG00000270727	0	0	0.410807	0	ENSG00000270727	AL590032.1
ENSG00000270728	2.27734	1.63052	1.80149	2.45274	ENSG00000270728	AL035413.2
ENSG00000270729	0	0	0	0.104097	ENSG00000270729	AC004853.1
ENSG00000270733	0.513269	1.95695	0.885021	1.61931	ENSG00000270733	AL355877.2
ENSG00000270734	0.242767	0.779641	1.09655	0.352161	ENSG00000270734	AC136443.5
ENSG00000270736	0	0	0	0	ENSG00000270736	AL670379.7
ENSG00000270737	0.0306141	0	0	0	ENSG00000270737	ELK2AP
ENSG00000270738	0	0	0	0	ENSG00000270738	PFN1P4
ENSG00000270739	0.336055	1.40191	1.76078	1.80265	ENSG00000270739	AC090953.1
ENSG00000270741	0.409243	3.82745	3.54458	7.15552	ENSG00000270741	PRELID3BP8
ENSG00000270745	0	0	0	0	ENSG00000270745	AL731768.1
ENSG00000270746	0	0	0.0606778	0.300223	ENSG00000270746	RP4-725K1.1
ENSG00000270747	0.212075	0	0.180082	0.217836	ENSG00000270747	AL606490.9
ENSG00000270748	0	0	0	0	ENSG00000270748	IGKV2OR2-1
ENSG00000270749	0	0.22953	0	0.264889	ENSG00000270749	AC064862.7
ENSG00000270753	0	0	0	0	ENSG00000270753	AP001836.1
ENSG00000270754	0	0	0	0	ENSG00000270754	NEK4P3
ENSG00000270756	0.284177	0.431107	0.0259567	0.338158	ENSG00000270756	LILRB1
ENSG00000270757	5.9829	0.134938	2.34017	1.31114	ENSG00000270757	HSPE1-MOB4
ENSG00000270759	0	0.865657	0.260842	0	ENSG00000270759	AC091810.1
ENSG00000270762	0	0	0	0	ENSG00000270762	FXYD6P1
ENSG00000270763	0.0868629	0	0.0378816	0	ENSG00000270763	DDX43P2
ENSG00000270764	0.520958	2.70232	1.77127	1.86978	ENSG00000270764	AC005070.1
ENSG00000270765	0.0818642	0.200377	0.153824	0.182836	ENSG00000270765	GAS2L2
ENSG00000270766	0	0.48182	0	0	ENSG00000270766	AC024940.4
ENSG00000270767	0	0	0	0	ENSG00000270767	AL356157.2
ENSG00000270771	0	0	0	0	ENSG00000270771	AL670379.8
ENSG00000270772	1.13977	2.85192	1.50004	2.86964	ENSG00000270772	AC099777.1
ENSG00000270773	0.49322	0.696913	0.655258	0.433968	ENSG00000270773	AC137695.2
ENSG00000270774	0	0	0	0	ENSG00000270774	IGHV3-20
ENSG00000270775	0.243	0.15575	0.211716	0.351381	ENSG00000270775	AP000436.1
ENSG00000270776	0.5775	7.05334	2.90687	4.08649	ENSG00000270776	AC012443.1
ENSG00000270778	0	0	0	0	ENSG00000270778	BUB1P1
ENSG00000270779	0	0	0	0	ENSG00000270779	AC008782.1
ENSG00000270780	0	0	0	0	ENSG00000270780	AL591742.1
ENSG00000270781	0.697371	1.57299	0.901788	0.723694	ENSG00000270781	AC091133.5
ENSG00000270782	0	0	0	0	ENSG00000270782	AC072026.1
ENSG00000270783	0	0	0	0	ENSG00000270783	IGHD3OR15-3A
ENSG00000270784	0	0.105855	0.0665227	0.436923	ENSG00000270784	CRIP1
ENSG00000270785	0.428706	0	0	0	ENSG00000270785	AC010518.3
ENSG00000270786	0	0	0	0	ENSG00000270786	IGHV3-49
ENSG00000270787	0	0	0.0124249	0.0198593	ENSG00000270787	KIR2DL3
ENSG00000270788	0	0	0	0.0699514	ENSG00000270788	PDLIM1P1
ENSG00000270789	4.18044	15.8297	11.3085	8.74226	ENSG00000270789	AC135983.5

ENSG00000270790	0	0	0	0	ENSG00000270790	AC025588.3
ENSG00000270791	0	0.121716	0	0	ENSG00000270791	AC092474.3
ENSG00000270793	0	0	0	0	ENSG00000270793	LLPHP1
ENSG00000270794	0	0	0	0	ENSG00000270794	AC005185.1
ENSG00000270796	0	0	0	0	ENSG00000270796	IGHD3-16
ENSG00000270797	1.00101	5.61846	4.10742	11.4442	ENSG00000270797	AC004987.4
ENSG00000270798	0	0	0	0	ENSG00000270798	AC018737.1
ENSG00000270799	0.614407	2.95684	1.67308	3.00187	ENSG00000270799	AC013467.2
ENSG00000270800	8.1083	4.99018	5.10235	3.27935	ENSG00000270800	RPS10-NUDT3
ENSG00000270802	2.77139	1.9136	5.36779	1.56219	ENSG00000270802	AC005776.1
ENSG00000270803	0.382714	0.689972	0.500865	0.444952	ENSG00000270803	CTD-2522E6.4
ENSG00000270804	6.64935	7.94562	10.3069	14.3212	ENSG00000270804	AC010326.4
ENSG00000270805	0	0	0	0	ENSG00000270805	IGHD4-23
ENSG00000270806	0.181329	0.145398	0.449884	0.137648	ENSG00000270806	C17orf50
ENSG00000270807	0	0	0	0	ENSG00000270807	AC024153.1
ENSG00000270808	0.669203	1.68757	1.36923	1.52863	ENSG00000270808	AC022400.4
ENSG00000270809	0.173689	1.6628	1.62454	1.87557	ENSG00000270809	CHCHD2P11
ENSG00000270811	0	0	0	0	ENSG00000270811	AL590095.2
ENSG00000270812	0	0	0.0623145	0.0779163	ENSG00000270812	AC002069.2
ENSG00000270813	0.856315	1.1707	1.43805	1.53423	ENSG00000270813	AL035422.2
ENSG00000270814	0.841897	0.800424	0	0	ENSG00000270814	TMEM261P1
ENSG00000270815	0	0	0	0	ENSG00000270815	AC019159.1
ENSG00000270816	5.77828	10.5596	8.62179	16.5585	ENSG00000270816	LINC00221
ENSG00000270818	0.0415632	0.0802573	0.187247	0.0515401	ENSG00000270818	AL445675.1
ENSG00000270819	0.147819	0.280889	0.126933	0	ENSG00000270819	IGHV7-27
ENSG00000270822	2.42198	1.13236	0.996885	5.98379	ENSG00000270822	AC092032.1
ENSG00000270824	0	0	0	0	ENSG00000270824	IGHD5OR15-5B
ENSG00000270825	0	0	0	0	ENSG00000270825	AC012314.3
ENSG00000270826	0.164396	0.157512	0.142185	0	ENSG00000270826	Z94722.1
ENSG00000270827	1.83986	7.54592	2.14069	2.30046	ENSG00000270827	HIST2H3C
ENSG00000270830	0	0	0	0	ENSG00000270830	AC022441.3
ENSG00000270831	0	0	0	0	ENSG00000270831	NF1P1
ENSG00000270832	1.0147	6.57266	6.48463	5.99447	ENSG00000270832	AC092120.3
ENSG00000270835	0.459443	0.110537	0.199799	0.375641	ENSG00000270835	AP001425.1
ENSG00000270836	13.9514	3.86813	5.63883	3.16433	ENSG00000270836	EPS8L1
ENSG00000270837	0	0.330482	0.596349	0.361847	ENSG00000270837	HNRNPDLP4
ENSG00000270838	0	0	0	0	ENSG00000270838	AL121912.1
ENSG00000270839	0.590997	1.4747	0.512214	0.890208	ENSG00000270839	AC091393.1
ENSG00000270841	0	0	0	0	ENSG00000270841	IGHV3-57
ENSG00000270842	6.35682	1.69626	3.72566	3.51612	ENSG00000270842	AC073413.2
ENSG00000270846	0.169107	0.37975	0.490297	0.799036	ENSG00000270846	AC021171.2
ENSG00000270848	0	0	0	0	ENSG00000270848	AC245052.1
ENSG00000270849	0	0.169628	0.306361	0.377033	ENSG00000270849	CHCHD2P3
ENSG00000270850	0	0	0	0	ENSG00000270850	AL356986.1
ENSG00000270851	0	0	0	0.0513024	ENSG00000270851	AF146191.8
ENSG00000270852	0	0	0.0995699	0	ENSG00000270852	AL390816.3
ENSG00000270855	0	0	0	0	ENSG00000270855	AC099849.1
ENSG00000270856	0	0	0	0	ENSG00000270856	AL353765.1
ENSG00000270857	0.185988	0.541043	0.330328	0.203709	ENSG00000270857	AC007621.1
ENSG00000270858	0.0806216	0.0832469	0.0788637	0.336785	ENSG00000270858	VDAC1P5
ENSG00000270859	0	0.355938	0	0	ENSG00000270859	AC099785.1
ENSG00000270861	0	0.533493	0	0.573937	ENSG00000270861	AP002906.1
ENSG00000270863	0.207379	0.400546	0.293617	0.361939	ENSG00000270863	DDX55P1
ENSG00000270864	0	0	0	0	ENSG00000270864	IGHV3OR16-6

ENSG00000270865	0	0	0	0	ENSG00000270865	RPL12P48
ENSG00000270868	0	1.21271	1.07366	2.56913	ENSG00000270868	AP000942.3
ENSG00000270870	0	0.46102	0	0.684688	ENSG00000270870	AC004805.2
ENSG00000270872	3.90838	7.22353	7.20408	6.03608	ENSG00000270872	SRGAP2D
ENSG00000270873	0	0	0	0	ENSG00000270873	IGHVIII-13-1
ENSG00000270874	0.258142	1.08249	0.996794	1.57758	ENSG00000270874	RPAP2P1
ENSG00000270877	0	0	0	0	ENSG00000270877	IGHVIII-5-2
ENSG00000270878	0.531882	0.608267	0.949533	1.37612	ENSG00000270878	AL136038.4
ENSG00000270879	19.5784	62.6045	73.0994	90.3035	ENSG00000270879	RP11-210K20.4
ENSG00000270880	0.225599	0.108294	0.195606	0	ENSG00000270880	AC128687.1
ENSG00000270881	0	0	0	0	ENSG00000270881	IGHV3-66
ENSG00000270882	22.4704	99.2338	23.9434	24.1079	ENSG00000270882	HIST2H4A
ENSG00000270884	0.00591224	0.0414758	0	0	ENSG00000270884	NLRP7
ENSG00000270885	6.76921	21.0509	21.2527	41.4554	ENSG00000270885	RASL10B
ENSG00000270886	0.133284	0.247489	0.256662	0.413123	ENSG00000270886	GP6
ENSG00000270888	0	0	0	0	ENSG00000270888	IGHD2-15
ENSG00000270889	0	0	0	0	ENSG00000270889	AC087072.1
ENSG00000270890	1.43823	3.52714	4.54458	2.28777	ENSG00000270890	AL049844.2
ENSG00000270891	0.162847	0.312076	0.140857	1.21614	ENSG00000270891	AC012507.3
ENSG00000270892	0.27626	0.262793	1.18771	0.289479	ENSG00000270892	AC006077.1
ENSG00000270893	0.325526	1.0207	1.13073	1.32352	ENSG00000270893	AC008277.2
ENSG00000270895	0	0	0	0	ENSG00000270895	IGHG2
ENSG00000270896	0	3.48429	2.06821	0.903026	ENSG00000270896	AL645939.4
ENSG00000270897	0.672832	0	0	1.56145	ENSG00000270897	AC111188.3
ENSG00000270898	0.315653	1.71421	0.476093	0.566677	ENSG00000270898	GPR75-ASB3
ENSG00000270899	0	0	0	0	ENSG00000270899	IGHD3-9
ENSG00000270900	0	0.467532	0.745107	1.7024	ENSG00000270900	AL360272.1
ENSG00000270901	36.2584	63.7198	62.1545	106.259	ENSG00000270901	RP11-592P9.1
ENSG00000270902	0	0	2.99065	1.19676	ENSG00000270902	AL160290.3
ENSG00000270903	0.910341	1.37746	2.33338	1.25214	ENSG00000270903	HNRNPA3P9
ENSG00000270904	0	1.01458	0	0.282053	ENSG00000270904	AC008385.1
ENSG00000270906	0	0.123316	0.0743215	0.23347	ENSG00000270906	MTND4P35
ENSG00000270908	0	0	0	0	ENSG00000270908	AC098789.1
ENSG00000270909	0.928211	2.18645	1.97921	2.22284	ENSG00000270909	CR788268.1
ENSG00000270911	0	0.138247	0.0827311	1.03862	ENSG00000270911	AC114878.2
ENSG00000270912	0	0	0	0	ENSG00000270912	RPS28P1
ENSG00000270913	0	0.243112	0.118486	0.198619	ENSG00000270913	PPIAL4D
ENSG00000270914	0	0	0	0	ENSG00000270914	AL096840.1
ENSG00000270915	0.620872	1.11176	1.50782	0.917761	ENSG00000270915	AC073410.2
ENSG00000270916	0	0	0	0	ENSG00000270916	RPL12P50
ENSG00000270917	0.724907	1.61349	0.833433	1.0188	ENSG00000270917	AL161911.2
ENSG00000270920	0	0	0	0	ENSG00000270920	MCRIP2P2
ENSG00000270921	0	0	0	0	ENSG00000270921	CICP23
ENSG00000270923	1.01463	1.0985	3.18988	1.58651	ENSG00000270923	TAS2R6P
ENSG00000270924	0	0	0	0	ENSG00000270924	AC140658.5
ENSG00000270925	0	0	0	0	ENSG00000270925	IGHV3-22
ENSG00000270926	0	1.02989	0.29025	0.280498	ENSG00000270926	AC008013.3
ENSG00000270927	0	0	0	0.165722	ENSG00000270927	AL645944.1
ENSG00000270928	0	0	0	0	ENSG00000270928	GAGE12F
ENSG00000270929	0	0.18965	0.0571285	0	ENSG00000270929	SRD5A3P1
ENSG00000270930	0	0	0	0.0592385	ENSG00000270930	GRAMD4P8
ENSG00000270931	0.58451	10.2779	6.43028	3.79823	ENSG00000270931	CRIP2
ENSG00000270934	0	0.109708	0	0.369216	ENSG00000270934	AL512430.4
ENSG00000270935	0	0	0.0979042	0.303902	ENSG00000270935	AL021808.1

ENSG00000270936	0.203905	1.07734	0.62019	1.21101	ENSG00000270936	AL034351.1
ENSG00000270938	0.324674	0	0	0.231278	ENSG00000270938	RAP2CP1
ENSG00000270939	0	0	0	0	ENSG00000270939	IGHV3-50
ENSG00000270940	0	0	0	0	ENSG00000270940	IGHJ1P
ENSG00000270941	1.55825	1.19657	1.08245	0.833822	ENSG00000270941	AC006254.2
ENSG00000270942	4.64461	0	7.14477	1.00631	ENSG00000270942	AC245052.2
ENSG00000270943	0	0	0	0	ENSG00000270943	AL928654.2
ENSG00000270945	0	0	0.543684	0	ENSG00000270945	HSPE1P7
ENSG00000270946	0	0	0	0	ENSG00000270946	CT45A9
ENSG00000270948	0.332307	0.479576	0.363089	0.540231	ENSG00000270948	MTDHP1
ENSG00000270950	0	3.48429	2.06821	0.903026	ENSG00000270950	Xxbac-BPG170G13.31
ENSG00000270954	0	0	0	0	ENSG00000270954	RPSAP75
ENSG00000270955	0	0.0257889	0.079531	0	ENSG00000270955	AC135731.2
ENSG00000270957	0	0	0	0	ENSG00000270957	AC092175.1
ENSG00000270958	0	0	0	0	ENSG00000270958	
ENSG00000270960	0	0	0	0	ENSG00000270960	AC106872.11
ENSG00000270961	0	0	0	0	ENSG00000270961	IGHD5OR15-5A
ENSG00000270962	0	0	0	0	ENSG00000270962	AC239800.4
ENSG00000270963	0	0	0	0	ENSG00000270963	IGHD6-25
ENSG00000270965	0	0.0511679	0.0462051	0.0574712	ENSG00000270965	NTAN1P1
ENSG00000270966	0	0	0.866083	0.53992	ENSG00000270966	AC087763.1
ENSG00000270969	0.184556	0.295955	0.21397	0.268011	ENSG00000270969	AP001823.1
ENSG00000270971	0	0	0	0	ENSG00000270971	REXO1L8P
ENSG00000270973	0	0	0	0	ENSG00000270973	SMARCE1P7
ENSG00000270975	0.858051	0.524986	0.678237	1.57307	ENSG00000270975	MAGOH3P
ENSG00000270976	0	0	0.570064	0	ENSG00000270976	AL596327.1
ENSG00000270978	0.0543729	0.104534	0	0.0592385	ENSG00000270978	AC091982.3
ENSG00000270979	0	0	0	0	ENSG00000270979	RP11-403I13.10
ENSG00000270980	0	0	0	0	ENSG00000270980	AC060764.1
ENSG00000270981	0	0.136803	0.0618038	0	ENSG00000270981	AC092944.2
ENSG00000270982	0	0	0	0	ENSG00000270982	AL353621.2
ENSG00000270983	0	0	0	0	ENSG00000270983	AL589674.2
ENSG00000270984	0	0	0	0	ENSG00000270984	GS1-115M3.4
ENSG00000270985	6.72781	10.1063	9.9895	15.292	ENSG00000270985	AC245884.3
ENSG00000270986	2.2626	4.08199	2.69267	8.35868	ENSG00000270986	HMGB1P51
ENSG00000270987	0	0	0	0	ENSG00000270987	AL133338.2
ENSG00000270989	0	0	0	0	ENSG00000270989	AC139493.1
ENSG00000270990	0	0	0	0	ENSG00000270990	AC069304.2
ENSG00000270992	0	0	0.251204	0	ENSG00000270992	AC024085.1
ENSG00000270993	3.72544	5.85276	2.32067	1.9441	ENSG00000270993	AC111186.1
ENSG00000270994	0	0.0642722	0.0580758	0.508868	ENSG00000270994	AL157899.1
ENSG00000270995	0.505818	1.61515	1.45792	1.25788	ENSG00000270995	AL137072.1
ENSG00000270997	0.109235	0.1049	0	0.353304	ENSG00000270997	AC073137.1
ENSG00000270998	3.73612	2.69337	3.04044	3.60671	ENSG00000270998	RDH13
ENSG00000270999	0	0	0	0	ENSG00000270999	IGKV1OR2-118
ENSG00000271000	0.0173935	0.0653909	0.0528049	0.105118	ENSG00000271000	NCR1
ENSG00000271001	0	1.09788	0	0	ENSG00000271001	AC243756.1
ENSG00000271002	0.642199	0.609267	0.826112	1.00392	ENSG00000271002	AC129492.5
ENSG00000271003	0	0	0	0	ENSG00000271003	AC009237.13
ENSG00000271004	0	0	0	0	ENSG00000271004	AB019438.66
ENSG00000271005	0	0	0	0	ENSG00000271005	CTHRC1P1
ENSG00000271008	0	6.8238	14.0934	8.67027	ENSG00000271008	IGHJ6
ENSG00000271010	1.59402	3.67033	3.3406	7.82558	ENSG00000271010	AC011475.1
ENSG00000271013	0.0578262	0.153975	0.162496	0.255638	ENSG00000271013	LRRC37A9P

ENSG00000271014	0	7.69689	0	2.37832	ENSG00000271014	AC062037.1
ENSG00000271015	0	0	0	0	ENSG00000271015	IGKV2OR2-7D
ENSG00000271016	6.65526	7.37127	5.58789	8.42543	ENSG00000271016	NDUFA3
ENSG00000271018	0	0	0	0	ENSG00000271018	AC013244.1
ENSG00000271019	24.0879	22.1499	22.3581	4.72986	ENSG00000271019	MBOAT7
ENSG00000271021	0	0.0818136	0.147696	0	ENSG00000271021	AC239600.1
ENSG00000271022	0.0855097	0.0824135	0.147084	0.18643	ENSG00000271022	AP002365.1
ENSG00000271023	0	0	0	0	ENSG00000271023	IGHV4-34
ENSG00000271024	0	0.342775	0	0.37509	ENSG00000271024	HSPE1P19
ENSG00000271025	0.550262	1.29237	0.2307	0	ENSG00000271025	AP000907.4
ENSG00000271026	0.582701	0.451569	0.172301	0.88595	ENSG00000271026	KATNBL1P1
ENSG00000271027	0	0	0	0	ENSG00000271027	AC006380.1
ENSG00000271028	0.120784	0	0.0350531	0	ENSG00000271028	AC009643.2
ENSG00000271029	0	0.618144	0.186165	0.914146	ENSG00000271029	AC135178.6
ENSG00000271030	0	0	0	0	ENSG00000271030	AC008746.9
ENSG00000271031	0	0	0	0	ENSG00000271031	IGHD3-3
ENSG00000271034	0	0.112373	0.0333231	0.172041	ENSG00000271034	AC139700.1
ENSG00000271035	0	0	0	0	ENSG00000271035	AC010385.2
ENSG00000271036	0	0.305818	0.139721	0.340309	ENSG00000271036	CLPTM1LP1
ENSG00000271037	0	0	0	0	ENSG00000271037	AC008746.10
ENSG00000271039	0	0	0	0	ENSG00000271039	KIR3DL1
ENSG00000271041	0.250088	0	0	0	ENSG00000271041	AL670379.9
ENSG00000271042	0.649515	0.924115	0.834911	1.01538	ENSG00000271042	AL078603.1
ENSG00000271043	37388.5	38681.4	47961.9	48105.9	ENSG00000271043	MTRNR2L2
ENSG00000271044	0.771142	0.952082	0.482003	2.49364	ENSG00000271044	AC087468.1
ENSG00000271045	0.2215	0.283176	0.639161	0.315962	ENSG00000271045	NDUFB9P1
ENSG00000271047	0	0	0	0	ENSG00000271047	AC092447.9
ENSG00000271048	0.230238	0	0	0.729234	ENSG00000271048	AC087045.1
ENSG00000271049	0.704908	1.65749	1.46485	0.821666	ENSG00000271049	AC020910.3
ENSG00000271050	0	0	0	0	ENSG00000271050	IGHV3-30-2
ENSG00000271052	2.20105	3.61862	3.6912	1.16448	ENSG00000271052	AC108738.1
ENSG00000271053	0	0	0	0	ENSG00000271053	AC093765.1
ENSG00000271056	0	0.144283	0.159737	0	ENSG00000271056	AL136363.2
ENSG00000271057	0	0	0	0	ENSG00000271057	AC073648.5
ENSG00000271058	0	0	0	0	ENSG00000271058	IGHV3-15
ENSG00000271060	0	0	0	0	ENSG00000271060	IGHV3-71
ENSG00000271062	0	0	0	0	ENSG00000271062	IGHV2-5
ENSG00000271063	0	0	0	0	ENSG00000271063	SNRPGP17
ENSG00000271064	8.62576	14.3183	21.063	21.6117	ENSG00000271064	AC027644.2
ENSG00000271069	0	0.0818136	0.147696	0	ENSG00000271069	RP5-878I13.2
ENSG00000271070	0.156381	0.152224	0.135826	0	ENSG00000271070	GMCL1P2
ENSG00000271071	0.0645014	0.185871	0.252694	0.459643	ENSG00000271071	AL513548.2
ENSG00000271072	0.0790762	0	0.068873	0	ENSG00000271072	PHBP20
ENSG00000271074	0.0811269	0.391472	0.211352	0.175927	ENSG00000271074	AC012491.1
ENSG00000271075	0.259171	1.95593	0.907315	4.16009	ENSG00000271075	AL139317.4
ENSG00000271077	0.232469	0.676747	0.547616	0.562093	ENSG00000271077	AC096553.1
ENSG00000271078	0.0546122	0	0.0853835	0.0299683	ENSG00000271078	AC139426.3
ENSG00000271079	0	0	0	0	ENSG00000271079	CTAGE15
ENSG00000271080	0	0	0	0	ENSG00000271080	IGHV1-58
ENSG00000271081	0	0.347914	0	1.49711	ENSG00000271081	AC009314.1
ENSG00000271082	0	0	0	0	ENSG00000271082	IGHVII-67-1
ENSG00000271083	0	0	0	0	ENSG00000271083	IGHV4-39
ENSG00000271088	0	0.0708443	0.0640513	0.0605977	ENSG00000271088	AL161722.3
ENSG00000271089	0.126528	0.121421	0.219282	0.407744	ENSG00000271089	IGHV3-53

ENSG00000271091	5.04355	3.24984	2.43234	2.91572	ENSG00000271091	RP2
ENSG00000271092	0	0	0	0	ENSG00000271092	TMEM56-RWDD3
ENSG00000271093	0	0	0	0	ENSG00000271093	IGLCOR22-2
ENSG00000271094	0	0	0.570064	0	ENSG00000271094	AL022161.1
ENSG00000271095	4.06796	5.78199	5.59417	8.71484	ENSG00000271095	BNIP3P28
ENSG00000271096	1.46575	6.71362	5.63027	5.6934	ENSG00000271096	SUMO2P14
ENSG00000271097	0	0	0	0.0052235	ENSG00000271097	AC083899.3
ENSG00000271098	0	1.78297	0.515716	2.75389	ENSG00000271098	IMMP1LP3
ENSG00000271099	0.484965	1.96847	1.67137	3.6275	ENSG00000271099	AL357315.2
ENSG00000271100	3.44005	6.4376	6.606	2.26292	ENSG00000271100	AP000753.3
ENSG00000271101	0.141947	0.0455575	0.123532	0	ENSG00000271101	AC005181.1
ENSG00000271105	0.816731	0.914182	0.235756	1.16959	ENSG00000271105	AC133552.5
ENSG00000271107	0.23394	0.38731	0.32465	0.694744	ENSG00000271107	AC009892.10
ENSG00000271108	0	0	0	0	ENSG00000271108	KATNBL1P5
ENSG00000271111	0	0.288768	0.400297	0.785446	ENSG00000271111	AL365503.1
ENSG00000271112	0	0	0	0	ENSG00000271112	RP11-666A1.7
ENSG00000271113	0	0	0	0.109054	ENSG00000271113	AC079089.3
ENSG00000271114	0	0	0	0	ENSG00000271114	AL590392.1
ENSG00000271115	0	0	0	0	ENSG00000271115	AC010738.1
ENSG00000271116	0	0	0	0.0366664	ENSG00000271116	LAIR2
ENSG00000271117	0	0	0	0	ENSG00000271117	AC078841.1
ENSG00000271118	0	0	0	0	ENSG00000271118	AC012119.1
ENSG00000271121	1.28616	1.12793	0	9.51E-05	ENSG00000271121	NUDT4P2
ENSG00000271123	0	0	0	0	ENSG00000271123	ELOCP5
ENSG00000271124	0	0	0	0	ENSG00000271124	KIR3DL3
ENSG00000271126	0	0	0	0	ENSG00000271126	AC008984.7
ENSG00000271128	0	0	0	0	ENSG00000271128	AC008608.1
ENSG00000271129	0.647322	0.312078	0.14	1.04019	ENSG00000271129	AC009027.1
ENSG00000271130	0	0.255427	0	0.281347	ENSG00000271130	IGHV3OR16-8
ENSG00000271131	0	0	0	0	ENSG00000271131	AC024220.1
ENSG00000271132	0.165299	0	0	0	ENSG00000271132	RP1-241P17.7
ENSG00000271134	0	0.229634	0.416874	0	ENSG00000271134	AC012498.2
ENSG00000271136	0	0	0	0	ENSG00000271136	AL592504.1
ENSG00000271137	0.286472	0.688721	0.45757	0.544673	ENSG00000271137	AC006254.3
ENSG00000271138	0.216322	0	0	0.228747	ENSG00000271138	IGLVIVOR22-1
ENSG00000271140	0	0	0	0	ENSG00000271140	PRR20FP
ENSG00000271142	0.731752	0.81443	0.811959	3.01445	ENSG00000271142	YWHAQP7
ENSG00000271143	0	0.70597	0	0	ENSG00000271143	AL357137.1
ENSG00000271144	0	0	0	0	ENSG00000271144	IGHD2-8
ENSG00000271146	0.654583	1.2401	2.23976	3.92037	ENSG00000271146	AC018889.1
ENSG00000271149	0	0.296471	0	0	ENSG00000271149	AC011467.6
ENSG00000271150	0.424149	0.455783	0	0	ENSG00000271150	AC008745.1
ENSG00000271153	0.546611	0	0	0	ENSG00000271153	RPL23AP88
ENSG00000271154	0.250088	0	0	0	ENSG00000271154	AL670379.10
ENSG00000271157	0	0.318875	0.144041	0	ENSG00000271157	AL022154.1
ENSG00000271158	0.0535284	0.0807321	0.049474	0.091395	ENSG00000271158	AL450472.2
ENSG00000271159	0	0	0	0	ENSG00000271159	HINT1P2
ENSG00000271161	1.56046	3.26828	3.59978	3.78877	ENSG00000271161	BOLA2P2
ENSG00000271162	0	0.0902001	0	0.101513	ENSG00000271162	AL022099.1
ENSG00000271163	0.385406	0	0	0	ENSG00000271163	AC004840.2
ENSG00000271164	0	0	0	0.170662	ENSG00000271164	AL139286.1
ENSG00000271165	0.0917625	0.0886634	0.0801124	0.0506041	ENSG00000271165	RP11-42L13.3
ENSG00000271166	0	0.258496	0	0	ENSG00000271166	AL671309.1

ENSG00000271169	0	0	0	0	ENSG00000271169	IGHJ2
ENSG00000271173	0	0	0	0	ENSG00000271173	AL355989.2
ENSG00000271174	0	0.525586	0.237542	0	ENSG00000271174	AC104440.1
ENSG00000271175	0	0	0	0	ENSG00000271175	AC016925.2
ENSG00000271176	0	0	0	0	ENSG00000271176	IGHV3-33-2
ENSG00000271177	0	0	0	1.12889	ENSG00000271177	AC010200.2
ENSG00000271178	0	0	0	0	ENSG00000271178	IGHV3OR16-13
ENSG00000271179	0	0	0	0	ENSG00000271179	AC098826.3
ENSG00000271180	0	0	0	0	ENSG00000271180	AL158801.4
ENSG00000271181	0	2.07283	1.0093	0.579579	ENSG00000271181	Z99916.2
ENSG00000271182	0	0.267028	0	0	ENSG00000271182	AC123912.5
ENSG00000271184	0	0	0.0499498	0	ENSG00000271184	AC005252.1
ENSG00000271186	0	0	0	0	ENSG00000271186	IGHV3-38
ENSG00000271187	0	0	0	0	ENSG00000271187	AL713866.2
ENSG00000271188	0.059703	0.108637	0.0554507	0.139663	ENSG00000271188	LILRA1
ENSG00000271189	0	0	0	0	ENSG00000271189	IGHA1
ENSG00000271190	0.219072	0.367042	0.451025	0.449868	ENSG00000271190	RPP40P2
ENSG00000271193	0	0.250391	0	0	ENSG00000271193	IGHVIII-25-1
ENSG00000271194	0	0	0	0	ENSG00000271194	RNF138P2
ENSG00000271195	0.18026	1.04092	1.09017	0.191672	ENSG00000271195	AC018618.2
ENSG00000271196	0	0	0	0	ENSG00000271196	AC113403.1
ENSG00000271197	0	0	0	0	ENSG00000271197	IGHD2OR15-2A
ENSG00000271198	0	0	0	0	ENSG00000271198	VDAC3P1
ENSG00000271202	0	0	0	0	ENSG00000271202	PRR13P7
ENSG00000271203	0.586232	0.553337	0.745755	0.452985	ENSG00000271203	TFPT
ENSG00000271205	0	0	0	0	ENSG00000271205	Z83818.1
ENSG00000271207	0	0	0	0.189047	ENSG00000271207	MTCO1P22
ENSG00000271209	0.20036	0.192489	0.0869335	0.108229	ENSG00000271209	BRDTP1
ENSG00000271210	0.508036	0.828791	1.10703	2.11598	ENSG00000271210	FCAR
ENSG00000271211	0.250088	0	0	0	ENSG00000271211	AL670379.11
ENSG00000271212	0	0	0	0	ENSG00000271212	RP11-810O3.2
ENSG00000271214	0	0	0	3.04091	ENSG00000271214	AL138895.2
ENSG00000271215	0	1.0377	0.571627	0.465819	ENSG00000271215	RPL21P136
ENSG00000271217	0	0	0	0	ENSG00000271217	RP11-301J7.9
ENSG00000271219	0.257453	0	0.22302	0.552845	ENSG00000271219	AC011626.1
ENSG00000271220	0	0	0	0.538948	ENSG00000271220	AL355376.2
ENSG00000271221	0	0	0	0	ENSG00000271221	IGHVII-26-2
ENSG00000271222	0	0	0	0.634573	ENSG00000271222	AC091152.3
ENSG00000271223	0	0	0	0	ENSG00000271223	RP6-137J22.3
ENSG00000271224	0	0	0	0	ENSG00000271224	IGHV1-46
ENSG00000271225	3.47643	16.5983	0.332109	1.23496	ENSG00000271225	BNIP3P4
ENSG00000271226	0	0	0	0	ENSG00000271226	IGKV2OR2-10
ENSG00000271227	0	0.821967	0.510387	0.642072	ENSG00000271227	AL109918.3
ENSG00000271229	0	0	0	0	ENSG00000271229	AC008984.6
ENSG00000271230	0.330598	0	0.283065	0.688367	ENSG00000271230	AC027334.1
ENSG00000271231	0	0	0	0	ENSG00000271231	KRT18P9
ENSG00000271232	0	0	0.0618038	0.0772929	ENSG00000271232	CARSP1
ENSG00000271235	0	0	0	0	ENSG00000271235	AC114477.1
ENSG00000271236	0	0.381924	0	0.416374	ENSG00000271236	SUMO2P15
ENSG00000271237	0.115823	0.67339	0	0.872761	ENSG00000271237	HMGB1P50
ENSG00000271238	0	0	0	0	ENSG00000271238	AC023932.2
ENSG00000271240	0	0	0	0	ENSG00000271240	AC110741.2
ENSG00000271242	0	0	0	0	ENSG00000271242	PRELID3BP2
ENSG00000271243	0.113621	0.492094	0.292155	0.324606	ENSG00000271243	AC016727.2

ENSG00000271245	0	2.34543	1.57359	1.26197	ENSG00000271245	AL136139.1
ENSG00000271246	0	0	0	0	ENSG00000271246	AC010492.5
ENSG00000271247	0	0	0	0	ENSG00000271247	AC009892.9
ENSG00000271248	0	0	0	0	ENSG00000271248	AC091193.1
ENSG00000271249	0.0859606	0	0.149267	0.0931134	ENSG00000271249	DIMT1P1
ENSG00000271250	0	0	0	0	ENSG00000271250	AL158032.1
ENSG00000271251	0	0	0	0	ENSG00000271251	AC025946.2
ENSG00000271253	0	0.206683	0	0.228747	ENSG00000271253	AC011891.2
ENSG00000271254	3.31801	4.1489	1.9445	4.05354	ENSG00000271254	AC240274.1
ENSG00000271255	0	0	0	0	ENSG00000271255	IGHD3OR15-3B
ENSG00000271257	0	0	0	0	ENSG00000271257	AC008814.1
ENSG00000271258	0	0	0	0	ENSG00000271258	IGHJ3P
ENSG00000271261	0	0	0	0	ENSG00000271261	IGHV1-18
ENSG00000271263	3.23556	4.09435	5.9765	10.8875	ENSG00000271263	RP11-450H5.4
ENSG00000271264	2.55643	2.22838	1.38707	6.77155	ENSG00000271264	MZT1P1
ENSG00000271266	0	0	0	0	ENSG00000271266	LAPTM4BP2
ENSG00000271267	2.82287	2.21336	6.34197	1.43675	ENSG00000271267	AL353807.4
ENSG00000271268	0	0.0807274	0.220588	0.178339	ENSG00000271268	AC015849.6
ENSG00000271269	0	0	0.178793	0	ENSG00000271269	AL353778.1
ENSG00000271271	0.112405	0.299791	0.261014	0.246167	ENSG00000271271	UGT2A2
ENSG00000271272	0	0.0870615	0	0.392147	ENSG00000271272	AC068802.1
ENSG00000271273	0.130271	0	0	0	ENSG00000271273	RP11-157B13.9
ENSG00000271274	0	0	0	0	ENSG00000271274	IGHV1-14
ENSG00000271275	0	0.497236	0.75871	0.385574	ENSG00000271275	AC007326.1
ENSG00000271276	0	0	0	0	ENSG00000271276	IGHD4-4
ENSG00000271277	0	0	0	0.246214	ENSG00000271277	AL356280.1
ENSG00000271278	4.5993	10.0837	11.3812	17.0152	ENSG00000271278	ELOCP33
ENSG00000271279	0	0	0.0384919	0	ENSG00000271279	CTC-550B14.1
ENSG00000271281	0.0645014	0.185871	0.252694	0.459643	ENSG00000271281	RP11-457M11.6
ENSG00000271282	0	0	0	0	ENSG00000271282	RP11-417P24.1
ENSG00000271283	0.723502	0.678588	0	3.11627	ENSG00000271283	AC011458.2
ENSG00000271284	0	0.392519	0.353021	1.28248	ENSG00000271284	SMIM12P1
ENSG00000271285	1.07724	4.79285	3.17575	6.05441	ENSG00000271285	CTD-2542C24.9
ENSG00000271286	0	0.0921942	0.0832791	0.20744	ENSG00000271286	U73023.1
ENSG00000271287	0.673728	0.857689	0.444715	2.13442	ENSG00000271287	BCRP9
ENSG00000271288	0	0	0	0	ENSG00000271288	IGHV1OR15-3
ENSG00000271289	0	0	0	0	ENSG00000271289	IGHV1-67
ENSG00000271290	0	0	0.0957338	0	ENSG00000271290	AL390058.1
ENSG00000271291	0	0	0	0	ENSG00000271291	AC245014.2
ENSG00000271292	0	0.0203302	0.0523175	0.0655454	ENSG00000271292	IGHG1
ENSG00000271294	0	0	0	0	ENSG00000271294	IGHV7-56
ENSG00000271295	0.141779	0	0	0	ENSG00000271295	IGHVIV-44-1
ENSG00000271296	0	0	0	0	ENSG00000271296	AC233724.14
ENSG00000271298	0	0	0	0	ENSG00000271298	AL080274.1
ENSG00000271299	0	0.324658	0	0.711163	ENSG00000271299	AC008962.1
ENSG00000271300	0	0	0	0	ENSG00000271300	IGHVII-49-1
ENSG00000271302	0	0	0	0	ENSG00000271302	AC105254.2
ENSG00000271303	16.4854	15.9221	16.2821	8.45846	ENSG00000271303	SRXN1
ENSG00000271304	0.130345	0	0	0.142421	ENSG00000271304	AL133507.1
ENSG00000271305	0	0	0	0	ENSG00000271305	IGHD2OR15-2B
ENSG00000271306	0	0	0	0	ENSG00000271306	RAC1P9
ENSG00000271307	0	0	0	0.0513024	ENSG00000271307	AF146191.1
ENSG00000271309	0	0.823092	0	0	ENSG00000271309	AC140113.2
ENSG00000271310	49.4773	43.219	41.0307	52.1638	ENSG00000271310	UBA1

ENSG00000271312	0	0	0	0	ENSG00000271312	IGHD3-10
ENSG00000271313	0	0	0	0	ENSG00000271313	AC069114.2
ENSG00000271315	0	3.05171	1.30938	1.5956	ENSG00000271315	AC174048.1
ENSG00000271317	0	0	0	0	ENSG00000271317	IGHD4OR15-4A
ENSG00000271318	0.12337	0.122939	0.618995	0	ENSG00000271318	AP000654.2
ENSG00000271321	0.0638631	0	0	0.204932	ENSG00000271321	CTAGE6
ENSG00000271322	0	0	0	0	ENSG00000271322	AL357312.1
ENSG00000271323	0	0	0	0	ENSG00000271323	IGHJ1
ENSG00000271325	0.342873	0.218115	0.375649	0.0612136	ENSG00000271325	CRIP1
ENSG00000271326	0.745233	1.657	1.50797	2.75599	ENSG00000271326	LILRB4
ENSG00000271328	0	0	0	0	ENSG00000271328	B3GNTL1P2
ENSG00000271329	0.244529	0	0.0707812	0.0883708	ENSG00000271329	AL035417.2
ENSG00000271330	0	0.324658	0.292932	3.55581	ENSG00000271330	AC005084.1
ENSG00000271331	0	0	0	0	ENSG00000271331	IGHVIII-67-2
ENSG00000271332	0.710172	4.56657	3.40059	3.03417	ENSG00000271332	AC023206.1
ENSG00000271333	0	0	0	0	ENSG00000271333	AC019322.2
ENSG00000271336	0	0	0	0	ENSG00000271336	IGHD1OR15-1A
ENSG00000271337	1.03169	3.384	2.75751	4.17299	ENSG00000271337	NDE1P2
ENSG00000271338	0	0	0	0	ENSG00000271338	AL591034.3
ENSG00000271339	0	0	0	0	ENSG00000271339	AL683813.2
ENSG00000271340	0	0	0	0	ENSG00000271340	AC120024.3
ENSG00000271342	16.5862	16.4265	5.48014	8.0662	ENSG00000271342	SLC9A7
ENSG00000271343	0.769707	1.50141	3.06278	3.81799	ENSG00000271343	AL355598.1
ENSG00000271346	1.08E-08	0	0	0	ENSG00000271346	AC008162.1
ENSG00000271349	0	0	0	0	ENSG00000271349	AC007992.2
ENSG00000271350	0.068322	0	0.118742	0.297167	ENSG00000271350	AC103792.1
ENSG00000271351	0	0	0	0	ENSG00000271351	IGKV1OR2-9
ENSG00000271352	9.32348	8.94532	9.53297	6.48352	ENSG00000271352	RBM10
ENSG00000271353	0.190662	0.912101	0.658921	0.202458	ENSG00000271353	AC012468.1
ENSG00000271354	0	0	0	0	ENSG00000271354	GAGE12H
ENSG00000271355	0	0	0	0	ENSG00000271355	AL356458.1
ENSG00000271356	0.138839	0.200276	0.244323	0.2264	ENSG00000271356	AC073091.2
ENSG00000271357	0	0	0.413933	1.5003	ENSG00000271357	AC048344.3
ENSG00000271358	0	0	0	0	ENSG00000271358	AL137190.1
ENSG00000271361	0.989366	0.950073	2.28793	0.829494	ENSG00000271361	AL133351.4
ENSG00000271362	0.552352	0	0.886705	0	ENSG00000271362	AL138889.2
ENSG00000271363	2.15126	3.07472	2.91267	4.47535	ENSG00000271363	PHF16
ENSG00000271364	0.0658136	0.0632967	0.114401	0.143209	ENSG00000271364	AC015871.2
ENSG00000271365	0	0	0.870729	2.51807	ENSG00000271365	AC140113.3
ENSG00000271368	0	0	0	0	ENSG00000271368	AC073387.2
ENSG00000271369	1.15854	0.370556	0.22302	0.691056	ENSG00000271369	AC087783.2
ENSG00000271370	0	1.55939	1.01541	1.7235	ENSG00000271370	AC007619.2
ENSG00000271371	0	0	0	0	ENSG00000271371	IGHD6-6
ENSG00000271372	1.37498	1.26931	0.900864	2.28672	ENSG00000271372	PFN1P3
ENSG00000271373	0	0	0	0	ENSG00000271373	NANOGP3
ENSG00000271374	11.8685	18.0217	17.1114	14.4571	ENSG00000271374	PACS2
ENSG00000271375	0.477383	0.688694	0.623068	0.287205	ENSG00000271375	AC134879.2
ENSG00000271377	0	0	0	0	ENSG00000271377	AC113143.2
ENSG00000271378	1.13625	0.927384	1.44066	1.95207	ENSG00000271378	C8orf59P2
ENSG00000271379	0	0	0	0	ENSG00000271379	AC023513.1
ENSG00000271381	0	0	0	0	ENSG00000271381	REXO1L9P
ENSG00000271383	7.09149	5.27422	8.01628	8.50085	ENSG00000271383	NBPF19
ENSG00000271385	0	1.88647	1.59006	1.92661	ENSG00000271385	AL161798.1
ENSG00000271386	0	0	0	0.188517	ENSG00000271386	SRGNP1

ENSG00000271389	0.0792307	0.228948	0.104656	0.174238	ENSG00000271389	OSBPL9P1
ENSG00000271391	0	0	0	0	ENSG00000271391	IGHD7-27
ENSG00000271393	0	0	0	0	ENSG00000271393	IGHD3-22
ENSG00000271396	0.0706493	0.135874	0.246649	0.307099	ENSG00000271396	AC091167.5
ENSG00000271397	0	0	0	0	ENSG00000271397	AL109837.1
ENSG00000271399	0	0	0	0	ENSG00000271399	AL078624.1
ENSG00000271400	0	0	0	0	ENSG00000271400	AL392112.1
ENSG00000271402	0	0	0	0	ENSG00000271402	IGKV2OR2-2
ENSG00000271403	0	0	0	0	ENSG00000271403	HOMER2P2
ENSG00000271404	0	0	0	0	ENSG00000271404	MZT1P2
ENSG00000271408	0	0	0.0804654	0.100269	ENSG00000271408	NAPGP1
ENSG00000271410	0.638406	1.41838	1.28198	1.44811	ENSG00000271410	AC020728.1
ENSG00000271411	0	0	0	0	ENSG00000271411	IGHGP
ENSG00000271412	0.236298	0.682361	1.2362	1.32136	ENSG00000271412	PRR13P3
ENSG00000271413	0	0	0	0	ENSG00000271413	AC104640.2
ENSG00000271414	0	1.03858	0.468831	0.576948	ENSG00000271414	AC093107.2
ENSG00000271415	0	2.45671	1.39403	2.24283	ENSG00000271415	RPL23AP90
ENSG00000271416	0	0	0	0	ENSG00000271416	IGHVII-60-1
ENSG00000271418	0	1.32193	0.927476	0.382533	ENSG00000271418	AC092747.3
ENSG00000271419	0	0	0.127977	0	ENSG00000271419	AL035410.2
ENSG00000271421	0	0	0	0	ENSG00000271421	AC005191.1
ENSG00000271422	0	0	0.028314	0	ENSG00000271422	SLC20A1P1
ENSG00000271423	0	0	0	0	ENSG00000271423	CYCSP1
ENSG00000271424	0.487011	1.55553	3.37009	1.55888	ENSG00000271424	AL157791.2
ENSG00000271425	2.54282	3.70867	2.59268	4.48144	ENSG00000271425	NBPF10
ENSG00000271426	0.432718	0.531736	1.19782	1.03448	ENSG00000271426	AL109983.1
ENSG00000271428	2.67675	4.97996	7.7661	10.0893	ENSG00000271428	AL031281.1
ENSG00000271429	0	0	0	0	ENSG00000271429	RPL17P51
ENSG00000271432	0	0	0	0	ENSG00000271432	IGHD1-1
ENSG00000271433	0.148512	0.581617	1.28656	0.635367	ENSG00000271433	PPATP2
ENSG00000271435	0	0	0	0	ENSG00000271435	AC068137.2
ENSG00000271437	1.74293	5.53088	6.28953	7.32807	ENSG00000271437	AL356423.1
ENSG00000271438	0	0.0332544	0.0446284	0.0758869	ENSG00000271438	IGHD
ENSG00000271439	0	0	0	0	ENSG00000271439	AC246785.4
ENSG00000271440	0	0	0	0	ENSG00000271440	AL121932.1
ENSG00000271442	2.36758	1.90678	2.11706	1.49956	ENSG00000271442	PRPF31
ENSG00000271443	0.12622	0.121127	0.109376	0	ENSG00000271443	AC011247.3
ENSG00000271444	0	0	0	0	ENSG00000271444	IGHD2-21
ENSG00000271445	0.106859	0.106157	0.0747939	0.24089	ENSG00000271445	CTC-575C13.1
ENSG00000271446	0	0	0	0	ENSG00000271446	IGHVIII-22-2
ENSG00000271447	12.0464	7.31347	13.1868	2.29736	ENSG00000271447	MMP28
ENSG00000271448	0	0	0	0	ENSG00000271448	IGHV3-52
ENSG00000271449	0	0	0	0	ENSG00000271449	CT45A2
ENSG00000271450	0	0	0	0	ENSG00000271450	IGHV3-64
ENSG00000271453	0.546611	0	0	0	ENSG00000271453	ABC7-43041399I9.1
ENSG00000271454	1.55775	3.39144	2.1765	4.50712	ENSG00000271454	AL353729.2
ENSG00000271455	0	1.10912	0	0.805663	ENSG00000271455	AC112187.2
ENSG00000271456	0	0	0	0	ENSG00000271456	AC108081.1
ENSG00000271457	0	0.129919	0.117267	0	ENSG00000271457	AL590229.1
ENSG00000271459	0	0.549421	0.248008	0.306655	ENSG00000271459	Z98751.3
ENSG00000271461	0.541033	0.692601	0.638314	1.10376	ENSG00000271461	AL109809.4
ENSG00000271462	0	0	0.468273	0	ENSG00000271462	AC091805.2
ENSG00000271464	0	0	0	0	ENSG00000271464	AL031176.1
ENSG00000271465	0	0	0	0	ENSG00000271465	SQSTM1P1

ENSG00000271466	0	0.0831778	0.0184761	0	ENSG00000271466	CICP24
ENSG00000271467	0	0	0	0	ENSG00000271467	GAGE12G
ENSG00000271468	0	0	0	0.164567	ENSG00000271468	AL357094.1
ENSG00000271469	0	0	0	0	ENSG00000271469	IGHV1-69
ENSG00000271475	0	0	0	0.422799	ENSG00000271475	AL078624.2
ENSG00000271476	0.0535284	0.0807321	0.049474	0.091395	ENSG00000271476	RP11-265D19.7
ENSG00000271477	0.105899	0	0.183713	0.347505	ENSG00000271477	AC010591.1
ENSG00000271479	0.174343	0	0	0	ENSG00000271479	CTC-260E6.11
ENSG00000271480	0	0	0	0	ENSG00000271480	MTND3P19
ENSG00000271481	0.716329	0.0396943	0.124052	0.490191	ENSG00000271481	LILRB2
ENSG00000271482	0	2.16647	0.775177	2.3453	ENSG00000271482	AC005070.2
ENSG00000271483	3.74178	4.6621	7.1719	25.8998	ENSG00000271483	AC108676.2
ENSG00000271484	0	0.156456	0.235304	0.353602	ENSG00000271484	ABI1P1
ENSG00000271486	0	0.0721415	0	0	ENSG00000271486	AP000403.1
ENSG00000271487	0	0	0	0	ENSG00000271487	VN1R105P
ENSG00000271488	0	0.0779797	0.0704506	0	ENSG00000271488	RBM11P1
ENSG00000271489	0.103648	0.148175	0	0.0544578	ENSG00000271489	AC008984.5
ENSG00000271490	3.51787	3.31026	0	0.0285578	ENSG00000271490	AC013244.2
ENSG00000271491	0.0971854	0.186779	0	0	ENSG00000271491	AC100767.2
ENSG00000271492	0	0	0.180163	0	ENSG00000271492	MEMO1P5
ENSG00000271493	0	0	0.084493	0.103777	ENSG00000271493	IGHV4-28
ENSG00000271494	0.127937	0.164282	0.0371236	0.0932859	ENSG00000271494	AC034205.3
ENSG00000271495	0	0	0	0	ENSG00000271495	AC020765.1
ENSG00000271496	0.737421	0.691847	0.612331	0.739592	ENSG00000271496	SNRPGP20
ENSG00000271497	0	0	0	0	ENSG00000271497	IGHVII-15-1
ENSG00000271498	0	0	0.120387	0	ENSG00000271498	AL360085.1
ENSG00000271499	0.176077	0.0565623	0.0511332	0.12877	ENSG00000271499	AC011477.6
ENSG00000271500	1.45707	2.21045	2.15773	2.46578	ENSG00000271500	AC005183.1
ENSG00000271501	0	0	0	0	ENSG00000271501	RP1-73A14.2
ENSG00000271502	0.250088	0	0	0	ENSG00000271502	AL670379.12
ENSG00000271503	2.44643	6.42515	6.40949	15.2325	ENSG00000271503	CCL5
ENSG00000271504	0	0	0	0	ENSG00000271504	IGHV4-55
ENSG00000271506	0.368711	0	0.306166	0.369796	ENSG00000271506	RP11-535E8.2
ENSG00000271507	0	0	0	0	ENSG00000271507	AC025884.3
ENSG00000271508	0	0	0	0	ENSG00000271508	AC090525.3
ENSG00000271509	1.43352	1.34256	1.78837	1.43766	ENSG00000271509	AC018714.1
ENSG00000271510	0.065495	0.495595	0.45387	0.23425	ENSG00000271510	RPL17P42
ENSG00000271511	0	0.96364	0	0.519212	ENSG00000271511	AL161756.2
ENSG00000271516	0.00527241	0.0101636	0.00924141	0.017363	ENSG00000271516	LILRP2
ENSG00000271517	0	0	0	0	ENSG00000271517	RP11-434J24.3
ENSG00000271519	2.90613	5.84835	5.51695	11.0714	ENSG00000271519	AL590065.1
ENSG00000271520	0	0	0	0	ENSG00000271520	IGHVII-33-1
ENSG00000271523	0	0	0	0	ENSG00000271523	AL049634.3
ENSG00000271524	0.442603	1.45097	0.227368	0.329992	ENSG00000271524	BNIP3P17
ENSG00000271525	0	0	0	0	ENSG00000271525	ARF4P1
ENSG00000271526	0	0	0	0	ENSG00000271526	AC004852.1
ENSG00000271527	0	0	0.119434	0	ENSG00000271527	AL606495.2
ENSG00000271529	4.73387	7.20972	10.8398	12.0385	ENSG00000271529	CICP14
ENSG00000271530	0	0	0.798771	0.537478	ENSG00000271530	WBP1LP12
ENSG00000271531	0.205433	0.0981906	0.396165	0.435371	ENSG00000271531	IGHV5-51
ENSG00000271532	0	3.08949	1.08022	2.30507	ENSG00000271532	BBIP1P1
ENSG00000271534	0	0	0	0	ENSG00000271534	IGHD5-18
ENSG00000271535	0	0	0	0	ENSG00000271535	IGHV1-3
ENSG00000271536	0	0	0	0.150903	ENSG00000271536	AC073046.2

ENSG00000271537	0.242999	0.349832	0.215248	1.04524	ENSG00000271537	AC009220.3
ENSG00000271539	0	0	0	0	ENSG00000271539	IGHVII-30-1
ENSG00000271541	0	0	0	0	ENSG00000271541	IGHM
ENSG00000271542	0	0.273981	0	0	ENSG00000271542	LENG1
ENSG00000271543	0	0	2.31852	2.78809	ENSG00000271543	AC021443.1
ENSG00000271544	0	0	0	0	ENSG00000271544	AC006499.8
ENSG00000271545	0	0	0	0	ENSG00000271545	RP11-301J7.9
ENSG00000271546	0	0	0.0606778	0.300223	ENSG00000271546	AC245389.1
ENSG00000271547	0.441741	0.564755	1.27472	0.472639	ENSG00000271547	AC117498.3
ENSG00000271548	0	0	0	0	ENSG00000271548	IGHVIII-67-4
ENSG00000271550	1.41249	3.00486	2.27679	1.82882	ENSG00000271550	BNIP3P11
ENSG00000271556	0	0.0378823	0.0687374	0	ENSG00000271556	CTD-M5.32
ENSG00000271557	0.257131	0.246181	0.220223	0.824669	ENSG00000271557	YPEL5P2
ENSG00000271558	0	0	0	0	ENSG00000271558	AL391813.1
ENSG00000271559	0	0	0	0	ENSG00000271559	AL138966.1
ENSG00000271560	0	0	0	0	ENSG00000271560	AP001330.4
ENSG00000271562	0	0	0	0	ENSG00000271562	IGHV3-23
ENSG00000271563	0	0	0	0.0896156	ENSG00000271563	HIRAP1
ENSG00000271565	0	0	0	0	ENSG00000271565	AL109618.2
ENSG00000271567	0	0.243112	0.118486	0.198619	ENSG00000271567	PPIAL4E
ENSG00000271568	0	0.49086	0	0	ENSG00000271568	AC069304.3
ENSG00000271569	0	0	0	0	ENSG00000271569	IGKV1OR2-6
ENSG00000271571	0	0	0	0	ENSG00000271571	IGHD2-2
ENSG00000271572	7.97041	24.3743	28.76	14.848	ENSG00000271572	RPS9
ENSG00000271573	1.33508	0.89581	0	1.36214	ENSG00000271573	AL136982.5
ENSG00000271574	0	0	0	0	ENSG00000271574	IGHV1-12
ENSG00000271575	0	0	0	0	ENSG00000271575	IGHVII-62-1
ENSG00000271577	0	0	0	0	ENSG00000271577	IGHVII-1-1
ENSG00000271578	0	0.157017	0	0	ENSG00000271578	AC119501.1
ENSG00000271580	1.00239	1.51707	2.4526	1.62069	ENSG00000271580	AL583832.1
ENSG00000271581	1.37422	7.40894	6.19608	3.13827	ENSG00000271581	AL671883.3
ENSG00000271582	0.170031	0	0.492968	0.681614	ENSG00000271582	AC073111.2
ENSG00000271583	0	0	0.76091	0.146666	ENSG00000271583	AC103881.1
ENSG00000271585	0	0	0	0	ENSG00000271585	AC011416.3
ENSG00000271586	0	0.333668	0	0	ENSG00000271586	AC011894.1
ENSG00000271587	0.330598	0	0.283065	0.344184	ENSG00000271587	AC004805.3
ENSG00000271588	0	0	0	0	ENSG00000271588	LARP7P1
ENSG00000271589	0	0	0	0	ENSG00000271589	AL139395.1
ENSG00000271592	0	0	0	0	ENSG00000271592	IGHV7-40
ENSG00000271594	0	0	0	0	ENSG00000271594	RP11-277L2.6
ENSG00000271595	0	0	0	0	ENSG00000271595	ELOCP35
ENSG00000271596	0	0	0	1.77794	ENSG00000271596	AC008121.1
ENSG00000271597	0	0.641272	0.34737	1.7205	ENSG00000271597	AC112230.1
ENSG00000271598	1.07724	4.79285	3.17575	6.05441	ENSG00000271598	AC008739.3
ENSG00000271600	0	0	0	0	ENSG00000271600	AP000942.4
ENSG00000271601	2.09251	3.77069	3.4948	7.98612	ENSG00000271601	LIX1L
ENSG00000271602	0	0	0	0	ENSG00000271602	KRT8P49
ENSG00000271605	3.85609	9.15344	10.5899	19.5735	ENSG00000271605	MILR1
ENSG00000271606	0	0	0	0	ENSG00000271606	AC097467.4
ENSG00000271607	0.657209	0.311555	0	0	ENSG00000271607	Z84480.1
ENSG00000271608	0	0	0	0	ENSG00000271608	AL391646.1
ENSG00000271609	0	0.317451	0	0	ENSG00000271609	AC005632.3
ENSG00000271611	3.08652	0	2.61876	1.5956	ENSG00000271611	AC006006.1
ENSG00000271612	0	0	0	0	ENSG00000271612	HSPE1P14

ENSG00000271613	0.0131325	0.00949554	0.0125962	0.044165	ENSG00000271613	KIR3DL2
ENSG00000271615	1.07366	1.46954	2.05892	2.99651	ENSG00000271615	ACTG1P22
ENSG00000271616	0	0	0.39047	0.47213	ENSG00000271616	AC055876.5
ENSG00000271618	0	0	0	0.959565	ENSG00000271618	AL359821.1
ENSG00000271620	0	0	0	0	ENSG00000271620	IGHV3OR16-7
ENSG00000271621	0	0.643267	0.193664	0.711473	ENSG00000271621	AC013244.3
ENSG00000271622	0	0	0	0	ENSG00000271622	IGHD5-24
ENSG00000271623	0.764643	0	0	0	ENSG00000271623	AC138894.3
ENSG00000271624	0	0	0	0	ENSG00000271624	AP004372.1
ENSG00000271625	0.0929649	0	0	0	ENSG00000271625	PSMA6P4
ENSG00000271626	1.15119	1.32972	1.19176	2.58519	ENSG00000271626	AC104763.2
ENSG00000271627	0	0	0	0	ENSG00000271627	AC027612.4
ENSG00000271629	0	0	0	0.246214	ENSG00000271629	AC067959.1
ENSG00000271630	0	0	0	0	ENSG00000271630	IGKV2OR2-8
ENSG00000271632	0	0.138866	0	0	ENSG00000271632	AL589743.3
ENSG00000271634	0	0	0	0	ENSG00000271634	IGHD6-13
ENSG00000271635	0.0379899	0	0.0661599	0.123089	ENSG00000271635	AC017002.4
ENSG00000271638	0.124117	0.304113	0.107556	0	ENSG00000271638	BNIP3P19
ENSG00000271639	0.820154	2.51388	1.94778	2.81679	ENSG00000271639	AC019072.1
ENSG00000271641	0	0	0	0	ENSG00000271641	GAGE12D
ENSG00000271642	0.321638	1.38392	1.3947	3.00661	ENSG00000271642	MARK3P1
ENSG00000271644	0	0	0	0.997561	ENSG00000271644	AC242498.1
ENSG00000271647	0.0839259	0.0808468	0.036548	0.0458311	ENSG00000271647	KRT8P47
ENSG00000271648	0	0	0	0	ENSG00000271648	IGHV3-11
ENSG00000271650	0	0	0	0.249163	ENSG00000271650	AL031601.1
ENSG00000271652	0	0	0	0	ENSG00000271652	AL356052.1
ENSG00000271654	0	0.0975577	0	0.109681	ENSG00000271654	AC025062.2
ENSG00000271655	0	0.518451	0.138494	1.05152	ENSG00000271655	BNIP3P35
ENSG00000271656	0	0	0.266392	0	ENSG00000271656	AC007262.1
ENSG00000271657	0	0.213194	0.188327	0.461133	ENSG00000271657	AC018462.2
ENSG00000271658	0.396553	0.807641	1.03707	1.14122	ENSG00000271658	OSCAR
ENSG00000271660	0	0	0	0	ENSG00000271660	Z99497.2
ENSG00000271661	0.166686	0.370344	0	0.136404	ENSG00000271661	BNIP3P36
ENSG00000271662	0.176808	0.0793858	0.256065	0.186055	ENSG00000271662	AC233280.2
ENSG00000271664	1.82589	2.18404	2.77902	2.93753	ENSG00000271664	AC004890.3
ENSG00000271666	0	0	0.212088	0	ENSG00000271666	AC008555.7
ENSG00000271667	0	0	0	0	ENSG00000271667	AC104408.1
ENSG00000271668	0	0	0	0	ENSG00000271668	RP11-1324A7.2
ENSG00000271671	0	0	0	0	ENSG00000271671	AC107304.1
ENSG00000271672	0	0	0	0	ENSG00000271672	DUXAP8
ENSG00000271676	0	0	0	0.288139	ENSG00000271676	AC104771.1
ENSG00000271677	0	0	0	0	ENSG00000271677	Z82195.1
ENSG00000271679	0	0	0	0	ENSG00000271679	LSM1P2
ENSG00000271680	0.168673	1.93951	0.463604	1.2594	ENSG00000271680	AC098935.2
ENSG00000271681	0.164396	0	0	0.175313	ENSG00000271681	AC136601.2
ENSG00000271682	0	0	0	0	ENSG00000271682	AC092960.1
ENSG00000271686	0	0.0378823	0.0687374	0	ENSG00000271686	AL953862.2
ENSG00000271687	0	0.0606039	0.0273975	0	ENSG00000271687	MTND5P10
ENSG00000271688	0	0	0	0	ENSG00000271688	IGHD5-12
ENSG00000271689	0	0	0	0	ENSG00000271689	IGHV1-24
ENSG00000271691	0	0	0	0	ENSG00000271691	AC140658.6
ENSG00000271692	0	0	0	0	ENSG00000271692	IGHVII-53-1
ENSG00000271693	0	0	0	0	ENSG00000271693	AL929325.1
ENSG00000271694	0.647719	1.21463	0.66435	2.60377	ENSG00000271694	TMEM121

ENSG00000271695	0	0	0	0	ENSG00000271695	IGHV3-72
ENSG00000271696	0	0	0	0	ENSG00000271696	AC023141.13
ENSG00000271697	2.44184	1.75297	0	6.05873	ENSG00000271697	AL049779.4
ENSG00000271698	0	0.365764	0.823507	0.211381	ENSG00000271698	AC233992.2
ENSG00000271699	1.38043	4.47241	3.80079	6.41876	ENSG00000271699	SNX29P2
ENSG00000271701	0	0	0	0	ENSG00000271701	AC098483.2
ENSG00000271702	0	0	0.350769	1.27416	ENSG00000271702	AC123786.2
ENSG00000271703	0	0.13592	0.0491362	0.123193	ENSG00000271703	QTRT1P1
ENSG00000271704	0.106859	0.106157	0.0747939	0.24089	ENSG00000271704	BNIP3P20
ENSG00000271705	0	0	0	0	ENSG00000271705	RPL17P3
ENSG00000271707	0	0	0	0	ENSG00000271707	ATP1B3P1
ENSG00000271710	0.492402	4.69411	4.03144	3.36936	ENSG00000271710	NDUFA8P1
ENSG00000271711	1.79627	1.28653	1.46941	2.11716	ENSG00000271711	AC069236.1
ENSG00000271712	0	0.34855	0.262498	0.0657713	ENSG00000271712	AL163642.2
ENSG00000271713	0	0	0	0	ENSG00000271713	KIR2DL4
ENSG00000271719	0	0	0	0	ENSG00000271719	OR13Z2P
ENSG00000271723	0.0386186	0.171566	0.303819	0.519816	ENSG00000271723	MROH7-TTC4
ENSG00000271741	3.1396	2.31328	0.975389	0.58791	ENSG00000271741	AC114490.2
ENSG00000271749	3.50818	6.28516	9.65818	9.26054	ENSG00000271749	AC005828.6
ENSG00000271753	1.4174	1.30568	1.91125	3.07241	ENSG00000271753	BEND3
ENSG00000271760	0.992572	1.70669	1.46649	2.25281	ENSG00000271760	ADD2
ENSG00000271772	0.10834	0.0760753	0.120245	0.216199	ENSG00000271772	VAX2
ENSG00000271779	0.968695	1.36827	0.612264	9.33838	ENSG00000271779	AC009994.1
ENSG00000271786	0.372473	2.6619	2.38955	2.16514	ENSG00000271786	RP11-139J15.7
ENSG00000271793	2.78713	1.0388	1.23517	1.7792	ENSG00000271793	AL589666.1
ENSG00000271799	1.44614	1.23374	1.39403	1.5094	ENSG00000271799	ANKRD53
ENSG00000271801	0.466241	0.88347	0.892285	0.969875	ENSG00000271801	MORN3
ENSG00000271809	0.283739	0.397602	0.569339	1.18897	ENSG00000271809	ATP6V1B1
ENSG00000271810	1.38274	2.33559	1.56275	1.42364	ENSG00000271810	AL603832.3
ENSG00000271812	0.968695	1.36827	0.612264	9.33838	ENSG00000271812	RP11-87N3.6
ENSG00000271829	12.4768	13.008	14.3746	12.4229	ENSG00000271829	RNF34
ENSG00000271831	0	0	1.61611	0	ENSG00000271831	AL022345.9
ENSG00000271846	9.82988	34.7284	24.9487	14.8922	ENSG00000271846	CTD-3113P16.9
ENSG00000271867	5.07486	7.82054	6.91028	9.51424	ENSG00000271867	C6orf203
ENSG00000271885	7.5596	2.577	5.22862	0	ENSG00000271885	SRSF8
ENSG00000271890	0.992531	1.27138	1.09993	1.81066	ENSG00000271890	OR10AE1P
ENSG00000271900	0	8.70567	11.4837	3.19849	ENSG00000271900	AC025627.4
ENSG00000271910	6.2193	8.24655	8.75348	8.18597	ENSG00000271910	PARG
ENSG00000271915	0.0299349	0	0	0.0246767	ENSG00000271915	EEF1GP5
ENSG00000271919	0.791083	1.76282	3.26177	4.08159	ENSG00000271919	AC005828.7
ENSG00000271928	0	0	0	0	ENSG00000271928	OR12Z3P
ENSG00000271934	0	0	0	0	ENSG00000271934	OR2AS2P
ENSG00000271942	0	0.073843	0.173748	0.0797615	ENSG00000271942	OR7E91P
ENSG00000271949	0	0	0	0	ENSG00000271949	AC093423.3
ENSG00000271961	1.52278	4.51389	3.4346	6.32105	ENSG00000271961	AC007040.11
ENSG00000271962	3.22219	3.73673	5.77481	4.16157	ENSG00000271962	AGAP6
ENSG00000271968	0	0	0.0269845	0	ENSG00000271968	ADAM6
ENSG00000271974	6.06674	13.6579	27.2026	20.8087	ENSG00000271974	AC103810.6
ENSG00000271977	0	0.134084	0	0	ENSG00000271977	AC226119.2
ENSG00000271985	0	0	1.05671	0	ENSG00000271985	BX248123.2
ENSG00000272000	0.359802	0.83875	1.28428	1.30607	ENSG00000272000	AC236040.1
ENSG00000272006	5.84205	21.7493	0	2.73363	ENSG00000272006	AC037487.3
ENSG00000272014	0.0806506	0.336378	0.129506	0.24472	ENSG00000272014	ABBA01057584.1
ENSG00000272031	21.7893	44.5821	48.6563	80.7071	ENSG00000272031	ANKRD34A

ENSG00000272032	0.193451	0.370202	0.501342	0.308013	ENSG00000272032	C20orf166
ENSG00000272047	4.25173	6.26829	5.34695	8.82405	ENSG00000272047	GTF2H5
ENSG00000272058	1.81405	3.21304	5.02639	3.85113	ENSG00000272058	AC243772.2
ENSG00000272064	8.24995	5.79653	5.87196	6.77653	ENSG00000272064	FAM21A
ENSG00000272067	0.321475	0.396715	0.291511	0.207562	ENSG00000272067	CCDC120
ENSG00000272089	0.435196	0.655948	1.19586	1.22919	ENSG00000272089	AC244669.1
ENSG00000272095	0	0.0962443	0.101121	0.162418	ENSG00000272095	AC007395.4
ENSG00000272098	0.962103	5.53597	6.22307	7.23938	ENSG00000272098	AC092299.8
ENSG00000272101	0	0	0	0	ENSG00000272101	AC243587.1
ENSG00000272104	0.442641	0.266844	0	0.310729	ENSG00000272104	Z84492.1
ENSG00000272111	0	0.136101	0.24594	0.14988	ENSG00000272111	TCEB1P21
ENSG00000272120	0.914306	1.35958	1.51305	1.99595	ENSG00000272120	ZNF275
ENSG00000272125	10.1529	9.91141	8.97219	4.26757	ENSG00000272125	TEX261
ENSG00000272134	17.0313	30.3062	76.384	54.6091	ENSG00000272134	AC103810.7
ENSG00000272135	0	0	0	0.147406	ENSG00000272135	AL359747.1
ENSG00000272150	0.624007	0.685837	1.22956	0.641088	ENSG00000272150	NBPF25P
ENSG00000272151	0	0	0.63768	1.15623	ENSG00000272151	RP11-526K21.2
ENSG00000272162	0.0455707	0.228272	0	0.443101	ENSG00000272162	AL024498.2
ENSG00000272164	0.161399	1.2366	2.87268	3.7868	ENSG00000272164	AC005972.3
ENSG00000272165	1.37347	3.50809	2.44933	4.83572	ENSG00000272165	AC010614.1
ENSG00000272171	5.39888	6.77075	5.05227	3.7659	ENSG00000272171	ORAI1
ENSG00000272185	0.0762185	0.122445	0.0221393	0.16737	ENSG00000272185	AC233297.1
ENSG00000272195	0.300251	0.7708	0.612519	0.594108	ENSG00000272195	AL356512.1
ENSG00000272196	0	57.4369	25.7512	2.00222	ENSG00000272196	HIST2H2AA4
ENSG00000272204	34.6337	43.4402	41.685	53.8922	ENSG00000272204	ANAPC5
ENSG00000272207	2.98396	1.27661	1.10377	4.63158	ENSG00000272207	PLEKHO1
ENSG00000272210	0.0151889	0.0585476	0.0396956	0.0999496	ENSG00000272210	CD207
ENSG00000272214	1.39484	3.74973	3.50768	5.81407	ENSG00000272214	AC079602.1
ENSG00000272220	12.8251	3.53903	37.801	7.78309	ENSG00000272220	AC103810.8
ENSG00000272228	0.0503901	0.140843	0.0159481	0.0685824	ENSG00000272228	SLC9A3P3
ENSG00000272242	0.450634	1.11471	0.808279	1.01331	ENSG00000272242	ACTG1P10
ENSG00000272245	0.279761	0.352985	0.522896	0.506146	ENSG00000272245	RP11-324H6.5
ENSG00000272246	0	0	0	0	ENSG00000272246	AC245177.2
ENSG00000272252	0.523216	1.91975	3.16768	3.31814	ENSG00000272252	AC242426.1
ENSG00000272268	0.670751	0.953913	1.10433	1.78786	ENSG00000272268	DKFZp761K2322
ENSG00000272281	1.92612	3.97118	3.57785	5.52056	ENSG00000272281	TPTE2P2
ENSG00000272284	0.346939	0	1.50646	0.55639	ENSG00000272284	RP4-669P10.19
ENSG00000272295	0	0	0.754031	2.10E-05	ENSG00000272295	AL844853.2
ENSG00000272297	0.104524	0	0.206594	0.2324	ENSG00000272297	AC018709.1
ENSG00000272305	0.44054	3.19164	2.97407	3.49645	ENSG00000272305	AC096887.1
ENSG00000272309	2.94032	3.56079	2.30386	2.41259	ENSG00000272309	PDSS2
ENSG00000272311	0	0	0.12113	0	ENSG00000272311	IFNL4P1
ENSG00000272319	1.23164	5.34254	3.61929	1.89605	ENSG00000272319	AL022345.1
ENSG00000272325	8.81975	10.5043	10.3646	10.373	ENSG00000272325	NUDT3
ENSG00000272333	7.08066	7.49944	9.13794	9.74298	ENSG00000272333	KMT2B
ENSG00000272352	0	0.0134924	0.024395	0.0123049	ENSG00000272352	CLEC4F
ENSG00000272358	3.87698	6.46592	6.01116	8.14294	ENSG00000272358	KDM2B
ENSG00000272383	0.919369	1.31599	2.21382	2.38692	ENSG00000272383	AC006270.3
ENSG00000272387	0	1.33883	1.17863	0	ENSG00000272387	AL022345.2
ENSG00000272391	1.17236	0.848804	1.26489	1.53631	ENSG00000272391	POM121C
ENSG00000272395	0.135765	0	0	0.145547	ENSG00000272395	IFNL4
ENSG00000272398	1278.7	158.632	221.952	160.879	ENSG00000272398	CD24
ENSG00000272400	0.730914	0	0	1.38234	ENSG00000272400	AC103810.10
ENSG00000272407	1.42378	1.86686	3.63666	3.7967	ENSG00000272407	AL022394.1

ENSG00000272410	2.21271	1.96509	1.56455	2.33286	ENSG00000272410	AC022384.1
ENSG00000272414	2.85735	2.21846	2.1417	1.99761	ENSG00000272414	FAM47E-STBD1
ENSG00000272419	3.44427	4.75325	7.25367	4.00247	ENSG00000272419	AC241585.2
ENSG00000272427	0.112609	0.0969925	0.0789754	0.19091	ENSG00000272427	AC241929.1
ENSG00000272433	0	0	0	0	ENSG00000272433	HMGN2P21
ENSG00000272436	0	0	0	0	ENSG00000272436	CUX2P1
ENSG00000272442	0.989429	1.79424	1.90479	2.95128	ENSG00000272442	AL353588.1
ENSG00000272443	0	0	0	0	ENSG00000272443	OR13Z2P
ENSG00000272475	3.57685	0	0	0	ENSG00000272475	RP11-342M3.2
ENSG00000272480	0	0	0	0	ENSG00000272480	AC242628.1
ENSG00000272494	0	0	0	0	ENSG00000272494	OR1X1P
ENSG00000272497	0.435196	0.655948	1.19586	1.22919	ENSG00000272497	AC247039.1
ENSG00000272503	0.0461054	0.132904	0.240115	0.249362	ENSG00000272503	FIGLA
ENSG00000272514	0.308142	0.930951	1.02265	1.38022	ENSG00000272514	CFAP206
ENSG00000272517	81.5611	49.4237	18.4597	27.8866	ENSG00000272517	TGFA
ENSG00000272532	0	0	0	0	ENSG00000272532	CYP2D6
ENSG00000272546	0	0	0	0	ENSG00000272546	OR3A5P
ENSG00000272547	3.84836	4.9837	4.23204	3.57993	ENSG00000272547	TMEM242
ENSG00000272548	0.485299	2.34072	0.994225	0.736066	ENSG00000272548	PCDHAC2
ENSG00000272550	0.274869	0.248648	0.131412	0.312068	ENSG00000272550	PCDHAC1
ENSG00000272553	6.25364	4.86093	4.30662	4.47814	ENSG00000272553	NDUFA3
ENSG00000272557	0.365268	1.29583	0.805208	0.884098	ENSG00000272557	RP11-478C6.6
ENSG00000272559	0	0	0	0	ENSG00000272559	AC103710.1
ENSG00000272560	0.586232	0.553337	0.745755	0.452985	ENSG00000272560	TFPT
ENSG00000272561	1.51921	0.0206544	0.0163054	0	ENSG00000272561	TSEN34
ENSG00000272569	0	0	0	0.120241	ENSG00000272569	AP004247.3
ENSG00000272570	0	2.70928	0	2.13813	ENSG00000272570	RP11-2H3.2
ENSG00000272571	0	0.0462886	0.0208964	0.103325	ENSG00000272571	H2AFB3
ENSG00000272573	0.419313	0.853059	0.099939	1.42734	ENSG00000272573	MUSTN1
ENSG00000272577	0	0.0570873	0.328356	0.0814314	ENSG00000272577	AC012314.19
ENSG00000272578	20.2729	33.6552	35.4164	35.0314	ENSG00000272578	AP000347.1
ENSG00000272580	7.46909	9.86603	10.0577	9.57384	ENSG00000272580	ZNF721
ENSG00000272584	1.23656	2.89502	1.74787	4.92945	ENSG00000272584	ATP1A3
ENSG00000272585	0.0853093	0.0812371	0.0651443	0.0979091	ENSG00000272585	PCDHB3
ENSG00000272586	0	0	0	0	ENSG00000272586	KRTAP10-9
ENSG00000272587	1.81E-09	0.340825	0	0.000218358	ENSG00000272587	PCDHB9
ENSG00000272590	0.199466	0.64254	0.388092	0.647228	ENSG00000272590	TAS2R12
ENSG00000272591	0	0	0.580008	0.104487	ENSG00000272591	F8A2
ENSG00000272594	0	0	0	0.0394956	ENSG00000272594	KRTAP10-12
ENSG00000272595	0	0	0	0	ENSG00000272595	AC092028.1
ENSG00000272598	0.11044	0.300606	0.169699	0.607346	ENSG00000272598	VSTM1
ENSG00000272601	0.711223	0.680819	2.42716	0.953516	ENSG00000272601	AC010655.3
ENSG00000272602	4.28397	7.85708	8.24303	7.83019	ENSG00000272602	ZNF595
ENSG00000272603	0.164412	0	0.108894	0.250929	ENSG00000272603	NOP56P1
ENSG00000272607	25.922	33.7518	43.7219	31.5658	ENSG00000272607	PIGG
ENSG00000272611	0.236641	0.184136	0.307697	0.706281	ENSG00000272611	CEACAM3
ENSG00000272613	0	0	0	0	ENSG00000272613	CR759954.1
ENSG00000272614	42.0117	41.4846	22.7681	25.3501	ENSG00000272614	RPS9
ENSG00000272615	0.0134697	0.0232998	0.0306727	0.0813906	ENSG00000272615	PCDHA7
ENSG00000272616	0	0	0	0.0365034	ENSG00000272616	HNRNPA1P52
ENSG00000272617	0.464515	0	0	0	ENSG00000272617	COG8
ENSG00000272618	0	0	0	2.10042	ENSG00000272618	AC091738.3
ENSG00000272621	3.42339	4.64329	1.72368	1.68632	ENSG00000272621	TMC4
ENSG00000272623	1.53474	0.972714	0.48334	1.6718	ENSG00000272623	F8A1

ENSG00000272624	6.66548	15.6718	17.4284	35.9506	ENSG00000272624	AC091390.2
ENSG00000272628	0	0	0	0	ENSG00000272628	REXO1L3P
ENSG00000272633	0.0648944	0.0371863	0.0471534	0.124347	ENSG00000272633	PCDHB4
ENSG00000272634	0	0	0	0	ENSG00000272634	AC103710.2
ENSG00000272636	0.093871	0.225483	0.288268	0.46572	ENSG00000272636	DOC2B
ENSG00000272637	0	1.48184	0.675563	0	ENSG00000272637	RP11-478C6.4
ENSG00000272641	0.140585	0.0717563	0.220912	0.141507	ENSG00000272641	PCDHB15
ENSG00000272643	42.0117	41.4846	22.7681	25.3501	ENSG00000272643	RPS9
ENSG00000272647	2.57803	2.61254	2.26728	6.81323	ENSG00000272647	AC005020.2
ENSG00000272649	0.11044	0.300606	0.169699	0.607346	ENSG00000272649	VSTM1
ENSG00000272651	0	0	0	0.0393328	ENSG00000272651	KRTAP10-8
ENSG00000272652	15.9969	0	11.1927	0	ENSG00000272652	AL662890.5
ENSG00000272653	0.0412544	0	0.107747	0.180542	ENSG00000272653	SLC25A2
ENSG00000272655	8.03318	11.6092	10.5138	16.8225	ENSG00000272655	POLR2J4
ENSG00000272658	3.36459	6.34347	9.49038	3.76148	ENSG00000272658	LTB4R2
ENSG00000272664	0	0	0	0	ENSG00000272664	AC103710.3
ENSG00000272670	0.093871	0.225483	0.288268	0.46572	ENSG00000272670	DOC2B
ENSG00000272673	0	0.0570873	0.328356	0.0814314	ENSG00000272673	AC012314.19
ENSG00000272674	0.7796	0.583489	0.823492	0.728641	ENSG00000272674	PCDHB16
ENSG00000272676	0	0	0.29981	0	ENSG00000272676	AP001521.1
ENSG00000272680	0.586232	0.553337	0.745755	0.452985	ENSG00000272680	TFPT
ENSG00000272681	1.08429	2.46922	1.67569	2.7479	ENSG00000272681	FAM223B
ENSG00000272684	0	0.316787	0.116813	0.510046	ENSG00000272684	CEACAM7
ENSG00000272685	0.447934	0.0637807	0	0.0721459	ENSG00000272685	AP004247.4
ENSG00000272687	77.6426	109.172	57.4746	54.6368	ENSG00000272687	TKT
ENSG00000272693	0	0	0	0	ENSG00000272693	AC073107.1
ENSG00000272697	0	0.120834	0	0	ENSG00000272697	KRTAP10-13P
ENSG00000272704	0.110574	0.239452	0.0961836	0.211263	ENSG00000272704	KRTAP10-10
ENSG00000272705	1.51921	0.0206544	0.0163054	0	ENSG00000272705	TSEN34
ENSG00000272706	0.036254	0.17709	0.0989798	0.154913	ENSG00000272706	GRIK5
ENSG00000272708	0	0.067479	0.0613045	0.148222	ENSG00000272708	CEACAM4
ENSG00000272712	0	0	0.0277802	0.0174369	ENSG00000272712	TAS2R8
ENSG00000272714	0.462483	1.54578	1.59569	1.22057	ENSG00000272714	AL139098.2
ENSG00000272718	0.066234	0.360964	0.327636	0.504386	ENSG00000272718	AC006518.3
ENSG00000272722	0.586232	0.553337	0.745755	0.452985	ENSG00000272722	TFPT
ENSG00000272723	3.42339	4.64329	1.72368	1.68632	ENSG00000272723	TMC4
ENSG00000272725	0	0	0	0	ENSG00000272725	RP11-667F9.1
ENSG00000272726	0.418188	0.39575	0.408938	0.372155	ENSG00000272726	LENG1
ENSG00000272728	0.0612907	0.0525447	0.0595143	0.0917732	ENSG00000272728	TSPEAR
ENSG00000272731	0.0109211	0.0105287	0.00951881	0.0120005	ENSG00000272731	PCDHB1
ENSG00000272738	0	0.0570873	0.328356	0.0814314	ENSG00000272738	AC012314.19
ENSG00000272739	1.51921	0.0206544	0.0163054	0	ENSG00000272739	TSEN34
ENSG00000272741	0.655766	0.235212	0.523879	0	ENSG00000272741	AC069257.3
ENSG00000272743	3.56569	0.82951	0.6994	1.6044	ENSG00000272743	CEACAM5
ENSG00000272749	0.122457	0.259933	0.247953	0.628477	ENSG00000272749	TARM1
ENSG00000272751	0.199466	0.64254	0.388092	0.647228	ENSG00000272751	AC006518.4
ENSG00000272753	0	0	0.0167605	0.0842905	ENSG00000272753	RP11-285M22.2
ENSG00000272756	0.116349	0.0439262	0.0964955	0.0663163	ENSG00000272756	PCDHA4
ENSG00000272757	3.42339	4.64329	1.72368	1.68632	ENSG00000272757	TMC4
ENSG00000272759	0.11044	0.300606	0.169699	0.607346	ENSG00000272759	VSTM1
ENSG00000272762	0	0	0	0	ENSG00000272762	AC115284.1
ENSG00000272765	6.85869	6.86074	6.16687	4.47528	ENSG00000272765	NDUFA6
ENSG00000272766	0.0447613	0.129021	0.0777097	0.145328	ENSG00000272766	KRTAP12-2
ENSG00000272772	0	0.444252	0	0	ENSG00000272772	AC104109.3

ENSG00000272773	13.0309	20.8878	26.5074	26.4309	ENSG00000272773	UBE2G2
ENSG00000272779	23.8994	18.1076	19.927	13.1547	ENSG00000272779	AC245060.4
ENSG00000272781	0	0	0	0	ENSG00000272781	MDGA2
ENSG00000272786	15.9969	0	11.1927	0	ENSG00000272786	AL662890.8
ENSG00000272790	0	0	0	0	ENSG00000272790	AP002884.3
ENSG00000272794	0.168364	0.363334	0.267812	0.433784	ENSG00000272794	PCDHA9
ENSG00000272803	0.301483	0.748608	0.79526	1.42681	ENSG00000272803	PRH2
ENSG00000272804	0	0	0	0	ENSG00000272804	KRTAP10-7
ENSG00000272805	0.137195	0.226324	0.340901	0.448548	ENSG00000272805	TAS2R10
ENSG00000272809	5.20344	3.88437	1.75536	1.72367	ENSG00000272809	MBOAT7
ENSG00000272811	0	0	0	0.165374	ENSG00000272811	ATRNL1
ENSG00000272813	0.0555412	0.0541928	0.0958004	0.281774	ENSG00000272813	OLA1P1
ENSG00000272816	0.021805	0.27787	0.407957	0.25065	ENSG00000272816	CEACAMP3
ENSG00000272818	0	0.0228668	0.0488055	0.0861342	ENSG00000272818	PCDHA3
ENSG00000272822	1.46642	0.788102	0.412459	1.8512	ENSG00000272822	AC073610.3
ENSG00000272833	0.0673209	0.124011	0.116879	0.167476	ENSG00000272833	OSCAR
ENSG00000272835	1.13065	1.83608	1.49104	1.44355	ENSG00000272835	SMDT1
ENSG00000272837	0	0.159982	0.144426	0	ENSG00000272837	AC009779.7
ENSG00000272838	0.122457	0.259933	0.247953	0.628477	ENSG00000272838	TARM1
ENSG00000272845	0.0306789	0.0604342	0.0831789	0.084722	ENSG00000272845	PCDHB7
ENSG00000272852	592.487	454.598	402.971	250.223	ENSG00000272852	RPS19
ENSG00000272863	0	0	0	0	ENSG00000272863	KRTAP12-1
ENSG00000272867	0.196941	0.352475	0.890245	0.332637	ENSG00000272867	RP11-1365D11.1
ENSG00000272868	0.066234	0.360964	0.327636	0.504386	ENSG00000272868	RP11-144O23.8
ENSG00000272869	2.69806	2.88124	3.47826	3.75892	ENSG00000272869	AC008575.2
ENSG00000272873	0.0990988	1.0311	0.455987	0.727775	ENSG00000272873	TAS2R20
ENSG00000272875	0.122457	0.259933	0.247953	0.628477	ENSG00000272875	TARM1
ENSG00000272876	0	0	0	0	ENSG00000272876	CEACAM21
ENSG00000272877	0	0.253197	0.117158	0.086778	ENSG00000272877	DDX11L8
ENSG00000272878	0	0	0	0	ENSG00000272878	AC005894.1
ENSG00000272879	20.7231	12.7746	6.91756	11.7833	ENSG00000272879	ARHGEF1
ENSG00000272881	71.8721	51.0539	19.744	28.2056	ENSG00000272881	RABAC1
ENSG00000272882	0	0	0	0	ENSG00000272882	OR2BH1P
ENSG00000272883	0.451388	0.355499	0.725781	0.459573	ENSG00000272883	CNOT3
ENSG00000272886	6.55525	5.17198	5.91727	5.45385	ENSG00000272886	DCP1A
ENSG00000272887	0	0.0470529	0	0	ENSG00000272887	CSPG4P5
ENSG00000272889	0.483555	1.72463	0.490668	1.15399	ENSG00000272889	ZNF732
ENSG00000272890	0	0	0	0	ENSG00000272890	RP11-846F4.11
ENSG00000272891	0.0673209	0.124011	0.116879	0.167476	ENSG00000272891	OSCAR
ENSG00000272896	0.261543	0.121429	0.104271	0	ENSG00000272896	AL355987.3
ENSG00000272897	0	0	0	0	ENSG00000272897	AL109827.1
ENSG00000272898	0.11044	0.300606	0.169699	0.607346	ENSG00000272898	VSTM1
ENSG00000272900	0	0.127887	0.0641489	0.0821625	ENSG00000272900	AP000435.2
ENSG00000272901	1.13065	1.83608	1.49104	1.44355	ENSG00000272901	SMDT1
ENSG00000272903	0.137383	0.0578632	0.120017	0.111703	ENSG00000272903	PCDHB12
ENSG00000272916	1.4875	2.09311	2.99458	2.3451	ENSG00000272916	AC022400.6
ENSG00000272919	0.0673209	0.124011	0.116879	0.167476	ENSG00000272919	OSCAR
ENSG00000272921	2.49315	1.06346	1.10393	0.499903	ENSG00000272921	AC005832.4
ENSG00000272929	0.171398	0.244924	0.249708	0.719514	ENSG00000272929	C21orf90
ENSG00000272930	0	0.0858419	0	0.0648035	ENSG00000272930	TAS2R9
ENSG00000272932	2.36758	1.90677	2.11706	1.49956	ENSG00000272932	PRPF31
ENSG00000272935	0.0591208	0.00809258	0.0525104	0.0844322	ENSG00000272935	PCDHA10
ENSG00000272937	0	0	0	0	ENSG00000272937	AC009779.8

ENSG00000272939	0.789524	0.406053	1.05134	6.91843	ENSG00000272939	CEACAM6
ENSG00000272943	42.0117	41.4846	22.7681	25.3501	ENSG00000272943	RPS9
ENSG00000272946	3.42339	4.64329	1.72368	1.68632	ENSG00000272946	TMC4
ENSG00000272951	0.0898179	0	0	0	ENSG00000272951	KRTAP12-4
ENSG00000272952	0.102898	0.718323	0.447358	0.403433	ENSG00000272952	TAS2R50
ENSG00000272957	8.02876	11.2801	13.3659	17.4726	ENSG00000272957	ZNF141
ENSG00000272959	0	0	0	0	ENSG00000272959	RP13-157F18.2
ENSG00000272961	0.114115	0.176745	0.253605	0.231801	ENSG00000272961	KRTAP10-6
ENSG00000272962	8.55491	15.8513	8.95637	11.9958	ENSG00000272962	SLC5A3
ENSG00000272963	1.07633	4.19586	1.72458	4.75652	ENSG00000272963	OR7A19P
ENSG00000272964	2.36758	1.90677	2.11706	1.49956	ENSG00000272964	PRPF31
ENSG00000272968	0.288194	0.361531	0.305914	0.58089	ENSG00000272968	RBAK-RBAKDN
ENSG00000272972	14.9916	33.2176	25.3162	40.9457	ENSG00000272972	SPIDR
ENSG00000272974	0.0865499	0.0682183	0.0623268	0.109141	ENSG00000272974	PCDHA13
ENSG00000272976	1.08429	2.46922	1.67569	2.7479	ENSG00000272976	FAM223B
ENSG00000272978	1.53642	2.42545	3.23556	2.2952	ENSG00000272978	RP11-478C6.2
ENSG00000272985	0.165303	0.183125	0.330569	0.273126	ENSG00000272985	CD79A
ENSG00000272987	0	0	0	0	ENSG00000272987	AP002512.3
ENSG00000272996	0.418188	0.39575	0.408938	0.372155	ENSG00000272996	LENG1
ENSG00000272997	7.87635	9.30261	7.95609	7.57048	ENSG00000272997	ATP5SL
ENSG00000272998	15.9969	0	11.1927	0	ENSG00000272998	AL662890.9
ENSG00000273003	0.54071	0.652235	0.150717	0.389948	ENSG00000273003	ARL2-SNX15
ENSG00000273016	0	0.0570873	0.328356	0.0814314	ENSG00000273016	AC012314.19
ENSG00000273020	0	0	0	0.0665423	ENSG00000273020	CEA
ENSG00000273022	0.014225	0	0.0247501	0.0310757	ENSG00000273022	ATF4P1
ENSG00000273024	0	0.0539349	0.177005	0.0537363	ENSG00000273024	INTS4P2
ENSG00000273025	0	0	0	0	ENSG00000273025	AC009690.3
ENSG00000273028	0.231439	0	0.166581	0.467608	ENSG00000273028	IFRD2
ENSG00000273029	0.138589	0.159596	0.133905	0.222201	ENSG00000273029	AC005609.3
ENSG00000273031	0.586232	0.553337	0.745755	0.452985	ENSG00000273031	TFPT
ENSG00000273037	0.586232	0.553337	0.745755	0.452985	ENSG00000273037	TFPT
ENSG00000273039	0	0	0	0	ENSG00000273039	PCDHB17
ENSG00000273041	0.014225	0	0.0247501	0.0310757	ENSG00000273041	ATF4P2
ENSG00000273045	1.65764	1.12612	1.9194	2.44175	ENSG00000273045	C2orf15
ENSG00000273047	0	2.22141	0	0	ENSG00000273047	AL121845.2
ENSG00000273049	0	0	0.774787	0.491487	ENSG00000273049	AC012531.3
ENSG00000273050	0.301483	0.748608	0.79526	1.42681	ENSG00000273050	PRH1
ENSG00000273051	0	0.067479	0	0.076271	ENSG00000273051	AC103710.4
ENSG00000273052	6.25364	4.86093	4.30662	4.47814	ENSG00000273052	NDUFA3
ENSG00000273053	1.51921	0.0206544	0.0163054	0	ENSG00000273053	TSEN34
ENSG00000273054	0	0	0	0	ENSG00000273054	KRTAP10-3
ENSG00000273057	5.20344	3.88437	1.75536	1.72367	ENSG00000273057	MBOAT7
ENSG00000273060	2.36758	1.90677	2.11706	1.49956	ENSG00000273060	PRPF31
ENSG00000273067	0.0448865	0.00841702	0.0559991	0.0871754	ENSG00000273067	PCDHB18
ENSG00000273074	0.0673209	0.124011	0.116879	0.167476	ENSG00000273074	OSCAR
ENSG00000273078	0.0537674	0.0103695	0	0.0456136	ENSG00000273078	PCDHA1
ENSG00000273079	0.151832	0.225387	0.152256	0.458603	ENSG00000273079	GRIN2B
ENSG00000273083	0.164412	0	0.108894	0.250929	ENSG00000273083	NOP56P1
ENSG00000273085	0	0	0	0	ENSG00000273085	AC113331.2
ENSG00000273086	0	0.0858419	0	0.0648035	ENSG00000273086	TAS2R9
ENSG00000273088	0.195072	0	0	0	ENSG00000273088	AL713999.1
ENSG00000273089	2.24367	4.04489	6.17979	7.96233	ENSG00000273089	AC0240565.2
ENSG00000273092	0.0990988	1.0311	0.455987	0.727775	ENSG00000273092	TAS2R20

ENSG00000273095	6.25364	4.86093	4.30662	4.47814	ENSG00000273095	NDUFA3
ENSG00000273099	3.42339	4.64329	1.72368	1.68632	ENSG00000273099	TMC4
ENSG00000273101	0	0	0	0	ENSG00000273101	AC005626.3
ENSG00000273103	0.122457	0.259933	0.247953	0.628477	ENSG00000273103	TARM1
ENSG00000273105	0.0819205	0.586298	0.37711	0.820575	ENSG00000273105	TAS2R13
ENSG00000273109	2.36758	1.90677	2.11706	1.49956	ENSG00000273109	PRPF31
ENSG00000273111	0.141558	0.000489657	0.246337	0.536782	ENSG00000273111	LYPD4
ENSG00000273114	0	0	0	0	ENSG00000273114	KRTAP12-3
ENSG00000273121	2.04277	0.779898	0.971565	1.54972	ENSG00000273121	FAM109B
ENSG00000273122	0	0	0	0	ENSG00000273122	AL844539.2
ENSG00000273126	6.25364	4.86093	4.30662	4.47814	ENSG00000273126	NDUFA3
ENSG00000273127	0	0.253197	0.117158	0.086778	ENSG00000273127	DDX11L8
ENSG00000273128	0.418188	0.39575	0.408938	0.372155	ENSG00000273128	LENG1
ENSG00000273130	5.20344	3.88437	1.75536	1.72367	ENSG00000273130	MBOAT7
ENSG00000273135	42.0117	41.4846	22.7681	25.3501	ENSG00000273135	RPS9
ENSG00000273136	1.39957	0.16924	2.46408	0	ENSG00000273136	NBPF26
ENSG00000273140	1.95394	2.26574	3.32935	2.17489	ENSG00000273140	CCT6P1
ENSG00000273144	0.292621	1.27252	1.10461	1.53197	ENSG00000273144	TAS2R15P
ENSG00000273146	0.0238848	0.0331103	0.0197264	0.0792427	ENSG00000273146	PCDHA5
ENSG00000273150	0.2825	0.283479	0.220893	0	ENSG00000273150	AC245150.1
ENSG00000273154	2.51036	1.90415	3.42702	2.15726	ENSG00000273154	AL121845.3
ENSG00000273155	0.850383	1.15838	1.30124	0.79141	ENSG00000273155	AC092587.1
ENSG00000273157	0	0	0.106579	0.650835	ENSG00000273157	KRTAP10-2
ENSG00000273158	0.298672	0.768449	0.499456	1.08207	ENSG00000273158	CTD-2575K13.6
ENSG00000273159	0.451388	0.355499	0.725781	0.459573	ENSG00000273159	CNOT3
ENSG00000273161	0.407195	0.313898	0.748127	0.20931	ENSG00000273161	RP11-479O9.2
ENSG00000273166	0	0	0	0	ENSG00000273166	DNAJC19P2
ENSG00000273167	0.0508784	0	0	0.167938	ENSG00000273167	AL359736.1
ENSG00000273168	0	0	0	0	ENSG00000273168	DNAJC19P3
ENSG00000273169	0	0	0	0	ENSG00000273169	IMMTP1
ENSG00000273170	0.662779	2.53183	0.977268	0.628522	ENSG00000273170	ANKRD18A
ENSG00000273171	0	0	0	0	ENSG00000273171	AC002094.3
ENSG00000273173	40.3555	27.2278	25.5491	12.9378	ENSG00000273173	SNURF
ENSG00000273178	6.25364	4.86093	4.30662	4.47814	ENSG00000273178	NDUFA3
ENSG00000273182	0.418188	0.39575	0.408938	0.372155	ENSG00000273182	LENG1
ENSG00000273191	0.292621	1.27252	1.10461	1.53197	ENSG00000273191	TAS2R15
ENSG00000273194	0.0555412	0.0541928	0.0958004	0.281774	ENSG00000273194	OLA1P1
ENSG00000273195	2.00188	2.45461	3.62439	1.74328	ENSG00000273195	ABCA11P
ENSG00000273201	0.0279167	0.109821	0.0708882	0.151641	ENSG00000273201	PCDHA2
ENSG00000273202	0.451388	0.355499	0.725781	0.459573	ENSG00000273202	CNOT3
ENSG00000273205	0.265745	0.774309	0.999446	1.23192	ENSG00000273205	C19orf69
ENSG00000273206	0	0	0	0	ENSG00000273206	RP5-933K21.2
ENSG00000273207	0	0	0.580008	0.104487	ENSG00000273207	F8A3
ENSG00000273208	0.0724045	0.0462886	0.0208964	0.103325	ENSG00000273208	H2AFB1
ENSG00000273215	0.122457	0.259933	0.247953	0.628477	ENSG00000273215	TARM1
ENSG00000273217	0	0	0.0675916	0	ENSG00000273217	AC008695.1
ENSG00000273220	0.25311	0.0931596	0.0524582	0.0642875	ENSG00000273220	PCDHA11
ENSG00000273222	0.0673209	0.124011	0.116879	0.167476	ENSG00000273222	OSCAR
ENSG00000273223	0.451388	0.355499	0.725781	0.459573	ENSG00000273223	CNOT3
ENSG00000273224	2.36758	1.90678	2.11706	1.49956	ENSG00000273224	PRPF31
ENSG00000273225	0.728072	0	0	3.35932	ENSG00000273225	FAM25BP
ENSG00000273227	0.139488	0.0109423	0.0808673	0	ENSG00000273227	PCDHB8
ENSG00000273228	0	0	0	0	ENSG00000273228	AP002826.1
ENSG00000273229	0.073732	0.023662	0.0215792	0.0820157	ENSG00000273229	KRTAP10-1

ENSG00000273231	0	0.0570873	0.328356	0.0814314	ENSG00000273231	AC012314.19
ENSG00000273234	0.202057	0.4534	0.468212	0.366268	ENSG00000273234	AC091768.1
ENSG00000273235	1.51921	0.0206544	0.0163054	0	ENSG00000273235	TSEN34
ENSG00000273239	0.0673209	0.124011	0.116879	0.167476	ENSG00000273239	OSCAR
ENSG00000273242	0.11044	0.300606	0.169699	0.607346	ENSG00000273242	VSTM1
ENSG00000273246	1.22489	1.79959	2.48136	2.00213	ENSG00000273246	AC118758.8
ENSG00000273252	0	0	0	0	ENSG00000273252	AC079882.1
ENSG00000273255	0	0.128584	0	0.14372	ENSG00000273255	AP001521.2
ENSG00000273256	0.0823114	0.097346	0.0523417	0.107388	ENSG00000273256	PCDHA6
ENSG00000273259	0.350809	0.28477	0.367398	0.416187	ENSG00000273259	AL049839.2
ENSG00000273260	0.052067	0.100241	0.181198	0.171326	ENSG00000273260	Z95704.3
ENSG00000273263	0	0	0	0.0138936	ENSG00000273263	PCDHA8
ENSG00000273266	0.0713149	0.12878	0.221906	3.2905	ENSG00000273266	HOXC4
ENSG00000273268	0.0673209	0.124011	0.116879	0.167476	ENSG00000273268	OSCAR
ENSG00000273269	0.0694134	0.0737938	0.0669843	0.0999296	ENSG00000273269	STPG4
ENSG00000273273	0.451388	0.355499	0.725781	0.459573	ENSG00000273273	CNOT3
ENSG00000273274	1.38612	2.82787	2.5568	4.66864	ENSG00000273274	ZBTB8B
ENSG00000273276	0.122457	0.259933	0.247953	0.628477	ENSG00000273276	TARM1
ENSG00000273278	0.490444	0.134444	0.606778	0.150111	ENSG00000273278	RP11-478C6.1
ENSG00000273279	0.137195	0.226324	0.340901	0.448548	ENSG00000273279	TAS2R10
ENSG00000273280	0	0	0	0	ENSG00000273280	PLEKHA3P1
ENSG00000273286	0	0	0	0	ENSG00000273286	BX908720.2
ENSG00000273291	1.06983	3.82378	2.18395	0.837209	ENSG00000273291	AC092042.3
ENSG00000273292	0.418188	0.39575	0.408938	0.372155	ENSG00000273292	LENG1
ENSG00000273294	0.284607	0.537923	0.657323	0.73113	ENSG00000273294	C1QTNF3-AMACR
ENSG00000273296	0	0	0	0	ENSG00000273296	FP700107.1
ENSG00000273303	0	0	0	0	ENSG00000273303	RP11-944L7.5
ENSG00000273310	0.422639	0.159446	0.510084	0.263305	ENSG00000273310	PCDHB14
ENSG00000273315	0.418188	0.39575	0.408938	0.372155	ENSG00000273315	LENG1
ENSG00000273316	5.20344	3.88437	1.75536	1.72367	ENSG00000273316	MBOAT7
ENSG00000273317	0.312453	0.162931	0.105318	0.0865265	ENSG00000273317	PCDHB12
ENSG00000273318	2.74701	4.04566	3.57703	3.9498	ENSG00000273318	AC018755.2
ENSG00000273322	0.0523826	0.0756352	0.138032	0.178617	ENSG00000273322	KRTAP10-5
ENSG00000273323	0.164412	0	0.108894	0.250929	ENSG00000273323	NOP56P1
ENSG00000273324	4.69864	6.28399	6.30994	4.92456	ENSG00000273324	AC253576.3
ENSG00000273326	0	0.03555	0	0.0201421	ENSG00000273326	TAS2R7
ENSG00000273327	0.435909	0.777123	2.8609	1.08736	ENSG00000273327	OR6L2P
ENSG00000273330	0	0	0	0.914483	ENSG00000273330	CYP4F36P
ENSG00000273331	2.4999	0.27902	0	0	ENSG00000273331	TM4SF19
ENSG00000273332	0.0207546	0	0	0	ENSG00000273332	PCDHB14
ENSG00000273336	0.554513	0.665138	0.600338	1.48553	ENSG00000273336	OR7M1P
ENSG00000273339	2.35423	10.4071	8.85686	14.5964	ENSG00000273339	AC138827.2
ENSG00000273340	2.30915	0	0	0	ENSG00000273340	MICE
ENSG00000273347	3.42339	4.64329	1.72368	1.68632	ENSG00000273347	TMC4
ENSG00000273349	0.11044	0.300606	0.169699	0.607346	ENSG00000273349	VSTM1
ENSG00000273351	0	0.0440913	0	0	ENSG00000273351	KRTAP10-4
ENSG00000273354	0	0.0570873	0.328356	0.0814314	ENSG00000273354	AC012314.19
ENSG00000273357	0.315309	0.0828291	0.237716	0.364214	ENSG00000273357	PCDHB13
ENSG00000273358	0.122457	0.259933	0.247953	0.628477	ENSG00000273358	TARM1
ENSG00000273359	0	0	0.0277802	0.0174369	ENSG00000273359	TAS2R8
ENSG00000273376	2.36758	1.90678	2.11706	1.49956	ENSG00000273376	PRPF31
ENSG00000273377	0	0	0.0596058	0	ENSG00000273377	OR2Q1P
ENSG00000273378	2.04277	0.779898	0.971565	1.54972	ENSG00000273378	FAM109B
ENSG00000273380	0.0673209	0.124011	0.116879	0.167476	ENSG00000273380	OSCAR

ENSG00000273383	0	0	0	0	ENSG00000273383	PCDHB5
ENSG00000273385	42.0117	41.4846	22.7681	25.3501	ENSG00000273385	RPS9
ENSG00000273392	0.0378828	0.178853	0.48614	0.403366	ENSG00000273392	PCDHB6
ENSG00000273395	0	0	0	0	ENSG00000273395	FLJ00388
ENSG00000273397	6.85869	6.86074	6.16687	4.47528	ENSG00000273397	NDUFA6
ENSG00000273398	0.15339	0.0928079	0.0947077	0	ENSG00000273398	RP11-474G23.1
ENSG00000273400	15.9969	0	11.1927	0	ENSG00000273400	AL662890.15
ENSG00000273404	0	0.03555	0	0.0201421	ENSG00000273404	TAS2R7
ENSG00000273408	0	0	0	0	ENSG00000273408	OR5B15P
ENSG00000273410	0	0.0511679	0.0462051	0.0574712	ENSG00000273410	RP11-169K19.1
ENSG00000273412	0	0	0	0	ENSG00000273412	KRTAP10-11
ENSG00000273414	0.11044	0.300606	0.169699	0.607346	ENSG00000273414	VSTM1
ENSG00000273417	0.586232	0.553337	0.745755	0.452985	ENSG00000273417	TFPT
ENSG00000273418	0.122457	0.259933	0.247953	0.628477	ENSG00000273418	TARM1
ENSG00000273421	0.11044	0.300606	0.169699	0.607346	ENSG00000273421	VSTM1
ENSG00000273422	0.697168	1.94566	1.60176	2.1243	ENSG00000273422	ZNF876P
ENSG00000273423	0.643397	2.01685	1.58317	2.99836	ENSG00000273423	OR13I1P
ENSG00000273425	0.79966	1.15155	1.3439	2.29132	ENSG00000273425	AC073107.1
ENSG00000273426	6.25364	4.86093	4.30662	4.47814	ENSG00000273426	NDUFA3
ENSG00000273427	6.25364	4.86093	4.30662	4.47814	ENSG00000273427	NDUFA3
ENSG00000273429	12.5191	8.75674	15.9159	9.76696	ENSG00000273429	AC253572.2
ENSG00000273430	0.586232	0.553337	0.745755	0.452985	ENSG00000273430	TFPT
ENSG00000273431	0.102898	0.718323	0.447358	0.403433	ENSG00000273431	TAS2R50
ENSG00000273434	0	0	0	0	ENSG00000273434	AC090115.4
ENSG00000273436	0.459625	0.428689	0.469558	0.202455	ENSG00000273436	DMRTC2
ENSG00000273439	1.42474	1.73424	3.77E-09	0	ENSG00000273439	ZNF8
ENSG00000273440	0	0.0462886	0.0208964	0.103325	ENSG00000273440	H2AFB2
ENSG00000273441	0.441462	1.64169	2.31387	2.29425	ENSG00000273441	RP11-822E23.6
ENSG00000273444	8.24364	1.10127	6.70646	2.51633	ENSG00000273444	RP5-114A1.2
ENSG00000273446	5.20344	3.88437	1.75536	1.72367	ENSG00000273446	MBOAT7
ENSG00000273452	0	0	0	0	ENSG00000273452	AC005358.1
ENSG00000273453	6.25364	4.86093	4.30662	4.47814	ENSG00000273453	NDUFA3
ENSG00000273457	0.0819205	0.586298	0.37711	0.820575	ENSG00000273457	TAS2R13
ENSG00000273458	0.586232	0.553337	0.745755	0.452985	ENSG00000273458	TFPT
ENSG00000273459	0.451388	0.355499	0.725781	0.459573	ENSG00000273459	CNOT3
ENSG00000273460	0.11044	0.300606	0.169699	0.607346	ENSG00000273460	VSTM1
ENSG00000273462	2.36758	1.90678	2.11706	1.49956	ENSG00000273462	PRPF31
ENSG00000273463	0	0	0	0	ENSG00000273463	AL138834.1
ENSG00000273465	1.21075	1.44437	0.319386	1.07726	ENSG00000273465	RP11-478C6.5
ENSG00000273467	42.0117	41.4846	22.7681	25.3501	ENSG00000273467	RPS9
ENSG00000273468	0.106695	0.0458805	0.0312506	0.143234	ENSG00000273468	PCDHB19P
ENSG00000273469	2.36758	1.90677	2.11706	1.49956	ENSG00000273469	PRPF31
ENSG00000273470	5.20344	3.88437	1.75536	1.72367	ENSG00000273470	MBOAT7
ENSG00000273475	0.224987	0.293343	0.330485	0.856166	ENSG00000273475	LDHAL6FP
ENSG00000273479	0.0485048	0	0	0	ENSG00000273479	AC005795.1
ENSG00000273482	2.60026	2.37243	3.38802	3.58456	ENSG00000273482	PRKCD
ENSG00000273484	0.441035	1.25921	1.74637	3.79971	ENSG00000273484	OR6R2P
ENSG00000273490	1.51921	0.0206544	0.0163054	0	ENSG00000273490	TSEN34

Supplemental Table S3 - Complete list of potential extracellular proteome
SILAC protein ratios of ECM isolated from primary human keratinocytes derived from two RDEB and two healthy donors. Annotated spectra of single peptide identifications are available as supplemental information.
Protein IDs Protein names Gene names Fasta headers Ctrl1_1 Ctrl1_2 Ctrl2_1 Ctrl2_2 RDEB1_1 RDEB1_2 RDEB2_1 RDEB2_2 PEP Peptides Sequence coverage [%] GOBP name GOMF name GOCC name KEGG name
P25054-2;P25054 Adenomatous polyposis coli protein APC >sp|P25054-2|APC_HUMAN Isoform Short of Adenomatous polyposis coli protein OS=Homo sapiens GN=APC;>sp|P25054|APC_HUMAN Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2 1.03 NaN 0.66 0.73 0.89 1.34 1.02 NaN 0.0010609 1 0.6 anatomical structure development;anatomical structure homeostasis;anatomical structure morphogenesis;anterior/posterior pattern specification;axis specification;axonogenesis;biological adhesion;biological regulation;canonical Wnt receptor signaling pathway;cell activation;cell adhesion;cell cycle arrest;cell cycle checkpoint;cell cycle cytokinesis;cell cycle process;cell differentiation;cell junction assembly;cell junction organization;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;cytokinesis;cytokinesis after mitosis;cytoplasmic microtubule organization;cytoskeleton organization;developmental process;dorsal/ventral pattern formation;epidermis development;hair cycle process;hair follicle development;hemopoietic or lymphoid organ development;homeostatic process;immune system process;kidney development;leukocyte activation;leukocyte differentiation;locomotion;lymphocyte activation;lymphocyte differentiation;macromolecular complex assembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule-based process;mitotic cell cycle checkpoint;mitotic cell cycle spindle assembly checkpoint;mitotic cell cycle spindle checkpoint;mitotic metaphase/anaphase transition;molting cycle;molting cycle process;multicellular organismal process;muscle cell homeostasis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cyclin-dependent protein kinase activity;negative regulation of cytoskeleton organization;negative regulation of developmental process;negative regulation of epithelial cell proliferation;negative regulation of epithelial cell proliferation involved in prostate gland development;negative regulation of intracellular protein kinase cascade;negative regulation of kinase activity;negative regulation of MAPKKK cascade;negative regulation of microtubule depolymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of mitosis;negative regulation of mitotic metaphase/anaphase transition;negative regulation of molecular function;negative regulation of nuclear division;negative regulation of odontogenesis;negative regulation of organelle organization;negative regulation of programmed cell death;negative regulation of protein complex disassembly;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of reproductive process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transferase activity;negative regulation of Wnt receptor signaling pathway;neuron projection morphogenesis;organ development;organelle organization;pattern specification process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell adhesion;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of epithelial cell differentiation;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of microtubule polymerization;positive regulation of microtubule polymerization or depolymerization;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of protein catabolic process;positive regulation of protein complex assembly;positive regulation of protein metabolic process;positive regulation of protein polymerization;positive regulation of pseudopodium assembly;protein complex assembly;protein complex subunit organization;proximal/distal pattern formation;regionalization;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of attachment of spindle microtubules to kinetochore;regulation of biological process;regulation of biological quality;regulation of canonical Wnt receptor signaling pathway;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell differentiation;regulation of cell division;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome segregation;regulation of cyclin-dependent protein kinase activity;regulation of cytoskeleton organization;regulation of developmental process;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of epithelial cell proliferation involved in prostate gland development;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule depolymerization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic metaphase/anaphase transition;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of odontogenesis;regulation of organ morphogenesis;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoclast differentiation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of protein serine/threonine kinase activity;regulation of pseudopodium assembly;regulation of reproductive process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of Wnt receptor signaling pathway;response to DNA damage stimulus;response

to stimulus;response to stress;retina development in camera-type eye;signal transduction;skin development;somatic stem cell maintenance;spindle assembly checkpoint;spindle checkpoint;stem cell maintenance;T cell activation;T cell differentiation;T cell differentiation in thymus;thymus development;tight junction assembly;tissue development;Wnt receptor signaling pathway binding;cytoskeletal protein binding;enzyme regulator activity;kinase regulator activity;microtubule binding;microtubule plus-end binding;protein binding;protein kinase regulator activity;tubulin binding adherens junction;anchoring junction;axon part;axonal growth cone;beta-catenin destruction complex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;centrosome;chromosomal part;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytosol;growth cone;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;lamellipodium;lateral plasma membrane;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;microtubule;microtubule organizing center;microtubule plus end;non-membrane-bounded organelle;nucleus;occluding junction;organelle;organelle part;plasma membrane part;protein complex;ruffle membrane;site of polarized growth;tight junction Basal cell carcinoma;Colorectal cancer;Endometrial cancer;Pathways in cancer;Regulation of actin cytoskeleton;Wnt signaling pathway

G3V1B6;H7C1U8;C9J574;Q9BUR5-2;Q9BUR5 Apolipoprotein O APOO >tr|G3V1B6|G3V1B6_HUMAN Apolipoprotein O OS=Homo sapiens GN=APOO PE=2 SV=1;>tr|H7C1U8|H7C1U8_HUMAN Apolipoprotein O (Fragment) OS=Homo sapiens GN=APOO PE=2 SV=1;>tr|C9J574|C9J574_HUMAN Apolipoprotein O OS=Homo sapiens GN=APOO PE=2 SV=1;>sp|Q9BUR5-2|APOO_HU NaN NaN 1.78 NaN 18.56 NaN NaN NaN 0.00079091 1 9.6 establishment of localization;lipid transport;organic substance transport;transport cell part;extracellular region part;extracellular space;high-density lipoprotein particle;integral to membrane;intrinsic to membrane;low-density lipoprotein particle;macromolecular complex;membrane part;plasma lipoprotein particle;protein-lipid complex;triglyceride-rich lipoprotein particle;very-low-density lipoprotein particle

H0YDI1;P19256-2;B1AMW1;P19256-3;P19256 Lymphocyte function-associated antigen 3 CD58 ">tr|H0YDI1|H0YDI1_HUMAN Lymphocyte function-associated antigen 3 (Fragment) OS=Homo sapiens GN=CD58 PE=2 SV=1;>sp|P19256-2|LFA3_HUMAN Isoform 2 of Lymphocyte function-associated antigen 3 OS=Homo sapiens GN=CD58;>tr|B1AMW1|B1AMW1_HUMAN CD58 antigen, (Lymph" NaN NaN 1.41 NaN 7.24 NaN NaN NaN 0.0010377 1 7.6 biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell-cell adhesion;cellular component movement;cellular process;coagulation;hemostasis;immune system process;leukocyte migration;locomotion;multicellular organismal process;regulation of biological quality;regulation of body fluid levels anchored to membrane;cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Cell adhesion molecules (CAMs)

Q15517;G8JLG2 Corneodesmosin CDSN >sp|Q15517|CDSN_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=1 SV=3;>tr|G8JLG2|G8JLG2_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=2 SV=1 0.38 NaN 0.13 NaN 2.86 NaN 1.88 NaN 8.80E-07 1 4.7 anatomical structure morphogenesis;biological adhesion;cell adhesion;cell differentiation;cell-cell adhesion;cellular developmental process;cellular process;developmental process;epidermal cell differentiation;epidermis morphogenesis;epithelial cell differentiation;keratinocyte differentiation;skin morphogenesis;tissue morphogenesis binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity anchoring junction;cell junction;cell part;cell-cell junction;cornified envelope;cytoskeleton;desmosome;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

H0YAS8;P10909-3;P10909-4;P10909;P10909-5;P10909-2 Clusterin;Clusterin beta chain;Clusterin alpha chain CLU >tr|H0YAS8|H0YAS8_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1;>sp|P10909-3|CLUS_HUMAN Isoform 3 of Clusterin OS=Homo sapiens GN=CLU;>sp|P10909-4|CLUS_HUMAN Isoform 4 of Clusterin OS=Homo sapiens GN=CLU;>sp|P10909|CLUS_HUMAN Clust NaN NaN NaN NaN NaN NaN NaN NaN 6.00E-06 1 12.1 "activation of immune response;apoptotic mitochondrial changes;biological regulation;cell activation;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone-mediated protein folding;cholesterol transport;complement activation;complement activation, classical pathway;death;defense response;establishment of localization;establishment of localization in cell;exocytosis;humoral immune response;immune effector process;immune response;immune system process;innate immune response;lipid metabolic process;lipid transport;macromolecule metabolic process;metabolic process;mitochondrion organization;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of programmed cell death;negative regulation of protein complex assembly;negative regulation of protein homooligomerization;negative regulation of protein oligomerization;organelle organization;organic substance transport;platelet activation;platelet degranulation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell death;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of immune response;positive regulation of immune system process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of programmed cell death;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;positive regulation of proteolysis;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;posttranscriptional regulation of gene expression;primary metabolic process;protein activation cascade;protein folding;protein metabolic process;protein stabilization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catabolic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of immune response;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein homooligomerization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein oligomerization;regulation of protein stability;regulation of protein ubiquitination;regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of proteolysis;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;release of cytochrome c from mitochondria;response to biotic stimulus;response to chemical stimulus;response to misfolded protein;response to organic substance;response to other organism;response to stimulus;response to stress;response to topologically incorrect protein;response to virus;reverse cholesterol transport;secretion;secretion by cell;sterol transport;transport;vesicle-mediated transport" binding;enzyme binding;misfolded protein binding;protein binding;ubiquitin protein ligase binding cell part;chromaffin granule;cytoplasmic membrane-bounded vesicle;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle part;cytosol;endoplasmic reticulum;extracellular region part;high-density lipoprotein particle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma lipoprotein particle;platelet alpha granule lumen;protein-lipid complex;secretory granule lumen;spherical high-density lipoprotein particle;stored secretory granule;vesicle;vesicle lumen

A6NCT7;Q07092-2;Q07092;A6NDR9 Collagen alpha-1(XVI) chain COL16A1 >tr|A6NCT7|A6NCT7_HUMAN Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL16A1 PE=2 SV=1;>sp|Q07092-2|COGA1_HUMAN Isoform 2 of Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL16A1;>sp|Q07092|COGA1_HUMAN Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL1 NaN NaN NaN NaN NaN NaN NaN NaN 9.00E-06 1 1.8 biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;collagen catabolic process;collagen metabolic process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;female pregnancy;integrin-mediated signaling pathway;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;multi-organism process;regulation of biological process;regulation of cellular process;reproductive process;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to organic nitrogen;response to organic substance;response to stimulus;signal transduction binding;integrin binding;protein binding;protein complex binding;receptor binding anchoring collagen;cell part;collagen;collagen type XVI;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;FACIT collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part

Q02388-2;Q02388 Collagen alpha-1(VII) chain COL7A1 >sp|Q02388-2|CO7A1_HUMAN Isoform 2 of Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1;>sp|Q02388|CO7A1_HUMAN Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2 NaN NaN 0.02 NaN 0.01 NaN NaN NaN 2.70E-09 1 0.5 anatomical structure development;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;developmental process;epidermis development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;tissue development endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity anchoring collagen;basement membrane;cell part;collagen;collagen type VII;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part

O94919 Endonuclease domain-containing 1 protein ENDOD1>sp|O94919|ENDD1_HUMAN Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2 0.76 NaN 1.06 0.87 1.28 1.64 1.23 NaN 2.38E-09 1 2.6 cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process "binding;catalytic activity;cation binding;endonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nuclease activity;nucleic acid binding" extracellular region Apoptosis

P01834 Ig kappa chain C region IGKC >sp|P01834|IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 NaN NaN NaN NaN NaN NaN NaN NaN 0.00074596 1 18.9 "activation of immune response;biological regulation;complement activation;complement activation, classical pathway;defense response;humoral immune response;immune effector process;immune response;immune system process;innate immune response;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of immune response;positive regulation of immune system process;positive regulation of response to stimulus;primary metabolic process;protein activation cascade;protein metabolic process;regulation of biological process;regulation of immune response;regulation of immune system process;regulation of response to stimulus;response to stimulus;response to stress" antigen binding;binding cell part;extracellular region;membrane;plasma membrane

P06756-3;P06756-2;P06756 Integrin alpha-V;Integrin alpha-V heavy chain;Integrin alpha-V light chain ITGAV >sp|P06756-3|ITAV_HUMAN Isoform 3 of Integrin alpha-V OS=Homo sapiens GN=ITGAV;>sp|P06756-2|ITAV_HUMAN Isoform 2 of Integrin alpha-V OS=Homo sapiens GN=ITGAV;>sp|P06756|ITAV_HUMAN Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2 NaN 1.21 NaN NaN NaN NaN NaN 0.8 0.00068122 1 1.4 "anatomical structure formation involved in morphogenesis;angiogenesis;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptotic cell clearance;axon guidance;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;coagulation;developmental process;endocytosis;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of organism into cell of other organism by promotion of phagocytosis in other organism involved in symbiotic interaction;entry of symbiont into host cell by promotion of host phagocytosis;entry of virus into host cell;ERK1 and ERK2 cascade;establishment of localization;extracellular matrix organization;extracellular structure organization;hemostasis;immune system process;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;leukocyte migration;locomotion;MAPKKK cascade;membrane invagination;membrane organization;modification by symbiont of host morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by symbiont of host cellular process;modulation by symbiont of host phagocytosis;modulation of phagocytosis in other organism involved in symbiotic interaction;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multicellular organismal process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of entry of bacterium into host cell;negative regulation of lipid storage;negative regulation of lipid transport;negative regulation of lipoprotein metabolic process;negative regulation of locomotion;negative regulation of low-density lipoprotein particle receptor biosynthetic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of macrophage derived foam cell differentiation;negative regulation of metabolic process;negative regulation of multi-organism process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of receptor biosynthetic process;negative regulation of transport;phagocytosis;positive regulation by organism of phagocytosis in other organism involved in symbiotic interaction;positive regulation by symbiont of host phagocytosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of locomotion;positive regulation of osteoblast proliferation;positive regulation of phagocytosis;positive regulation of transport;regulation of apoptosis;regulation of apoptotic cell clearance;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell adhesion;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of endocytosis;regulation of entry of bacterium into host cell;regulation of lipid storage;regulation of lipid transport;regulation of lipoprotein metabolic process;regulation of localization;regulation of locomotion;regulation of low-density lipoprotein particle receptor biosynthetic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of macrophage derived foam cell differentiation;regulation of metabolic process;regulation of multi-organism process;regulation of osteoblast proliferation;regulation of phagocytosis;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of receptor biosynthetic process;regulation of symbiosis, encompassing mutualism through parasitism;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis;transport;vesicle-mediated transport" binding;calcium channel activity;cation binding;cation channel activity;cation transmembrane transporter activity;channel activity;cytokine binding;gated channel activity;growth factor binding;ion binding;ion channel activity;ion transmembrane transporter activity;metal ion binding;passive transmembrane transporter activity;protein binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transforming growth factor beta binding;transmembrane transporter activity;transporter activity;voltage-gated calcium channel activity;voltage-gated cation channel activity;voltage-gated channel activity;voltage-gated ion channel activity alphav-beta3 integrin-IGF-1-IGF1R complex;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;external side of plasma membrane;integrin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;phagocytic vesicle;plasma membrane part;protein complex;receptor complex;vesicle Arrhythmogenic right ventricular cardiomyopathy (ARVC);Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Small cell lung cancer

H7C0L5;Q14624-4;Q14624-3;Q14624-2;Q14624;B7ZKJ8 Inter-alpha-trypsin inhibitor heavy chain H4;70 kDa inter-alpha-trypsin inhibitor heavy chain H4;35 kDa inter-alpha-trypsin inhibitor heavy chain H4ITIH4 >tr|H7C0L5|H7C0L5_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 (Fragment) OS=Homo sapiens GN=ITIH4 PE=4 SV=1;>sp|Q14624-4|ITIH4_HUMAN Isoform 4 of Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4;>sp|Q14624-3|ITIH4_HUMAN I 0.05 102.64 0 NaN 0.02 NaN 0.05 0.85 0.001212 1 1.5 acute inflammatory response;acute-phase response;amine metabolic process;aminoglycan metabolic process;carbohydrate metabolic process;defense response;glycosaminoglycan metabolic process;hyaluronan metabolic process;inflammatory response;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;polysaccharide metabolic process;primary metabolic process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;response to stress;response to wounding endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasm;extracellular region;intracellular part;membrane;plasma membrane

C9JD84;Q14766-3;E7EV71;Q14766-2;Q14766-5;Q14766;Q14766-4 Latent-transforming growth factor beta-binding protein 1 LTBP1 >tr|C9JD84|C9JD84_HUMAN Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=2 SV=1;>sp|Q14766-3|LTBP1_HUMAN Isoform 3 of Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1;>tr|E7EV71|E7EV71_HU 0.89 1.3 0.91 0.85 0.57 0.68 0.97 1.2 0.00062768 1 1.3 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular sequestering of receptor ligand;extracellular structure organization;maintenance of location;maintenance of location in cell;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;maintenance of protein location in extracellular region;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transforming growth factor beta receptor signaling pathway by extracellular sequestering of TGFbeta;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway "binding;calcium ion binding;catalytic activity;cation binding;ion binding;kinase activity;metal ion binding;molecular transducer activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;receptor activity;signal transducer activity;signaling receptor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transforming growth factor beta-activated receptor activity;transmembrane receptor protein kinase activity;transmembrane receptor protein serine/threonine kinase activity;transmembrane signaling receptor activity" extracellular matrix;extracellular region part;proteinaceous extracellular matrix

Q14210 Lymphocyte antigen 6D LY6D >sp|Q14210|LY6D_HUMAN Lymphocyte antigen 6D OS=Homo sapiens GN=LY6D PE=1 SV=1 0.97 1.9 2.65 2.31 0.52 0.56 0.27 0.17 0.00017169 1 7 biological adhesion;cell activation;cell adhesion;cell differentiation;cellular developmental process;cellular process;developmental process;immune system

process;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;response to chemical stimulus;response to organic substance;response to stilbenoid;response to stimulus	anchored to membrane;cell part;cell surface;intrinsic to membrane;membrane;membrane part;plasma membrane
H0YAH0;O60245;O60245-2;O60245-3;F5GWJ1	Protocadherin-7	PCDH7	>tr|H0YAH0|H0YAH0_HUMAN Protocadherin-7 (Fragment) OS=Homo sapiens GN=PCDH7 PE=4 SV=1;>sp|O60245|PCDH7_HUMAN Protocadherin-7 OS=Homo sapiens GN=PCDH7 PE=1 SV=2;>sp|O60245-2|PCDH7_HUMAN Isoform B of Protocadherin-7 OS=Homo sapiens GN=PCDH7;>sp|O60245-3|PCDH	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	2.19E-05	1	1.7	biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion	binding;calcium ion binding;cation binding;ion binding;metal ion binding	cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane;plasma membrane part
H0Y8D1;Q8NHM4;P07478;P07477;CON__P07477;E7EQ64	Putative trypsin-6;Trypsin-2;Trypsin-1;Alpha-trypsin chain 1;Alpha-trypsin chain 2	PRSS1;TRY6;PRSS2	>tr|H0Y8D1|H0Y8D1_HUMAN Trypsin-1 (Fragment) OS=Homo sapiens GN=PRSS1 PE=2 SV=1;>sp|Q8NHM4|TRY6_HUMAN Putative trypsin-6 OS=Homo sapiens GN=TRY6 PE=5 SV=1;>sp|P07478|TRY2_HUMAN Trypsin-2 OS=Homo sapiens GN=PRSS2 PE=1 SV=1;>sp|P07477|TRY1_HUMAN Trypsin-1 OS	NaN	NaN	0.12	NaN	0	NaN	NaN	NaN	1.45E-10	1	14.1	biological regulation;cell migration;cell motility;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;defense response;digestion;endothelial cell migration;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune response;immune system process;innate immune response;locomotion;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of cell adhesion;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;response to stimulus;response to stress	"binding;calcium ion binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity"	extracellular matrix;extracellular region;extracellular region part;extracellular space	Neuroactive ligand-receptor interaction;Pancreatic secretion;Protein digestion and absorption
B1AN99;F8W7P3;P35030-3;P35030-2;P35030-4;P35030	Trypsin-3	PRSS3	>tr|B1AN99|B1AN99_HUMAN Trypsin-3 (Fragment) OS=Homo sapiens GN=PRSS3 PE=2 SV=1;>tr|F8W7P3|F8W7P3_HUMAN Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=2 SV=1;>sp|P35030-3|TRY3_HUMAN Isoform C of Trypsin-3 OS=Homo sapiens GN=PRSS3;>sp|P35030-2|TRY3_HUMAN Isoform B o	NaN	25.58	0.09	14.26	0.06	0.58	NaN	4.68	1.48E-26	1	7.3	cell migration;cell motility;cellular component movement;cellular process;defense response;digestion;endothelial cell migration;immune response;immune system process;innate immune response;locomotion;macromolecule metabolic process;metabolic process;multicellular organismal process;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;response to stimulus;response to stress;zymogen activation	"binding;calcium ion binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity"	extracellular region part;extracellular space	Neuroactive ligand-receptor interaction;Pancreatic secretion;Protein digestion and absorption
H0Y4H1;H0Y7Z9;H0Y6Z7;P10586-2;P10586	Receptor-type tyrosine-protein phosphatase F	PTPRF	>tr|H0Y4H1|H0Y4H1_HUMAN Receptor-type tyrosine-protein phosphatase F (Fragment) OS=Homo sapiens GN=PTPRF PE=4 SV=1;>tr|H0Y7Z9|H0Y7Z9_HUMAN Receptor-type tyrosine-protein phosphatase F (Fragment) OS=Homo sapiens GN=PTPRF PE=4 SV=1;>tr|H0Y6Z7|H0Y6Z7_HUMAN Re	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	0.00073052	1	1.6	biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;dephosphorylation;enzyme linked receptor protein signaling pathway;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;transmembrane receptor protein tyrosine phosphatase signaling pathway	"binding;carbohydrate binding;catalytic activity;glycosaminoglycan binding;heparin binding;hydrolase activity;hydrolase activity, acting on ester bonds;molecular transducer activity;pattern binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;polysaccharide binding;protein tyrosine phosphatase activity;receptor activity;signal transducer activity;signaling receptor activity;transmembrane receptor protein phosphatase activity;transmembrane receptor protein tyrosine phosphatase activity;transmembrane signaling receptor activity"	cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part	Adherens junction;Cell adhesion molecules (CAMs);Insulin signaling pathway
O95197-3;O95197-4;O95197-7;O95197-2;O95197	Reticulon-3	RTN3	>sp|O95197-3|RTN3_HUMAN Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3;>sp|O95197-4|RTN3_HUMAN Isoform 4 of Reticulon-3 OS=Homo sapiens GN=RTN3;>sp|O95197-7|RTN3_HUMAN Isoform 7 of Reticulon-3 OS=Homo sapiens GN=RTN3;>sp|O95197-2|RTN3_HUMAN Isoform 2 of	NaN	NaN	NaN	0.33	NaN	2.24	NaN	NaN	0.0010692	1	4.7	apoptosis;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;death;endoplasmic reticulum organization;endoplasmic reticulum tubular network organization;establishment of localization;interaction with host;interspecies interaction between organisms;multi-organism process;organelle organization;programmed cell death;reproductive process;response to stimulus;response to stress;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction		cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular region part;extracellular space;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part
P31151	Protein S100-A7	S100A7	>sp|P31151|S10A7_HUMAN Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	NaN	17.03	NaN	NaN	NaN	NaN	NaN	1.35	0.0011997	1	10.9	anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;cell differentiation;cellular developmental process;cellular process;defense response;defense response to bacterium;defense response to Gram-negative bacterium;developmental process;epidermal cell differentiation;epithelial cell differentiation;immune response;immune system process;innate immune response;keratinocyte differentiation;maintenance of location;multi-organism process;positive regulation of behavior;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell migration;positive regulation of cell motility;positive regulation of

cellular component movement;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of ERK1 and ERK2 cascade;positive regulation of granulocyte chemotaxis;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of lymphocyte migration;positive regulation of MAPKKK cascade;positive regulation of monocyte chemotaxis;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of T cell chemotaxis;positive regulation of T cell migration;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of chemotaxis;regulation of ERK1 and ERK2 cascade;regulation of granulocyte chemotaxis;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of lymphocyte migration;regulation of MAPKKK cascade;regulation of monocyte chemotaxis;regulation of response to external stimulus;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell chemotaxis;regulation of T cell migration;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to inorganic substance;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to other organism;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;sequestering of metal ion binding;calcium ion binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytosol;endoplasmic reticulum;extracellular region;focal adhesion;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

P10599-2;P10599 Thioredoxin TXN >sp|P10599-2|THIO_HUMAN Isoform 2 of Thioredoxin OS=Homo sapiens GN=TXN;>sp|P10599|THIO_HUMAN Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 NaN NaN NaN NaN NaN NaN NaN NaN 4.59E-09 1 15.3 "antibiotic metabolic process;biological regulation;biosynthetic process;carbohydrate homeostasis;cell communication;cell proliferation;cell redox homeostasis;cell-cell signaling;cellular biosynthetic process;cellular chemical homeostasis;cellular component movement;cellular glucose homeostasis;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to drug;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to hyperoxia;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;chemical homeostasis;defense response;drug metabolic process;electron transport chain;generation of precursor metabolites and energy;glucose homeostasis;glycerol ether metabolic process;homeostatic process;immune response;immune system process;innate immune response;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of protein export from nucleus;negative regulation of protein transport;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;organic ether metabolic process;oxidation-reduction process;positive regulation of binding;positive regulation of DNA binding;positive regulation of molecular function;primary metabolic process;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA binding;regulation of establishment of protein localization;regulation of gene expression;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein localization;regulation of protein transport;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;response to abiotic stimulus;response to activity;response to axon injury;response to carbohydrate stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to dexamethasone stimulus;response to drug;response to endogenous stimulus;response to glucocorticoid stimulus;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to hyperoxia;response to inorganic substance;response to metal ion;response to monosaccharide stimulus;response to organic substance;response to oxygen levels;response to radiation;response to selenium ion;response to steroid hormone stimulus;response to stimulus;response to stress;response to thyroid hormone stimulus;response to thyroxine stimulus;response to wounding;RNA biosynthetic process;RNA metabolic process;signal transduction;signaling;small molecule metabolic process;transcription, DNA-dependent" "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;peptide disulfide oxidoreductase activity;protein disulfide oxidoreductase activity" axon;cell body;cell part;cell projection;cytoplasmic part;cytosol;dendrite;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;neuronal cell body;nuclear part;nucleoplasm;organelle;organelle part

Q5JQ13;P18206-2;P18206 Vinculin VCL >tr|Q5JQ13|Q5JQ13_HUMAN Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=2 SV=1;>sp|P18206-2|VINC_HUMAN Isoform 1 of Vinculin OS=Homo sapiens GN=VCL;>sp|P18206|VINC_HUMAN Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 NaN 1.44 NaN NaN NaN NaN NaN 0.99 1.02E-07 1 1.7 adherens junction assembly;adherens junction organization;anatomical structure morphogenesis;apical junction assembly;biological adhesion;biological regulation;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell projection assembly;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;developmental process;epithelial cell-cell adhesion;establishment of localization;establishment of localization in cell;exocytosis;lamellipodium assembly;localization;macromolecule localization;morphogenesis of an epithelium;multicellular organismal process;muscle contraction;muscle system process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;platelet activation;platelet degranulation;protein localization;protein localization at cell surface;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of locomotion;secretion;secretion by cell;system process;tissue morphogenesis;transport;vesicle-mediated transport actin binding;beta-catenin binding;binding;cadherin binding;cell adhesion molecule binding;cytoskeletal protein binding;protein binding;structural molecule activity actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;costamere;cytoplasmic part;cytoskeleton;cytosol;extracellular region;fascia adherens;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;sarcolemma;Z disc Adherens junction;Amoebiasis;Bacterial invasion of epithelial cells;Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Shigellosis

Q8NE71-2;Q8NE71;F5GYK6;Q5STZ8;H0YGW7 ATP-binding cassette sub-family F member 1 ABCF1 >sp|Q8NE71-2|ABCF1_HUMAN Isoform 2 of ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1;>sp|Q8NE71|ABCF1_HUMAN ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2;>tr|F5GYK6|F5GYK6_HUMAN ATP-binding cassette sub- NaN NaN 0.52 NaN 2.15 NaN NaN NaN 3.20E-21 2 3 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;heterocycle catabolic process;heterocycle metabolic process;inflammatory response;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;response to stimulus;response to stress;response to wounding;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;translational initiation"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleoprotein binding;ribonucleotide binding;ribosome binding;RNA binding;translation activator activity;translation factor activity, nucleic acid binding;translation regulator activity;translation regulator activity, nucleic acid binding" cell part;cytoplasmic part;envelope;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleoplasm;organelle;organelle envelope;organelle part;polysomal ribosome;ribonucleoprotein complex;ribosome

P42765 "3-ketoacyl-CoA thiolase, mitochondrial" ACAA2 ">sp|P42765|THIM_HUMAN 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2" NaN 0.04 1.35 0.05 2.9 0.33 NaN 0.2 4.61E-14 2 6 alcohol metabolic process;biological regulation;biosynthetic process;carboxylic acid metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "acetyl-CoA C-acyltransferase activity;C-acyltransferase activity;catalytic activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part "Benzoate degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Valine, leucine and isoleucine degradation"

P24752 "Acetyl-CoA acetyltransferase, mitochondrial" ACAT1 ">sp|P24752|THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1" NaN NaN NaN NaN NaN NaN NaN NaN 0.00013637 2 6.1 adipose tissue development;amine catabolic process;amine metabolic process;anatomical structure development;biosynthetic process;brain development;branched chain family amino acid catabolic process;branched chain family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone body metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;ketone body biosynthetic process;ketone body catabolic process;lipid metabolic process;liver development;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;metanephric proximal convoluted tubule development;nitrogen compound metabolic process;organ development;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;proximal convoluted tubule development;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to nutrient levels;response to organic cyclic compound;response to organic substance;response to starvation;response to stimulus;response to stress;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;tissue development "acetyl-CoA C-acetyltransferase activity;acetyl-CoA C-acyltransferase activity;acetyltransferase activity;binding;C-acetyltransferase activity;C-acyltransferase activity;catalytic activity;cation binding;coenzyme binding;cofactor binding;ion binding;metal ion binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part "Benzoate degradation;Butanoate metabolism;Carbon fixation pathways in prokaryotes;Fatty acid metabolism;Glyoxylate and dicarboxylate metabolism;Lysine degradation;Propanoate metabolism;Pyruvate metabolism;Synthesis and degradation of ketone bodies;Terpenoid backbone biosynthesis;Tryptophan metabolism;Two-component system;Valine, leucine and isoleucine degradation"

R4GMT0;P61163;F5H3I4;B4DXP9;P42025 Alpha-centractin;Beta-centractin ACTR1A;ACTR1B >tr|R4GMT0|R4GMT0_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=4 SV=1;>sp|P61163|ACTZ_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1;>tr|F5H3I4|F5H3I4_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=2 SV=1;>tr|B4DXP9|B4DXP9_HUMAN Alp 0.7 NaN NaN 1.11 NaN 1.02 1.08 NaN 6.88E-05 2 8.1 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cell cycle process;cellular process;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;transport;vesicle-mediated transport adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;dynactin complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex

O00116;B8ZZ81 "Alkyldihydroxyacetonephosphate synthase, peroxisomal" AGPS ">sp|O00116|ADAS_HUMAN Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1;>tr|B8ZZ81|B8ZZ81_HUMAN Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=2 SV=1" NaN NaN 1.29 NaN 1.31 NaN NaN NaN 5.04E-05 2 3.6 biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;ether lipid biosynthetic process;ether lipid metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;organic ether metabolic process;primary metabolic process;small molecule metabolic process "alkylglycerone-phosphate synthase activity;binding;catalytic activity;coenzyme binding;cofactor binding;FAD binding;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups;UDP-N-acetylmuramate dehydrogenase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part Ether lipid metabolism;Peroxisome

Q12904;Q12904-2;D6R937 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;Endothelial monocyte-activating polypeptide 2 AIMP1 >sp|Q12904|AIMP1_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2;>sp|Q12904-2|AIMP1_HUMAN Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=A 1.03 0.94 0.59 0.73 1.02 0.92 1.53 1.01 3.32E-17 2 7.7 alcohol metabolic process;amine metabolic process;amino acid activation;anatomical structure formation involved in morphogenesis;angiogenesis;apoptosis;biological adhesion;biological regulation;carbohydrate metabolic process;carboxylic acid metabolic process;cell adhesion;cell communication;cell death;cell migration;cell motility;cell-cell signaling;cellular amine metabolic process;cellular amino acid metabolic process;cellular carbohydrate metabolic process;cellular component movement;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chemotaxis;death;defense response;developmental process;glucose metabolic process;hexose metabolic process;immune system process;inflammatory response;leukocyte migration;locomotion;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;response to wounding;RNA metabolic process;signal transduction;signaling;small molecule metabolic process;taxis;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process binding;cell surface binding;cytokine activity;identical protein binding;nucleic acid binding;protein binding;protein dimerization activity;protein homodimerization activity;receptor binding;RNA binding;tRNA binding aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;extracellular region part;extracellular space;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;protein complex;transport vesicle;vesicle

J3QRD1;P51648;P51648-2;J3QS00;I3L1M4 Fatty aldehyde dehydrogenase ALDH3A2 >tr|J3QRD1|J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=3 SV=1;>sp|P51648|AL3A2_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1;>sp|P51648-2|AL3A2_HUMAN Isoform 2 of Fatty aldehyde dehydrogenase OS=Homo sa NaN NaN NaN NaN NaN NaN NaN NaN 0.00027123 2 5.6 alcohol metabolic process;anatomical structure development;cellular aldehyde metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;central nervous system development;developmental process;epidermis development;isoprenoid metabolic process;lipid metabolic process;metabolic process;peripheral nervous system development;phytol metabolic process;primary metabolic process;sesquiterpene metabolic process;sesquiterpenoid metabolic process;small molecule metabolic process;system development;terpene metabolic process;terpenoid metabolic process;tissue development "aldehyde dehydrogenase (NAD) activity;aldehyde dehydrogenase [NAD(P)+] activity;catalytic activity;long-chain-alcohol oxidase activity;long-chain-aldehyde dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, oxygen as acceptor" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microbody;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle membrane;organelle part;peroxisome "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Chloroalkane and chloroalkene degradation;Fatty acid metabolism;Glycerolipid metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Limonene and pinene degradation;Lysine degradation;Pentose and glucuronate interconversions;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation"

B4DXY7;P49189 4-trimethylaminobutyraldehyde dehydrogenase ALDH9A1 >tr|B4DXY7|B4DXY7_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=2 SV=1;>sp|P49189|AL9A1_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 0.14 4.48 NaN 2.59 NaN 1.75

0.31 1.13 6.69E-06 2 4.5 amine biosynthetic process;amine metabolic process;betaine biosynthetic process;betaine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carnitine biosynthetic process;carnitine metabolic process;cellular aldehyde metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;hormone metabolic process;metabolic process;neurotransmitter biosynthetic process;neurotransmitter metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of biological quality;regulation of hormone levels;regulation of neurotransmitter levels;small molecule biosynthetic process;small molecule metabolic process "1-pyrroline dehydrogenase activity;3-chloroallyl aldehyde dehydrogenase activity;4-trimethylammoniobutyraldehyde dehydrogenase activity;aminobutyraldehyde dehydrogenase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor"cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle;plasma membrane "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Fatty acid metabolism;Glycerolipid metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Lysine degradation;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation"

B4DT77;P20073-2;P20073 Annexin;Annexin A7 ANXA7 >tr|B4DT77|B4DT77_HUMAN Annexin OS=Homo sapiens GN=ANXA7 PE=2 SV=1;>sp|P20073-2|ANXA7_HUMAN Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7;>sp|P20073|ANXA7_HUMAN Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 NaN 0.83 NaN 0.24 NaN 2 NaN 0.57 2.09E-29 2 7.4 behavior;behavioral interaction between organisms;biological regulation;calcium ion homeostasis;cation homeostasis;cell proliferation;cell volume homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular water homeostasis;chemical homeostasis;divalent inorganic cation homeostasis;hemostasis;homeostatic process;ion homeostasis;metal ion homeostasis;multicellular organismal process;multi-organism process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to abiotic stimulus;response to osmotic stress;response to salt stress;response to stimulus;response to stress;social behavior;water homeostasis binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;ion binding;lipid binding;metal ion binding;phospholipid binding cell part;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;nuclear envelope;nuclear part;nucleus;organelle;organelle envelope;organelle membrane;organelle part;plasma membrane;vesicle

O76027 Annexin A9 ANXA9 >sp|O76027|ANXA9_HUMAN Annexin A9 OS=Homo sapiens GN=ANXA9 PE=1 SV=3 NaN NaN NaN 0.17 NaN 2.41 NaN NaN 2.12E-05 2 6.7 biological adhesion;cell adhesion;cell-cell adhesion;cellular process acetylcholine binding;acetylcholine receptor activity;amine binding;binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;identical protein binding;ion binding;lipid binding;metal ion binding;molecular transducer activity;neurotransmitter binding;neurotransmitter receptor activity;phosphatidylserine binding;phospholipid binding;protein binding;protein dimerization activity;protein homodimerization activity;receptor activity;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity cell part;cell surface;cytoplasmic part;cytosol;intracellular part

E5RJ68;O00203 AP-3 complex subunit beta-1 AP3B1 >tr|E5RJ68|E5RJ68_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=2 SV=1;>sp|O00203|AP3B1_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3 0.79 NaN 0.47 0.82 1.11 1.29 1.19 NaN 8.39E-05 2 2.1 "anterograde axon cargo transport;anterograde synaptic vesicle transport;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of lipid antigen via MHC class Ib;antigen processing and presentation via MHC class Ib;antigen processing and presentation, exogenous lipid antigen via MHC class Ib;axon cargo transport;biological regulation;blood coagulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;coagulation;cytoskeleton-dependent intracellular transport;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;hemostasis;immune system process;intracellular protein transport;intracellular transport;lysosomal transport;melanosome organization;membrane invagination;membrane organization;microtubule-based movement;microtubule-based process;microtubule-based transport;multicellular organismal process;organelle organization;pigment granule organization;positive regulation of alpha-beta T cell activation;positive regulation of alpha-beta T cell differentiation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of NK T cell differentiation;positive regulation of T cell activation;positive regulation of T cell differentiation;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;regulation of alpha-beta T cell activation;regulation of alpha-beta T cell differentiation;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell activation;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of NK T cell differentiation;regulation of T cell activation;regulation of T cell differentiation;synaptic vesicle transport;transport;vacuolar transport;vesicle organization;vesicle-mediated transport" AP-3 adaptor complex;AP-type membrane coat adaptor complex;cell part;clathrin coated vesicle membrane;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex;vesicle membrane Lysosome

Q9HDC9-2;H0Y512;Q9HDC9 Adipocyte plasma membrane-associated protein APMAP >sp|Q9HDC9-2|APMAP_HUMAN Isoform 2 of Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP;>tr|H0Y512|H0Y512_HUMAN Adipocyte plasma membrane-associated protein (Fragment) OS=Homo sapiens GN=APMAP PE=4 SV=1;>sp|Q9HDC9|APMAP_HUMAN Adipocyte NaN NaN NaN NaN NaN 0.77 NaN NaN 5.25E-05 2 7.3 biosynthetic process;metabolic process "amine-lyase activity;arylesterase activity;carbon-nitrogen lyase activity;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;lyase activity;strictosidine synthase activity" cell part;cell surface;integral to membrane;intrinsic to membrane;membrane;membrane part

P07741-2;H3BQF1;P07741;H3BSW3;H3BQZ9;H3BQB1 Adenine phosphoribosyltransferase APRT >sp|P07741-2|APT_HUMAN Isoform 2 of Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT;>tr|H3BQF1|H3BQF1_HUMAN Adenine phosphoribosyltransferase (Fragment) OS=Homo sapiens GN=APRT PE=2 SV=1;>sp|P07741|APT_HUMAN Adenine phosphoribosyltransferase OS=H NaN NaN 0.04 1.03 0.31 2.25 NaN NaN 2.35E-05 2 15.7 adenine biosynthetic process;adenine metabolic process;adenine salvage;AMP biosynthetic process;AMP metabolic process;AMP salvage;behavior;biological regulation;biosynthetic process;body fluid secretion;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;establishment of localization;grooming behavior;heterocycle biosynthetic process;heterocycle metabolic process;lactation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside salvage;nucleotide biosynthetic process;nucleotide metabolic process;nucleotide salvage;pigment biosynthetic process;pigment metabolic process;primary metabolic process;purine base biosynthetic process;purine base metabolic process;purine base salvage;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine nucleotide salvage;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleoside salvage;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;purine-containing compound salvage;regulation of biological quality;regulation of body fluid levels;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside biosynthetic process;ribonucleoside metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;small molecule metabolic process;transport "adenine binding;adenine phosphoribosyltransferase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;AMP binding;binding;catalytic activity;nucleobase binding;nucleotide binding;purine base binding;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Purine metabolism

P62330 ADP-ribosylation factor 6 ARF6 >sp|P62330|ARF6_HUMAN ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 1.13 NaN 1.02 0.7 1.11 1.57 0.91 NaN 3.60E-06 2 18.3 actin cytoskeleton organization;actin filament-based process;anatomical structure development;apoptosis;biological adhesion;biological regulation;cell adhesion;cell death;cell projection organization;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to stimulus;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;death;developmental process;establishment of cell polarity;establishment of epithelial cell polarity;establishment of localization;establishment of protein localization;establishment or maintenance of cell polarity;intracellular signal transduction;liver development;localization;macromolecule localization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of endocytosis;negative regulation of receptor-mediated endocytosis;negative regulation of transport;organ development;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of establishment of protein localization in plasma membrane;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;programmed cell death;protein localization;protein localization at cell surface;protein transport;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular localization;regulation of cellular process;regulation of cytoskeleton organization;regulation of dendrite development;regulation of dendritic spine development;regulation of developmental process;regulation of endocytosis;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of filopodium assembly;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organelle organization;regulation of protein complex assembly;regulation of protein localization;regulation of protein polymerization;regulation of Rac protein signal transduction;regulation of Ras protein signal transduction;regulation of receptor-mediated endocytosis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;ruffle organization;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell cortex;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome;endocytic vesicle;endosomal part;endosome;endosome membrane;filopodium membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane part;recycling endosome;ruffle;vesicle Endocytosis;Fc gamma R-mediated phagocytosis

O15145;F8VR50;C9JZD1 Actin-related protein 2/3 complex subunit 3 ARPC3 >sp|O15145|ARPC3_HUMAN Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3;>tr|F8VR50|F8VR50_HUMAN Actin-related protein 2/3 complex subunit 3 (Fragment) OS=Homo sapiens GN=ARPC3 PE=2 SV=1;>tr|C9JZD1|C9JZD1_HUMAN Actin-related pr 0.55 2.14 0.75 2.96 0.28 0.71 0.43 0.92 2.94E-48 2 11.2 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin nucleation;Arp2/3 complex-mediated actin nucleation;biological regulation;cellular component movement;cellular component organization;cellular component

organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stress structural constituent of cytoskeleton;structural molecule activity Arp2/3 protein complex;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;organelle part;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis
O15511;O15511-2;B1ALC0 Actin-related protein 2/3 complex subunit 5 ARPC5 >sp|O15511|ARPC5_HUMAN Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3;>sp|O15511-2|ARPC5_HUMAN Isoform 2 of Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5;>tr|B1ALC0|B1ALC0_HUMAN Actin-related protein 2 0.78 1.5 1.23 2.43 0.98 0.53 0.52 0.9 4.47E-56 2 14.6 actin cytoskeleton organization;actin filament-based process;biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stressstructural constituent of cytoskeleton;structural molecule activity Arp2/3 protein complex;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis
P56385 "ATP synthase subunit e, mitochondrial" ATP5I ">sp|P56385|ATP5I_HUMAN ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2" 0.87 1.61 1.81 1.35 0.43 0.53 0.7 0.82 1.01E-06 2 30.4 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity "cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle part;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain"Oxidative phosphorylation
Q15904 V-type proton ATPase subunit S1 ATP6AP1 >sp|Q15904|VAS1_HUMAN V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2 NaN NaN NaN NaN NaN NaN NaN NaN 3.10E-06 2 6 "ATP hydrolysis coupled proton transport;cation transport;cellular process;energy coupled proton transport, against electrochemical gradient;establishment of localization;hydrogen transport;ion transmembrane transport;ion transport;monovalent inorganic cation transport;proton transport;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to

membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain;proton-transporting V-type ATPase, V1 domain;vacuolar membrane;vacuolar part" Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

O75348;O95670-2;F2Z307;O95670;C9JRT2 V-type proton ATPase subunit G 1;V-type proton ATPase subunit G 2 ATP6V1G1;ATP6V1G2-DDX39B;ATP6V1G2 >sp|O75348|VATG1_HUMAN V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3;>sp|O95670-2|VATG2_HUMAN Isoform 2 of V-type proton ATPase subunit G 2 OS=Homo sapiens GN=ATP6V1G2;>tr|F2Z307|F2Z307_HUMAN Protein ATP6V1G2-DDX39B OS=Homo sapiens 0.8 1.35 1.23 0.97 0.89 1.29 0.81 1.28 5.77E-14 2 22 biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organelle organization;phagosome maturation;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport "catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;transmembrane transporter activity;transporter activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle part;pigment granule;plasma membrane;protein complex;proton-transporting two-sector ATPase complex;proton-transporting V-type ATPase complex;vacuolar part;vacuolar proton-transporting V-type ATPase complex;vesicle Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

O95817 BAG family molecular chaperone regulator 3 BAG3 >sp|O95817|BAG3_HUMAN BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 0.99 0.77 0.81 0.41 1.8 1.64 1.35 0.97 1.75E-10 2 4.7 anatomical structure development;apoptosis;biological regulation;brain development;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;developmental process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organ development;primary metabolic process;programmed cell death;protein folding;protein metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;spinal cord development cell part;cell projection;cytoplasmic part;cytosol;intracellular part;membrane;neuron projection;plasma membrane

Q9UIG0-2;Q9UIG0 Tyrosine-protein kinase BAZ1B BAZ1B >sp|Q9UIG0-2|BAZ1B_HUMAN Isoform 2 of Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B;>sp|Q9UIG0|BAZ1B_HUMAN Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2 1.21 1.25 NaN 3.16 NaN 0.28 0.38 0.38 0.00019029 2 1.8 "anatomical structure morphogenesis;ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin-mediated maintenance of transcription;chromosome organization;developmental process;DNA metabolic process;DNA repair;DNA replication-dependent nucleosome disassembly;DNA replication-dependent nucleosome organization;double-strand break repair;heart morphogenesis;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;organ morphogenesis;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of gene expression, epigenetic;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "acetylcholine receptor regulator activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;chromatin binding;histone acetyl-lysine binding;histone binding;histone kinase activity;ion binding;kinase activity;metal ion binding;non-membrane spanning protein tyrosine kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein complex scaffold;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activator activity;receptor regulator activity;ribonucleotide binding;structural molecule activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;vitamin D receptor activator activity;zinc ion binding" cell part;centromeric heterochromatin;chromatin;chromatin remodeling complex;chromosomal part;chromosome;condensed chromosome;heterochromatin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;organelle;organelle part;protein complex;SWI/SNF-type complex;WINAC complex

C9J1S9;C9J8G3;Q9Y276 Mitochondrial chaperone BCS1 BCS1L >tr|C9J1S9|C9J1S9_HUMAN Mitochondrial chaperone BCS1 (Fragment) OS=Homo sapiens GN=BCS1L PE=2 SV=1;>tr|C9J8G3|C9J8G3_HUMAN Mitochondrial chaperone BCS1 (Fragment) OS=Homo sapiens GN=BCS1L PE=2 SV=1;>sp|Q9Y276|BCS1_HUMAN Mitochondrial chaperone BCS1 OS=Homo NaN NaN 2.72 NaN 1.42 NaN NaN NaN 3.84E-05 2 16.7 cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytochrome complex assembly;macromolecular complex assembly;macromolecular complex subunit organization;mitochondrial respiratory chain complex assembly;mitochondrial respiratory chain complex I assembly;mitochondrial respiratory chain complex I biogenesis;mitochondrial respiratory chain complex III assembly;mitochondrial respiratory chain complex III biogenesis;mitochondrial respiratory chain complex IV assembly;mitochondrial respiratory chain complex IV biogenesis;NADH dehydrogenase complex assembly;protein complex assembly;protein complex biogenesis;protein complex subunit organization;respiratory chain complex III assembly;respiratory chain complex IV assembly "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex III;mitochondrion;organelle;organelle part;protein complex;respiratory chain complex III

A6NLG9;P21810;C9JKG1 Biglycan BGN >tr|A6NLG9|A6NLG9_HUMAN Biglycan OS=Homo sapiens GN=BGN PE=2 SV=1;>sp|P21810|PGS1_HUMAN Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2;>tr|C9JKG1|C9JKG1_HUMAN Biglycan (Fragment) OS=Homo sapiens GN=BGN PE=2 SV=1 NaN NaN NaN NaN NaN NaN NaN NaN 0.00019258 2 10.1 amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;biosynthetic process;blood vessel remodeling;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chondroitin sulfate biosynthetic process;chondroitin sulfate catabolic process;chondroitin sulfate metabolic process;dermatan sulfate biosynthetic process;dermatan sulfate metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;nitrogen compound metabolic process;peptide cross-linking;peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan;peptidyl-amino acid modification;peptidyl-serine modification;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;protein metabolic process;protein modification process;sulfur compound biosynthetic process;sulfur compound catabolic process;sulfur compound metabolic process;tissue remodeling binding;carbohydrate binding;extracellular matrix binding;extracellular matrix structural constituent;glycosaminoglycan binding;pattern binding;polysaccharide binding;structural molecule activity cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular matrix;extracellular region part;Golgi apparatus part;Golgi lumen;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;proteinaceous extracellular matrix;sarcolemma;transport vesicle;vacuolar lumen;vacuolar part;vesicle

Q9UKR5 Probable ergosterol biosynthetic protein 28 C14orf1 >sp|Q9UKR5|ERG28_HUMAN Probable ergosterol biosynthetic protein 28 OS=Homo sapiens GN=C14orf1 PE=1 SV=1 1.06 NaN 1.96 1.11 1.02 0.64 0.9 NaN 0.00028209 2 12.1 alcohol metabolic process;biosynthetic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;transport vesicle;vesicle

A8MQ03;B8A4K4 UPF0574 protein C9orf169 C9orf169 >sp|A8MQ03|CI169_HUMAN UPF0574 protein C9orf169 OS=Homo sapiens GN=C9orf169 PE=1 SV=1;>tr|B8A4K4|B8A4K4_HUMAN UPF0574 protein C9orf169 OS=Homo sapiens GN=C9orf169 PE=2 SV=1 NaN NaN 1.35 NaN 1.3 NaN NaN NaN 1.46E-11 2 25

Q9NZT1 Calmodulin-like protein 5 CALML5 >sp|Q9NZT1|CALL5_HUMAN Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2 NaN NaN NaN 7.98 NaN 1.44 NaN NaN 9.41E-06 2 24.7 anatomical structure development;biological regulation;cellular process;cellular response to stimulus;developmental process;epidermis development;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;tissue development binding;calcium ion binding;cation binding;ion binding;metal ion binding Alzheimer's disease;Calcium signaling pathway;Gastric acid secretion;Glioma;GnRH signaling pathway;Insulin signaling pathway;ko05152;Long-term potentiation;Melanogenesis;Neurotrophin signaling pathway;Olfactory transduction;Oocyte meiosis;Phosphatidylinositol signaling system;Phototransduction;Phototransduction - fly;Plant-pathogen interaction;Salivary secretion;Vascular smooth muscle contraction

Q13557-8;Q13557-12;Q13557-10;D6R938;Q13557;E9PBG7;Q13557-6;Q13557-11;E9PF82;H0Y9J2;Q13557-9;Q13557-5;Q13557-3;Q13557-4 Calcium/calmodulin-dependent protein kinase type II subunit delta CAMK2D >sp|Q13557-8|KCC2D_HUMAN Isoform Delta 6 of Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D;>sp|Q13557-12|KCC2D_HUMAN Isoform Delta 12 of Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo 0.94 0.58 0.18 0.37 1.73 2.63 1.45 1.25 3.60E-06 2 6.1 biological regulation;calcium ion transport;calcium-mediated signaling;cardiac muscle contraction;cation transport;cell communication;cell cycle process;cell surface receptor linked signaling pathway;cell-cell signaling;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;G1/S transition of mitotic cell cycle;interferon-gamma-mediated signaling pathway;intracellular signal transduction;ion transport;macromolecule metabolic process;macromolecule modification;metabolic process;metal ion transport;multicellular organismal process;muscle contraction;muscle system process;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cardiac muscle hypertrophy;positive regulation of multicellular organismal process;positive regulation of muscle hypertrophy;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cardiac muscle hypertrophy;regulation of cell growth;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of growth;regulation of heart contraction;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle adaptation;regulation of muscle contraction;regulation of muscle hypertrophy;regulation of muscle system process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of sodium ion transport;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;second-messenger-mediated signaling;signal transduction;signaling;striated muscle contraction;synaptic transmission;system process;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calmodulin-dependent protein kinase activity;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" axon part;calcium- and calmodulin-dependent protein kinase complex;cell body;cell junction;cell part;cell projection part;cell-cell contact zone;cell-cell junction;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endocytic vesicle membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;initial segment;intercalated disc;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;neuromuscular junction;neuronal cell body;nuclear part;nucleoplasm;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;sarcoplasmic reticulum membrane;synapse;T-tubule;vesicle membrane Calcium signaling pathway;ErbB signaling pathway;Gastric acid secretion;Glioma;GnRH signaling pathway;ko05152;Long-term potentiation;Melanogenesis;Neurotrophin signaling pathway;Olfactory transduction;Oocyte meiosis;Phototransduction - fly;Wnt signaling pathway

Q5T0R7;Q5T0R6;Q5T0R5;Q5T0R4;Q5T0R3;Q5T0R2;Q5T0R1;Q5T0R9;Q01518-2;Q01518;Q5T0R8;Q5T0S3 Adenylyl cyclase-associated protein 1 CAP1 >tr|Q5T0R7|Q5T0R7_HUMAN Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens GN=CAP1 PE=2 SV=1;>tr|Q5T0R6|Q5T0R6_HUMAN Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens GN=CAP1 PE=2 SV=1;>tr|Q5T0R5|Q5T0R5_HUMAN Adenylyl cyclase-a 1.03 0.36 0.72 0.31 1.81 0.97 2.15 1.29 5.03E-16 2 12.6 actin cytoskeleton organization;actin filament-based process;activation of adenylate cyclase activity;ameboidal cell migration;anatomical structure morphogenesis;axon guidance;biological regulation;cell activation;cell migration;cell morphogenesis;cell motility;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;endocytosis;establishment of localization;establishment of localization in cell;establishment or maintenance of cell polarity;exocytosis;locomotion;membrane invagination;membrane organization;organelle organization;platelet activation;platelet degranulation;positive regulation of adenylate cyclase activity;positive regulation of catalytic activity;positive regulation of cyclase activity;positive regulation of lyase activity;positive regulation of molecular function;receptor-mediated endocytosis;regulation of adenylate cyclase activity;regulation of biological process;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;response to chemical stimulus;response to external stimulus;response to stimulus;secretion;secretion by cell;signal transduction;taxis;transport;vesicle-mediated transport cell cortex part;cell part;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane

C9JUG7;B4DG50;F8W9N7;P47755;F8WED3 F-actin-capping protein subunit alpha-2 CAPZA2 >tr|C9JUG7|C9JUG7_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=2 SV=1;>tr|B4DG50|B4DG50_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=2 SV=1;>tr|F8W9N7|F8W9N7_HUMAN F-actin-capping protein subunit NaN 1.58 0.85 2.27 0.37 0.67 NaN 0.84 8.19E-34 2 15.1 actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;defense response;hemostasis;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;protein complex assembly;protein complex subunit organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to stimulus;response to stress cell cortex part;cell part;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular region;F-actin capping protein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;protein complex

Q13185;C9JMM0;B8ZZ43 Chromobox protein homolog 3 CBX3 ">sp|Q13185|CBX3_HUMAN Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4;>tr|C9JMM0|C9JMM0_HUMAN Chromobox protein homolog 3 (Fragment) OS=Homo sapiens GN=CBX3 PE=2 SV=1;>tr|B8ZZ43|B8ZZ43_HUMAN Chromobox homolog 3

(HP1 gamma homolog, Drosophila)" 1.26 1.08 1.82 2.28 0.5 0.42 0.82 0.87 7.99E-13 2 13.7 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "cell part;centromeric heterochromatin;chromatin;chromosomal part;chromosome, centromeric region;condensed chromosome, centromeric region;cytoskeletal part;euchromatin;heterochromatin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nuclear centromeric heterochromatin;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear heterochromatin;nuclear inner membrane;nuclear membrane;nuclear part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;spindle"

Q9H6F5;H0YG79;B4DY99 Coiled-coil domain-containing protein 86 CCDC86 >sp|Q9H6F5|CCD86_HUMAN Coiled-coil domain-containing protein 86 OS=Homo sapiens GN=CCDC86 PE=1 SV=1;>tr|H0YG79|H0YG79_HUMAN Coiled-coil domain-containing protein 86 (Fragment) OS=Homo sapiens GN=CCDC86 PE=4 SV=1;>tr|B4DY99|B4DY99_HUMAN Coiled-coil domain-c NaN NaN 0.7 NaN NaN NaN NaN NaN 0.00020456 2 5.8 interaction with host;interspecies interaction between organisms;multi-organism process;reproductive process;viral reproductive process;virus-host interaction cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

P27701-2;P27701;E9PJC7 CD82 antigen CD82 >sp|P27701-2|CD82_HUMAN Isoform 2 of CD82 antigen OS=Homo sapiens GN=CD82;>sp|P27701|CD82_HUMAN CD82 antigen OS=Homo sapiens GN=CD82 PE=1 SV=1;>tr|E9PJC7|E9PJC7_HUMAN CD82 antigen (Fragment) OS=Homo sapiens GN=CD82 PE=2 SV=1 NaN NaN 1.02 NaN 0.67 NaN NaN NaN 1.26E-10 2 10.7 cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part p53 signaling pathway

A6NNI4;P21926;G8JLH6;F5GXT1 CD9 antigen CD9 >tr|A6NNI4|A6NNI4_HUMAN CD9 antigen OS=Homo sapiens GN=CD9 PE=2 SV=1;>sp|P21926|CD9_HUMAN CD9 antigen OS=Homo sapiens GN=CD9 PE=1 SV=4;>tr|G8JLH6|G8JLH6_HUMAN CD9 antigen (Fragment) OS=Homo sapiens GN=CD9 PE=2 SV=1;>tr|F5GXT1|F5GXT1_HUMAN CD9 antigen (Frag 0.79 1.3 1.85 NaN 0.66 NaN 0.81 0.75 0.00020285 2 10.1 anatomical structure development;anatomical structure formation involved in morphogenesis;biological adhesion;biological regulation;brain development;cell activation;cell adhesion;cell development;cell junction assembly;cell junction organization;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane fusion;cellular membrane organization;cellular process;cellular process involved in reproduction;cellular process involved in reproduction in multicellular organism;developmental process;establishment of localization;establishment of localization in cell;exocytosis;fusion of sperm to egg plasma membrane;glial cell development;membrane fusion;membrane organization;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;oligodendrocyte development;organ development;paranodal junction assembly;plasma membrane fusion;platelet activation;platelet degranulation;regulation of biological process;regulation of cell proliferation;regulation of cellular process;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to stimulus;response to stress;response to water;response to water deprivation;secretion;secretion by cell;transport;vesicle-mediated transport apical plasma membrane;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;external side of plasma membrane;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;organelle membrane;organelle part;plasma membrane part;platelet alpha granule membrane;secretory granule membrane;vesicle membrane Hematopoietic cell lineage

P60953;E7ETU3;P60953-1 Cell division control protein 42 homolog CDC42 >sp|P60953|CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2;>tr|E7ETU3|E7ETU3_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=2 SV=1;>sp|P60953-1|CDC42_HUMAN Isoform 1 of Cell division contr 0.69 1.9 0.69 1.33 0.61 1.17 0.68 1.02 6.81E-14 2 13.6 actin cytoskeleton organization;actin filament branching;actin filament bundle assembly;actin filament organization;actin filament-based process;adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;axon guidance;biological adhesion;biological regulation;blood coagulation;canonical Wnt receptor signaling pathway;cardiac conduction system development;cell adhesion;cell communication;cell development;cell differentiation;cell fate determination;cell junction organization;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell junction organization;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to stimulus;chemotaxis;circulatory system process;coagulation;cytoskeleton organization;cytoskeleton-dependent intracellular transport;defense response;developmental process;ectodermal placode formation;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epithelial cell development;epithelial cell-cell adhesion;epithelial-mesenchymal cell signaling;establishment of Golgi localization;establishment of localization;establishment of localization in cell;establishment of nucleus localization;establishment of organelle localization;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;filopodium assembly;Golgi organization;growth;hair cycle process;hair follicle morphogenesis;hair follicle placode formation;heart contraction;heart process;hemostasis;immune response;immune system process;innate immune response;intracellular signal transduction;intracellular transport;keratinization;keratinocyte development;leukocyte differentiation;localization;locomotion;lymphocyte costimulation;macromolecule localization;macrophage differentiation;microspike assembly;microtubule-based movement;microtubule-based process;microtubule-based transport;molting cycle;molting cycle process;multicellular organism growth;multicellular organismal process;muscle cell differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein complex assembly;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;neuron fate determination;nuclear migration;organelle organization;organelle transport along microtubule;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell cycle cytokinesis;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokinesis;positive regulation of developmental process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of gene expression;positive regulation of hair follicle cell proliferation;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JNK cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of metalloenzyme activity;positive regulation of molecular function;positive regulation of muscle cell differentiation;positive regulation of neuron apoptosis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidyl-serine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein transport;positive regulation of pseudopodium assembly;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of synapse structural plasticity;positive regulation of T cell activation;positive regulation of transferase activity;positive regulation of transport;posttranscriptional regulation of gene expression;protein localization;regulation of apoptosis;regulation of attachment of spindle microtubules to kinetochore;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell cycle cytokinesis;regulation of cell cycle process;regulation of cell death;regulation of cell differentiation;regulation of cell division;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome segregation;regulation of cytokinesis;regulation of cytoskeleton organization;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of epidermal growth factor receptor signaling pathway;regulation of establishment of protein localization;regulation of filopodium assembly;regulation of gene expression;regulation of hair follicle cell proliferation;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JNK cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of metalloenzyme activity;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of mitosis;regulation of mitotic cell cycle;regulation of molecular function;regulation of muscle cell differentiation;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein binding;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein heterodimerization activity;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein transport;regulation of pseudopodium assembly;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of stress-activated protein kinase signaling cascade;regulation of synapse organization;regulation of synapse structural plasticity;regulation of T cell activation;regulation of transferase activity;regulation of transport;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;signal transduction;signaling;small GTPase mediated signal transduction;sprouting angiogenesis;submandibular salivary gland formation;system process;T cell costimulation;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;Wnt receptor signaling pathway "binding;catalytic activity;enzyme binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;kinase binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein kinase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" apical part of cell;cell body;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;filopodium;Golgi apparatus part;Golgi membrane;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;midbody;mitotic spindle;neuron projection;neuronal cell body;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;spindle;spindle midzone;stored secretory granule;vesicle Adherens junction;Axon guidance;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Endocytosis;Epithelial cell signaling in Helicobacter pylori infection;Fc gamma R-mediated phagocytosis;Focal adhesion;GnRH signaling pathway;Leukocyte transendothelial migration;MAPK signaling pathway;MAPK signaling pathway - yeast;Neurotrophin signaling pathway;Pancreatic cancer;Pathogenic Escherichia coli infection;Pathways in cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;T cell receptor signaling pathway;Tight junction;VEGF signaling pathway

P49454 Centromere protein F CENPF >sp|P49454|CENPF_HUMAN Centromere protein F OS=Homo sapiens GN=CENPF PE=1 SV=2 NaN NaN 0.91 NaN 1.2 NaN NaN NaN 0.00094264 2 0.6 "anaphase;anatomical structure development;biological regulation;biosynthetic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell differentiation;cell division;cell proliferation;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;chromosome organization;developmental process;DNA metabolic process;DNA replication;establishment of chromosome localization;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of protein localization;G2 phase;G2 phase of mitotic cell cycle;kinetochore assembly;kinetochore organization;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;metaphase plate congression;mitotic anaphase;mitotic cell cycle checkpoint;mitotic cell cycle spindle assembly checkpoint;mitotic cell cycle spindle checkpoint;mitotic prometaphase;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitosis;negative regulation of mitotic metaphase/anaphase transition;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear division;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle assembly;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of G2/M transition of mitotic cell cycle;regulation of gene expression;regulation of interphase of mitotic cell cycle;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic metaphase/anaphase transition;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of striated muscle tissue development;regulation of transcription, DNA-dependent;response to chemical stimulus;response to drug;response to stimulus;spindle assembly checkpoint;spindle checkpoint;transport" binding;chromatin binding;dynein binding;protein binding cell part;chromosomal part;condensed chromosome outer kinetochore;cytoplasmic part;cytoskeletal part;cytosol;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;midbody;nuclear envelope;nuclear matrix;nuclear part;nucleus;organelle;organelle envelope;organelle part;perinuclear region of cytoplasm;pronucleus;protein complex;spindle pole

O14646-2;O14646 Chromodomain-helicase-DNA-binding protein 1 CHD1 >sp|O14646-2|CHD1_HUMAN Isoform 2 of Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1;>sp|O14646|CHD1_HUMAN Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens GN=CHD1 PE=1 SV=2 NaN 53.72 NaN NaN NaN NaN NaN 2.26 8.26E-07 2 2 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;histone binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;methylated histone residue binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q14011;K7ELV6;K7ENX8;K7EJV5;K7ELT6;K7EMY9;K7EPM4;K7ER40;K7EQR7;B4E2X2;D6W5Y5 Cold-inducible RNA-binding protein CIRBP >sp|Q14011|CIRBP_HUMAN Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=1 SV=1;>tr|K7ELV6|K7ELV6_HUMAN Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens GN=CIRBP PE=4 SV=1;>tr|K7ENX8|K7ENX8_HUMAN Cold-inducible RNA-binding protein NaN NaN 2.22 NaN 0.92 NaN NaN NaN 1.06E-06 2 14.5 biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA stabilization;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of translation;response to abiotic stimulus;response to cold;response to light stimulus;response to radiation;response to stimulus;response to stress;response to temperature stimulus;response to UV;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA stabilization;stress granule assembly binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;rRNA binding;SSU rRNA binding;translation regulator activity;translation repressor activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;RNA granule;stress granule

G3V4N7;P12277;G3V461 Creatine kinase B-type CKB >tr|G3V4N7|G3V4N7_HUMAN Creatine kinase B-type (Fragment) OS=Homo sapiens GN=CKB PE=2 SV=1;>sp|P12277|KCRB_HUMAN Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1;>tr|G3V461|G3V461_HUMAN Creatine kinase B-type (Fragment) OS=Homo sapiens GN=CKB PE=2 S NaN 2.52 NaN NaN NaN NaN NaN 1.11 1.58E-07 2 12.4 amine metabolic process;anatomical structure development;anion homeostasis;biological regulation;brain development;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular anion homeostasis;cellular chemical homeostasis;cellular chloride ion homeostasis;cellular homeostasis;cellular ion homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular monovalent inorganic anion homeostasis;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;chloride ion homeostasis;creatine metabolic process;developmental process;homeostatic process;ion homeostasis;metabolic process;monovalent inorganic anion homeostasis;nitrogen compound metabolic process;organ development;organic acid metabolic process;oxoacid metabolic process;phosphagen metabolic process;primary metabolic process;regulation of biological quality;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;creatine kinase activity;kinase activity;nucleotide binding;phosphotransferase activity, nitrogenous group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Arginine and proline metabolism

J3KP58;F5H0N7;P30622-2;P30622-1;P30622;F5H6A0 CAP-Gly domain-containing linker protein 1 CLIP1 >tr|J3KP58|J3KP58_HUMAN CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1 PE=4 SV=1;>tr|F5H0N7|F5H0N7_HUMAN CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1 PE=2 SV=1;>sp|P30622-2|CLIP1_HUMAN Isoform 3 of CAP-Gly domain NaN NaN 0.25 NaN 4.26 NaN NaN NaN 9.16E-05 2 3.4 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;M phase;M phase of mitotic cell cycle;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;organelle organization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of microtubule polymerization;positive regulation of microtubule polymerization or depolymerization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;transport binding;cation binding;cytoskeletal protein binding;identical protein binding;ion binding;metal ion binding;microtubule binding;microtubule plus-end binding;nucleic acid binding;protein binding;protein dimerization activity;protein homodimerization activity;transition metal ion binding;tubulin binding;zinc ion binding cell part;cell projection;centrosome;chromosomal part;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endosome;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane-bounded organelle;microtubule;microtubule organizing center;microtubule plus end;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex;ruffle;vesicle membrane

O76031 "ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial" CLPX ">sp|O76031|CLPX_HUMAN ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2" NaN NaN 1.24 NaN 0.58 NaN NaN NaN 6.99E-05 2 3.3 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;peptidase activator activity;peptidase regulator activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endopeptidase Clp complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial endopeptidase Clp complex;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;protein complex Cell cycle - Caulobacter

Q12860-2;Q12860;H0YIJ1;Q12860-3 Contactin-1 CNTN1 >sp|Q12860-2|CNTN1_HUMAN Isoform 2 of Contactin-1 OS=Homo sapiens GN=CNTN1;>sp|Q12860|CNTN1_HUMAN Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1;>tr|H0YIJ1|H0YIJ1_HUMAN Contactin-1 (Fragment) OS=Homo sapiens GN=CNTN1 PE=2 SV=1;>sp|Q12860-3|CNTN1_HUMAN Isof NaN NaN 0.97 NaN 2.86 NaN NaN NaN 0.00084369 2 1.9 anatomical structure development;axon guidance;biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cerebellum development;chemotaxis;developmental process;locomotion;Notch signaling pathway;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of gene expression;positive regulation of ion transport;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of neuron projection development;positive regulation of sodium ion transport;positive regulation of transport;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of ion transport;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of sodium ion transport;regulation of transport;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis binding;carbohydrate binding anchored to membrane;cell part;intrinsic to membrane;membrane;membrane part;plasma membrane Cell adhesion molecules (CAMs)

H0YHL7;B4E3S0;Q9ULV4;A7MAP0;A7MAP1 Coronin;Coronin-1C CORO1C >tr|H0YHL7|H0YHL7_HUMAN Coronin-1C (Fragment) OS=Homo sapiens GN=CORO1C PE=2 SV=1;>tr|B4E3S0|B4E3S0_HUMAN Coronin OS=Homo sapiens GN=CORO1C PE=2 SV=1;>sp|Q9ULV4|COR1C_HUMAN Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1;>tr|A7MAP0|A7MAP0_HUMAN Coronin OS=H 1.79 0.71 NaN NaN NaN NaN 1.03 0.89 0.00021261 2 13.3 actin cytoskeleton organization;actin filament-based process;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular response to stimulus;cytoskeleton organization;endocytosis;establishment of localization;membrane invagination;membrane organization;organelle organization;phagocytosis;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;transport;vesicle-mediated transport actin binding;actin filament binding;binding;cytoskeletal protein binding;protein binding actin cytoskeleton;cell part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P10606 "Cytochrome c oxidase subunit 5B, mitochondrial" COX5B ">sp|P10606|COX5B_HUMAN Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2" 1.17 1.71 1.24 1.76 0.34 0.43 0.62 1.06 2.72E-08 2 17.8 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;multicellular organismal process;oxidation-reduction process;respiratory electron transport chain;respiratory gaseous exchange;small molecule metabolic process "binding;catalytic activity;cation binding;cation transmembrane transporter activity;cytochrome-c oxidase activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P09669 Cytochrome c oxidase subunit 6C COX6C >sp|P09669|COX6C_HUMAN Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2 1.32 1.49 1.39 2.22 0.85 0.52 0.62 0.89 3.08E-05 2 20 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process "catalytic activity;cation transmembrane transporter activity;cytochrome-c oxidase activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P14406;D6RIE3;D6RGV5;H0UI06;D6R9C3 "Cytochrome c oxidase subunit 7A2, mitochondrial" COX7A2 ">sp|P14406|CX7A2_HUMAN Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=1 SV=1;>tr|D6RIE3|D6RIE3_HUMAN Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=2 SV=1;>tr|D6RGV5|D6RGV5_HUMAN Cytochrome c oxid" 1.44 1.65 1.15 1.63 0.52 0.65 0.65 1.04 3.40E-32 2 27.7 "catalytic activity;cation transmembrane transporter activity;cytochrome-c oxidase activity;electron carrier activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain;organelle part;respiratory chain Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

E5RJZ1;H0YBD2;O14548 "Cytochrome c oxidase subunit 7A-related protein, mitochondrial" COX7A2L ">tr|E5RJZ1|E5RJZ1_HUMAN Cytochrome c oxidase subunit 7A-related protein, mitochondrial OS=Homo sapiens GN=COX7A2L PE=2 SV=1;>tr|H0YBD2|H0YBD2_HUMAN Cytochrome c oxidase subunit 7A-related protein, mitochondrial (Fragment) OS=Homo sapiens GN=COX7A2L PE=2 SV" 1.56 1.76 1.45 1.83 0.31 0.73 0.65 1.32 1.26E-05 2 38 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process "catalytic activity;cation transmembrane transporter activity;cytochrome-c oxidase activity;electron carrier activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain;organelle inner membrane;organelle membrane;organelle part;respiratory chain Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

D6R9Z7;P15954 "Cytochrome c oxidase subunit 7C, mitochondrial" COX7C ">tr|D6R9Z7|D6R9Z7_HUMAN Cytochrome c oxidase subunit 7C, mitochondrial OS=Homo sapiens GN=COX7C PE=2 SV=1;>sp|P15954|COX7C_HUMAN Cytochrome c oxidase subunit 7C, mitochondrial OS=Homo sapiens GN=COX7C PE=1 SV=1" 1.06 NaN 1.6 NaN 0.48 NaN 0.62 NaN 6.84E-05 2 32.1 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process "catalytic activity;cation transmembrane transporter activity;cytochrome-c oxidase activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

B4DJV2;O75390;F8W642;F8VZK9;F8VX07;F8VRP1;F8VX68;H0YIC4;F8VPF9;F8VPA1;F8VTT8;F8W1S4;F8W4S1;H0YH82 "Citrate synthase;Citrate synthase, mitochondrial" CS ">tr|B4DJV2|B4DJV2_HUMAN Citrate synthase OS=Homo sapiens GN=CS PE=2 SV=1;>sp|O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2;>tr|F8W642|F8W642_HUMAN Citrate synthase, mitochondrial (Fragment) OS=Homo sapiens GN=CS PE=2 SV=" NaN NaN 0.25 1.61 1.08 2.26 NaN NaN 2.46E-11 2 6 acetyl-CoA catabolic process;acetyl-CoA metabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;citrate (Si)-synthase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism

H0Y9X2;P48729;P48729-2 Casein kinase I isoform alpha CSNK1A1 >tr|H0Y9X2|H0Y9X2_HUMAN Casein kinase I isoform alpha (Fragment) OS=Homo sapiens GN=CSNK1A1 PE=4 SV=1;>sp|P48729|KC1A_HUMAN Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2;>sp|P48729-2|KC1A_HUMAN Isoform 2 of Casein kinase I isoform alph 1.02 1.32 1.23 1.44 0.51 0.6 0.68 0.82 3.94E-10 2 18 biological regulation;cell cycle phase;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;mitosis;nuclear division;organelle fission;organelle organization;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;Wnt receptor signaling pathway "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;centrosome;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;microtubule organizing center;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part;protein complex Hedgehog signaling pathway;Wnt signaling pathway

D6REM4;E7ETM0;Q71TU5 CSNK1A1 ">tr|D6REM4|D6REM4_HUMAN Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=2 SV=1;>tr|E7ETM0|E7ETM0_HUMAN Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=2 SV=1;>tr|Q71TU5|Q71TU5_HUMAN Casein kinase 1, alpha 1, isoform CRA_g OS=Homo sa" NaN NaN NaN NaN NaN NaN NaN NaN 1.15E-05 2 12.7 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" Hedgehog signaling pathway;Wnt signaling pathway

P48730-2;P48730;H7BYT1;J3KRM8;H0Y645;B0QY35;B0QY34;P49674 Casein kinase I isoform delta;Casein kinase I isoform epsilon CSNK1D;CSNK1E>sp|P48730-2|KC1D_HUMAN Isoform 2 of Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D;>sp|P48730|KC1D_HUMAN Casein kinase I isoform delta OS=Homo sapiens GN=CSNK1D PE=1 SV=2;>tr|H7BYT1|H7BYT1_HUMAN Casein kinase I isoform delta OS=Homo sapiens GN=CS 1.32 1.37 1.22 1.75 1 0.71 0.57 0.67 5.31E-05 2 6.1 biological regulation;cell cycle process;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular response to stimulus;cellular response to stress;circadian regulation of gene expression;circadian rhythm;cytoskeleton organization;DNA metabolic process;DNA repair;G2/M transition of mitotic cell cycle;localization;macromolecule localization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle assembly;organelle organization;positive regulation of biological process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of proteolysis;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of Wnt receptor signaling pathway;primary metabolic process;protein localization;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of circadian rhythm;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of proteolysis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of Wnt receptor signaling pathway;response to DNA damage stimulus;response to stimulus;response to stress;rhythmic process;signal transduction;spindle assembly;spindle organization;Wnt receptor signaling pathway "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;tau-protein kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex;ribonucleoprotein complex;spindle microtubule Circadian rhythm - fly;Circadian rhythm - mammal;Gap junction;Hedgehog signaling pathway;Wnt signaling pathway

H7C469;P07339;H7C1V0;F8WD96;C9JH19 Cathepsin D;Cathepsin D light chain;Cathepsin D heavy chain CTSD >tr|H7C469|H7C469_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=3 SV=1;>sp|P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1;>tr|H7C1V0|H7C1V0_HUMAN Cathepsin D light chain (Fragment) OS=Homo sapiens GN=CTSD PE=2 SV=1;>tr|F8WD96 0.83 0.55 0.54 0.29 2.93 1.37 2.48 1.05 6.83E-05 2 7.4 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;autophagic vacuole assembly;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;death;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune system process;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;organelle assembly;organelle organization;primary metabolic process;protein metabolic process;proteolysis;response to biotic stimulus;response to stimulus;vacuole organization "aspartic-type endopeptidase activity;aspartic-type peptidase activity;catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular region part;extracellular space;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal lumen;lysosome;lytic vacuole;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrion;organelle;organelle lumen;organelle part;pigment granule;vacuolar lumen;vacuolar part;vacuole;vesicle ko05152;Lysosome

Q13620-3;Q13620-1;K4DI93;Q13620;A6NE76;Q13619-2;Q13619 Cullin-4B;Cullin-4A CUL4B;CUL4A ">sp|Q13620-3|CUL4B_HUMAN Isoform 3 of Cullin-4B OS=Homo sapiens GN=CUL4B;>sp|Q13620-1|CUL4B_HUMAN Isoform 2 of Cullin-4B OS=Homo sapiens GN=CUL4B;>tr|K4DI93|K4DI93_HUMAN Cullin 4B, isoform CRA_e OS=Homo sapiens GN=CUL4B PE=3 SV=1;>sp|Q13620|CUL4B_HUMAN Cul" NaN NaN 0.14 NaN 0.11 NaN NaN NaN 0.00023308 2 3.2 biological regulation;catabolic process;cell cycle;cell cycle arrest;cell cycle process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;G1/S transition of mitotic cell cycle;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multi-organism process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell proliferation;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell cycle;positive regulation of cell cycle process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitotic cell cycle;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of S phase of mitotic cell cycle;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catabolic process;regulation of cell cycle;regulation of cell cycle process;regulation of cell proliferation;regulation of cellular process;regulation of interphase of mitotic cell cycle;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of S phase;regulation of S phase of mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;ubiquitin-dependent protein catabolic process;viral reproductive process;virus-host interaction cell part;CUL4 RING ubiquitin ligase complex;Cul4A-RING ubiquitin ligase complex;Cul4B-RING ubiquitin ligase complex;cullin-RING ubiquitin ligase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane;protein complex;ubiquitin ligase complex Nucleotide excision repair;Ubiquitin mediated proteolysis

P39880-2;P39880;P39880-3;P39880-4;P39880-5;O14529 Homeobox protein cut-like 1;Homeobox protein cut-like 2 CUX1;CUX2 >sp|P39880-2|CUX1_HUMAN Isoform 2 of Homeobox protein cut-like 1 OS=Homo sapiens GN=CUX1;>sp|P39880|CUX1_HUMAN Homeobox protein cut-like 1 OS=Homo sapiens GN=CUX1 PE=1 SV=3;>sp|P39880-3|CUX1_HUMAN Isoform 3 of Homeobox protein cut-like 1 OS=Homo sapiens GN 0.9 0.71 NaN 0.33 NaN 1.98 1.42 1.12 0.00085104 2 1.2 "anatomical structure development;auditory receptor cell differentiation;biological regulation;biosynthetic process;cell differentiation;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;developmental process;establishment of localization;establishment of localization in cell;Golgi vesicle transport;inner ear receptor cell differentiation;intracellular transport;intra-Golgi vesicle-mediated transport;lung development;macromolecule biosynthetic process;macromolecule metabolic process;mechanoreceptor differentiation;metabolic process;multicellular organismal development;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;neuron differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to organic substance;response to stimulus;retrograde transport, vesicle recycling within Golgi;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;transport;vesicle-mediated transport"   binding;chromatin binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity   cell part;cytoplasmic part;cytosol;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part

H3BUX2;O43169;J3KNF8;D6RFH4   Cytochrome b5 type B   CYB5B   >tr|H3BUX2|H3BUX2_HUMAN Cytochrome b5 type B OS=Homo sapiens GN=CYB5B PE=2 SV=1;>sp|O43169|CYB5B_HUMAN Cytochrome b5 type B OS=Homo sapiens GN=CYB5B PE=1 SV=2;>tr|J3KNF8|J3KNF8_HUMAN Cytochrome b5 type B OS=Homo sapiens GN=CYB5B PE=3 SV=1;>tr|D6RFH4|D6RFH4 1.01 1.52 1.21 0.69 0.65 0.62 0.85 0.99 2.55E-20 2   22.1 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process   binding;cation binding;enzyme activator activity;enzyme regulator activity;heme binding;ion binding;iron ion binding;metal ion binding;tetrapyrrole binding;transition metal ion binding   cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane

P08574   "Cytochrome c1, heme protein, mitochondrial"   CYC1   ">sp|P08574|CY1_HUMAN Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3" 0.91 1.39 1.66 1.99 11.8 0.48 0.53 0.9   0.00050416   2   4.9   cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process "binding;cation binding;electron carrier activity;electron transporter, transferring electrons from CoQH2-cytochrome c reductase complex and cytochrome c oxidase complex activity;heme binding;ion binding;iron ion binding;metal ion binding;tetrapyrrole binding;transition metal ion binding"   cell junction;cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;respiratory chain   Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q16850-2;Q16850;H7C0D0 Lanosterol 14-alpha demethylase   CYP51A1   >sp|Q16850-2|CP51A_HUMAN Isoform 2 of Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1;>sp|Q16850|CP51A_HUMAN Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1 PE=1 SV=3;>tr|H7C0D0|H7C0D0_HUMAN Lanosterol 14-alpha demethylase (Fragment) NaN NaN 1.24 NaN 1.01 NaN NaN NaN 1.25E-05 2   12.4 "alcohol metabolic process;biosynthetic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol biosynthetic process via 24,25-dihydrolanosterol;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;xenobiotic metabolic process"   "binding;catalytic activity;cation binding;demethylase activity;electron carrier activity;heme binding;ion binding;iron ion binding;metal ion binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;sterol 14-demethylase activity;tetrapyrrole binding;transition metal ion binding"   cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part   Steroid biosynthesis

F5H895;F5GXX5;P61803   Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 DAD1   >tr|F5H895|F5H895_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=2 SV=1;>tr|F5GXX5|F5GXX5_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD   1.18 1.21 1.98 0.81 0.75 0.56 1.03 1.08 8.21E-35 2   33.8 anatomical structure development;apoptosis;biological regulation;blastocyst development;carbohydrate metabolic process;cell death;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;developmental process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;programmed cell death;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to chemical stimulus;response to drug;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to stimulus   "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups"   cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;oligosaccharyltransferase complex;organelle part;protein complex   N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis

Q9NV06;Q9NV06-2;E5RJ28;E5RHM4;E7EVM5   DDB1- and CUL4-associated factor 13 DCAF13 >sp|Q9NV06|DCA13_HUMAN DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13 PE=1 SV=2;>sp|Q9NV06-2|DCA13_HUMAN Isoform 2 of DDB1- and CUL4-associated factor 13 OS=Homo sapiens GN=DCAF13;>tr|E5RJ28|E5RJ28_HUMAN

DDB1- and CUL4-associated factor 13 O NaN NaN 1.55 NaN 0.86 NaN NaN NaN 4.91E-05 2 5.2 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;CUL4 RING ubiquitin ligase complex;cullin-RING ubiquitin ligase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex;ribonucleoprotein complex;ubiquitin ligase complex

P81605;P81605-2 Dermcidin;Survival-promoting peptide;DCD-1 DCD >sp|P81605|DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2;>sp|P81605-2|DCD_HUMAN Isoform 2 of Dermcidin OS=Homo sapiens GN=DCD 0.43 7.84 0.05 14.52 0.34 0.76 0.11 1.48 7.55E-11 2 20 cell killing;defense response;defense response to bacterium;defense response to fungus;killing of cells of other organism;macromolecule metabolic process;metabolic process;multi-organism process;primary metabolic process;protein metabolic process;proteolysis;response to bacterium;response to biotic stimulus;response to fungus;response to other organism;response to stimulus;response to stress catalytic activity;hydrolase activity;peptidase activity extracellular region

Q8TDD1;Q8TDD1-2;H0YHH7 ATP-dependent RNA helicase DDX54 DDX54 >sp|Q8TDD1|DDX54_HUMAN ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2;>sp|Q8TDD1-2|DDX54_HUMAN Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54;>tr|H0YHH7|H0YHH7_HUMAN ATP-dependent RNA helicase DDX54 (Fragment) O NaN NaN 1.12 NaN 1.66 NaN NaN NaN 7.42E-05 2 2 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;estrogen receptor signaling pathway;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;signal transduction;steroid hormone receptor signaling pathway;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;estrogen receptor binding;helicase activity;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;steroid hormone receptor binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity" cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part

P26196 Probable ATP-dependent RNA helicase DDX6 DDX6 >sp|P26196|DDX6_HUMAN Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 NaN 1.52 0.64 1.33 0.7 1.04 NaN 0.85 7.62E-06 2 5.6 "catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoplasmic mRNA processing body assembly;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;gene expression;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA catabolic process;RNA metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity" cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;RNA granule;RNAi effector complex;RNA-induced silencing complex;stress granule RNA degradation

E9PNR5;O75907 Diacylglycerol O-acyltransferase 1DGAT1 >tr|E9PNR5|E9PNR5_HUMAN Diacylglycerol O-acyltransferase 1 OS=Homo sapiens GN=DGAT1 PE=2 SV=1;>sp|O75907|DGAT1_HUMAN Diacylglycerol O-acyltransferase 1 OS=Homo sapiens GN=DGAT1 PE=1 SV=2 0.91 NaN 1.62 NaN 0.75 NaN 0.62 NaN 1.57E-10 2 11.8 acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular metabolic process;cellular process;chemical homeostasis;coenzyme metabolic process;cofactor metabolic process;diacylglycerol metabolic process;fatty acid homeostasis;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;homeostatic process;lipid biosynthetic process;lipid homeostasis;lipid localization;lipid metabolic process;lipid storage;localization;long-chain fatty-acyl-CoA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;metabolic process;multicellular organismal process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic ether metabolic process;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;plasma lipoprotein particle assembly;plasma lipoprotein particle organization;primary metabolic process;protein-lipid complex assembly;protein-lipid complex subunit organization;regulation of biological quality;small molecule metabolic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process;very-low-density lipoprotein particle assembly "2-acylglycerol O-acyltransferase activity;acylglycerol O-acyltransferase activity;catalytic activity;diacylglycerol O-acyltransferase activity;O-acyltransferase activity;retinol O-fatty-acyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Fat digestion and absorption;Glycerolipid metabolism;Retinol metabolism

Q9Y394-2;Q9Y394;H0YJE4;H0YJ66 Dehydrogenase/reductase SDR family member 7 DHRS7 >sp|Q9Y394-2|DHRS7_HUMAN Isoform 2 of Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7;>sp|Q9Y394|DHRS7_HUMAN Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7 PE=1 SV=1;>tr|H0YJE4|H0YJE4_HUMAN Dehydrogenase/reductase NaN NaN NaN 0.16 NaN 2.54 NaN NaN 1.09E-05 2 10.7 metabolic process;oxidation-reduction process catalytic activity;oxidoreductase activity

P31689-2;P31689 DnaJ homolog subfamily A member 1 DNAJA1 >sp|P31689-2|DNJA1_HUMAN Isoform 2 of DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1;>sp|P31689|DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2 1.27 NaN NaN NaN NaN NaN 0.79 NaN 1.35E-05 2 7.3 androgen receptor signaling pathway;biological regulation;cell motility;cellular component movement;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;gamete generation;intracellular receptor mediated signaling pathway;locomotion;macromolecule metabolic process;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to heat;response to organic substance;response to stimulus;response to stress;response to temperature stimulus;response to topologically incorrect protein;response to unfolded protein;signal transduction;sperm motility;spermatogenesis;steroid hormone receptor signaling pathwayadenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cation binding;ion binding;lipoprotein particle receptor binding;low-density lipoprotein particle receptor binding;metal ion binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding cell part;membrane Protein processing in endoplasmic reticulum

O60884 DnaJ homolog subfamily A member 2 DNAJA2 >sp|O60884|DNJA2_HUMAN DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1 NaN 1.27 0.74 NaN 0.95 NaN NaN 0.78 1.38E-09 2 9.5 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cation binding;ion binding;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;membrane Protein processing in endoplasmic reticulum

Q96EY1-2;Q96EY1 "DnaJ homolog subfamily A member 3, mitochondrial" DNAJA3 ">sp|Q96EY1-2|DNJA3_HUMAN Isoform 2 of DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3;>sp|Q96EY1|DNJA3_HUMAN DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3 PE=1 SV=2" 1.1 1.2 1.12 1.43 0.76 0.41 0.71 0.62 5.46E-25 2 6.2 "activation of caspase activity;activation-induced cell death of T cells;aging;apoptosis;biological regulation;biosynthetic process;cell activation;cell aging;cell death;cell differentiation;cellular biosynthetic process;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to stimulus;death;developmental process;DNA metabolic process;DNA replication;DNA-dependent DNA replication;embryo development;immune system process;intracellular signal transduction;leukocyte activation;leukocyte apoptosis;leukocyte differentiation;localization;lymphocyte activation;lymphocyte apoptosis;lymphocyte differentiation;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial DNA metabolic process;mitochondrial DNA replication;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine-mediated signaling pathway;negative regulation of gene expression;negative regulation of hydrolase activity;negative regulation of I-kappaB kinase/NF-kappaB cascade;negative regulation of interferon-gamma-mediated signaling pathway;negative regulation of intracellular protein kinase cascade;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of response to cytokine stimulus;negative regulation of response to interferon-gamma;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;neuromuscular junction development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of hydrolase activity;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of leukocyte proliferation;positive regulation of lymphocyte activation;positive regulation of lymphocyte proliferation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of mononuclear cell proliferation;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of T cell activation;positive regulation of T cell proliferation;postsynaptic membrane organization;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein folding;protein localization;protein localization in membrane;protein metabolic process;protein stabilization;receptor clustering;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-gamma-mediated signaling pathway;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein ubiquitination;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of T cell activation;regulation of T cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;response to abiotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to heat;response to interferon-gamma;response to organic substance;response to stimulus;response to stress;response to temperature stimulus;signal transduction;skeletal muscle nicotinic acetylcholine receptor clustering;small GTPase mediated signal transduction;synapse organization;T cell activation;T cell apoptosis;T cell differentiation;T cell differentiation in thymus" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cation binding;cytokine receptor binding;enzyme regulator activity;GTPase regulator activity;interferon-gamma receptor binding;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;small GTPase regulator activity cell junction;cell part;cytoplasmic part;cytosol;extrinsic to membrane;extrinsic to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial nucleoid;mitochondrial part;neuromuscular junction;non-membrane-bounded organelle;nucleoid;nucleus;organelle;organelle lumen;organelle part;plasma membrane part;postsynaptic membrane;synapse;synapse part;synaptic membrane

E9PHH5;O60762;Q5QPK2;H0Y368 Dolichol-phosphate mannosyltransferase DPM1 >tr|E9PHH5|E9PHH5_HUMAN Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=2 SV=1;>sp|O60762|DPM1_HUMAN Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=1 SV=1;>tr|Q5QPK2|Q5QPK2_HUMAN Dolichol-phosphate mannosyltransferase O NaN NaN 2.48 NaN 1.35 NaN NaN NaN 0.00018206 2 10.6 alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;C-terminal protein amino acid modification;C-terminal protein lipidation;dolichol metabolic process;dolichol-linked oligosaccharide biosynthetic process;GDP-mannose metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;glycosylation;GPI anchor biosynthetic process;GPI anchor metabolic process;hexose metabolic process;isoprenoid metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;mannose metabolic process;metabolic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;organophosphate metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;polyprenol metabolic process;post-translational protein modification;prenol metabolic process;primary metabolic process;protein glycosylation;protein lipidation;protein mannosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein O-linked glycosylation;protein O-linked mannosylation;small molecule metabolic process "alcohol binding;binding;carbohydrate binding;catalytic activity;dolichyl-phosphate beta-D-mannosyltransferase activity;dolichyl-phosphate-mannose-protein mannosyltransferase activity;mannose binding;mannosyltransferase activity;monosaccharide binding;sugar binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;dolichol-phosphate-mannose synthase complex;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;macromolecular complex;mannosyltransferase complex;membrane;membrane part;organelle membrane;organelle part;protein complex N-Glycan biosynthesis

F6RFD5;P60981-2;P60981 Destrin DSTN >tr|F6RFD5|F6RFD5_HUMAN Destrin OS=Homo sapiens GN=DSTN PE=2 SV=1;>sp|P60981-2|DEST_HUMAN Isoform 2 of Destrin OS=Homo sapiens GN=DSTN;>sp|P60981|DEST_HUMAN Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3 0.29 1.68 0.1 1.15 1.02 2.59 0.81 1.31 1.01E-05 2 14.8 actin cytoskeleton organization;actin filament depolymerization;actin filament organization;actin filament severing;actin filament-based process;actin polymerization or depolymerization;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex disassembly;cytokinesis;cytoskeleton organization;macromolecular complex disassembly;macromolecular complex subunit organization;organelle organization;positive regulation of actin filament depolymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex disassembly;protein complex disassembly;protein complex subunit organization;protein depolymerization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex disassembly actin cytoskeleton;cell cortex part;cell part;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part

A2BED6;A2BED7;Q96KQ7-2;B0UZY3;Q96KQ7;B0UZY0;A2ABF8;B0UZY1;A2ABF9 Histone-lysine N-methyltransferase EHMT2 EHMT2 >tr|A2BED6|A2BED6_HUMAN
Histone-lysine N-methyltransferase EHMT2 (Fragment) OS=Homo sapiens GN=EHMT2 PE=2 SV=1;>tr|A2BED7|A2BED7_HUMAN Histone-lysine N-methyltransferase EHMT2
(Fragment) OS=Homo sapiens GN=EHMT2 PE=2 SV=1;>sp|Q96KQ7-2|EHMT2_HUMAN Isoform 2 NaN NaN NaN NaN NaN NaN NaN NaN 2.53E-05 2 6.9 "anatomical structure
development;biological regulation;cell cycle phase;cell cycle process;cell development;cellular component assembly;cellular component assembly at cellular level;cellular component
organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular
developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in
reproduction;cellular protein metabolic process;chromosome organization;chromosome organization involved in meiosis;developmental process;developmental process involved in
reproduction;DNA alkylation;DNA metabolic process;DNA methylation;DNA methylation on cytosine;DNA methylation on cytosine within a CG sequence;DNA
modification;fertilization;germ cell development;growth;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic
process;methylation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular
macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of
macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic
process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase
II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic
process;one-carbon metabolic process;organ growth;organelle organization;pachytene;peptidyl-amino acid modification;peptidyl-lysine dimethylation;peptidyl-lysine methylation;peptidyl-
lysine modification;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;regulation of biological process;regulation of
biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular
process;regulation of DNA metabolic process;regulation of DNA replication;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule
biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing
compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of
transcription, DNA-dependent;reproductive process;small molecule metabolic process;spermatid development;synaptonemal complex assembly;synaptonemal complex organization"
"binding;catalytic activity;cation binding;histone methyltransferase activity;histone methyltransferase activity (H3-K27 specific);histone methyltransferase activity (H3-K9 specific);histone-
lysine N-methyltransferase activity;ion binding;lysine N-methyltransferase activity;metal ion binding;methyltransferase activity;N-methyltransferase activity;protein methyltransferase
activity;protein-lysine N-methyltransferase activity;S-adenosylmethionine-dependent methyltransferase activity;transferase activity;transferase activity, transferring one-carbon
groups;transition metal ion binding;zinc ion binding" cell part;chromosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular
organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle Lysine degradation
P05198;H0YJS4;G3V4T5 Eukaryotic translation initiation factor 2 subunit 1EIF2S1 >sp|P05198|IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens
GN=EIF2S1 PE=1 SV=3;>tr|H0YJS4|H0YJS4_HUMAN Eukaryotic translation initiation factor 2 subunit 1 (Fragment) OS=Homo sapiens GN=EIF2S1 PE=4
SV=1;>tr|G3V4T5|G3V4T5_HUM 1.36 0.91 1.19 0.77 1.11 0.82 1.37 1.04 4.30E-07 2 6.3 activation of signaling protein activity involved in unfolded protein response;biological
regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to
stress;macromolecule metabolic process;macromolecule modification;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic
process;phosphorylation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular
function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;posttranscriptional regulation of gene
expression;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological
process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of
cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of hydrolase activity;regulation of kinase
activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of
nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of
protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;regulation of
translation;regulation of translation in response to stress;regulation of translational initiation;regulation of translational initiation in response to stress;response to stimulus;response to
stress;translational initiation "binding;nucleic acid binding;ribonucleoprotein binding;ribosome binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation
factor activity"cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 2 complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded
organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;polysome;protein
complex;ribonucleoprotein complex;RNA granule;stress granule Hepatitis C;Measles;Protein processing in endoplasmic reticulum;RNA transport
P60228;E5RIT4;H0YBR5;E5RHS5;E5RGA2 Eukaryotic translation initiation factor 3 subunit E EIF3E >sp|P60228|EIF3E_HUMAN Eukaryotic translation initiation factor 3
subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1;>tr|E5RIT4|E5RIT4_HUMAN Eukaryotic translation initiation factor 3 subunit E (Fragment) OS=Homo sapiens GN=EIF3E PE=2
SV=1;>tr|H0YBR5|H0YBR5_HUMA 1 NaN NaN NaN NaN NaN 1.38 NaN 0.00056886 2 4.9 "biological regulation;catabolic process;cellular catabolic process;cellular
macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule
catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of
biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic
process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of
macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;negative regulation of
translational initiation;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic
acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological
process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic

process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;RNA catabolic process;RNA metabolic process;translational initiation" "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;PML body;protein complex Hepatitis C;RNA transport

P56537;P56537-2 Eukaryotic translation initiation factor 6 EIF6 >sp|P56537|IF6_HUMAN Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1;>sp|P56537-2|IF6_HUMAN Isoform 2 of Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 1.01 1.22 1.38 1.4 1.16 1.05 0.73 0.88 1.66E-06 2 14.3 cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of ribosome localization;intracellular transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;mature ribosome assembly;nuclear export;nuclear transport;nucleocytoplasmic transport;organelle assembly;ribonucleoprotein complex assembly;ribonucleoprotein complex biogenesis;ribonucleoprotein complex export from nucleus;ribonucleoprotein complex localization;ribonucleoprotein complex subunit organization;ribosomal large subunit biogenesis;ribosomal subunit export from nucleus;ribosome assembly;rRNA-containing ribonucleoprotein complex export from nucleus;transport "binding;nucleic acid binding;ribonucleoprotein binding;ribosomal large subunit binding;ribosome binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;protein complex Ribosome biogenesis in eukaryotes

Q9P0I2-2;Q9P0I2;C9JLM9 ER membrane protein complex subunit 3 EMC3 >sp|Q9P0I2-2|EMC3_HUMAN Isoform 2 of ER membrane protein complex subunit 3 OS=Homo sapiens GN=EMC3;>sp|Q9P0I2|EMC3_HUMAN ER membrane protein complex subunit 3 OS=Homo sapiens GN=EMC3 PE=1 SV=3;>tr|C9JLM9|C9JLM9_HUMAN ER membrane protein complex subunit 3 O 1 1.39 2.01 1.31 0.88 0.66 0.73 0.87 3.87E-10 2 11.9 cell part;ER membrane protein complex;macromolecular complex;membrane;protein complex

H0YDT8;Q9NPA0;H0YDX2 ER membrane protein complex subunit 7 EMC7 >tr|H0YDT8|H0YDT8_HUMAN ER membrane protein complex subunit 7 (Fragment) OS=Homo sapiens GN=EMC7 PE=4 SV=1;>sp|Q9NPA0|EMC7_HUMAN ER membrane protein complex subunit 7 OS=Homo sapiens GN=EMC7 PE=1 SV=1;>tr|H0YDX2|H0YDX2_HUMAN ER membrane protein complex sub NaN NaN 1.65 NaN 0.66 NaN NaN NaN 7.04E-05 2 12 binding;carbohydrate binding;nucleotide binding;purine nucleotide binding ER membrane protein complex;macromolecular complex;protein complex

P84090;G3V279 Enhancer of rudimentary homolog ERH >sp|P84090|ERH_HUMAN Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1;>tr|G3V279|G3V279_HUMAN Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=2 SV=1 NaN 1.21 1.44 1.79 0.43 0.34 NaN 0.74 5.29E-60 2 21.2 cell cycle;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;primary metabolic process;pyrimidine nucleoside metabolic process;pyrimidine-containing compound metabolic process;small molecule metabolic process cell part;midbody

H7BY36;Q01844-2;C9JGE3;Q01844-6;B0QYK0;Q01844-3;Q01844;Q01844-5 RNA-binding protein EWS EWSR1 ">tr|H7BY36|H7BY36_HUMAN RNA-binding protein EWS (Fragment) OS=Homo sapiens GN=EWSR1 PE=4 SV=1;>sp|Q01844-2|EWS_HUMAN Isoform EWS-B of RNA-binding protein EWS OS=Homo sapiens GN=EWSR1;>tr|C9JGE3|C9JGE3_HUMAN Ewing sarcoma breakpoint region 1, isoform CRA_e"1.51 0.93 0.98 1.03 0.53 0.3 1.17 0.84 1.39E-12 2 7.5 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane

Q9NVH0-2;Q9NVH0;C9JLF4 Exonuclease 3-5 domain-containing protein 2 EXD2 >sp|Q9NVH0-2|EXD2_HUMAN Isoform 2 of Exonuclease 3-5 domain-containing protein 2 OS=Homo sapiens GN=EXD2;>sp|Q9NVH0|EXD2_HUMAN Exonuclease 3-5 domain-containing protein 2 OS=Homo sapiens GN=EXD2 PE=1 SV=2;>tr|C9JLF4|C9JLF4_HUMAN Exonuclease 3-5 domai NaN NaN NaN NaN NaN NaN NaN NaN 0.00016141 2 5.2 cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process "3'-5' exonuclease activity;binding;catalytic activity;exonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding"

P13726;P13726-2 Tissue factor F3 >sp|P13726|TF_HUMAN Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1;>sp|P13726-2|TF_HUMAN Isoform 2 of Tissue factor OS=Homo sapiens GN=F3 1.38 1.45 1.02 0.52 0.54 0.41 0.98 1.4 1.15E-16 2 8.5 "activation of blood coagulation via clotting cascade;activation of caspase activity;activation of plasma proteins involved in acute inflammatory response;biological regulation;blood coagulation, extrinsic pathway;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;positive regulation of angiogenesis;positive regulation of behavior;positive regulation of biological process;positive regulation of blood coagulation;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of coagulation;positive regulation of developmental process;positive regulation of endothelial cell proliferation;positive regulation of epithelial cell proliferation;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of locomotion;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of peptidase activity;positive regulation of platelet-derived growth factor receptor signaling pathway;positive regulation of positive chemotaxis;positive regulation of protein kinase B signaling cascade;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein activation cascade;protein maturation;protein metabolic process;protein processing;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of blood coagulation;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of chemotaxis;regulation of coagulation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of peptidase activity;regulation of platelet-derived growth factor receptor signaling pathway;regulation of positive chemotaxis;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of wound healing;response to stimulus" binding;cell surface binding;lipid binding;phospholipid binding cell part;extracellular matrix;extracellular region part;extracellular space;integral to membrane;intrinsic to external side of plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Complement and coagulation cascades

Q9BQN1 Protein FAM83C FAM83C >sp|Q9BQN1|FA83C_HUMAN Protein FAM83C OS=Homo sapiens GN=FAM83C PE=1 SV=3 NaN NaN 1.94 NaN 1.43 NaN NaN NaN 1.16E-08 2 3.6

B3KQ95;B4DT56;B7Z1J3;B4DJE5;E9PNM1;P37268 Squalene synthase FDFT1 >tr|B3KQ95|B3KQ95_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1;>tr|B4DT56|B4DT56_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1;>tr|B7Z1J3|B7Z1J3_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1;>tr|B4DJE5|B4DJE5_HUMAN S 1.03 0.9 1.64 0.39 0.83 1.34 1.23 0.98 2.73E-14 2 9.2 alcohol metabolic process;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;farnesyl diphosphate metabolic process;isoprenoid biosynthetic process;isoprenoid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;organophosphate metabolic process;phospholipid metabolic process;prenol metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "catalytic activity;farnesyl-diphosphate farnesyltransferase activity;farnesyltranstransferase activity;oxidoreductase activity;prenyltransferase activity;squalene synthase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Steroid biosynthesis

A9Z1Z3-3;A9Z1Z3 Fer-1-like protein 4 FER1L4 >sp|A9Z1Z3-3|FR1L4_HUMAN Isoform 3 of Fer-1-like protein 4 OS=Homo sapiens GN=FER1L4;>sp|A9Z1Z3|FR1L4_HUMAN Fer-1-like protein 4 OS=Homo sapiens GN=FER1L4 PE=2 SV=1 NaN NaN 1.01 NaN 0.93 NaN NaN NaN 0.00010818 2 0.7 cell part;integral to membrane;intrinsic to membrane;membrane part

Q9NYL4-2;F8VU90;Q9NYL4;H0YHM7 Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase FKBP11 FKBP11 >sp|Q9NYL4-2|FKB11_HUMAN Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP11 OS=Homo sapiens GN=FKBP11;>tr|F8VU90|F8VU90_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=FKBP11 PE=2 SV=1;>sp|Q9NYL4|FKB11_HUMAN Peptidyl-prolyl cis-trans isom 1.15 1.39 1.7 1.12 0.3 0.21 0.85 0.89 0.00014202 2 12.3 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-proline modification;primary metabolic process;protein folding;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization binding;catalytic activity;cis-trans isomerase activity;drug binding;FK506 binding;isomerase activity;macrolide binding;peptidyl-prolyl cis-trans isomerase activity cell part;integral to membrane;intrinsic to membrane;membrane;membrane part

Q9NY12-2;Q9NY12 H/ACA ribonucleoprotein complex subunit 1 GAR1 >sp|Q9NY12-2|GAR1_HUMAN Isoform 2 of H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens GN=GAR1;>sp|Q9NY12|GAR1_HUMAN H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens GN=GAR1 PE=1 SV=1 1.32 1 1.95 1.43 0.74 0.52 1.17 0.8 0.00021165 2 11.1 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;macromolecule modification;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;pseudouridine synthesis;RNA metabolic process;RNA modification;RNA processing;rRNA metabolic process;rRNA processing;snRNA metabolic process;snRNA modification;snRNA pseudouridine synthesis binding;catalytic activity;cation channel activity;cation transmembrane transporter activity;channel activity;intramolecular transferase activity;ion channel activity;ion transmembrane transporter activity;isomerase activity;nucleic acid binding;passive transmembrane transporter activity;pseudouridine synthase activity;RNA binding;snoRNA binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity box H/ACA RNP complex;box H/ACA snoRNP complex;Cajal body;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nucleolar part;nucleoplasm part;organelle part;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes

K7EM11;O14908-2;O14908 PDZ domain-containing protein GIPC1 GIPC1 >tr|K7EM11|K7EM11_HUMAN PDZ domain-containing protein GIPC1 (Fragment) OS=Homo sapiens GN=GIPC1 PE=4 SV=1;>sp|O14908-2|GIPC1_HUMAN Isoform 2 of PDZ domain-containing protein GIPC1 OS=Homo sapiens GN=GIPC1;>sp|O14908|GIPC1_HUMAN PDZ domain-containing protei NaN NaN 0.65 NaN 2.25 NaN NaN NaN 8.12E-07 2 21.9 biological regulation;cell communication;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component movement;cellular process;cellular response to stimulus;endothelial cell migration;establishment of localization;establishment of localization in cell;establishment of protein localization;glutamate secretion;G-protein coupled receptor protein signaling pathway;intracellular protein transport;intracellular transport;locomotion;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of proteasomal ubiquitin-dependent protein catabolic process;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transforming growth factor beta receptor signaling pathway;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;posttranscriptional regulation of gene expression;protein targeting;protein transport;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein stability;regulation of proteolysis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmission of nerve impulse;response to stimulus;secretion;secretion by cell;signal release;signal transduction;signaling;synaptic transmission;transport actin binding;binding;cytoskeletal protein binding;identical protein binding;myosin binding;protein binding;protein dimerization activity;protein homodimerization activity brush border;cell cortex;cell part;cell projection;cell projection part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;cytosolic part;dendritic shaft;dendritic spine;endocytic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;neuron projection;neuron spine;organelle;organelle membrane;organelle part;synapse part;synaptic vesicle;vesicle;vesicle membrane

Q9NZM5 Glioma tumor suppressor candidate region gene 2 protein GLTSCR2 >sp|Q9NZM5|GSCR2_HUMAN Glioma tumor suppressor candidate region gene 2 protein OS=Homo sapiens GN=GLTSCR2 PE=1 SV=2 NaN NaN 1.44 NaN 0.51 NaN NaN NaN 3.05E-09 2 6.5 cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

P29992;K7EL62;O95837 Guanine nucleotide-binding protein subunit alpha-11;Guanine nucleotide-binding protein subunit alpha-14 GNA11;GNA14 >sp|P29992|GNA11_HUMAN Guanine nucleotide-binding protein subunit alpha-11 OS=Homo sapiens GN=GNA11 PE=1 SV=2;>tr|K7EL62|K7EL62_HUMAN Guanine nucleotide-binding protein subunit alpha-11 (Fragment) OS=Homo sapiens GN=GNA11 PE=4 SV=1;>sp|O95837|GNA14_HUMAN G 1.07 1.47 0.85 0.9 0.63 0.88 0.67 1.13 3.16E-06 2 7.2 "activation of phospholipase C activity;activation of phospholipase C activity by dopamine receptor signaling pathway;activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger;anatomical structure development;biological regulation;cAMP-mediated signaling;cell activation;cell surface receptor linked signaling pathway;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;cyclic-nucleotide-mediated signaling;developmental pigmentation;developmental process;dopamine receptor signaling pathway;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;heart development;homeostatic process;inositol phosphate-mediated signaling;intracellular signal transduction;ion homeostasis;organ development;pigmentation;platelet activation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;regulation of action potential;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell differentiation;regulation of cellular process;regulation of developmental pigmentation;regulation of developmental process;regulation of hydrolase activity;regulation of lipase activity;regulation of melanocyte differentiation;regulation of membrane potential;regulation of metabolic process;regulation of molecular function;regulation of phospholipase activity;regulation of pigment cell differentiation;response to stimulus;second-messenger-mediated signaling;signal transduction;skeletal system development;system development" "binding;catalytic activity;cation binding;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity" cell part;cytoplasm;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular part;macromolecular complex;membrane part;plasma membrane part;protein complex

Amoebiasis;Calcium signaling pathway;Chagas disease (American trypanosomiasis);Gap junction;GnRH signaling pathway;Long-term depression;Vascular smooth muscle contraction

D6RAU2;E9PD14;D6RFX4;D6RFZ9;D6RHH4;D6R9Z1;D6R9L0;P63244;D6RGK8;D6R909;D6RBD0;H0YAF8;D6RAC2;J3KPE3;H0Y8W2;D6REE5 Guanine nucleotide-binding protein subunit beta-2-like 1 GNB2L1 >tr|D6RAU2|D6RAU2_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=2 SV=1;>tr|E9PD14|E9PD14_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=2 SV=1;>tr|D6RFX4|D6RFX4_HUMA 0.78 NaN 0.29 0.57 1.38 1.41 1.46 NaN 2.43E-05 2 14.3 anatomical structure morphogenesis;biological regulation;cell cycle;cellular process;developmental process;embryonic morphogenesis;gastrulation;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of endocytosis;negative regulation of growth;negative regulation of intracellular protein kinase cascade;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phagocytosis;negative regulation of protein kinase B signaling cascade;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of translation;negative regulation of transport;negative regulation of Wnt receptor signaling pathway;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular catabolic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of gastrulation;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein complex assembly;positive regulation of protein homooligomerization;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein oligomerization;positive regulation of protein phosphorylation;positive regulation of proteolysis;posttranscriptional regulation of gene expression;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell division;regulation of cell growth;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of embryonic development;regulation of endocytosis;regulation of establishment of cell polarity;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of establishment or maintenance of cell polarity;regulation of gastrulation;regulation of gene expression;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein homooligomerization;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein oligomerization;regulation of protein phosphorylation;regulation of proteolysis;regulation of purine nucleotide catabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of translation;regulation of transport;regulation of vesicle-mediated transport;regulation of Wnt receptor signaling pathway;reproductive process;rhythmic process;viral reproductive process;virus-host interaction apoptotic protease activator activity;binding;caspase activator activity;caspase regulator activity;channel inhibitor activity;channel regulator activity;enzyme activator activity;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;ion channel inhibitor activity;kinase binding;kinase inhibitor activity;kinase regulator activity;peptidase activator activity;peptidase regulator activity;protein binding;protein domain specific binding;protein kinase binding;protein kinase C binding;protein kinase inhibitor activity;protein kinase regulator activity;protein tyrosine kinase inhibitor activity;receptor binding;receptor tyrosine kinase binding;SH2 domain binding cell body;cell part;cell projection;cytoplasmic part;cytoskeleton;dendrite;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;midbody;neuron projection;neuronal cell body;non-membrane-bounded organelle;nucleus;organelle;organelle part;perikaryon;perinuclear region of cytoplasm;phagocytic cup;plasma membrane part;ribonucleoprotein complex;small ribosomal subunit Measles

Q9UBI6 Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 GNG12 >sp|Q9UBI6|GBG12_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=3 1.12 1.57 1.21 1.06 0.6 0.64 0.6 0.89 1.18E-32 2 37.5 biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to glucagon stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;G-protein coupled receptor protein signaling pathway;metabolic process;oxidation-reduction process;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to glucagon stimulus;response to hormone stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;signaling;small molecule metabolic process;synaptic transmission molecular transducer activity;signal transducer activitycell part;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular part;macromolecular complex;membrane;membrane part;plasma membrane;plasma membrane part;protein complex Chemokine signaling pathway;MAPK signaling pathway;Regulation of actin cytoskeleton

E7ERW2;P00505 "Aspartate aminotransferase;Aspartate aminotransferase, mitochondrial" GOT2 ">tr|E7ERW2|E7ERW2_HUMAN Aspartate aminotransferase OS=Homo sapiens GN=GOT2 PE=2 SV=1;>sp|P00505|AATM_HUMAN Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3" 0.96 0.37 1.05 NaN 3.11 NaN 2.21 1.37 1.91E-44 2 6.7 2-oxoglutarate metabolic process;4-hydroxyproline catabolic process;4-hydroxyproline metabolic process;alcohol biosynthetic process;alcohol metabolic process;amine biosynthetic process;amine catabolic process;amine metabolic process;aspartate biosynthetic process;aspartate catabolic process;aspartate family amino acid biosynthetic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;aspartate metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;carboxylic acid transport;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid catabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;dicarboxylic acid metabolic process;establishment of localization;fatty acid transport;fumarate metabolic process;gluconeogenesis;glucose metabolic process;glutamate catabolic process;glutamate catabolic process to 2-oxoglutarate;glutamate catabolic process to aspartate;glutamate metabolic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;heterocycle catabolic process;heterocycle metabolic process;hexose biosynthetic process;hexose metabolic process;lipid transport;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;organic acid transport;organic substance transport;oxaloacetate metabolic process;oxoacid metabolic process;primary metabolic process;response to chemical stimulus;response to ethanol;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;transport "binding;catalytic activity;cofactor binding;kynurenine-oxoglutarate transaminase activity;L-aspartate:2-oxoglutarate aminotransferase activity;L-phenylalanine aminotransferase activity;L-phenylalanine:2-oxoglutarate aminotransferase activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;Cysteine and methionine metabolism;Fat digestion and absorption;Phenylalanine metabolism;Phenylalanine, tyrosine and tryptophan biosynthesis;Tyrosine metabolism"

H7C024;P35052;H7C410;C9J4Y6;H7BZE9 Glypican-1;Secreted glypican-1 GPC1 >tr|H7C024|H7C024_HUMAN Glypican-1 (Fragment) OS=Homo sapiens GN=GPC1 PE=3 SV=1;>sp|P35052|GPC1_HUMAN Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2;>tr|H7C410|H7C410_HUMAN Glypican-1 (Fragment) OS=Homo sapiens GN=GPC1 PE=3 SV=1;>tr|C9J4Y6|C9J4Y6_HUMAN Glypi NaN NaN 1.58 NaN 1.17 NaN NaN NaN 9.04E-12 2 6.9 "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure formation involved in morphogenesis;axon guidance;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell differentiation;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chemotaxis;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;glial cell differentiation;glycoprotein metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;heparan sulfate proteoglycan catabolic process;heparan sulfate proteoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;locomotion;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;myelin assembly;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of fibroblast growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nitrogen compound metabolic process;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle cell differentiation;positive regulation of skeletal muscle cell differentiation;positive regulation of striated muscle cell differentiation;primary metabolic process;proteoglycan catabolic process;proteoglycan metabolic process;regulation of biological process;regulation of cell communication;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of fibroblast growth factor receptor signaling pathway;regulation of muscle cell differentiation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of striated muscle cell differentiation;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;Schwann cell differentiation;signal transduction;sulfur compound catabolic process;sulfur compound metabolic process;taxis;terpenoid metabolic process" binding;cation binding;copper ion binding;extracellular matrix binding;fibroblast growth factor binding;growth factor binding;ion binding;laminin binding;metal ion binding;protein binding;transition metal ion binding anchored to membrane;cell part;cytoplasmic part;endosome;extracellular matrix;extracellular region part;extracellular space;Golgi apparatus part;Golgi lumen;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;plasma membrane part;proteinaceous extracellular matrix;vacuolar lumen;vacuolar part

P07203;P07203-2 Glutathione peroxidase 1 GPX1 >sp|P07203|GPX1_HUMAN Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4;>sp|P07203-2|GPX1_HUMAN Isoform 2 of Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 0.94 0.9 0.87 0.67 0.89 0.99 0.9 1.01 0.00042078 2 12.3 "acylglycerol metabolic process;amine metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;angiogenesis involved in wound healing;apoptotic mitochondrial changes;arachidonic acid metabolic process;biological regulation;blood vessel endothelial cell migration;carboxylic acid metabolic process;catabolic process;cell development;cell differentiation;cell migration;cell motility;cell proliferation;cell redox homeostasis;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;circulatory system process;developmental growth;developmental process;endothelial cell development;endothelial cell migration;epithelial cell development;fat cell differentiation;fatty acid metabolic process;glutathione metabolic process;glycerol ether metabolic process;glycerolipid metabolic process;growth;heart contraction;heart process;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;icosanoid metabolic process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of apoptosis by oxidative stress;induction of programmed cell death;interaction with symbiont;interspecies interaction between organisms;lipid metabolic process;lipoxygenase pathway;locomotion;macromolecule metabolic process;macromolecule modification;metabolic process;mitochondrion organization;monocarboxylic acid metabolic process;multicellular organismal homeostasis;multicellular organismal process;multi-organism process;muscle cell development;muscle cell differentiation;muscle fiber development;myoblast proliferation;myotube differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of defense response;negative regulation of hydrolase activity;negative regulation of immune response;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of inflammatory response to antigenic stimulus;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of response to external stimulus;negative regulation of response to stimulus;neurological system process;neutral lipid metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;peptide metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein metabolic process;protein modification process;protein oxidation;purine base metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;reactive oxygen species metabolic process;regeneration;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of blood vessel size;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of defense response;regulation of developmental process;regulation of endopeptidase activity;regulation of epithelial cell proliferation;regulation of gene expression;regulation of gene expression, epigenetic;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of inflammatory response to antigenic stimulus;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of mammary gland epithelial cell proliferation;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of neuron apoptosis;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of protein catabolic process;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of proteolysis;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of tube size;release of cytochrome c from mitochondria;response to abiotic stimulus;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to gamma radiation;response to hydrogen peroxide;response to hydroperoxide;response to inorganic substance;response to ionizing radiation;response to light stimulus;response to metal ion;response to other organism;response to oxidative stress;response to radiation;response to reactive oxygen species;response to selenium ion;response to stimulus;response to stress;response to symbiont;response to symbiotic bacterium;response to toxin;response to UV;response to xenobiotic stimulus;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;skeletal muscle cell differentiation;skeletal muscle fiber development;skeletal muscle tissue regeneration;small molecule metabolic process;striated muscle cell development;striated muscle cell differentiation;sulfur compound metabolic process;system process;temperature homeostasis;tissue development;tissue regeneration;triglyceride metabolic process;unsaturated fatty acid metabolic process;UV protection;vascular process in circulatory system;vasodilation;very long-chain fatty acid metabolic process" "antioxidant activity;catalytic activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;glutathione peroxidase activity;oxidoreductase activity;oxidoreductase activity, acting on peroxide as acceptor;peptidase inhibitor activity;peptidase regulator activity;peroxidase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Arachidonic acid metabolism;Glutathione metabolism E9PLF1;E9PHN7;P28161-2;E9PHN6;P28161;F6XZQ7;Q5T8Q9;P46439;P21266;Q5T8R1 Glutathione S-transferase Mu 2;Glutathione S-transferase Mu 5;Glutathione S-transferase Mu 3 GSTM2;GSTM5;GSTM3 >tr|E9PLF1|E9PLF1_HUMAN Glutathione S-transferase Mu 2 (Fragment) OS=Homo sapiens GN=GSTM2 PE=2 SV=2;>tr|E9PHN7|E9PHN7_HUMAN Glutathione S-transferase Mu 2 OS=Homo sapiens GN=GSTM2 PE=2 SV=1;>sp|P28161-2|GSTM2_HUMAN Isoform 2 of Glutathione S-transferase M NaN NaN NaN NaN NaN NaN NaN NaN 1.07E-06 2 17.7 amine metabolic process;anatomical structure development;benzene-containing compound metabolic process;biological regulation;calcium-mediated signaling;carboxylic acid metabolic process;catabolic process;cell development;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular detoxification of nitrogen compound;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to alkaloid;cellular response to caffeine;cellular response to chemical stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to purine-containing compound;cellular response to stimulus;cellular response to stress;detoxification of nitrogen compound;developmental process;endothelial cell development;epithelial cell development;establishment of blood-nerve barrier;glutathione metabolic process;intracellular signal transduction;metabolic process;multicellular organismal process;muscle system process;negative regulation of biological process;negative regulation of cardiac muscle contraction;negative regulation of ion transmembrane transporter activity;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of muscle contraction;negative regulation of ryanodine-sensitive calcium-release channel activity;negative regulation of striated muscle contraction;negative regulation of transport;negative regulation of transporter activity;nitrobenzene metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;peptide metabolic process;positive regulation of biological process;positive regulation of ion transmembrane transporter activity;positive regulation of molecular function;positive regulation of ryanodine-sensitive calcium-release channel activity;positive regulation of transport;positive regulation of transporter activity;primary metabolic process;regulation of biological process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cellular localization;regulation of cellular process;regulation of heart contraction;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of skeletal muscle contraction;regulation of skeletal muscle contraction by calcium ion signaling;regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;relaxation of cardiac muscle;relaxation of muscle;response to alkaloid;response to caffeine;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to nitrosative stress;response to organic cyclic compound;response to organic substance;response to purine-containing compound;response to steroid hormone stimulus;response to stimulus;response to stress;response to toxin;second-messenger-mediated signaling;signal transduction;small molecule metabolic process;sulfur compound metabolic process;system process;xenobiotic catabolic process;xenobiotic metabolic process "amine binding;amino acid binding;binding;carboxylic acid binding;catalytic activity;glutathione binding;glutathione transferase activity;identical protein binding;modified amino acid binding;peptide binding;protein binding;protein dimerization activity;protein homodimerization activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;sarcoplasmic reticulum Drug metabolism - cytochrome

P450;Glutathione metabolism;Metabolism of xenobiotics by cytochrome P450

P53701 Cytochrome c-type heme lyase HCCS >sp|P53701|CCHL_HUMAN Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1 NaN NaN 1.79 NaN 2.5 NaN NaN NaN 6.74E-06 2 8.6 anatomical structure morphogenesis;developmental process;metabolic process;organ morphogenesis;oxidation-reduction process binding;carbon-sulfur lyase activity;catalytic activity;cation binding;holocytochrome-c synthase activity;ion binding;lyase activity;metal ion binding cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Porphyrin and chlorophyll metabolism

P05204 Non-histone chromosomal protein HMG-17 HMGN2 >sp|P05204|HMGN2_HUMAN Non-histone chromosomal protein HMG-17 OS=Homo sapiens GN=HMGN2 PE=1 SV=3 0.72 1.54 NaN 3.67 NaN 0.18 0.28 0.25 1.50E-05 2 23.3 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chromatin organization;chromosome organization;organelle organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent" binding;chromatin binding;chromatin DNA binding;DNA binding;nucleic acid binding;nucleosomal DNA binding;nucleosome binding;structure-specific DNA binding cell part;chromatin;chromosomal part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nucleus;organelle;organelle part

Q99714;Q5H928;Q99714-2 3-hydroxyacyl-CoA dehydrogenase type-2 HSD17B10 >sp|Q99714|HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3;>tr|Q5H928|Q5H928_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=2 SV=1;>sp|Q99714-2|HCD2_HUMAN Isoform 2 of 3-hydroxyacyl-CoA d 0.96 0.64 0.53 0.19 0.52 1.75 1.6 1.41 6.72E-16 2 11.9 amine catabolic process;amine metabolic process;branched chain family amino acid catabolic process;branched chain family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;lipid metabolic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;RNA processing;small molecule catabolic process;small molecule metabolic process;tRNA metabolic process;tRNA processing "3-hydroxy-2-methylbutyryl-CoA dehydrogenase activity;3-hydroxyacyl-CoA dehydrogenase activity;catalytic activity;cholate 7-alpha-dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane "Alzheimer's disease;Valine, leucine and isoleucine degradation"

D6RJ96;E9PDE8;O95757;E7ES43;B4DY72 Heat shock 70 kDa protein 4L HSPA4L;HSPH1 >tr|D6RJ96|D6RJ96_HUMAN Heat shock 70 kDa protein 4L (Fragment) OS=Homo sapiens GN=HSPA4L PE=2 SV=1;>tr|E9PDE8|E9PDE8_HUMAN Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=2 SV=1;>sp|O95757|HS74L_HUMAN Heat shock 70 kDa protein 4L OS=Homo sapiens 0.9 NaN 0.78 1.45 0.85 1.1 0.99 NaN 2.79E-05 2 5.1 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Protein processing in endoplasmic reticulum

B9A008;E7ENR5;H0Y714;Q96G21;B8ZZ47 U3 small nucleolar ribonucleoprotein protein IMP4 IMP4 >tr|B9A008|B9A008_HUMAN U3 small nucleolar ribonucleoprotein protein IMP4 (Fragment) OS=Homo sapiens GN=IMP4 PE=2 SV=1;>tr|E7ENR5|E7ENR5_HUMAN U3 small nucleolar ribonucleoprotein protein IMP4 (Fragment) OS=Homo sapiens GN=IMP4 PE=2 SV=1;>tr|H0Y714|H0Y714_ NaN NaN 1.44 NaN 0.84 NaN NaN NaN 5.92E-06 2 14 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complexRibosome biogenesis in eukaryotes

Q5VZ66;Q5VZ66-2 Janus kinase and microtubule-interacting protein 3 JAKMIP3 >sp|Q5VZ66|JKIP3_HUMAN Janus kinase and microtubule-interacting protein 3 OS=Homo sapiens GN=JAKMIP3 PE=2 SV=2;>sp|Q5VZ66-2|JKIP3_HUMAN Isoform 2 of Janus kinase and microtubule-interacting protein 3 OS=Homo sapiens GN=JAKMIP3 NaN 0.88 NaN NaN NaN NaN NaN 0.75 0.00086722 2 1.9 cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle

B3KSG2;P50748 Kinetochore-associated protein 1 KNTC1 >tr|B3KSG2|B3KSG2_HUMAN Kinetochore-associated protein 1 OS=Homo sapiens GN=KNTC1 PE=2 SV=1;>sp|P50748|KNTC1_HUMAN Kinetochore-associated protein 1 OS=Homo sapiens GN=KNTC1 PE=1 SV=1 1.14 NaN NaN NaN NaN NaN 0.65 NaN 0.0008622 2 4.5 anaphase;biological regulation;cell cycle checkpoint;cell cycle phase;cell cycle process;cell division;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular process;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;mitotic anaphase;mitotic cell cycle checkpoint;mitotic prometaphase;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;regulation of exit from mitosis;regulation of mitotic cell cycle cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;kinetochore microtubule;macromolecular complex;membrane-bounded organelle;microtubule;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;spindle microtubule;spindle pole

P01116-2;G3V4K2;G3V5T7;P01112-2;P01116;P01112;P01111 "GTPase KRas;GTPase KRas, N-terminally processed;GTPase HRas;GTPase HRas, N-terminally processed;GTPase NRas" KRAS;HRAS;NRAS >sp|P01116-2|RASK_HUMAN Isoform 2B of GTPase KRas OS=Homo sapiens GN=KRAS;>tr|G3V4K2|G3V4K2_HUMAN GTPase KRas OS=Homo sapiens GN=KRAS PE=2 SV=1;>tr|G3V5T7|G3V5T7_HUMAN GTPase KRas OS=Homo sapiens GN=KRAS PE=2 SV=1;>sp|P01112-2|RASH_HUMAN Isoform 2 of GTPas 0.8 1.23 1.27 NaN 0.89 NaN 0.77 0.89 3.47E-05 2 12.2 "actin cytoskeleton organization;actin filament-based process;activation of MAPKK activity;activation of protein kinase activity;aging;anatomical structure morphogenesis;associative learning;axon guidance;behavior;behavioral interaction between organisms;biological regulation;blood coagulation;cell aging;cell communication;cell cycle arrest;cell cycle checkpoint;cell cycle process;cell differentiation;cell migration;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;cellular senescence;chemotaxis;coagulation;cognition;cytokine-mediated signaling pathway;cytoskeleton organization;defense response;developmental process;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;fibroblast growth factor receptor signaling pathway;hemostasis;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;insulin receptor signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;learning;learning or memory;leukocyte migration;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;membrane invagination;membrane organization;metabolic process;mitotic cell cycle checkpoint;multicellular organismal process;multi-organism process;muscle cell differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of gene expression;negative regulation of GTPase activity;negative regulation of hydrolase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of Ras GTPase activity;negative regulation of Rho GTPase activity;nerve growth factor receptor signaling pathway;neurological system process;organ morphogenesis;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of actin cytoskeleton reorganization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of epithelial cell proliferation;positive regulation of ERK1 and ERK2 cascade;positive regulation of gene expression;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of JNK cascade;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of miRNA metabolic process;positive regulation of molecular function;positive regulation of monooxygenase activity;positive regulation of NF-kappaB transcription factor activity;positive regulation of nitric-oxide synthase activity;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of oxidoreductase activity;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of Rac GTPase activity;positive regulation of Rac protein signal transduction;positive regulation of Ras GTPase activity;positive regulation of Ras protein signal transduction;positive regulation of response to stimulus;positive regulation of Rho GTPase activity;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of small GTPase mediated signal transduction;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of wound healing;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein metabolic process;protein modification process;protein oligomerization;protein phosphorylation;Ras protein signal transduction;regulation of actin cytoskeleton organization;regulation of actin cytoskeleton reorganization;regulation of actin filament-based process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cytoskeleton organization;regulation of DNA metabolic process;regulation of DNA replication;regulation of epithelial cell proliferation;regulation of ERK1 and ERK2 cascade;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of long-term neuronal synaptic plasticity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of miRNA metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal process;regulation of neurological system process;regulation of neuron apoptosis;regulation of neuronal synaptic plasticity;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of oxidoreductase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of purine nucleotide catabolic process;regulation of Rac protein signal transduction;regulation of Ras GTPase activity;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of stress-activated protein kinase signaling cascade;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of synaptic transmission, GABAergic;regulation of system process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of wound healing;response to abiotic stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to cytokine stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to glucocorticoid stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to light stimulus;response to mineralocorticoid stimulus;response to organic substance;response to peptide hormone stimulus;response to radiation;response to steroid hormone stimulus;response to stimulus;response to stress;signal transduction;signaling;small GTPase mediated signal transduction;social behavior;striated muscle cell differentiation;synaptic transmission;system process;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport;visual behavior;visual learning" "binding;catalytic activity;GDP binding;GMP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;membrane-bounded organelle;mitochondrion;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane Acute myeloid leukemia;Aldosterone-regulated sodium reabsorption;Axon guidance;B cell receptor signaling pathway;Bladder cancer;Chemokine signaling pathway;Chronic myeloid leukemia;Colorectal cancer;Dorso-ventral axis formation;Endocytosis;Endometrial cancer;ErbB signaling pathway;Fc epsilon RI signaling pathway;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;Hepatitis C;Insulin signaling pathway;Long-term depression;Long-term potentiation;MAPK signaling pathway;MAPK signaling pathway - fly;Melanogenesis;Melanoma;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Non-small cell lung cancer;Pancreatic cancer;Pathways in cancer;Progesterone-mediated oocyte maturation;Prostate cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;T cell receptor signaling pathway;Thyroid cancer;Tight junction;VEGF signaling pathway

Q13601-2;Q13601 KRR1 small subunit processome component homolog KRR1 >sp|Q13601-2|KRR1_HUMAN Isoform 2 of KRR1 small subunit processome component homolog OS=Homo sapiens GN=KRR1;>sp|Q13601|KRR1_HUMAN KRR1 small subunit processome component homolog OS=Homo sapiens GN=KRR1 PE=1 SV=4 0.92 0.88 1.69 2.11 0.39 0.43 0.62 0.7 3.30E-07 2 8 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing binding;nucleic acid binding;RNA binding cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex

B4E2S7;P13473-2;P13473;P13473-3;B7Z2R9 Lysosome-associated membrane glycoprotein 2 LAMP2 >tr|B4E2S7|B4E2S7_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1;>sp|P13473-2|LAMP2_HUMAN Isoform LAMP-2B of Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2;>sp|P13473|LAMP2_HUMAN Lysosome-associat 0.77 0.59 0.6 0.2 4.21 0.92 2.41 1.56 1.76E-06 2 5.5 cell activation;cellular process;establishment of localization;establishment of localization in cell;exocytosis;platelet activation;platelet degranulation;secretion;secretion by cell;transport;vesicle-mediated transport cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosomal part;endosome membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;late endosome membrane;lysosomal membrane;membrane;membrane part;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;platelet dense granule membrane;secretory granule membrane;vacuolar membrane;vacuolar part;vesicle membrane ko05152;Lysosome;Phagosome

H0YFI1;F5H479;F5GX19;F5H3Y3;Q6IAA8 Ragulator complex protein LAMTOR1 LAMTOR1 >tr|H0YFI1|H0YFI1_HUMAN Ragulator complex protein LAMTOR1 (Fragment) OS=Homo sapiens GN=LAMTOR1 PE=4 SV=1;>tr|F5H479|F5H479_HUMAN Ragulator complex protein LAMTOR1 OS=Homo sapiens GN=LAMTOR1 PE=2 SV=1;>tr|F5GX19|F5GX19_HUMAN Ragulator complex protein LAMTO 0.87 1.3 0.22 1.14 0.61 0.58 0.9 0.9 5.00E-14 2 30.4 biological regulation;cell growth;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cholesterol homeostasis;endosome localization;endosome organization;growth;homeostatic process;lipid homeostasis;localization;lysosome localization;lysosome organization;macromolecule localization;organelle localization;organelle organization;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of MAPKKK cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of TOR signaling cascade;protein localization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular metabolic process;regulation of cellular process;regulation of cholesterol efflux;regulation of cholesterol esterification;regulation of cholesterol import;regulation of cholesterol transport;regulation of intracellular protein kinase cascade;regulation of lipid metabolic process;regulation of lipid transport;regulation of localization;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of primary metabolic process;regulation of receptor recycling;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of steroid metabolic process;regulation of sterol import;regulation of sterol transport;regulation of TOR signaling cascade;regulation of transmembrane transport;regulation of transport;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to organic nitrogen;response to organic substance;response to stimulus;sterol homeostasis;vacuole organization cell part;cytoplasmic part;endosomal part;endosome membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome membrane;lysosomal membrane;lysosome;lytic vacuole;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;protein complex;Ragulator complex;vacuolar membrane;vacuolar part;vacuole

P28838-2;P28838;H0Y9Q1 Cytosol aminopeptidase LAP3 >sp|P28838-2|AMPL_HUMAN Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3;>sp|P28838|AMPL_HUMAN Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3;>tr|H0Y9Q1|H0Y9Q1_HUMAN Cytosol aminopeptidase (Fragment) OS=Homo sapiens GN=LAP3 PE=2 SV=1 0.16 6.98 NaN 4.51 NaN 1.42 0.36 0.95 1.39E-09 2 4.9 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;ion binding;magnesium ion binding;manganese ion binding;metal ion binding;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle;organelle part;trans-Golgi network Arginine and proline metabolism;Glutathione metabolism

P17931;G3V3R6 Galectin-3 LGALS3 >sp|P17931|LEG3_HUMAN Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5;>tr|G3V3R6|G3V3R6_HUMAN Galectin-3 OS=Homo sapiens GN=LGALS3 PE=2 SV=1 1.29 1.49 2.11 1.79 0.36 0.32 0.52 0.83 1.19E-07 2 8.8 anatomical structure development;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;developmental process;extracellular matrix organization;extracellular structure organization;immune response;immune system process;innate immune response;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;response to stimulus;response to stress;RNA metabolic process;RNA processing;RNA splicing;skeletal system development;system development binding;carbohydrate binding cell part;cytoplasmic part;extracellular matrix;extracellular region part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;nuclear part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane;proteinaceous extracellular matrix;ribonucleoprotein complex;spliceosomal complex

Q9Y5X9-2;J3QQQ0;Q9Y5X9;B4DTR8 Endothelial lipase LIPG >sp|Q9Y5X9-2|LIPE_HUMAN Isoform 2 of Endothelial lipase OS=Homo sapiens GN=LIPG;>tr|J3QQQ0|J3QQQ0_HUMAN Endothelial lipase OS=Homo sapiens GN=LIPG PE=3 SV=1;>sp|Q9Y5X9|LIPE_HUMAN Endothelial lipase OS=Homo sapiens GN=LIPG PE=1 SV=1;>tr|B4DTR8|B4DTR8_HUMAN 1.08 0.94 1.95 1.1 0.34 0.16 0.41 0.57 6.20E-10 2 8.8 biological regulation;catabolic process;cell proliferation;cellular catabolic process;cellular component organization;cellular component organization or biogenesis;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;chemical homeostasis;cholesterol homeostasis;cholesterol transport;establishment of localization;high-density lipoprotein particle remodeling;homeostatic process;lipid catabolic process;lipid homeostasis;lipid metabolic process;lipid transport;macromolecular complex remodeling;macromolecular complex subunit organization;metabolic process;multicellular organismal process;organic substance transport;organophosphate metabolic process;phospholipid catabolic process;phospholipid homeostasis;phospholipid metabolic process;plasma lipoprotein particle organization;plasma lipoprotein particle remodeling;positive regulation of biological process;positive regulation of cholesterol transport;positive regulation of high-density lipoprotein particle clearance;positive regulation of lipid transport;positive regulation of lipoprotein particle clearance;positive regulation of multicellular organismal process;positive regulation of sterol transport;positive regulation of transport;primary metabolic process;protein-lipid complex remodeling;protein-lipid complex subunit organization;regulation of biological process;regulation of biological quality;regulation of cellular metabolic process;regulation of cellular process;regulation of cholesterol transport;regulation of high-density lipoprotein particle clearance;regulation of lipid transport;regulation of lipoprotein metabolic process;regulation of lipoprotein particle clearance;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of sterol transport;regulation of transport;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to stimulus;reverse cholesterol transport;sterol homeostasis;sterol transport;transport "binding;carbohydrate binding;carboxylic ester hydrolase activity;catalytic activity;glycosaminoglycan binding;heparin binding;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;lipoprotein lipase activity;pattern binding;phosphatidylcholine 1-acylhydrolase activity;phospholipase activity;polysaccharide binding;retinyl-palmitate esterase activity;triglyceride lipase activity" extracellular region;extracellular region part;extracellular space Glycerolipid metabolism

Q12907;D6RIU4;D6RBH1;D6RBV2 Vesicular integral-membrane protein VIP36 LMAN2 >sp|Q12907|LMAN2_HUMAN Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1;>tr|D6RIU4|D6RIU4_HUMAN Vesicular integral-membrane protein VIP36 (Fragment) OS=Homo sapiens GN=LMAN2 PE=2 SV=1;>tr|D6RBH1|D6RBH1_HUMAN Vesicular integral-m NaN NaN 1.34 NaN 2.55 NaN NaN NaN 4.25E-05 2 5.9 establishment of localization;establishment of protein localization;protein transport;transport binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Protein processing in endoplasmic reticulum

Q8N1G4 Leucine-rich repeat-containing protein 47 LRRC47 >sp|Q8N1G4|LRC47_HUMAN Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1 0.97 0.96 NaN 0.83 NaN 1.75 1.31 1.1 1.58E-05 2 5.1 "aminoacyl-tRNA ligase activity;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;phenylalanine-tRNA ligase activity;RNA binding"

E7ETZ8;Q49MG5;Q49MG5-2;A2VCS9 Microtubule-associated protein 9 MAP9 >tr|E7ETZ8|E7ETZ8_HUMAN Microtubule-associated protein 9 OS=Homo sapiens GN=MAP9 PE=2 SV=1;>sp|Q49MG5|MAP9_HUMAN Microtubule-associated protein 9 OS=Homo sapiens GN=MAP9 PE=1 SV=3;>sp|Q49MG5-2|MAP9_HUMAN Isoform 2 of Microtubule-associated protein 9 OS=Hom 0.96 NaN 0.75 2.98 0.31 0.51 0.32 NaN 0.00040086 2 2.6 biological regulation;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytokinesis;cytoskeleton organization;microtubule cytoskeleton organization;microtubule-based process;mitosis;nuclear division;organelle assembly;organelle fission;organelle organization;regulation of biological process;regulation of cell cycle;regulation of cell cycle process;regulation of cellular component organization;regulation of cellular process;regulation of mitosis;regulation of mitotic cell cycle;regulation of nuclear division;regulation of organelle organization;spindle assembly;spindle organization cell part;cytoplasmic part;cytoskeletal part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;spindle

Q96N66-2;Q96N66;Q96N66-3 Lysophospholipid acyltransferase 7 MBOAT7 >sp|Q96N66-2|MBOA7_HUMAN Isoform 2 of Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7;>sp|Q96N66|MBOA7_HUMAN Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2;>sp|Q96N66-3|MBOA7_HUMAN Isoform 3 of Lysophospholipid acyltran 0.96 0.95 1.3 1.07 0.85 0.93 1.07 1.13 9.81E-09 2 6 anatomical structure development;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;developmental process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;small molecule metabolic process;system development;ventricular system development "catalytic activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Glycerophospholipid metabolism

Q8NE86-3;Q8NE86-2;Q8NE86 "Calcium uniporter protein, mitochondrial" MCU ">sp|Q8NE86-3|MCU_HUMAN Isoform 3 of Calcium uniporter protein, mitochondrial OS=Homo sapiens GN=MCU;>sp|Q8NE86-2|MCU_HUMAN Isoform 2 of Calcium uniporter protein, mitochondrial OS=Homo sapiens GN=MCU;>sp|Q8NE86|MCU_HUMAN Calcium uniporter protein, mitochon" 1.11 NaN 1.83 1.51 0.5 0.69 0.7 NaN 1.08E-05 2 6.6 biological regulation;calcium ion homeostasis;calcium ion transport;calcium-mediated signaling;carbohydrate homeostasis;cation homeostasis;cation transport;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of mitochondrial calcium ion concentration;establishment of localization;establishment of localization in cell;glucose homeostasis;homeostatic process;intracellular signal transduction;intracellular transport;ion homeostasis;ion transport;macromolecular complex assembly;macromolecular complex subunit organization;metal ion homeostasis;metal ion transport;mitochondrial calcium ion homeostasis;mitochondrial calcium ion transport;mitochondrial transport;positive regulation of biological process;positive regulation of cellular process;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of secretion;positive regulation of transport;protein complex assembly;protein complex oligomerization;protein complex subunit organization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;response to stimulus;second-messenger-mediated signaling;signal transduction;transport active transmembrane transporter activity;calcium channel activity;cation channel activity;cation transmembrane transporter activity;channel activity;ion channel activity;ion transmembrane transporter activity;passive transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;uniporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

Q08431-2;Q08431-3;F5GZN3;F5H7N9;Q08431;H0YKS8 Lactadherin;Lactadherin short form;Medin MFGE8 >sp|Q08431-2|MFGM_HUMAN Isoform 2 of Lactadherin OS=Homo sapiens GN=MFGE8;>sp|Q08431-3|MFGM_HUMAN Isoform 3 of Lactadherin OS=Homo sapiens GN=MFGE8;>tr|F5GZN3|F5GZN3_HUMAN Lactadherin short form OS=Homo sapiens GN=MFGE8 PE=2 SV=1;>tr|F5H7N9|F5H7N9_HUMAN La0.82 1.25 NaN 0.41 NaN 1.25 0.7 1.1 9.74E-12 2 9 "anatomical structure formation involved in morphogenesis;angiogenesis;biological adhesion;biological regulation;cell adhesion;cell recognition;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;developmental process;fertilization;interaction with host;interspecies interaction between organisms;membrane invagination;membrane organization;multi-organism process;phagocytosis, engulfment;phagocytosis, recognition;positive regulation of apoptotic cell clearance;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of phagocytosis;positive regulation of transport;regulation of apoptotic cell clearance;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of phagocytosis;regulation of transport;regulation of vesicle-mediated transport;reproductive process;single fertilization;viral reproductive process;virus-host interaction" binding;lipid binding;phosphatidylethanolamine binding;phosphatidylserine binding;phospholipid binding cell part;external side of plasma membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;extrinsic to membrane;extrinsic to plasma membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane part;vesicle

O14880;Q5VV89 Microsomal glutathione S-transferase 3 MGST3 >sp|O14880|MGST3_HUMAN Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1;>tr|Q5VV89|Q5VV89_HUMAN Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=2 SV=1 NaN NaN 1.08 NaN 0.85 NaN NaN NaN 2.15E-05 2 14.5 amine biosynthetic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;glutathione biosynthetic process;glutathione metabolic process;lipid metabolic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptide biosynthetic process;peptide metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small molecule biosynthetic process;small molecule metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;xenobiotic metabolic process "antioxidant activity;catalytic activity;glutathione peroxidase activity;glutathione transferase activity;oxidoreductase activity;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;nuclear envelope;nuclear part;organelle envelope;organelle membrane;organelle part Drug metabolism - cytochrome P450;Glutathione metabolism;Metabolism of xenobiotics by cytochrome P450

Q5TAQ0;Q9BRT2 Mitochondrial nucleoid factor 1 MNF1 >tr|Q5TAQ0|Q5TAQ0_HUMAN Mitochondrial nucleoid factor 1 OS=Homo sapiens GN=MNF1 PE=2 SV=1;>sp|Q9BRT2|MNF1_HUMAN Mitochondrial nucleoid factor 1 OS=Homo sapiens GN=MNF1 PE=1 SV=1 NaN 1.19 2.56 1.08 1 0.63 NaN 0.9 9.35E-11 2 24.8 cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;nucleus;organelle;organelle part

O60487 Myelin protein zero-like protein 2 MPZL2 >sp|O60487|MPZL2_HUMAN Myelin protein zero-like protein 2 OS=Homo sapiens GN=MPZL2 PE=1 SV=1 NaN NaN 1.51 NaN 1.21 NaN NaN NaN 0.00023955 2 10.2 anatomical structure morphogenesis;biological adhesion;cell activation;cell adhesion;cell differentiation;cell-cell adhesion;cellular developmental process;cellular process;developmental process;homophilic cell adhesion;immune system process;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;T cell activation;T cell differentiation;T cell differentiation in thymus cell part;cytoskeleton;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;non-membrane-bounded organelle;organelle;plasma membrane

Q9Y3B7-2;Q9Y3B7;H0YCD5;Q9Y3B7-3 "39S ribosomal protein L11, mitochondrial" MRPL11 ">sp|Q9Y3B7-2|RM11_HUMAN Isoform 2 of 39S ribosomal protein L11, mitochondrial OS=Homo sapiens GN=MRPL11;>sp|Q9Y3B7|RM11_HUMAN 39S ribosomal protein L11, mitochondrial OS=Homo sapiens GN=MRPL11 PE=1 SV=1;>tr|H0YCD5|H0YCD5_HUMAN 39S ribosomal protein L11, mi" NaN NaN 1.11 NaN 1.17 NaN NaN NaN 0.00058251 2 18.1 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial ribosome;non-membrane-bounded organelle;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome

E5RHF4;Q9P015 "39S ribosomal protein L15, mitochondrial" MRPL15 ">tr|E5RHF4|E5RHF4_HUMAN 39S ribosomal protein L15, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL15 PE=2 SV=1;>sp|Q9P015|RM15_HUMAN 39S ribosomal protein L15, mitochondrial OS=Homo sapiens GN=MRPL15 PE=1 SV=1" NaN NaN 2 NaN 0.63 NaN NaN NaN 0.00045051 2 9.6 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;mitochondrion;organelle;organelle part;ribonucleoprotein complex

Q9BZE1;H0Y4J2;A6NHR2 "39S ribosomal protein L37, mitochondrial" MRPL37 ">sp|Q9BZE1|RM37_HUMAN 39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2;>tr|H0Y4J2|H0Y4J2_HUMAN 39S ribosomal protein L37, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL37 PE=4 SV=1;>tr|A6NHR2|A6NHR2_HUMAN 39S ribosomal protein" 1.21 1.33 2.1 1.34 0.41 0.32 0.76 0.67 1.37E-09 2 7.3 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial part;mitochondrial ribosome;mitochondrion;non-membrane-bounded organelle;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome

Q96DV4 "39S ribosomal protein L38, mitochondrial" MRPL38 ">sp|Q96DV4|RM38_HUMAN 39S ribosomal protein L38, mitochondrial OS=Homo sapiens GN=MRPL38 PE=1 SV=2" NaN NaN 2.34 NaN 0.68 NaN NaN NaN 7.90E-06 2 5.3 actin cytoskeleton;cell part;cytoplasmic part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome

C9JG87;Q9NYK5;Q9NYK5-2 "39S ribosomal protein L39, mitochondrial" MRPL39 ">tr|C9JG87|C9JG87_HUMAN 39S ribosomal protein L39, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL39 PE=2 SV=1;>sp|Q9NYK5|RM39_HUMAN 39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3;>sp|Q9NYK5-2|RM39_HUMAN Isoform 2 of 39S ribo" NaN NaN 1.82 NaN 0.72 NaN NaN NaN 2.73E-06 2 8.8 binding;nucleotide binding cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial ribosome;non-membrane-bounded organelle;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome

K7EKI4;K7ELF1;K7ELQ0;Q9BYD3-2;K7ES61;Q9BYD3 "39S ribosomal protein L4, mitochondrial" MRPL4 ">tr|K7EKI4|K7EKI4_HUMAN 39S ribosomal protein L4, mitochondrial OS=Homo sapiens GN=MRPL4 PE=4 SV=1;>tr|K7ELF1|K7ELF1_HUMAN 39S ribosomal protein L4, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL4 PE=4 SV=1;>tr|K7ELQ0|K7ELQ0_HUMAN 39S ribosomal protein L" NaN NaN 1.59 NaN 0.7 NaN NaN NaN 8.95E-11 2 27.6 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome

H0YBU8;Q8N983-4;Q8N983-3;H0Y6Y8;B1AL05;Q8N983-2;Q8N983;C9J5Q3;B1AL06 "39S ribosomal protein L43, mitochondrial" MRPL43 ">tr|H0YBU8|H0YBU8_HUMAN 39S ribosomal protein L43, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL43 PE=4 SV=1;>sp|Q8N983-4|RM43_HUMAN Isoform 4 of 39S ribosomal protein L43, mitochondrial OS=Homo sapiens GN=MRPL43;>sp|Q8N983-3|RM43_HUMAN Isoform 3 of 39S" NaN NaN 1.85 NaN 0.49 NaN NaN NaN 1.01E-05 2 14.9 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial part;mitochondrial ribosome;mitochondrion;non-membrane-bounded organelle;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome

Q9H9J2 "39S ribosomal protein L44, mitochondrial" MRPL44 ">sp|Q9H9J2|RM44_HUMAN 39S ribosomal protein L44, mitochondrial OS=Homo sapiens GN=MRPL44 PE=1 SV=1" NaN NaN 1.84 NaN 0.78 NaN NaN NaN 1.04E-11 2 9 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing "binding;catalytic activity;double-stranded RNA binding;endonuclease activity;endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;endoribonuclease activity;endoribonuclease activity, producing 5'-phosphomonoesters;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding;ribonuclease activity;ribonuclease III activity;RNA binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome

P82914 "28S ribosomal protein S15, mitochondrial" MRPS15 ">sp|P82914|RT15_HUMAN 28S ribosomal protein S15, mitochondrial OS=Homo sapiens GN=MRPS15 PE=1 SV=1" NaN NaN 1.1 NaN 0.68 NaN NaN NaN 0.00032811 2 8.2 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial part;mitochondrial small ribosomal subunit;nuclear membrane;nuclear part;organellar small ribosomal subunit;organelle membrane;organelle part;ribonucleoprotein complex;small ribosomal subunit

B4DFG6;Q9Y676 "28S ribosomal protein S18b, mitochondrial" MRPS18B ">tr|B4DFG6|B4DFG6_HUMAN 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=2 SV=1;>sp|Q9Y676|RT18B_HUMAN 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=1 SV=1" NaN NaN 2.01 NaN 0.61 NaN NaN NaN 5.40E-07 2 22.3 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial small ribosomal subunit;non-membrane-bounded organelle;organellar small ribosomal subunit;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit

P82675;P82675-2 "28S ribosomal protein S5, mitochondrial" MRPS5 ">sp|P82675|RT05_HUMAN 28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5 PE=1 SV=2;>sp|P82675-2|RT05_HUMAN Isoform 2 of 28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5" NaN NaN 0.93 NaN 0.44 NaN NaN NaN 0.00086971 2 5.3 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome

P22033 "Methylmalonyl-CoA mutase, mitochondrial" MUT ">sp|P22033|MUTA_HUMAN Methylmalonyl-CoA mutase, mitochondrial OS=Homo sapiens GN=MUT PE=1 SV=4" NaN NaN 0.74 NaN 2.26 NaN NaN NaN 9.21E-06 2 3.6 amine metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;homocysteine metabolic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;post-embryonic development;primary metabolic process;short-chain fatty acid catabolic process;short-chain fatty acid metabolic process;small molecule catabolic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound metabolic process amine binding;amino acid binding;binding;carboxylic acid binding;catalytic activity;cation binding;cobalamin binding;intramolecular transferase activity;ion binding;isomerase activity;metal ion binding;methylmalonyl-CoA mutase activity;modified amino acid binding;tetrapyrrole binding;vitamin binding cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Carbon fixation pathways in prokaryotes;Glyoxylate and dicarboxylate metabolism;Propanoate metabolism;Valine, leucine and isoleucine degradation"

F8W8T1;P20591;H9KVC7;H9KVC9;P20591-2 "Interferon-induced GTP-binding protein Mx1;Interferon-induced GTP-binding protein Mx1, N-terminally processed" MX1 ">tr|F8W8T1|F8W8T1_HUMAN Interferon-induced GTP-binding protein Mx1, N-terminally processed OS=Homo sapiens GN=MX1 PE=2 SV=1;>sp|P20591|MX1_HUMAN Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=4;>tr|H9KVC7|H9KVC7_HUMAN Interferon-" 3.28 1.32 1.11 0.65 1.04 0.92 1.39 0.93 4.79E-06 2 3.8 biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;immune effector process;immune system process;induction of apoptosis;induction of programmed cell death;metabolic process;multi-organism process;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;regulation of reproductive process;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;type I interferon-mediated signaling pathway "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm Measles

E9PNW0;E9PJJ2;E9PS34;E9PNJ7;A8MXH2;C9J6D1;Q99733;F5HFY4;E9PKI2;E9PP22;E9PKT8;C9JZI7 Nucleosome assembly protein 1-like 4 NAP1L4;NAP1L4b >tr|E9PNW0|E9PNW0_HUMAN Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1;>tr|E9PJJ2|E9PJJ2_HUMAN Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1;>tr|E9PS34|E9PS34_HUMAN Nucleosome assem NaN NaN NaN NaN NaN NaN NaN NaN 1.66E-08 2 25.2 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;protein binding;unfolded protein binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

K7EMW4;Q969V3-2;Q969V3;K7ELZ9 Nicalin NCLN >tr|K7EMW4|K7EMW4_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=4 SV=1;>sp|Q969V3-2|NCLN_HUMAN Isoform 2 of Nicalin OS=Homo sapiens GN=NCLN;>sp|Q969V3|NCLN_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2;>tr|K7ELZ9|K7ELZ9_HUMAN Nicalin (Fragment) OS=Homo sapien NaN 0.98 1.91 NaN 3.41 NaN NaN 1.17 1.06E-05 2 4.7 biological regulation;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling catalytic activity;hydrolase activity;peptidase activity cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part

E7ENA9;F6Y097;Q92542-2;Q92542;Q5T205;Q5T209;H0Y6T7;H0Y3Z4 Nicastrin NCSTN >tr|E7ENA9|E7ENA9_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=2 SV=2;>tr|F6Y097|F6Y097_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=2 SV=1;>sp|Q92542-2|NICA_HUMAN Isoform 2 of Nicastrin OS=Homo sapiens GN=NCSTN;>sp|Q92542|NICA_HUMAN Nicastrin OS=Homo sapien NaN NaN NaN NaN NaN NaN NaN NaN 2.33E-08 2 7.3 amyloid precursor protein catabolic process;amyloid precursor protein metabolic process;beta-amyloid metabolic process;biological regulation;catabolic process;cell activation;cell proliferation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;epithelial cell proliferation;glycoprotein catabolic process;glycoprotein metabolic process;homeostasis of number of cells;homeostatic process;immune system process;leukocyte activation;leukocyte proliferation;lymphocyte activation;lymphocyte proliferation;macromolecule catabolic process;macromolecule metabolic process;membrane protein ectodomain proteolysis;membrane protein intracellular domain proteolysis;membrane protein proteolysis;metabolic process;mononuclear cell proliferation;myeloid cell homeostasis;nerve growth factor receptor signaling pathway;Notch receptor processing;Notch signaling pathway;positive regulation of catalytic activity;positive regulation of molecular function;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular process;regulation of metabolic process;regulation of molecular function;response to stimulus;signal transduction;T cell activation;T cell proliferation;transmembrane receptor protein tyrosine kinase signaling pathway "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;plasma membrane part;vacuolar membrane;vacuolar part;vesicle Alzheimer's disease;Notch signaling pathway

Q9UI09;H0YIT1;H0YID5;Q9UI09-2;F8VRD8 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 NDUFA12 >sp|Q9UI09|NDUAC_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Homo sapiens GN=NDUFA12 PE=1 SV=1;>tr|H0YIT1|H0YIT1_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 (Fragment) OS=Homo sapiens GN=NDUFA12 PE=2 SV=1; NaN NaN NaN NaN NaN NaN NaN NaN 0.00037372 2 17.9 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;multicellular organismal process;oxidation-reduction process;respiratory electron transport chain;respiratory gaseous exchange;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;small molecule metabolic process "catalytic activity;electron carrier activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;mitochondrion;NADH dehydrogenase complex;organelle;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

O43678;O43678-2 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 NDUFA2 >sp|O43678|NDUA2_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens GN=NDUFA2 PE=1 SV=3;>sp|O43678-2|NDUA2_HUMAN Isoform 2 of NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens GN=NDUFA2 1.16 1.74 1.27 2.17 0.6 0.37 0.48 0.85 1.03E-16 2 31.3 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

O75438;O75438-2 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 NDUFB1 >sp|O75438|NDUB1_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 OS=Homo sapiens GN=NDUFB1 PE=1 SV=1;>sp|O75438-2|NDUB1_HUMAN Isoform 2 of NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1 OS=Homo sapiens GN=NDUFB1 1.02 1.42 1.41 NaN 0.4 NaN 0.52 0.63 3.59E-06 2 34.5 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

O43676;C9JKQ2 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 NDUFB3 >sp|O43676|NDUB3_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 OS=Homo sapiens GN=NDUFB3 PE=1 SV=3;>tr|C9JKQ2|C9JKQ2_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 (Fragment) OS=Homo sapiens GN=NDUFB3 PE=2 SV=1 1.14 NaN 1.32 1.89 1.27 0.39 0.58 NaN 5.97E-05 2 21.4 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle inner membrane;organelle membrane;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q5W145;O95169;K9J7I2;E9PQ68;Q5W143"NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial" NDUFB8 ">tr|Q5W145|Q5W145_HUMAN NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 8, 19kDa, isoform CRA_a OS=Homo sapiens GN=NDUFB8 PE=2 SV=1;>sp|O95169|NDUB8_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial OS=Homo sapiens GN=NDUF" NaN NaN NaN NaN NaN NaN NaN NaN 2.57E-05 2 14.8 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;endoplasmic reticulum;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;mitochondrion;NADH dehydrogenase complex;organelle;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

E9PH64;Q9Y6M9;E7EWZ0;E9PF49 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 NDUFB9 >tr|E9PH64|E9PH64_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens GN=NDUFB9 PE=2 SV=1;>sp|Q9Y6M9|NDUB9_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens GN=NDUFB9 PE=1 SV=3;>tr|E7EWZ0|E7EWZ0 NaN NaN NaN NaN NaN NaN NaN NaN 4.77E-05 2 20.2 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;multicellular organismal process;neurological system process;oxidation-reduction process;respiratory electron transport chain;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;small molecule metabolic process;system process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;mitochondrion;NADH dehydrogenase complex;organelle;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

F5H5N1;B3KRI2;O75251;F5GXJ1 "NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial" NDUFS7 ">tr|F5H5N1|F5H5N1_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDUFS7 PE=2 SV=1;>tr|B3KRI2|B3KRI2_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDUFS7 PE=2 SV=" NaN NaN 1.48 NaN 0.79 NaN NaN NaN 0.00034603 2 9.9 "cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular metabolic process;cellular process;cellular protein complex assembly;electron transport chain;generation of precursor metabolites and energy;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;mitochondrial electron transport, NADH to ubiquinone;mitochondrial respiratory chain complex assembly;mitochondrial respiratory chain complex I assembly;mitochondrial respiratory chain complex I biogenesis;NADH dehydrogenase complex assembly;oxidation-reduction process;protein complex assembly;protein complex biogenesis;protein complex subunit organization;respiratory electron transport chain;small molecule metabolic process" "4 iron, 4 sulfur cluster binding;binding;catalytic activity;cation binding;cofactor binding;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;quinone binding" cell body;cell part;cell projection;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;neuron projection;neuronal cell body;organelle part;protein complex;respiratory chain complex I;synapse part;synaptic membrane Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q86UT6-2;Q86UT6;C9JLK8;C9JQE9;C9J0R6 NLR family member X1 NLRX1 >sp|Q86UT6-2|NLRX1_HUMAN Isoform 2 of NLR family member X1 OS=Homo sapiens GN=NLRX1;>sp|Q86UT6|NLRX1_HUMAN NLR family member X1 OS=Homo sapiens GN=NLRX1 PE=1 SV=1;>tr|C9JLK8|C9JLK8_HUMAN NLR family member X1 (Fragment)

OS=Homo sapiens GN=NLRX1 PE=2 SV=1;>t NaN NaN 0.9 NaN 2.79 NaN NaN NaN 0.00037221 2 2.5 biological regulation;defense response;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of type I interferon production;regulation of biological process;regulation of cytokine production;regulation of multicellular organismal process;regulation of type I interferon production;reproductive process;response to stimulus;response to stress;viral reproductive process;virus-host interaction adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane RIG-I-like receptor signaling pathway

C9K028;E5RHP0;E7ERL0;P22392;P15531;P15531-2;J3KPD9;P22392-2;Q32Q12 Nucleoside diphosphate kinase B;Nucleoside diphosphate kinase A;Nucleoside diphosphate kinase NME1;NME2;NME1-NME2 >tr|C9K028|C9K028_HUMAN Nucleoside diphosphate kinase A (Fragment) OS=Homo sapiens GN=NME1 PE=2 SV=1;>tr|E5RHP0|E5RHP0_HUMAN Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=2 SV=1;>tr|E7ERL0|E7ERL0_HUMAN Nucleoside diphosphate kinase A OS=Homo s 0.65 NaN NaN 0.97 NaN 0.74 1.15 NaN 0.00023936 2 33.3 "anatomical structure development;biological adhesion;biological regulation;biosynthetic process;carbohydrate homeostasis;cell adhesion;cellular biosynthetic process;cellular chemical homeostasis;cellular component organization;cellular component organization or biogenesis;cellular glucose homeostasis;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to drug;cellular response to fatty acid;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to lipid;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;CTP biosynthetic process;CTP metabolic process;developmental process;endocytosis;establishment of localization;glucose homeostasis;GTP biosynthetic process;GTP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;hippocampus development;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte differentiation;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;positive regulation of binding;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of DNA binding;positive regulation of epidermal cell differentiation;positive regulation of epidermis development;positive regulation of epithelial cell differentiation;positive regulation of epithelial cell proliferation;positive regulation of keratinocyte differentiation;positive regulation of molecular function;positive regulation of neuron projection development;primary metabolic process;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of DNA binding;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of gene expression;regulation of immune system process;regulation of keratinocyte differentiation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;response to amine stimulus;response to cAMP;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to fatty acid;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to lipid;response to monosaccharide stimulus;response to organic nitrogen;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to testosterone stimulus;ribonucleoside metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;transcription, DNA-dependent;transport;UTP biosynthetic process;UTP metabolic process;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;deoxyribonuclease activity;DNA binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;kinase activity;magnesium ion binding;metal ion binding;nuclease activity;nucleic acid binding;nucleic acid binding transcription factor activity;nucleobase-containing compound kinase activity;nucleoside diphosphate kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;phosphotransferase activity, nitrogenous group as acceptor;phosphotransferase activity, phosphate group as acceptor;protein histidine kinase activity;protein kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleoprotein binding;ribonucleotide binding;ribosomal small subunit binding;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cell projection;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;ruffle Purine metabolism;Pyrimidine metabolism

E9PFK5;P78316-2;P78316 Nucleolar protein 14 NOP14 >tr|E9PFK5|E9PFK5_HUMAN Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=2 SV=1;>sp|P78316-2|NOP14_HUMAN Isoform 2 of Nucleolar protein 14 OS=Homo sapiens GN=NOP14;>sp|P78316|NOP14_HUMAN Nucleolar protein 14 OS=Homo sapiens GN=NOP14 PE=1 SV=3 NaN 0.96 0.82 NaN 0.55 NaN NaN 0.56 9.01E-05 2 3.3 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cleavage involved in rRNA processing;endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage involved in rRNA processing;endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA);macromolecule metabolic process;metabolic process;ncRNA 5'-end processing;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;RNA 5'-end processing;RNA metabolic process;RNA processing;rRNA 5'-end processing" binding;nucleic acid binding;RNA binding;snoRNA binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;Noc complex;Noc4p-Nop14p complex;non-membrane-bounded organelle;nuclear part;nucleolar part;nucleolus;organelle;organelle part;preribosome;protein complex;ribonucleoprotein complex;small-subunit processome

O95478 Ribosome biogenesis protein NSA2 homolog NSA2 >sp|O95478|NSA2_HUMAN Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens GN=NSA2 PE=1 SV=1 NaN NaN NaN 2.22 NaN 0.43 NaN NaN 1.85E-05 2 8.8 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex

P49790;F6QR24 Nuclear pore complex protein Nup153 NUP153 >sp|P49790|NU153_HUMAN Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2;>tr|F6QR24|F6QR24_HUMAN Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=2 SV=1 NaN NaN 0.52 NaN 0.38 NaN NaN NaN 0.0010954 2 2 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of virus into host cell;establishment of localization;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;interaction with host;interspecies interaction between organisms;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide transport;movement in environment of other organism involved in symbiotic interaction;movement in host environment;mRNA transport;multi-organism process;negative regulation of biological process;negative regulation of intracellular transport;negative regulation of nucleobase-containing compound transport;negative regulation of nucleocytoplasmic transport;negative regulation of RNA export from nucleus;negative regulation of transport;nuclear pore complex assembly;nuclear pore organization;nucleic acid transport;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of glucose transport;regulation of intracellular transport;regulation of localization;regulation of nucleobase-containing compound transport;regulation of nucleocytoplasmic transport;regulation of RNA export from nucleus;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleocytoplasmic transporter activity;protein anchor;protein binding;structural constituent of nuclear pore;structural molecule activity;transition metal ion binding;transporter activity;zinc ion binding cell part;cytoplasm;inclusion body;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear inclusion body;nuclear membrane;nuclear part;nuclear periphery;nucleolus;nucleoplasm;organelle;organelle membrane;organelle part RNA transport

Q12769;E9PQY5;Q12769-2;E9PR16;G3V198 Nuclear pore complex protein Nup160 NUP160 >sp|Q12769|NU160_HUMAN Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3;>tr|E9PQY5|E9PQY5_HUMAN Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=2 SV=1;>sp|Q12769-2|NU160_HUMAN Isoform 2 of Nuclear pore complex protei NaN NaN 1.02 NaN 9.53 NaN NaN NaN 1.73E-05 2 1.5 anaphase;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular transport;M phase;M phase of mitotic cell cycle;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear export;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;organic substance transport;primary metabolic process;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process nucleocytoplasmic transporter activity;transporter activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;Nup107-160 complex;organelle part;protein complex RNA transport

F2Z2D0;Q92621 Nuclear pore complex protein Nup205 NUP205 >tr|F2Z2D0|F2Z2D0_HUMAN Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=2 SV=1;>sp|Q92621|NU205_HUMAN Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 NaN NaN 0.75 NaN 1.48 NaN NaN NaN 8.61E-06 2 13.5

"biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of RNA localization;glucose transport;hexose transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide transport;mRNA transport;nuclear pore complex assembly;nuclear pore organization;nucleic acid transport;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein import into nucleus, docking;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process" structural constituent of nuclear pore;structural molecule activity cell part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;organelle membrane;organelle part;pore complex;protein complex
RNA transport

P29728-2;P29728;F8W1C5 2-5-oligoadenylate synthase 2OAS2 >sp|P29728-2|OAS2_HUMAN Isoform p69 of 2-5-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2;>sp|P29728|OAS2_HUMAN 2-5-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2 PE=1 SV=3;>tr|F8W1C5|F8W1C5_HUMAN 2-5-oligoadenylate synthase 2 (Fragment) OS=Hom NaN NaN 1.57 NaN 0.78 NaN NaN NaN 3.74E-08 2 5.4 biological regulation;biosynthetic process;carbohydrate metabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;glycosylation;heterocycle biosynthetic process;heterocycle metabolic process;immune effector process;immune response;immune system process;interferon-gamma-mediated signaling pathway;macromolecule catabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;protein acylation;protein glycosylation;protein lipidation;protein metabolic process;protein modification process;protein myristoylation;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of cellular process;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;RNA catabolic process;RNA metabolic process;signal transduction;small molecule metabolic process;type I interferon-mediated signaling pathway "2'-5'-oligoadenylate synthetase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;adenylyltransferase activity;ATP binding;binding;catalytic activity;cation binding;double-stranded RNA binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;nucleotidyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;nucleus;organelle;perinuclear region of cytoplasm Hepatitis C;Measles

Q56VL3 OCIA domain-containing protein 2 OCIAD2 >sp|Q56VL3|OCAD2_HUMAN OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIAD2 PE=1 SV=1 1.02 1.2 1.38 1.4 0.29 0.56 0.84 1.33 2.12E-07 2 12.3 cell part;cytoplasmic part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle membrane;organelle part

P55809;Q8N5Z0;Q8N5Z0-2 "Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial;Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial" OXCT1;AADAT ">sp|P55809|SCOT1_HUMAN Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1;>sp|Q8N5Z0|AADAT_HUMAN Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial OS=Homo sapiens GN=AADAT PE=1 SV=2;>sp|Q8N5Z0-2|A" 1.2 2.48 0.19 5.83 0.5 1.57 1.06 0.89 0.0001166 2 3.3 2-oxoglutarate metabolic process;acetyl-CoA metabolic process;adipose tissue development;amine catabolic process;amine metabolic process;anatomical structure development;aromatic amino acid family catabolic process;aromatic amino acid family metabolic process;aromatic compound catabolic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;biological regulation;biosynthetic process;brain development;carbohydrate homeostasis;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular catabolic process;cellular chemical homeostasis;cellular glucose homeostasis;cellular homeostasis;cellular ketone body metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to acid;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;coenzyme metabolic process;cofactor metabolic process;developmental process;dicarboxylic acid metabolic process;glucose homeostasis;glutamate metabolic process;glutamine family amino acid metabolic process;heart development;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;indolalkylamine catabolic process;indolalkylamine metabolic process;indole-containing compound catabolic process;indole-containing compound metabolic process;ketone body catabolic process;ketone catabolic process;kynurenine metabolic process;lipid metabolic process;L-lysine catabolic process;L-lysine catabolic process to acetyl-CoA;L-lysine catabolic process to acetyl-CoA via saccharopine;L-lysine metabolic process;lysine catabolic process;lysine metabolic process;metabolic process;nitrogen compound metabolic process;organ development;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular process;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of secretion;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;response to acid;response to activity;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to monosaccharide stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to starvation;response to stimulus;response to stress;small molecule catabolic process;small molecule metabolic process;tissue development;tryptophan catabolic process;tryptophan catabolic process to kynurenine;tryptophan metabolic process "2-aminoadipate transaminase activity;3-oxoacid CoA-transferase activity;binding;catalytic activity;CoA-transferase activity;cofactor binding;identical protein binding;kynurenine-oxoglutarate transaminase activity;protein binding;protein dimerization activity;protein homodimerization activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;transferase activity, transferring sulfur-containing groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Butanoate metabolism;Lysine biosynthesis;Lysine degradation;Synthesis and degradation of ketone bodies;Tryptophan metabolism;Valine, leucine and isoleucine degradation"

P43034;B4DF38;I3L3N5 Platelet-activating factor acetylhydrolase IB subunit alpha PAFAH1B1 >sp|P43034|LIS1_HUMAN Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2;>tr|B4DF38|B4DF38_HUMAN Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=2 SV=1;>tr|I3L3N5|I3L NaN 4.43 NaN 3.08 NaN 1.68 NaN 1.03 2.42E-08 2 6.3 acrosome assembly;actin cytoskeleton organization;actin filament-based process;adult behavior;adult locomotory behavior;alcohol metabolic process;ameboidal cell migration;amine metabolic process;anaphase;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;axon cargo transport;axonogenesis;behavior;biological regulation;brain morphogenesis;catabolic process;cell communication;cell cycle phase;cell cycle process;cell differentiation;cell division;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell-cell signaling;cellular amine metabolic process;cellular biogenic amine metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular localization;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular process involved in reproduction in multicellular organism;central nervous system neuron axonogenesis;central nervous system neuron differentiation;central nervous system projection neuron axonogenesis;cerebral cortex neuron differentiation;cognition;corpus callosum morphogenesis;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;developmental process involved in reproduction;establishment of centrosome localization;establishment of localization;establishment of localization in cell;establishment of mitotic spindle localization;establishment of mitotic spindle orientation;establishment of nucleus localization;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;establishment of spindle orientation;ethanolamine-containing compound metabolic process;G2/M transition of mitotic cell cycle;glycerolipid metabolic process;glycerophospholipid metabolic process;hippocampus development;intracellular transport;layer formation in cerebral cortex;learning or memory;lipid catabolic process;lipid metabolic process;localization;locomotion;locomotory behavior;M phase;M phase of mitotic cell cycle;membrane disassembly;membrane organization;metabolic process;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based movement;microtubule-based process;microtubule-based transport;mitosis;mitotic anaphase;mitotic prometaphase;multicellular organismal process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of intracellular protein kinase cascade;negative regulation of JNK cascade;negative regulation of MAPKKK cascade;negative regulation of neuron projection development;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of stress-activated protein kinase signaling cascade;neural precursor cell proliferation;neuroblast proliferation;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;neuron migration;neuron projection morphogenesis;nitrogen compound metabolic process;nuclear division;nuclear envelope disassembly;nuclear envelope organization;nuclear migration;organ morphogenesis;organelle fission;organelle localization;organelle organization;organelle transport along microtubule;organophosphate metabolic process;phospholipid metabolic process;platelet activating factor metabolic process;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell cycle;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytokine-mediated signaling pathway;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of mitotic cell cycle;positive regulation of neurogenesis;positive regulation of response to cytokine stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein secretion;protein transport;regulation of anatomical structure morphogenesis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of cytokine-mediated signaling pathway;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of MAPKKK cascade;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to cytokine stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;reproductive process;response to stimulus;retrograde axon cargo transport;secretion;secretion by cell;signaling;small molecule metabolic process;stem cell division;synaptic transmission;system process;transport;vesicle localization;vesicle transport along microtubule binding;carbohydrate binding;catalytic activity;cytoskeletal protein binding;dynactin binding;dynein binding;enzyme binding;glycosaminoglycan binding;heparin binding;hydrolase activity;identical protein binding;microtubule binding;pattern binding;phospholipase binding;phosphoprotein binding;polysaccharide binding;protein binding;protein dimerization activity;protein homodimerization activity;tubulin binding astral microtubule;axon part;cell body;cell cortex;cell leading edge;cell part;cell projection;cell projection part;centrosome;chromosomal part;cilium;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytosol;envelope;growth cone;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinesin complex;kinetochore;macromolecular complex;membrane;microtubule;microtubule associated complex;microtubule organizing center;motile primary cilium;neuronal cell body;non-membrane-bounded organelle;nuclear envelope;nuclear membrane;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;perinuclear region of cytoplasm;primary cilium;protein complex;site of polarized growth;spindle microtubule;vesicle Ether lipid metabolism

E9PBS1;P22234;P22234-2 Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide synthase;Phosphoribosylaminoimidazole carboxylase PAICS >tr|E9PBS1|E9PBS1_HUMAN Phosphoribosylaminoimidazole carboxylase (Fragment) OS=Homo sapiens GN=PAICS PE=2 SV=1;>sp|P22234|PUR6_HUMAN Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3;>sp|P22234-2|PUR6_HUMAN Isoform 2 of Multifunctional protei 1.25 NaN NaN NaN NaN NaN 2.29 NaN 4.36E-05 2 5.1 biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;'de novo' IMP biosynthetic process;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;pigment biosynthetic process;pigment metabolic process;primary metabolic process;purine base biosynthetic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "5-(carboxyamino)imidazole ribonucleotide mutase activity;acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;intramolecular transferase activity;isomerase activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;lyase activity;nucleotide binding;phosphoribosylaminoimidazole carboxylase activity;phosphoribosylaminoimidazolesuccinocarboxamide synthase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part Purine metabolism

Q15365 Poly(rC)-binding protein 1 PCBP1 >sp|Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 0.84 1.14 0.53 0.74 1.69 1.71 1.05 0.83 5.43E-07 2 6.2 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;DNA binding;nucleic acid binding;RNA binding;single-stranded DNA binding;structure-specific DNA bindingcell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex Spliceosome

H3BRU6;G3V0E8;F8VZX2;B4DXP5;Q15366-4;Q15366-5;Q15366-6;Q15366-3;Q15366;Q15366-2;F8W0G4;F8VXH9;H3BSS4;F8W1G6;B4DLC0;F8VRH0 Poly(rC)-binding protein 2 PCBP2 ">tr|H3BRU6|H3BRU6_HUMAN Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=4 SV=1;>tr|G3V0E8|G3V0E8_HUMAN Poly(RC) binding protein 2, isoform CRA_f OS=Homo sapiens GN=PCBP2 PE=2 SV=1;>tr|F8VZX2|F8VZX2_HUMAN Poly(rC)-binding protein 2 OS=Homo" 1.3 1.18 0.74 0.99 1.22 0.95 0.97 0.75 2.78E-06 2 8 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of defense response;negative regulation of defense response to virus;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of multicellular organismal process;negative regulation of multi-organism process;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of type I interferon production;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of immune effector process;regulation of immune system process;regulation of multicellular organismal process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of type I interferon production;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;ubiquitin-dependent protein catabolic process" binding;DNA binding;nucleic acid binding;RNA binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex

F8WF02;P11177-3;P11177-2;C9J634;P11177 "Pyruvate dehydrogenase E1 component subunit beta, mitochondrial" PDHB ">tr|F8WF02|F8WF02_HUMAN Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=2 SV=1;>sp|P11177-3|ODPB_HUMAN Isoform 3 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB;>sp|P1117" 0.52 1.18 1.1 NaN 0.89 NaN 1.23 1.16 9.96E-09 2 9.6 acetyl-CoA biosynthetic process;acetyl-CoA biosynthetic process from pyruvate;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor catabolic process;cofactor metabolic process;glucose metabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of metabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor;pyruvate dehydrogenase (acetyl-transferring) activity;pyruvate dehydrogenase activity" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part;protein complex;pyruvate dehydrogenase complex "Butanoate metabolism;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Pyruvate metabolism;Valine, leucine and isoleucine biosynthesis"

P13667 Protein disulfide-isomerase A4 PDIA4 >sp|P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 NaN NaN 0.52 NaN 2.13 NaN NaN NaN 7.82E-05 2 3.6 biological regulation;cell redox homeostasis;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;glycerol ether metabolic process;homeostatic process;macromolecule metabolic process;metabolic process;organic ether metabolic process;primary metabolic process;protein folding;protein metabolic process;protein secretion;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;secretion;secretion by cell;small molecule metabolic process;transport "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;vesicle Protein processing in endoplasmic reticulum;Vibrio cholerae infection

B7Z254;Q15084;F8WA83;B5MCQ5;Q15084-2 Protein disulfide-isomerase A6 PDIA6 >tr|B7Z254|B7Z254_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=2 SV=1;>sp|Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1;>tr|F8WA83|F8WA83_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDI 1.12 0.43 0.84 0.23 1.21 0.61 2.55 1.17 1.71E-07 2 6.6 activation of signaling protein activity involved in unfolded protein response;biological regulation;cell redox homeostasis;cellular homeostasis;cellular process;glycerol ether metabolic process;homeostatic process;metabolic process;organic ether metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part;pigment granule;plasma membrane;vesicle Protein processing in endoplasmic reticulum

E9PBF5;Q96HC4-4;Q96HC4;D6RB78;H0Y929;H0YBI4;Q96HC4-3;F5H0X8;H0Y8Y3;Q96HC4-2;D3YTJ1;F5H7Y0 PDZ and LIM domain protein 5 PDLIM5 >tr|E9PBF5|E9PBF5_HUMAN PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=2 SV=1;>sp|Q96HC4-4|PDLI5_HUMAN Isoform 4 of PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5;>sp|Q96HC4|PDLI5_HUMAN PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDL NaN 0.25 0.41 NaN 2.52 NaN NaN 1.07 0.00022785 2 4.8 biological regulation;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of dendritic spine development;regulation of dendritic spine morphogenesis;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of synapse assembly;regulation of synapse organization actin binding;actinin binding;binding;cation binding;cytoskeletal protein binding;enzyme binding;ion binding;kinase binding;metal ion binding;protein binding;protein kinase binding;protein kinase C binding;transition metal ion binding;zinc ion binding actin cytoskeleton;cell junction;cell part;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;postsynaptic density;postsynaptic membrane;synapse part;synaptic membrane;Z disc

B5MCF9;O00541-2;O00541;C9JXJ1;H7C267;B3KXD6 Pescadillo homolog PES1 >tr|B5MCF9|B5MCF9_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1;>sp|O00541-2|PESC_HUMAN Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1;>sp|O00541|PESC_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1;>tr|C9JXJ1|C9JXJ1_HUMAN NaN NaN 1.17 NaN 1.4 NaN NaN NaN 0.00018009 2 3.2 "biological regulation;cell cycle phase;cell cycle process;cell proliferation;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;localization;macromolecule localization;macromolecule metabolic process;maturation of 5.8S rRNA;maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);maturation of LSU-rRNA;maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;metaphase;mitotic metaphase;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleolus organization;nucleus organization;organelle organization;primary metabolic process;protein localization;protein localization to organelle;regulation of biological process;regulation of cell cycle;regulation of cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing" "cell part;chromosome;condensed chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolar part;nucleolus;nucleoplasm;organelle;organelle part;PeBoW complex;preribosome;preribosome, large subunit precursor;protein complex;ribonucleoprotein complex"

O15173 Membrane-associated progesterone receptor component 2 PGRMC2 >sp|O15173|PGRC2_HUMAN Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1 1.02 0.99 1.9 0.43 1.24 1.12 1.17 1.16 2.44E-09 2 12.1 binding;cation binding;heme binding;ion binding;iron ion binding;ligand-dependent nuclear receptor activity;lipid binding;metal ion binding;molecular transducer activity;receptor activity;signal transducer activity;signaling receptor activity;steroid binding;steroid hormone receptor activity;tetrapyrrole binding;transition metal ion binding cell part;integral to membrane;intrinsic to membrane;membrane part

Q9HBL7 Plasminogen receptor (KT) PLGRKT >sp|Q9HBL7|PLRKT_HUMAN Plasminogen receptor (KT) OS=Homo sapiens GN=PLGRKT PE=1 SV=1 0.71 1.11 1.91 2.01 0.47 0.34 1.27 0.51 1.21E-08 2 14.3 biological regulation;chemotaxis;defense response;inflammatory response;locomotion;positive regulation of plasminogen activation;positive regulation of protein processing;regulation of biological process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of plasminogen activation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein processing;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;response to wounding;taxis cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;plasma membrane part

B7Z6M1;F8W8D8;B4DGB4;P13797;H7C4N2;B4DI60 Plastin-3 PLS3 >tr|B7Z6M1|B7Z6M1_HUMAN Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1;>tr|F8W8D8|F8W8D8_HUMAN Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1;>tr|B4DGB4|B4DGB4_HUMAN Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1;>sp|P13797|PLST_HUMAN Plastin-3 OS=Homo sapiens GN=P NaN NaN 1.16 NaN 3.21 NaN NaN NaN 0.00011686 2 4.1 binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasm;intracellular part

Q8IY17-5;Q8IY17-2;M0QYF5;M0QZK5;M0R2H4;M0R2K2;Q8IY17-3;Q8IY17;Q8IY17-4 Neuropathy target esterase PNPLA6 >sp|Q8IY17-5|PLPL6_HUMAN Isoform 5 of Neuropathy target esterase OS=Homo sapiens GN=PNPLA6;>sp|Q8IY17-2|PLPL6_HUMAN Isoform 2 of Neuropathy target esterase OS=Homo sapiens GN=PNPLA6;>tr|M0QYF5|M0QYF5_HUMAN Neuropathy target esterase (Fragment) OS=Homo sapi NaN NaN NaN NaN NaN NaN NaN NaN 3.42E-06 2 3.9 alcohol metabolic process;amine metabolic process;catabolic process;cell death;cellular amine metabolic process;cellular biogenic amine metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;ethanolamine-containing compound metabolic process;glycerolipid metabolic process;glycerophospholipid metabolic process;lipid catabolic process;lipid metabolic process;metabolic process;nitrogen compound metabolic process;organophosphate metabolic process;phosphatidylcholine metabolic process;phospholipid metabolic process;primary metabolic process;small molecule metabolic process "carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;lysophospholipase activity;phospholipase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Glycerophospholipid metabolism

P54098;H0YCV2 DNA polymerase subunit gamma-1 POLG >sp|P54098|DPOG1_HUMAN DNA polymerase subunit gamma-1 OS=Homo sapiens GN=POLG PE=1 SV=1;>tr|H0YCV2|H0YCV2_HUMAN DNA polymerase subunit gamma-1 (Fragment) OS=Homo sapiens GN=POLG PE=2 SV=1 1.24 1.83 2.34 1.2 0.51 0.55 0.86 1.06 0.00033347 2 1.5 "aging;base-excision repair, gap-filling;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;developmental process;DNA metabolic process;DNA replication;DNA-dependent DNA replication;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrial DNA metabolic process;mitochondrial DNA replication;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process" "binding;catalytic activity;chromatin binding;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;exonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding;nucleotidyltransferase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;DNA polymerase complex;gamma DNA polymerase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle part;protein complex

C9J4M6;C9J2Y9;P30876 DNA-directed RNA polymerase;DNA-directed RNA polymerase II subunit RPB2 POLR2B >tr|C9J4M6|C9J4M6_HUMAN DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=2 SV=2;>tr|C9J2Y9|C9J2Y9_HUMAN DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=2 SV=2;>sp|P30876|RPB2_HUMAN DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapien NaN NaN NaN NaN NaN NaN NaN NaN 5.20E-05 2 2.7 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA capping;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA capping;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent;transcription-coupled nucleotide-excision repair;viral reproductive process" "binding;catalytic activity;cation binding;chromatin binding;DNA binding;DNA-directed RNA polymerase activity;ion binding;metal ion binding;nucleic acid binding;nucleoside binding;nucleotidyltransferase activity;ribonucleoside binding;RNA polymerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" "cell part;DNA-directed RNA polymerase complex;DNA-directed RNA polymerase II, core complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear DNA-directed RNA polymerase complex;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;RNA polymerase complex" Huntington's disease;Purine metabolism;Pyrimidine metabolism;RNA polymerase

H7C446;A8MV53;Q9NQ55-2;Q9NQ55;Q9NQ55-3 Suppressor of SWI4 1 homolog PPAN ">tr|H7C446|H7C446_HUMAN Suppressor of SWI4 1 homolog (Fragment) OS=Homo sapiens GN=PPAN PE=4 SV=1;>tr|A8MV53|A8MV53_HUMAN HCG2033702, isoform CRA_a OS=Homo sapiens GN=PPAN PE=2 SV=1;>sp|Q9NQ55-2|SSF1_HUMAN Isoform 2 of Suppressor of SWI4 1 homolog OS=Homo" NaN NaN 0.62 NaN 1.33 NaN NaN NaN 2.33E-06 2 10.6 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

P62136-3;P62136;P62136-2;E9PMD7 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;Serine/threonine-protein phosphatase PPP1CA >sp|P62136-3|PP1A_HUMAN Isoform 3 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA;>sp|P62136|PP1A_HUMAN Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1;>sp|P NaN 1.38 0.79 1.38 0.45 0.75 NaN 0.86 1.69E-06 2 7.3 acylglycerol catabolic process;acylglycerol metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;branching morphogenesis of a tube;carbohydrate metabolic process;catabolic process;cell cycle;cell division;cell surface receptor linked signaling pathway;cellular carbohydrate metabolic process;cellular catabolic process;cellular glucan metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;dephosphorylation;developmental process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;generation of precursor metabolites and energy;glucan metabolic process;glycerol ether catabolic process;glycerol ether metabolic process;glycerolipid catabolic process;glycerolipid metabolic process;glycogen metabolic process;lipid catabolic process;lipid metabolic process;lung development;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of a branching structure;multicellular organismal process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;neutral lipid catabolic process;neutral lipid metabolic process;organ development;organic ether metabolic process;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;polysaccharide metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen biosynthetic process;regulation of glycogen catabolic process;regulation of glycogen metabolic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to stimulus;signal transduction;small molecule metabolic process;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;triglyceride catabolic process;triglyceride metabolic process;tube morphogenesis "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity;ribonucleoprotein binding" cell part;cell projection;cell projection part;cytoplasmic part;cytosol;dendritic spine;glycogen granule;histone methyltransferase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL5-L complex;neuron projection;neuron spine;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;organelle;organelle part;perikaryon;protein complex;protein phosphatase type 1 complex;protein serine/threonine phosphatase complex;PTW/PP1 phosphatase complex Focal adhesion;Insulin signaling pathway;Long-term potentiation;Meiosis - yeast;Oocyte meiosis;Regulation of actin cytoskeleton;Vascular smooth muscle contraction

C9J9S3;C9JP48;P62140 Serine/threonine-protein phosphatase;Serine/threonine-protein phosphatase PP1-beta catalytic subunit PPP1CB >tr|C9J9S3|C9J9S3_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CB PE=2 SV=1;>tr|C9JP48|C9JP48_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CB PE=2 SV=1;>sp|P62140|PP1B_HUMAN Serine/threonine-p 0.76 1.63 0.64 1.54 0.68 1.26 0.75 0.79 3.65E-06 2 18.4 acylglycerol catabolic process;acylglycerol metabolic process;biological regulation;carbohydrate metabolic process;catabolic process;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular carbohydrate metabolic process;cellular catabolic process;cellular glucan metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;dephosphorylation;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;G2/M transition of mitotic cell cycle;generation of precursor metabolites and energy;glucan metabolic process;glycerol ether catabolic process;glycerol ether metabolic process;glycerolipid catabolic process;glycerolipid metabolic process;glycogen metabolic process;lipid catabolic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal

transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;neutral lipid catabolic process;neutral lipid metabolic process;organic ether metabolic process;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;polysaccharide metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of cell adhesion;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen biosynthetic process;regulation of glycogen catabolic process;regulation of glycogen metabolic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to stimulus;signal transduction;small molecule metabolic process;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;triglyceride catabolic process;triglyceride metabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;myosin phosphatase activity;myosin-light-chain-phosphatase activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity" cell part;cytoplasmic part;glycogen granule;histone methyltransferase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL5-L complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;organelle;organelle part;protein complex;protein phosphatase type 1 complex;protein serine/threonine phosphatase complex;PTW/PP1 phosphatase complex
Focal adhesion;Insulin signaling pathway;Long-term potentiation;Meiosis - yeast;Oocyte meiosis;Regulation of actin cytoskeleton;Vascular smooth muscle contraction

P32119;A6NIW5 Peroxiredoxin-2 PRDX2 ">sp|P32119|PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5;>tr|A6NIW5|A6NIW5_HUMAN Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=2 SV=2"NaN NaN 0.11 3.76 0.37 1.63 NaN NaN 1.16E-06 2 14.1 biological regulation;catabolic process;cellular catabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to oxygen radical;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cellular response to superoxide;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of neuron apoptosis;regulation of programmed cell death;removal of superoxide radicals;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to oxygen radical;response to reactive oxygen species;response to stimulus;response to stress;response to superoxide;superoxide metabolic process "antioxidant activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;peroxiredoxin activity;thioredoxin peroxidase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part

P04156-2;A2A2V1;P04156 Major prion protein PRNP >sp|P04156-2|PRIO_HUMAN Isoform 2 of Major prion protein OS=Homo sapiens GN=PRNP;>tr|A2A2V1|A2A2V1_HUMAN Major prion protein (Fragment) OS=Homo sapiens GN=PRNP PE=2 SV=1;>sp|P04156|PRIO_HUMAN Major prion protein OS=Homo sapiens GN=PRNP PE=1 SV=1 1.38 2.22 1.49 1.24 0.39 0.21 0.51 0.97 7.29E-21 2 8.1 "axon guidance;behavior;biological regulation;cation homeostasis;cell cycle arrest;cell cycle process;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular copper ion homeostasis;cellular homeostasis;cellular ion homeostasis;cellular process;chemical homeostasis;chemotaxis;cognition;copper ion homeostasis;homeostatic process;ion homeostasis;learning or memory;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multicellular organismal process;negative regulation of activated T cell proliferation;negative regulation of antigen receptor-mediated signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of calcineurin-NFAT signaling pathway;negative regulation of calcium-mediated signaling;negative regulation of cell activation;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cytokine production;negative regulation of immune system process;negative regulation of interferon-gamma production;negative regulation of interleukin-17 production;negative regulation of interleukin-2 production;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of mononuclear cell proliferation;negative regulation of multicellular organismal process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of response to stimulus;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of T cell activation;negative regulation of T cell proliferation;negative regulation of T cell receptor signaling pathway;neurological system process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;regulation of activated T cell proliferation;regulation of antigen receptor-mediated signaling pathway;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcineurin-NFAT signaling pathway;regulation of calcium-mediated signaling;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of gene expression;regulation of immune system process;regulation of interferon-gamma production;regulation of interleukin-17 production;regulation of interleukin-2 production;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of T cell activation;regulation of T cell proliferation;regulation of T cell receptor signaling pathway;regulation of transcription, DNA-dependent;response to cadmium ion;response to chemical stimulus;response to copper ion;response to external stimulus;response to inorganic substance;response to metal ion;response to oxidative stress;response to stimulus;response to stress;system process;taxis"

binding;cation binding;copper ion binding;cytoskeletal protein binding;ion binding;metal ion binding;microtubule binding;protein binding;transition metal ion binding;tubulin binding

anchored to membrane;cell part;cytoplasmic part;endoplasmic reticulum;extrinsic to membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane raft;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane Prion diseases

G3V3U4;G3V3I1;G3V295;B4DXJ9;P60900;G3V5Z7 Proteasome subunit alpha type;Proteasome subunit alpha type-6 PSMA6 >tr|G3V3U4|G3V3U4_HUMAN Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1;>tr|G3V3I1|G3V3I1_HUMAN Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1;>tr|G3V295|G3V295_HUMAN Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 0.67 1.41 0.4 0.94 0.33 0.42 1.45 1.5 6.83E-07 2 23.4 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of gene expression;regulation of inflammatory response;regulation of ligase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" "binding;catalytic activity;endopeptidase activity;hydrolase activity;nucleic acid binding;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;contractile fiber part;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear matrix;nuclear part;nucleoplasm;nucleus;organelle;organelle part;polysome;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex;ribonucleoprotein complex;RNA granule;sarcomere" Proteasome

P20618 Proteasome subunit beta type-1 PSMB1 >sp|P20618|PSB1_HUMAN Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 1.16 0.75 NaN NaN NaN NaN 2.29 1.32 1.70E-09 2 9.5 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome core complex;protein complex Proteasome

B4DR63;P62191;G3V4X1 26S protease regulatory subunit 4 PSMC1 >tr|B4DR63|B4DR63_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=2 SV=1;>sp|P62191|PRS4_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1;>tr|G3V4X1|G3V4X1_HUMAN 26S protease regulatory subunit 4 (Fragment) OS= 0.81 1.25 NaN 0.44 NaN 0.75 2.88 1.47 2.01E-08 2 8.7 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome accessory complex;protein complex Proteasome

C9J7B7;Q15008;C9IZE4;C9J0E9;E9PHI9;Q6UV22 26S proteasome non-ATPase regulatory subunit 6PSMD6 >tr|C9J7B7|C9J7B7_HUMAN 26S proteasome non-ATPase regulatory subunit 6 (Fragment) OS=Homo sapiens GN=PSMD6 PE=2 SV=1;>sp|Q15008|PSMD6_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1;>tr|C9IZE4|C9IZE4_HUMAN 26S protea 0.86 1.83 0.36 1.23 0.44 1.53 1.13 1.67 4.13E-05 2 16 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction" "ATPase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;pyrophosphatase activity" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;proteasome complex;protein complex Proteasome

Q6Y1H2;H7C4K8;C9JWG1 Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 2 PTPLB >sp|Q6Y1H2|HACD2_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 2 OS=Homo sapiens GN=PTPLB PE=1 SV=1;>tr|H7C4K8|H7C4K8_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 2 (Fragment) OS=Homo sapiens GN= NaN 0.9 1.36 1.25 0.79 0.71 NaN 0.97 1.32E-05 2 8.7 biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid biosynthetic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process catalytic activity;lyase activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Biosynthesis of unsaturated fatty acids

Q00577 Transcriptional activator protein Pur-alpha PURA >sp|Q00577|PURA_HUMAN Transcriptional activator protein Pur-alpha OS=Homo sapiens GN=PURA PE=1 SV=2 NaN NaN NaN 3.18 NaN 0.83 NaN NaN 4.44E-12 2 14.9 "anatomical structure development;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA unwinding involved in replication;DNA-dependent DNA replication initiation;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;system development" "binding;DNA binding;double-stranded DNA binding;double-stranded telomeric DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;purine-rich negative regulatory element binding;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific distal enhancer binding RNA polymerase II transcription factor activity;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;telomeric DNA binding;transcription factor binding;transcription regulatory region DNA binding;translation regulator activity;translation regulator activity, nucleic acid binding;translation repressor activity;translation repressor activity, nucleic acid binding" "cell body;cell part;cell projection;chromosomal part;chromosome, telomeric region;cytoplasm;dendrite;DNA replication factor A complex;intracellular organelle part;intracellular part;macromolecular complex;neuron projection;neuronal cell body;nuclear chromosome part;nuclear chromosome, telomeric region;nuclear part;organelle part;protein complex"

Q9UL25 Ras-related protein Rab-21 RAB21 >sp|Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=31.15 NaN NaN NaN NaN NaN 0.9 NaN 1.64E-23 2 10.2 biological regulation;cellular process;cellular response to stimulus;establishment of localization;establishment of protein localization;intracellular signal transduction;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell division site part;cell part;cleavage furrow;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endosomal part;endosome;endosome membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;vesicle membrane

Q13637;O14966;P57729 Ras-related protein Rab-32;Ras-related protein Rab-7L1;Ras-related protein Rab-38 RAB32;RAB7L1;RAB38 >sp|Q13637|RAB32_HUMAN Ras-related protein Rab-32 OS=Homo sapiens GN=RAB32 PE=1 SV=3;>sp|O14966|RAB7L_HUMAN Ras-related protein Rab-7L1 OS=Homo sapiens GN=RAB7L1 PE=1 SV=1;>sp|P57729|RAB38_HUMAN Ras-related protein Rab-38 OS=Homo sapiens GN=RAB38 PE=1 SV=1 NaN NaN 1.62 NaN 1.53 NaN NaN NaN 6.55E-06 2 9.8 biological regulation;cation homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular monovalent inorganic cation homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;establishment of localization;establishment of protein localization;homeostatic process;intracellular pH reduction;intracellular signal transduction;ion homeostasis;monovalent inorganic cation homeostasis;organelle organization;pH reduction;phagosome acidification;phagosome maturation;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular pH;regulation of cellular process;regulation of intracellular pH;regulation of pH;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;organelle membrane;organelle part;phagocytic vesicle;phagocytic vesicle membrane;pigment granule;plasma membrane;vesicle;vesicle membrane

P51151;Q9NP90 Ras-related protein Rab-9A;Ras-related protein Rab-9B RAB9A;RAB9B >sp|P51151|RAB9A_HUMAN Ras-related protein Rab-9A OS=Homo sapiens GN=RAB9A PE=1 SV=1;>sp|Q9NP90|RAB9B_HUMAN Ras-related protein Rab-9B OS=Homo sapiens GN=RAB9B PE=1 SV=1 0.98 0.95 0.95 0.43 2.67 2.23 1.08 1.12 1.20E-14 2 12.4 biological regulation;cellular process;cellular response to stimulus;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi to endosome transport;Golgi vesicle transport;intracellular signal transduction;intracellular transport;positive regulation of biological process;positive regulation of cellular process;positive regulation of exocytosis;positive regulation of secretion;positive regulation of transport;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endosome;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;phagocytic vesicle;phagocytic vesicle membrane;plasma

membrane;vacuole;vesicle;vesicle membrane Measles
J3KSC4;J3QLK0;B1AH77;B1AH80;P63000;P60763;P15153;P63000-2;B1AH78 Ras-related C3 botulinum toxin substrate 1;Ras-related C3 botulinum toxin substrate 3;Ras-related C3 botulinum toxin substrate 2 RAC3;RAC2;RAC1 >tr|J3KSC4|J3KSC4_HUMAN Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens GN=RAC3 PE=3 SV=1;>tr|J3QLK0|J3QLK0_HUMAN Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens GN=RAC3 PE=3 SV=1;>tr|B1AH77|B1AH77_HUMAN Ras-rela 0.83 2.27 1.03 1.28 0.69 0.81 0.61 1.02 8.73E-128 2 19.2 "actin cytoskeleton organization;actin filament organization;actin filament polymerization;actin filament-based process;actin polymerization or depolymerization;anatomical structure arrangement;anatomical structure homeostasis;anatomical structure morphogenesis;auditory receptor cell morphogenesis;axon guidance;biological adhesion;biological regulation;bone resorption;cell activation;cell adhesion;cell chemotaxis;cell differentiation;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell morphogenesis involved in neuron differentiation;cell motility;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to stimulus;cerebral cortex cell migration;cerebral cortex radially oriented cell migration;chemotaxis;cochlea morphogenesis;cytoskeleton organization;defense response;dendrite morphogenesis;developmental process;dopaminergic neuron differentiation;embryonic morphogenesis;embryonic olfactory bulb interneuron precursor migration;engulfment of apoptotic cell;enzyme linked receptor protein signaling pathway;epithelial cell morphogenesis;forebrain cell migration;homeostatic process;hyperosmotic response;immune response;immune system process;inflammatory response;innate immune response;intracellular signal transduction;lamellipodium assembly;leukocyte chemotaxis;leukocyte migration;localization;localization within membrane;locomotion;lymphocyte costimulation;macromolecular complex assembly;macromolecular complex subunit organization;mast cell chemotaxis;membrane invagination;membrane organization;multicellular organismal process;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of endocytosis;negative regulation of interleukin-23 production;negative regulation of multicellular organismal process;negative regulation of receptor-mediated endocytosis;negative regulation of transport;nerve growth factor receptor signaling pathway;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;neuron projection development;neuron projection morphogenesis;non-canonical Wnt receptor signaling pathway;organelle organization;phagocytosis, engulfment;platelet activation;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of lamellipodium assembly;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of protein complex assembly;positive regulation of protein polymerization;positive regulation of Ras protein signal transduction;positive regulation of response to stimulus;positive regulation of Rho protein signal transduction;positive regulation of signal transduction;positive regulation of signaling;positive regulation of small GTPase mediated signal transduction;positive regulation of T cell activation;positive regulation of transferase activity;protein complex assembly;protein complex subunit organization;protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of cytoskeleton organization;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of endocytosis;regulation of establishment of planar polarity;regulation of hydrogen peroxide metabolic process;regulation of immune effector process;regulation of immune system process;regulation of interleukin-23 production;regulation of kinase activity;regulation of lamellipodium assembly;regulation of leukocyte activation;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein polymerization;regulation of Ras protein signal transduction;regulation of reactive oxygen species metabolic process;regulation of receptor-mediated endocytosis;regulation of respiratory burst;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of T cell activation;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to osmotic stress;response to stimulus;response to stress;response to wounding;ruffle organization;signal transduction;small GTPase mediated signal transduction;substrate adhesion-dependent cell spreading;substrate-independent telencephalic tangential interneuron migration;substrate-independent telencephalic tangential migration;system process;T cell costimulation;tangential migration from the subventricular zone to the olfactory bulb;taxis;telencephalon cell migration;tissue homeostasis;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproduction;Wnt receptor signaling pathway;Wnt receptor signaling pathway, planar cell polarity pathway" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl

ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell body;cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;endomembrane system;envelope;extrinsic to membrane;extrinsic to plasma membrane;filamentous actin;Golgi apparatus part;Golgi membrane;growth cone;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;leading edge membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuronal cell body;nuclear envelope;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;phagocytic cup;pigment granule;plasma membrane;plasma membrane part;protein complex;ruffle membrane;site of polarized growth;trans-Golgi network;vesicle Adherens junction;Amyotrophic lateral sclerosis (ALS);Axon guidance;B cell receptor signaling pathway;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Colorectal cancer;Epithelial cell signaling in Helicobacter pylori infection;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Leukocyte transendothelial migration;MAPK signaling pathway;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Osteoclast differentiation;Pancreatic cancer;Pancreatic secretion;Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;Toll-like receptor signaling pathway;VEGF signaling pathway;Viral myocarditis;Wnt signaling pathway

O60216 Double-strand-break repair protein rad21 homolog RAD21 >sp|O60216|RAD21_HUMAN Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2 1.13 1.15 1.38 3.02 0.6 0.43 0.39 0.54 2.39E-08 2 4.6 "anaphase;apoptosis;biological regulation;cell cycle phase;cell cycle process;cell death;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular response to stimulus;cellular response to stress;chromosome segregation;cytokinesis;death;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;localization;M phase;M phase of mitotic cell cycle;macromolecule localization;macromolecule metabolic process;metabolic process;mitotic anaphase;mitotic prometaphase;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;protein localization;protein localization to chromatin;protein localization to chromosome;protein localization to organelle;reciprocal DNA recombination;reciprocal meiotic recombination;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle" "cell part;chromosomal part;chromosome, centromeric region;cohesin complex;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;meiotic cohesin complex;nuclear chromosome part;nuclear cohesin complex;nuclear meiotic cohesin complex;nuclear part;nucleoplasm;organelle part;protein complex" Cell cycle;Cell cycle - yeast

F8W7I9;P46060;H0Y4Q3 Ran GTPase-activating protein 1 RANGAP1 >tr|F8W7I9|F8W7I9_HUMAN Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=2 SV=1;>sp|P46060|RAGP1_HUMAN Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1;>tr|H0Y4Q3|H0Y4Q3_HUMAN Ran GTPase-activating protein 1 (Fragment) OS=H NaN NaN 0.45 NaN 0.67 NaN NaN NaN 4.72E-06 2 5.1 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular process;cellular response to stimulus;M phase;M phase of mitotic cell cycle;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of nucleocytoplasmic transport;negative regulation of protein export from nucleus;negative regulation of protein transport;negative regulation of transport;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Ran GTPase activity;positive regulation of Ras GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of establishment of protein localization;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein localization;regulation of protein transport;regulation of purine nucleotide catabolic process;regulation of Ran GTPase activity;regulation of Ras GTPase activity;regulation of transport;response to stimulus;signal transduction enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Ran GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;nuclear pore;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;pore complex;protein complex;spindle pole RNA transport

A2A2V2;P42696;Q5TCT4;P42696-2 RNA-binding protein 34 RBM34 >tr|A2A2V2|A2A2V2_HUMAN RNA-binding protein 34 (Fragment) OS=Homo sapiens GN=RBM34 PE=2 SV=1;>sp|P42696|RBM34_HUMAN RNA-binding protein 34 OS=Homo sapiens GN=RBM34 PE=1 SV=2;>tr|Q5TCT4|Q5TCT4_HUMAN RNA-binding protein 34 (Fragment) OS=Homo sapiens GN=RBM34 NaN NaN 1.22 NaN 0.65 NaN NaN NaN 0.00011548 2 5.6 binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

Q14257;F8WCY5;H0YL43;A8MXP8 Reticulocalbin-2 RCN2 >sp|Q14257|RCN2_HUMAN Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=1 SV=1;>tr|F8WCY5|F8WCY5_HUMAN Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=2 SV=1;>tr|H0YL43|H0YL43_HUMAN Reticulocalbin-2 (Fragment) OS=Homo sapiens GN=RCN2 PE=4 SV=1;>tr|A8MXP8|A8MXP8_HUMA 0.89 NaN NaN 0.35 NaN 2.12 1.63 NaN 6.36E-11 2 12 binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part

Q96NR8 Retinol dehydrogenase 12 RDH12 >sp|Q96NR8|RDH12_HUMAN Retinol dehydrogenase 12 OS=Homo sapiens GN=RDH12 PE=1 SV=3 0.65 0.35 0.23 NaN 4.43 NaN 2.05 1.13 0.00013811 2 7.6 "biological regulation;cellular component maintenance;cellular component organization;cellular component organization or biogenesis;cellular hormone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;diterpenoid metabolic process;fat-soluble vitamin metabolic process;hormone metabolic process;isoprenoid metabolic process;lipid metabolic process;metabolic process;photoreceptor cell maintenance;phototransduction;phototransduction, visible light;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of hormone levels;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;retinol metabolic process;signal transduction;small molecule metabolic process;terpenoid metabolic process;vitamin A metabolic process;vitamin metabolic process" "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;retinol dehydrogenase activity" cell part;intracellular;membrane;photoreceptor inner segment membrane Retinol metabolism

P84095 Rho-related GTP-binding protein RhoGRHOG >sp|P84095|RHOG_HUMAN Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1 0.82 1.09 NaN 0.68 NaN 1.11 0.93 1.04 9.93E-05 2 13.6 "actin cytoskeleton organization;actin filament-based process;activation of Rac GTPase activity;activation of Ras GTPase activity;activation of Rho GTPase activity;axon guidance;biological regulation;cell activation;cell chemotaxis;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemotaxis;cytoskeleton organization;intracellular signal transduction;locomotion;organelle organization;platelet activation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of establishment of protein localization in plasma membrane;positive regulation of gene expression;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of Rac GTPase activity;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;Rac protein signal transduction;Ras protein signal transduction;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to chemical stimulus;response to external stimulus;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction;taxis" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Bacterial invasion of epithelial cells;Shigellosis

Q5UIP0-2;Q5UIP0;H7C2B5 Telomere-associated protein RIF1 RIF1 >sp|Q5UIP0-2|RIF1_HUMAN Isoform 2 of Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1;>sp|Q5UIP0|RIF1_HUMAN Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2;>tr|H7C2B5|H7C2B5_HUMAN Insulin-like peptide INSL6 (Fragment) OS=Homo sap NaN NaN 1.17 NaN NaN NaN NaN NaN 4.33E-07 2 1.2 biological regulation;cell cycle;cellular process;cellular response to stimulus;cellular response to stress;developmental process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;response to DNA damage stimulus;response to stimulus;response to stress;stem cell maintenance "cell part;chromosomal part;chromosome, telomeric region;cytoplasm;cytoskeletal part;female pronucleus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;male pronucleus;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;pronucleus;spindle"

O75695 Protein XRP2 RP2 >sp|O75695|XRP2_HUMAN Protein XRP2 OS=Homo sapiens GN=RP2 PE=1 SV=4 0.93 NaN NaN 0.89 NaN 0.74 0.75 NaN 0.00077205 2 5.1 anatomical structure morphogenesis;biosynthetic process;cell morphogenesis;cellular biosynthetic process;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;CTP biosynthetic process;CTP metabolic process;developmental process;establishment of localization;establishment of protein localization;GTP biosynthetic process;GTP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;multicellular organismal process;neurological system process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;protein folding;protein metabolic process;protein transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;ribonucleoside metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;sensory perception;sensory perception of light stimulus;small molecule metabolic process;system process;transport;UTP biosynthetic process;UTP metabolic process;visual perception "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;GTP binding;GTPase activator activity;GTPase regulator activity;guanyl nucleotide binding;guanyl ribonucleotide binding;kinase activity;nucleobase-containing compound kinase activity;nucleoside diphosphate kinase activity;nucleoside-triphosphatase regulator activity;nucleotide binding;phosphotransferase activity, phosphate group as acceptor;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups;unfolded protein binding" cell part;cell projection;cilium;cytoplasm;intracellular part;membrane;plasma membrane

Q5VXM9;Q5VXN0;Q9H7B2 Ribosome production factor 2 homolog RPF2 >tr|Q5VXM9|Q5VXM9_HUMAN Ribosome production factor 2 homolog (Fragment) OS=Homo sapiens GN=RPF2 PE=2 SV=1;>tr|Q5VXN0|Q5VXN0_HUMAN Ribosome production factor 2 homolog (Fragment) OS=Homo sapiens GN=RPF2 PE=2 SV=1;>sp|Q9H7B2|RPF2_HUMAN Ribosome production fa NaN NaN 0.19 NaN 0.15 NaN NaN NaN 0.0010548 2 13 cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

F8W7C6;P27635;H7C123;H7C2C5 60S ribosomal protein L10 RPL10 >tr|F8W7C6|F8W7C6_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=2 SV=1;>sp|P27635|RL10_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4;>tr|H7C123|H7C123_HUMAN 60S ribosomal protein L10 (Fragment) OS=Homo sapiens GN=RPL10 PE 1.46 0.89 0.32 0.66 0.84 0.73 1.08 0.72 8.84E-57 2 12.9 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P30050 60S ribosomal protein L12 RPL12 >sp|P30050|RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 0.98 0.81 1.14 0.86 0.51 0.68 1.35 1 3.82E-06 2 15.2 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

P61353;K7ERY7;K7EQQ9;K7ELC7 60S ribosomal protein L27 RPL27 >sp|P61353|RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2;>tr|K7ERY7|K7ERY7_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=4 SV=1;>tr|K7EQQ9|K7EQQ9_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=3 SV=1;>tr 1.5 0.74 0.66 0.66 1.18 0.78 1.32 0.94 1.94E-05 2 12.5 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

E9PJD9;E9PLL6;P46776;E9PLX7 60S ribosomal protein L27a RPL27A >tr|E9PJD9|E9PJD9_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1;>tr|E9PLL6|E9PLL6_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1;>sp|P46776|RL27A_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 S 1.49 0.89 0.64 0.71 0.93 1.02 1.44 0.98 9.65E-25 2 23.1 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

H0Y3A0;F2Z388;P42766 60S ribosomal protein L35 RPL35 >tr|H0Y3A0|H0Y3A0_HUMAN 60S ribosomal protein L35 (Fragment) OS=Homo sapiens GN=RPL35 PE=3 SV=1;>tr|F2Z388|F2Z388_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=2 SV=1;>sp|P42766|RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE 1.58 0.66 0.61 0.54 1.45 0.66 1.76 0.69 1.92E-95 2 16.7 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

C9K025;P18077;F8WBS5;F8WB72 60S ribosomal protein L35a RPL35A >tr|C9K025|C9K025_HUMAN 60S ribosomal protein L35a (Fragment) OS=Homo sapiens GN=RPL35A PE=2 SV=1;>sp|P18077|RL35A_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2;>tr|F8WBS5|F8WBS5_HUMAN 60S ribosomal protein L35a OS=Homo sapiens GN=RP 1.33 NaN 0.7 0.63 1.09 0.66 1.7 NaN 1.52E-10 2 19.1 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity;tRNA binding cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P83881;H7BZ11;H0Y5B4;J3KQN4;R4GN19;H7BY91;H0Y3V9 60S ribosomal protein L36a RPL36A >sp|P83881|RL36A_HUMAN 60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2;>tr|H7BZ11|H7BZ11_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=3 SV=1;>tr|H0Y5B4|H0Y5B4_HUMAN 60S ribosomal protein L36a (Fragment) OS=Homo sapiens GN=RPL3 1.28 0.92 0.28 NaN 0.79 NaN 1.25 0.9 4.15E-06 2 15.1 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P05386 60S acidic ribosomal protein P1 RPLP1 >sp|P05386|RLA1_HUMAN 60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 NaN NaN 0.92 NaN 0.65 NaN NaN NaN 9.77E-10 2 28.9 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

P60866;P60866-2;E5RIP1;E5RJX2;G3XAN0 40S ribosomal protein S20 RPS20 >sp|P60866|RS20_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1;>sp|P60866-2|RS20_HUMAN Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20;>tr|E5RIP1|E5RIP1_HUMAN 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=2 SV=1; 1.41 0.97 0.94 0.68 1.23 0.82 1.33 0.83 6.57E-13 2 19.3 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

P62847-2;E7ETK0;P62847-3;P62847;P62847-4 40S ribosomal protein S24 RPS24 >sp|P62847-2|RS24_HUMAN Isoform 2 of 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24;>tr|E7ETK0|E7ETK0_HUMAN 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=2 SV=1;>sp|P62847-3|RS24_HUMAN Isoform 3 of 40S ribosomal protein S24 OS=Homo sapiens GN=R 1.19 NaN NaN 1.16 NaN 0.95 1.29 NaN 4.85E-07 2 20 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;erythrocyte homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;homeostasis of number of cells;homeostatic process;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maturation of SSU-rRNA;maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological quality;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleotide binding;protein binding;structural constituent of ribosome;structural molecule activity;translation initiation factor binding cell part;cytoplasm;cytoplasmic part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

P62854;Q5JNZ5 40S ribosomal protein S26;Putative 40S ribosomal protein S26-like 1 RPS26;RPS26P11 >sp|P62854|RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3;>sp|Q5JNZ5|RS26L_HUMAN Putative 40S ribosomal protein S26-like 1 OS=Homo sapiens GN=RPS26P11 PE=5 SV=1 1.68 1.05 0.61 0.65 1.15 1.01 1.24 0.94 4.61E-35 2 20.9 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

P62857 40S ribosomal protein S28 RPS28 >sp|P62857|RS28_HUMAN 40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1 2.04 0.75 1.42 0.58 0.71 0.44 1.62 0.93 1.63E-40 2 30.4 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal small subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytosolic small ribosomal subunit;intracellular organelle part;intracellular part;macromolecular complex;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome

R4GN49;P29034 Protein S100-A2 S100A2 >tr|R4GN49|R4GN49_HUMAN Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=4 SV=1;>sp|P29034|S10A2_HUMAN Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=1 SV=3 0.62 0.43 0.43 0.36 2.37 1.48 1.56 1.16 0.00013229 2 25 cell migration;cell motility;cellular component

movement;cellular process;endothelial cell migration;locomotion	binding;calcium ion binding;cation binding;ion binding;metal ion binding
Q9NR31;D6RAA2;H0Y5E8;Q5SQT8;D6RDB2;B4DQ19;D6RD69;Q9Y6B6	GTP-binding protein SAR1a;GTP-binding protein SAR1b	SAR1A;SAR1B
>sp|Q9NR31|SAR1A_HUMAN GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1;>tr|D6RAA2|D6RAA2_HUMAN GTP-binding protein SAR1b (Fragment) OS=Homo sapiens GN=SAR1B PE=2 SV=1;>tr|H0Y5E8|H0Y5E8_HUMAN GTP-binding protein SAR1a (Fragment) OS=Homo sapiens	0.57 1.18 0.62 0.66 1.31 1.55 0.91 0.91 7.99E-07
2	11.6 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;transport;vesicle coating;vesicle organization;vesicle-mediated transport	"binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	cell part;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;ER to Golgi transport vesicle membrane;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;sarcoplasmic reticulum;transport vesicle membrane;vesicle membrane	Protein processing in endoplasmic reticulum
Q9BW04-2;Q9BW04	Specifically androgen-regulated gene protein	SARG	>sp|Q9BW04-2|SARG_HUMAN Isoform 2 of Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG;>sp|Q9BW04|SARG_HUMAN Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2	NaN NaN NaN 0.25 NaN 1.56 NaN NaN 1.52E-05 2	12.1		cell part;cytoplasm;intracellular part;membrane;plasma membrane
P31431;B4E1S6;P31431-2	Syndecan-4;Syndecan	SDC4	>sp|P31431|SDC4_HUMAN Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2;>tr|B4E1S6|B4E1S6_HUMAN Syndecan OS=Homo sapiens GN=SDC4 PE=2 SV=1;>sp|P31431-2|SDC4_HUMAN Isoform 2 of Syndecan-4 OS=Homo sapiens GN=SDC4	1.27 NaN 1.06 0.72 0.78 0.96 0.99 NaN 0.00028389	2	22.2 "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of actin filament bundle assembly;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of focal adhesion assembly;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of protein kinase activity;positive regulation of stress fiber assembly;positive regulation of transferase activity;primary metabolic process;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of biological process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of focal adhesion assembly;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of stress fiber assembly;regulation of transferase activity;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;sulfur compound metabolic process;terpenoid metabolic process;tube development;ureteric bud development"	molecular transducer activity;receptor activity;signal transducer activity;signaling receptor activity;thrombospondin receptor activity	adherens junction;anchoring junction;cell junction;cell part;cell surface;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;costamere;cytoplasmic part;extracellular region;focal adhesion;Golgi apparatus part;Golgi lumen;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;membrane part;membrane raft;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane part;vacuolar lumen;vacuolar part	Cell adhesion molecules (CAMs);ECM-receptor interaction;Malaria
O94979-7;H7BXG7;O94979-6;O94979-3;B7ZL00;O94979-4;O94979-9;O94979-2;O94979;O94979-8;D6REX3;H0YAF5;H0Y8W8;O94979-5;D6RHZ5 Protein transport protein Sec31A	SEC31A	>sp|O94979-7|SC31A_HUMAN Isoform 7 of Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A;>tr|H7BXG7|H7BXG7_HUMAN Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=2 SV=1;>sp|O94979-6|SC31A_HUMAN Isoform 6 of Protein transport protein Se NaN NaN 3.65 NaN 19.01	NaN NaN NaN 1.14E-05 2
2.3	activation of signaling protein activity involved in unfolded protein response;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular

component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;establishment of localization;establishment of protein localization;glycosylation;immune system process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;transport;vesicle coating;vesicle organization	cell part;COPII vesicle coat;cytoplasm;cytoplasmic part;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;vesicle coat	Protein processing in endoplasmic reticulum

K7EP23;K7EMT0;K7EKV8;Q15428	Splicing factor 3A subunit 2	SF3A2	>tr|K7EP23|K7EP23_HUMAN Splicing factor 3A subunit 2 (Fragment) OS=Homo sapiens GN=SF3A2 PE=4 SV=1;>tr|K7EMT0|K7EMT0_HUMAN Splicing factor 3A subunit 2 (Fragment) OS=Homo sapiens GN=SF3A2 PE=4 SV=1;>tr|K7EKV8|K7EKV8_HUMAN Splicing factor 3A subunit 2 OS=Ho	1.12	0.88	1.28	NaN	NaN	NaN	0.96	0.7	9.24E-07	2	18.5	cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;mRNA splice site selection;nuclear mRNA 3'-splice site recognition;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization	binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding	catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex	Spliceosome

Q9Y3B4	Pre-mRNA branch site protein p14	SF3B14	>sp|Q9Y3B4|PM14_HUMAN Pre-mRNA branch site protein p14 OS=Homo sapiens GN=SF3B14 PE=1 SV=1	NaN	NaN	1.41	NaN	0.83	NaN	NaN	NaN	2.00E-06	2	17.6	"cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile"	binding;nucleic acid binding;nucleotide binding;RNA binding	cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex	Spliceosome

P63208;E5RJR5;E5RGM3;E7ERH2;F8W8N3;P63208-2	S-phase kinase-associated protein 1	SKP1	>sp|P63208|SKP1_HUMAN S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2;>tr|E5RJR5|E5RJR5_HUMAN S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=2 SV=1;>tr|E5RGM3|E5RGM3_HUMAN S-phase kinase-associated protein 1 (Fragment)	NaN	NaN	1.05	NaN	1.01	NaN	NaN	NaN	2.23E-05	2	15.3	anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;G1 phase;G1 phase of mitotic cell cycle;G1/S transition of mitotic cell cycle;histone H2A monoubiquitination;histone H2A ubiquitination;histone modification;histone monoubiquitination;histone ubiquitination;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;Notch signaling pathway;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to stimulus;S phase;S phase of mitotic cell cycle;SCF-dependent proteasomal ubiquitin-dependent protein catabolic process;signal transduction;ubiquitin-dependent protein catabolic process;viral reproduction	"acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;ubiquitin-protein ligase activity"	cell part;cullin-RING ubiquitin ligase complex;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;protein complex;SCF ubiquitin ligase complex;ubiquitin ligase complex	Cell cycle;Cell cycle - yeast;Circadian rhythm - mammal;Oocyte meiosis;Protein processing in endoplasmic reticulum;TGF-beta signaling pathway;Ubiquitin mediated proteolysis;Wnt signaling pathway

O15427;J3QRP8;J3QLE3;J3KTM6;J3QRU2;J3KT83;J3QRA0;J3QQS9;J3QQV2;J3QSC3 Monocarboxylate transporter 4 SLC16A3 >sp|O15427|MOT4_HUMAN Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1;>tr|J3QRP8|J3QRP8_HUMAN Monocarboxylate transporter 4 (Fragment) OS=Homo sapiens GN=SLC16A3 PE=4 SV=1;>tr|J3QLE3|J3QLE3_HUMAN Monocarboxylate transporter 4 (Fragment) NaN 1.27 NaN 1.49 NaN 0.22 NaN 1.48 4.82E-05 2 5.4 biological regulation;blood coagulation;carboxylic acid metabolic process;cell migration;cell motility;cellular component movement;cellular ketone metabolic process;cellular metabolic process;cellular process;coagulation;establishment of localization;hemostasis;immune system process;leukocyte migration;locomotion;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;organic acid metabolic process;oxoacid metabolic process;pyruvate metabolic process;regulation of biological quality;regulation of body fluid levels;small molecule metabolic process;transmembrane transport;transport active transmembrane transporter activity;carboxylic acid transmembrane transporter activity;monocarboxylic acid transmembrane transporter activity;organic acid transmembrane transporter activity;secondary active monocarboxylate transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity actin cytoskeleton;cell part;cytoskeleton;integral to membrane;integral to plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;organelle;organelle membrane;organelle part;plasma membrane part

O00400;H7C562 Acetyl-coenzyme A transporter 1 SLC33A1 >sp|O00400|ACATN_HUMAN Acetyl-coenzyme A transporter 1 OS=Homo sapiens GN=SLC33A1 PE=1 SV=1;>tr|H7C562|H7C562_HUMAN Acetyl-coenzyme A transporter 1 (Fragment) OS=Homo sapiens GN=SLC33A1 PE=4 SV=1 NaN 3.26 0.16 1.75 0.66 0.87 NaN 0.71 3.08E-05 2 4 acetyl-CoA transport;cell death;cellular process;coenzyme transport;cofactor transport;death;establishment of localization;transmembrane transport;transport acetyl-CoA transporter activity;coenzyme transporter activity;cofactor transporter activity;transporter activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;organelle membrane;organelle part;plasma membrane part Glycosphingolipid biosynthesis - ganglio series

Q96QD8;F8VUY8;Q96QD8-2 Sodium-coupled neutral amino acid transporter 2 SLC38A2 >sp|Q96QD8|S38A2_HUMAN Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2;>tr|F8VUY8|F8VUY8_HUMAN Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=2 SV=1;>sp|Q96QD8-2|S38A2_HUMAN Isoform 2 of S 1.38 1.69 0.87 1.35 0.21 0.21 0.71 1.04 1.06E-48 2 7.3 biological regulation;cation transport;cellular process;establishment of localization;establishment of localization in cell;glutamate secretion;ion transport;metal ion transport;monovalent inorganic cation transport;neurotransmitter secretion;neurotransmitter transport;regulation of biological quality;regulation of neurotransmitter levels;secretion;secretion by cell;signal release;sodium ion transport;transmembrane transport;transport active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;carboxylic acid transmembrane transporter activity;organic acid transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Protein digestion and absorption

Q9GZT3-2;Q9GZT3;H0YJW7;H0YJ40;G3V4X6;G3V2S9 "SRA stem-loop-interacting RNA-binding protein, mitochondrial" SLIRP ">sp|Q9GZT3-2|SLIRP_HUMAN Isoform 2 of SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP;>sp|Q9GZT3|SLIRP_HUMAN SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1;>tr|H0YJW7|H0" NaN NaN 1.42 NaN 1.42 NaN NaN NaN 1.32E-05 2 21.5 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle

P51531-2;P51531;P51532-5;P51532-2;P51532-3;P51532-4;P51532;Q9HBD4;F6XE55;F6XDY1;F6UH26;B1ALG1;B1ALG2;F6XG14;B1ALF6;H0YGM3;F6VDE0 Probable global transcription activator SNF2L2;Transcription activator BRG1 SMARCA2;SMARCA4 >sp|P51531-2|SMCA2_HUMAN Isoform Short of Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2;>sp|P51531|SMCA2_HUMAN Probable global transcription activator SNF2L2 OS=Homo sapiens GN=SMARCA2 PE=1 SV=2;>sp|P51532-5|SMCA4_HUMAN Isoform NaN NaN NaN NaN NaN NaN NaN NaN 0.00052036 2 1.3 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;aortic smooth muscle cell differentiation;appendage morphogenesis;biological regulation;blastocyst growth;blastocyst hatching;cell differentiation;cell fate determination;cell morphogenesis;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromatin remodeling;chromatin silencing;chromosome organization;covalent chromatin modification;definitive erythrocyte differentiation;developmental growth;developmental process;DNA alkylation;DNA metabolic process;DNA methylation;DNA methylation on cytosine;DNA methylation on cytosine within a CG sequence;DNA modification;embryonic appendage morphogenesis;embryonic hindlimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;epidermal cell differentiation;epidermis morphogenesis;epithelial cell differentiation;erythrocyte differentiation;extracellular matrix organization;extracellular structure organization;forebrain development;gene silencing;glial cell fate determination;growth;hatching;heart trabecula formation;hindbrain development;hindlimb morphogenesis;histone acetylation;histone H3 acetylation;histone modification;interaction with symbiont;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;interspecies interaction between organisms;keratinocyte differentiation;limb morphogenesis;liver development;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;methylation-dependent chromatin silencing;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;multi-organism process;muscle cell differentiation;myeloid cell differentiation;negative regulation of androgen receptor signaling pathway;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of gene expression, epigenetic;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitotic cell cycle;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of S phase of mitotic cell cycle;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nervous system development;neural retina development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;one-carbon metabolic process;organ development;organ morphogenesis;organelle organization;organism emergence from protective structure;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;positive regulation by host of viral transcription;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA binding;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of androgen receptor signaling pathway;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell differentiation;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA binding;regulation of gene expression;regulation of gene expression, epigenetic;regulation of growth;regulation of interphase of mitotic cell cycle;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of S phase;regulation of S phase of mitotic cell cycle;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;small molecule metabolic process;smooth muscle cell differentiation;stem cell maintenance;system development;tissue morphogenesis;trabecula formation;vascular smooth muscle cell differentiation;vasculogenesis" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;chromatin binding;DNA binding;DNA-dependent ATPase activity;helicase activity;histone acetyl-lysine binding;histone binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;RNA polymerase II transcription coactivator activity;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;RNA polymerase II transcription factor binding transcription factor activity involved in positive regulation of transcription;sequence-specific DNA binding;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding" cell part;chromatin;chromatin remodeling complex;chromosomal part;cytoskeleton;euchromatin;heterochromatin;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nBAF complex;non-membrane-bounded organelle;npBAF complex;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleoplasm;nucleus;organelle;organelle part;perichromatin fibrils;protein complex;SWI/SNF complex;SWI/SNF-type complex;WINAC complex

B5MCL5;Q12824-2;Q12824;G5E975;C9JTA6 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 SMARCB1 >tr|B5MCL5|B5MCL5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=Homo sapiens GN=SMARCB1 PE=2 SV=1;>sp|Q12824-2|SNF5_HUMAN Isoform B of SWI/SNF-related matrix-associated actin-dependent regulator of c NaN NaN 1.57 NaN 0.91 NaN NaN NaN 0.00021008 2 9.7 "anatomical structure development;ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;blastocyst hatching;cell differentiation;cellular biosynthetic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;DNA integration;DNA metabolic process;DNA repair;hatching;interaction with host;interaction with symbiont;interspecies interaction between organisms;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;multi-organism process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;organelle organization;organism emergence from protective structure;positive regulation by host of viral transcription;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;retroviral genome replication;RNA biosynthetic process;RNA metabolic process;system development;transcription, DNA-dependent;viral genome replication;viral reproductive process;virus-host interaction" protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;chromatin remodeling complex;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;nBAF complex;non-membrane-bounded organelle;npBAF complex;nuclear chromosome;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;protein complex;sex chromosome;SWI/SNF complex;SWI/SNF-type complex;XY body

Q8TAQ2-2;Q8TAQ2-3;Q8TAQ2;F8VXC8;F8VZW6 SWI/SNF complex subunit SMARCC2 SMARCC2 >sp|Q8TAQ2-2|SMRC2_HUMAN Isoform 2 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2;>sp|Q8TAQ2-3|SMRC2_HUMAN Isoform 3 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2;>sp|Q8TAQ2|SMRC2_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo NaN NaN 0.93 NaN 3.14 NaN NaN NaN 2.19E-05 2 3.2 "anatomical structure development;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;system development;transcription, DNA-dependent" binding;chromatin binding;DNA binding;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;chromatin remodeling complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nBAF complex;npBAF complex;nuclear part;nucleus;organelle;organelle part;protein complex;SWI/SNF complex;SWI/SNF-type complex

J3KMX2;Q92925-3;Q92925-2;Q92925;J3QWB6 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 SMARCD2 >tr|J3KMX2|J3KMX2_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens GN=SMARCD2 PE=4 SV=1;>sp|Q92925-3|SMRD2_HUMAN Isoform 3 of SWI/SNF-related matrix-associated actin-dependent regulator of NaN NaN 1.75 NaN 0.51 NaN NaN NaN 2.09E-05 2 7.2 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;chromatin remodeling complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;protein complex;SWI/SNF complex;SWI/SNF-type complex

H7C048;K7EMQ8;J3QKS7;C0IMW7;C0IMW5;Q969G3-3;Q969G3-2;C0IMW4;B4DGM3;Q969G3 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 SMARCE1 >tr|H7C048|H7C048_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment) OS=Homo sapiens GN=SMARCE1 PE=2 SV=1;>tr|K7EMQ8|K7EMQ8_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chr NaN NaN 1.39 NaN 0.53 NaN NaN NaN 1.03E-05 2 16.6 "anatomical structure development;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;macromolecular complex disassembly;macromolecular complex subunit organization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nervous system development;nucleosome disassembly;nucleosome organization;organelle organization;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;system development" "acetyltransferase activity;binding;catalytic activity;chromatin binding;DNA binding;N-acetyltransferase activity;N-acyltransferase activity;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups"cell part;chromatin remodeling complex;chromosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nBAF complex;non-membrane-bounded organelle;npBAF complex;nuclear chromosome;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;SWI/SNF complex;SWI/SNF-type complex;transcriptional repressor complex

H3BNE1;H3BR18;H3BM38;H3BPJ0;O00161-2;O00161;H3BR99;H3BV99;H3BP15;H3BQY9 Synaptosomal-associated protein;Synaptosomal-associated protein 23 SNAP23 >tr|H3BNE1|H3BNE1_HUMAN Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=2 SV=1;>tr|H3BR18|H3BR18_HUMAN Synaptosomal-associated protein 23 (Fragment) OS=Homo sapiens GN=SNAP23 PE=2 SV=1;>tr|H3BM38|H3BM38_HUMAN Synaptosomal-associated protein 0.95 1.28 1.17 0.86 0.86 0.54 0.8 0.7 1.00E-06 2 24.7 cellular component organization;cellular component organization or biogenesis;cellular membrane fusion;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;Golgi vesicle transport;intracellular transport;membrane fusion;membrane organization;post-Golgi vesicle-mediated transport;protein transport;secretion;secretion by cell;transport;vesicle targeting;vesicle-mediated transport azurophil granule;cell junction;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane;membrane-bounded organelle;membrane-bounded vesicle;neuron projection;nucleus;organelle;plasma membrane;primary lysosome;specific granule;stored secretory granule;synapse;vacuole;vesicle SNARE interactions in vesicular transport

P08621-2;P08621;M0QYR1;P08621-3;P08621-4 U1 small nuclear ribonucleoprotein 70 kDa SNRNP70 >sp|P08621-2|RU17_HUMAN Isoform 2 of U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70;>sp|P08621|RU17_HUMAN U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2;>tr|M0QYR1|M0QYR1_HUMAN U1 small nuclear ribonucl 1.7 0.55 0.73 NaN 0.31 NaN 1.48 1.02 2.24E-05 2 6.8 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

P08579;M0R0G9;M0QXK2;M0R221;M0R2B8;M0QZG7;M0R268;P09012 U2 small nuclear ribonucleoprotein B;U1 small nuclear ribonucleoprotein A SNRPB2;SNRPA >sp|P08579|RU2B_HUMAN U2 small nuclear ribonucleoprotein B OS=Homo sapiens GN=SNRPB2 PE=1 SV=1;>tr|M0R0G9|M0R0G9_HUMAN U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=4 SV=1;>tr|M0QXK2|M0QXK2_HUMAN U1 small nuclear ribonucleoprotein A (F 1.14 NaN NaN 1.59 NaN 0.4 0.94 NaN 0.00031506 2 8.4 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding;snRNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U2 snRNP Spliceosome

J3QLI9;P62314 Small nuclear ribonucleoprotein Sm D1SNRPD1 >tr|J3QLI9|J3QLI9_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD1 PE=4 SV=1;>sp|P62314|SMD1_HUMAN Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 1.08 1.45 0.97 2.09 0.41 0.51 0.9 0.85 1.62E-09 2 17.3 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;spliceosomal snRNP assembly;spliceosome assembly binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome;Systemic lupus erythematosus

C9JBL0;P23497-7;P23497-6;E9PHV6;P23497-5;E9PBK3;P23497-2;P23497-3;E7EUA7;P23497;P23497-4;Q9H930-3;H7BYP4;Q9H930-1;Q9H930-2;Q9H930 Nuclear autoantigen Sp-100;Nuclear body protein SP140-like protein SP100;SP140L >tr|C9JBL0|C9JBL0_HUMAN Nuclear autoantigen Sp-100 (Fragment) OS=Homo sapiens GN=SP100 PE=2 SV=1;>sp|P23497-7|SP100_HUMAN Isoform 7 of Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100;>sp|P23497-6|SP100_HUMAN Isoform 6 of Nuclear autoantigen Sp-100 OS=H NaN NaN 0.91 2.62 0.33 0.29 NaN NaN 1.62E-05 2 13 "anatomical structure homeostasis;biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cellular response to type I interferon;chromosome organization;cytokine-mediated signaling pathway;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator;DNA damage response, signal transduction resulting in transcription;DNA metabolic process;homeostatic process;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;intracellular receptor mediated signaling pathway;intracellular signal transduction;macromolecule metabolic process;metabolic process;multi-organism process;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular biosynthetic process;negative regulation of cellular component movement;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA binding;negative regulation of endothelial cell migration;negative regulation of gene expression;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of locomotion;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of protein export from nucleus;negative regulation of protein transport;negative regulation of reproductive process;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transport;negative regulation of viral transcription;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA binding;regulation of endothelial cell migration;regulation of establishment of protein localization;regulation of gene expression;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein localization;regulation of protein transport;regulation of reproductive process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transport;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to external stimulus;response to extracellular stimulus;response to interferon-gamma;response to nutrient;response to nutrient levels;response to organic substance;response to retinoic acid;response to stimulus;response to stress;response to type I interferon;response to vitamin;response to vitamin A;retinoic acid receptor signaling pathway;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;telomere maintenance;telomere organization;type I interferon-mediated signaling pathway;viral reproductive process;virus-host interaction" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear periphery;nucleolus;nucleoplasm part;nucleus;organelle;organelle part;PML body

O15269;O15269-2 Serine palmitoyltransferase 1 SPTLC1 >sp|O15269|SPTC1_HUMAN Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1;>sp|O15269-2|SPTC1_HUMAN Isoform 2 of Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 0.92 1.23 1.1 0.24 2.01 1.74 1.36 1.17 3.08E-95 2 6.6 alcohol biosynthetic process;alcohol metabolic process;amine metabolic process;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;ceramide biosynthetic process;ceramide metabolic process;lipid biosynthetic process;lipid metabolic process;membrane lipid biosynthetic process;membrane lipid metabolic process;metabolic process;nitrogen compound metabolic process;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;sphinganine biosynthetic process;sphinganine metabolic process;sphingoid biosynthetic process;sphingoid metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process;sphingomyelin biosynthetic process;sphingomyelin metabolic process;sphingosine biosynthetic process;sphingosine metabolic process "binding;C-acyltransferase activity;catalytic activity;cofactor binding;C-palmitoyltransferase activity;palmitoyltransferase activity;pyridoxal phosphate binding;serine C-palmitoyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;endoplasmic reticulum palmitoyltransferase complex;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;organelle part;palmitoyltransferase complex;protein complex;serine C-palmitoyltransferase complex;SPOTS complex Sphingolipid metabolism

E7EVQ6;Q14534;E5RJH9 Squalene monooxygenase SQLE >tr|E7EVQ6|E7EVQ6_HUMAN Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=2 SV=1;>sp|Q14534|ERG1_HUMAN Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=1 SV=3;>tr|E5RJH9|E5RJH9_HUMAN Squalene monooxygenase (Fragment) OS=Homo sapiens GN=SQLE PE=2 SV=1 NaN NaN NaN NaN NaN NaN NaN NaN 0.00025322 2 7.3 alcohol metabolic process;biosynthetic process;cellular aromatic compound metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;response to chemical stimulus;response to organic substance;response to stimulus;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;squalene monooxygenase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Steroid biosynthesis

H0YLA2;P37108 Signal recognition particle 14 kDa protein SRP14 >tr|H0YLA2|H0YLA2_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=2 SV=1;>sp|P37108|SRP14_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 0.81 NaN 0.96 1.08 0.53 0.51 0.93 NaN 2.67E-06 2 22.6 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to drug;response to stimulus;SRP-dependent cotranslational protein targeting to membrane;translation;transport 7S RNA binding;binding;endoplasmic reticulum signal peptide binding;nucleic acid binding;peptide binding;RNA binding;signal sequence binding "cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;ribonucleoprotein complex;signal recognition particle;signal recognition particle, endoplasmic reticulum targeting" Protein export

Q08170;F6T1J1 Serine/arginine-rich splicing factor 4 SRSF4 >sp|Q08170|SRSF4_HUMAN Serine/arginine-rich splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=1 SV=2;>tr|F6T1J1|F6T1J1_HUMAN Serine/arginine-rich-splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=2 SV=1 2.19 0.74 0.74 0.95 0.67 0.52 1.49 0.89 5.78E-10 2 4.5 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part Spliceosome

B4DJK0;B4DUA4;Q13243-3;Q13243;G3V5K8;Q13243-2 Serine/arginine-rich splicing factor 5 SRSF5 >tr|B4DJK0|B4DJK0_HUMAN Serine/arginine-rich-splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=2 SV=1;>tr|B4DUA4|B4DUA4_HUMAN Serine/arginine-rich-splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=2 SV=1;>sp|Q13243-3|SRSF5_HUMAN Isoform SRP40-4 of Serine/arginine- 1.33 0.85 0.66 NaN 0.58 NaN 1.47 0.79 9.42E-09 2 16.9 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA splice site selection;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cellular process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part Spliceosome

H0YIB4;Q13242 Serine/arginine-rich splicing factor 9 SRSF9 >tr|H0YIB4|H0YIB4_HUMAN Serine/arginine-rich-splicing factor 9 (Fragment) OS=Homo sapiens GN=SRSF9 PE=4 SV=1;>sp|Q13242|SRSF9_HUMAN Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 1.19 1.09 1.34 NaN 0.67 NaN 0.77 0.55 6.73E-05 2 17.3 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA splice site selection;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part Spliceosome

C9K0U8;E7EUY5;Q04837 "Single-stranded DNA-binding protein, mitochondrial" SSBP1 ">tr|C9K0U8|C9K0U8_HUMAN Single-stranded DNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=SSBP1 PE=2 SV=1;>tr|E7EUY5|E7EUY5_HUMAN Single-stranded DNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=SSBP1 PE=2 SV=1;>sp|Q04837|SSB" 1.06 1.09 1.62 1.28 0.8 0.57 0.89 0.76 3.39E-43 2 19 anatomical structure morphogenesis;biological regulation;biosynthetic process;cell part morphogenesis;cellular biosynthetic process;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;DNA metabolic process;DNA replication;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrion morphogenesis;mitochondrion organization;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of catalytic activity;positive regulation of helicase activity;positive regulation of hydrolase activity;positive regulation of molecular function;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of helicase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function binding;chromatin binding;DNA binding;nucleic acid binding;single-stranded DNA binding;structure-specific DNA binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle part DNA replication;Homologous recombination;Mismatch repair

E7END2;P28290-2;E9PHV5;P28290-3;P28290;H7BZ26;E7EUL7 Sperm-specific antigen 2SSFA2 >tr|E7END2|E7END2_HUMAN Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2 PE=2 SV=1;>sp|P28290-2|SSFA2_HUMAN Isoform 2 of Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2;>tr|E9PHV5|E9PHV5_HUMAN Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2 PE=2 SV=1; NaN NaN 1.48 NaN 0.68 NaN NaN NaN 1.72E-05 2 2.8 cell part;cytoplasm;intracellular part;membrane;plasma membrane

Q5JW30;O95793-2;O95793-3;O95793;Q5JW28 Double-stranded RNA-binding protein Staufen homolog 1 STAU1 >tr|Q5JW30|Q5JW30_HUMAN Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=2 SV=1;>sp|O95793-2|STAU1_HUMAN Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1;>sp|O95793-3|STAU1_HUM 0.87 0.83 0.58 0.64 0.97 0.91 0.9 1.25 1.78E-06 2 5.5 cellular localization;cellular macromolecule localization;cellular process;intracellular mRNA localization;localization;macromolecule localization;RNA localization binding;double-stranded RNA binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule associated complex;non-membrane-bounded organelle;organelle;organelle part;protein complex;ribonucleoprotein complex;RNA granule;rough endoplasmic reticulum;stress granule

Q8TCJ2 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B STT3B >sp|Q8TCJ2|STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1 1.06 1.17 1.35 1.1 0.72 0.68 0.84 0.92 1.80E-05 2 2.3 carbohydrate metabolic process;catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;co-translational protein modification;ER-associated protein catabolic process;glycoprotein catabolic process;glycoprotein metabolic process;glycosylation;macromolecule catabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-

translational protein modification;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;proteolysis;proteolysis involved in cellular protein catabolic process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;ubiquitin-dependent protein catabolic process "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;oligosaccharyltransferase complex;organelle part;protein complex
N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis

Q86Y82;B1AJQ6 Syntaxin-12 STX12 >sp|Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1;>tr|B1AJQ6|B1AJQ6_HUMAN Syntaxin-12 (Fragment) OS=Homo sapiens GN=STX12 PE=2 SV=2 1.26 0.9 0.68 0.53 2.74 1.75 1.18 1.06 5.28E-19 2 10.5 biological regulation;cellular process;cholesterol efflux;cholesterol transport;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;intracellular protein transport;intracellular transport;lipid transport;organic substance transport;posttranscriptional regulation of gene expression;protein stabilization;protein transport;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability;secretion;secretion by cell;sterol transport;synaptic vesicle exocytosis;synaptic vesicle transport;transport;vesicle-mediated transport binding;protein binding;SNAP receptor activity;SNARE binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;endosomal part;endosome membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;phagocytic vesicle;protein complex;SNARE complex;vesicle Phagosome

O15400-2;O15400 Syntaxin-7 STX7 >sp|O15400-2|STX7_HUMAN Isoform 2 of Syntaxin-7 OS=Homo sapiens GN=STX7;>sp|O15400|STX7_HUMAN Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4 1.34 1.08 NaN 0.69 NaN 0.93 1.13 0.99 1.50E-14 2 11.7 cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;Golgi vesicle transport;intracellular protein transport;intracellular transport;post-Golgi vesicle-mediated transport;protein transport;secretion;secretion by cell;synaptic vesicle exocytosis;synaptic vesicle transport;transport;vesicle-mediated transport binding;protein binding;SNAP receptor activity;SNARE binding cell part;cytoplasmic part;early endosome membrane;endosomal part;endosome membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;SNARE complex
Phagosome;SNARE interactions in vesicular transport

P57105 Synaptojanin-2-binding protein SYNJ2BP >sp|P57105|SYJ2B_HUMAN Synaptojanin-2-binding protein OS=Homo sapiens GN=SYNJ2BP PE=1 SV=2 NaN NaN 1.66 NaN 0.99 NaN NaN NaN 1.99E-06 2 17.9 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular process;intracellular distribution of mitochondria;localization;mitochondrion distribution;mitochondrion localization;mitochondrion organization;organelle localization;organelle organization cell part;cytoplasmic part;integral to membrane;integral to mitochondrial membrane;integral to mitochondrial outer membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to mitochondrial outer membrane;intrinsic to organelle membrane;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrion;organelle;organelle part

P37802 Transgelin-2 TAGLN2 >sp|P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 NaN NaN NaN NaN NaN NaN NaN NaN 7.25E-05 2 12.6 anatomical structure development;developmental process;muscle organ development;muscle structure development;organ development

B4DJ45;Q13148;Q13148-2;K7EJM5;K7EN94;B1AKP7;G3V162 TAR DNA-binding protein 43 TARDBP >tr|B4DJ45|B4DJ45_HUMAN TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=2 SV=1;>sp|Q13148|TADBP_HUMAN TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1;>sp|Q13148-2|TADBP_HUMAN Isoform 2 of TAR DNA-binding protein 43 OS=Homo sapiens GN NaN NaN NaN NaN NaN NaN NaN NaN 1.66E-08 2 9.1 "3'-UTR-mediated mRNA stabilization;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;interaction with symbiont;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;mRNA metabolic process;mRNA processing;mRNA stabilization;multi-organism process;negative regulation by host of viral transcription;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of reproductive process;negative regulation of RNA metabolic process;negative regulation of viral transcription;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of viral reproduction;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of RNA stability;regulation of viral reproduction;regulation of viral transcription;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA stabilization;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;DNA binding;double-stranded DNA binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleotide binding;RNA binding;sequence-specific DNA binding transcription factor activity;structure-specific DNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

E7ERI3;G3XAN9;P26639;P26639-2 "Threonine--tRNA ligase, cytoplasmic" TARS ">tr|E7ERI3|E7ERI3_HUMAN Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens

GN=TARS PE=2 SV=1;>tr|G3XAN9|G3XAN9_HUMAN Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=2 SV=1;>sp|P26639|SYTC_HUMAN Threonine--tRNA ligase, cytoplasmic OS=Homo sa" NaN 1.65 0.06 NaN 0.21 NaN NaN 0.78 4.95E-05 2 3.7 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;threonyl-tRNA aminoacylation;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;identical protein binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;threonine-tRNA ligase activity" actin cytoskeleton;cell part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle Aminoacyl-tRNA biosynthesis

E9PF19;Q9Y4P3;C9JVF0 Transducin beta-like protein 2 TBL2 >tr|E9PF19|E9PF19_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=2 SV=1;>sp|Q9Y4P3|TBL2_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1;>tr|C9JVF0|C9JVF0_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 P NaN NaN 1.64 NaN 1.63 NaN NaN NaN 1.02E-09 2 7.3

E9PNA6;Q13488;E9PMC5;E9PM12;H0YCE3;Q13488-2 V-type proton ATPase 116 kDa subunit a isoform 3 TCIRG1 >tr|E9PNA6|E9PNA6_HUMAN V-type proton ATPase 116 kDa subunit a isoform 3 (Fragment) OS=Homo sapiens GN=TCIRG1 PE=2 SV=1;>sp|Q13488|VPP3_HUMAN V-type proton ATPase 116 kDa subunit a isoform 3 OS=Homo sapiens GN=TCIRG1 PE=1 SV=3;>tr|E9PMC5|E9PMC5_HUMAN V-typ NaN NaN NaN NaN NaN NaN NaN NaN 4.38E-08 2 11 "ATP hydrolysis coupled proton transport;biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular defense response;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;defense response;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organelle organization;phagosome maturation;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of cell proliferation;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity "apical plasma membrane;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosomal part;endosome membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex, proton-transporting domain;proton-transporting V-type ATPase, V0 domain;vacuolar part;vacuolar proton-transporting V-type ATPase, V0 domain;vesicle membrane" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

B4DIT7;F5H6P0;P21980 Protein-glutamine gamma-glutamyltransferase 2 TGM2 >tr|B4DIT7|B4DIT7_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=2 SV=1;>tr|F5H6P0|F5H6P0_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=2 SV=1;>sp|P21980|TGM2_HUMAN Protein-glutamine gamma-gl NaN NaN 2.13 NaN 3.48 NaN NaN NaN 0.00026627 2 3.8 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptotic cell clearance;biological regulation;blood vessel remodeling;branching involved in salivary gland morphogenesis;calcium ion homeostasis;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein metabolic process;chemical homeostasis;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion concentration;elevation of cytosolic calcium ion concentration involved in G-protein signaling coupled to IP3 second messenger;endocytosis;establishment of localization;homeostatic process;induction of apoptosis;induction of programmed cell death;ion homeostasis;isopeptide cross-linking;isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;peptide cross-linking;peptidyl-amino acid modification;peptidyl-glutamine modification;peptidyl-lysine modification;phagocytosis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of defense response;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of inflammatory response;positive regulation of intracellular protein kinase cascade;positive regulation of programmed cell death;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smooth muscle cell proliferation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein modification process;protein oligomerization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of defense response;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of inflammatory response;regulation of intracellular protein kinase cascade;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of smooth muscle cell proliferation;salivary gland cavitation;tissue morphogenesis;tissue remodeling;transport;tube formation;tube lumen cavitation;vesicle-mediated transport "binding;catalytic activity;cation binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ion binding;metal ion binding;nucleotide binding;protein-glutamine gamma-glutamyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle;plasma membrane Huntington's disease

Q6ZMP0;Q6ZMP0-2;B4DR13 Thrombospondin type-1 domain-containing protein 4 THSD4 >sp|Q6ZMP0|THSD4_HUMAN Thrombospondin type-1 domain-containing protein 4 OS=Homo sapiens GN=THSD4 PE=2 SV=2;>sp|Q6ZMP0-2|THSD4_HUMAN Isoform 2 of Thrombospondin type-1 domain-containing protein 4 OS=Homo sapiens GN=THSD4;>tr|B4DR13|B4DR13_HUMAN Thrombospon NaN NaN NaN NaN NaN NaN NaN NaN 0.00056304 2 1.9 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;elastic fiber assembly;extracellular matrix assembly;extracellular matrix organization;extracellular structure organization "catalytic activity;endopeptidase activity;hydrolase activity;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" extracellular matrix;extracellular matrix part;extracellular region part;fibril;microfibril

E9PB91;B1APJ0;O14925;H0Y6X5;E7EP42;Q5SRD1 Mitochondrial import inner membrane translocase subunit Tim23;Putative mitochondrial import inner membrane translocase subunit Tim23B TIMM23;TIMM23B >tr|E9PB91|E9PB91_HUMAN Mitochondrial import inner membrane translocase subunit Tim23 OS=Homo sapiens GN=TIMM23 PE=2 SV=2;>tr|B1APJ0|B1APJ0_HUMAN Mitochondrial import inner membrane translocase subunit Tim23 OS=Homo sapiens GN=TIMM23 PE=2 SV=1;>sp|O14925|T NaN 1.94 1.58 NaN 1.03 NaN NaN 1.02 9.31E-28 2 15.5 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transport active transmembrane transporter activity;macromolecule transmembrane transporter activity;P-P-bond-hydrolysis-driven protein transmembrane transporter activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;integral to mitochondrial inner membrane;integral to mitochondrial membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to mitochondrial inner membrane;intrinsic to organelle membrane;macromolecular complex;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane presequence translocase complex;mitochondrial intermembrane space;mitochondrial membrane part;mitochondrial part;mitochondrion;organelle;organelle envelope lumen;organelle part;protein complex

M0QXU7;O43615 Mitochondrial import inner membrane translocase subunit TIM44 TIMM44 >tr|M0QXU7|M0QXU7_HUMAN Mitochondrial import inner membrane translocase subunit TIM44 (Fragment) OS=Homo sapiens GN=TIMM44 PE=4 SV=1;>sp|O43615|TIM44_HUMAN Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=21.14 NaN 0.97 NaN 1.67 NaN 1.66 NaN 5.96E-05 2 9.5 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transport active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;macromolecule transmembrane transporter activity;nucleotide binding;P-P-bond-hydrolysis-driven protein transmembrane transporter activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein transmembrane transporter activity;protein transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part

Q9GZM7-3;Q9GZM7;B4DNS5;E7EUP2 Tubulointerstitial nephritis antigen-like TINAGL1 >sp|Q9GZM7-3|TINAL_HUMAN Isoform 3 of Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1;>sp|Q9GZM7|TINAL_HUMAN Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1 PE=1 SV=1;>tr|B4DNS5|B4DNS5_HUMAN Tubulointerstitial neph NaN 1.08 NaN NaN NaN NaN NaN 1.15 2.03E-05 2 5 cellular process;endosome transport;establishment of localization;establishment of localization in cell;immune response;immune system process;intracellular transport;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis;response to stimulus;transport;vesicle-mediated transport "binding;carbohydrate binding;cargo receptor activity;catalytic activity;cysteine-type peptidase activity;extracellular matrix structural constituent;hydrolase activity;pattern binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;polysaccharide binding;receptor activity;scavenger receptor activity;structural molecule activity" cell part;cytoplasm;extracellular region part;extracellular space;intracellular part

E9PSI1;H0YI89;E9PQI5;E9PJC4;E9PQ80;Q9BY43;E9PQY7;E9PS99;Q14D22;E9PL78;E9PJM1;O15321-2;E9PMQ9;O15321 Charged multivesicular body protein 4a;Transmembrane 9 superfamily member 1 TM9SF1;CHMP4A >tr|E9PSI1|E9PSI1_HUMAN Transmembrane 9 superfamily member 1 OS=Homo sapiens GN=TM9SF1 PE=4 SV=1;>tr|H0YI89|H0YI89_HUMAN Charged multivesicular body protein 4a (Fragment) OS=Homo sapiens GN=CHMP4A PE=4 SV=1;>tr|E9PQI5|E9PQI5_HUMAN Charged multivesicular bo NaN NaN 0.04 NaN 0.07 NaN NaN NaN 6.72E-10 2 2.3 autophagy;catabolic process;cellular catabolic process;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular metabolic process;cellular process;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;membrane organization;metabolic process;protein transport;transport;vesicle-mediated transport binding;lipid binding autophagic vacuole membrane;cell part;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endosomal part;endosome membrane;integral to membrane;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;late endosome membrane;lysosomal membrane;membrane;membrane part;organelle;organelle membrane;organelle part;vacuolar membrane;vacuolar part;vesicle;vesicle membrane Endocytosis

Q5TB53;Q9HD45 Transmembrane 9 superfamily member 3 TM9SF3 >tr|Q5TB53|Q5TB53_HUMAN Transmembrane 9 superfamily member 3 (Fragment) OS=Homo sapiens GN=TM9SF3 PE=2 SV=1;>sp|Q9HD45|TM9S3_HUMAN Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2 1.17 1.42 2.3 NaN 0.92 NaN 0.82 0.83 1.16E-05 2 7.5 cell part;integral to membrane;intrinsic to membrane;membrane part

Q92544 Transmembrane 9 superfamily member 4 TM9SF4 >sp|Q92544|TM9S4_HUMAN Transmembrane 9 superfamily member 4 OS=Homo sapiens GN=TM9SF4 PE=1 SV=2 1.22 1.17 1.24 1.05 0.82 0.62 0.9 0.88 6.34E-05 2 2.8 cell part;integral to membrane;intrinsic to membrane;membrane part

C9JEN3;C9IYT2;F8WDY4;C9IZ27;C9JW19;C9JWV9;B4DUD2;Q969X1;C9JAP5 Protein lifeguard 3 TMBIM1 >tr|C9JEN3|C9JEN3_HUMAN Protein lifeguard 3 (Fragment) OS=Homo sapiens GN=TMBIM1 PE=2 SV=1;>tr|C9IYT2|C9IYT2_HUMAN Protein lifeguard 3 (Fragment) OS=Homo sapiens GN=TMBIM1 PE=2 SV=1;>tr|F8WDY4|F8WDY4_HUMAN Protein lifeguard 3 OS=Homo sapiens GN=TMBIM1 PE=2 1.08 1.31 0.82 0.96 0.72 0.92 0.83 1.14 5.80E-31 2 14.2 cell part;cytoplasmic part;endosomal part;endosome membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal membrane;membrane;membrane part;organelle membrane;organelle part;vacuolar membrane;vacuolar part

Q9Y3A6;B1AKT3;Q9Y3A6-2 Transmembrane emp24 domain-containing protein 5 TMED5 >sp|Q9Y3A6|TMED5_HUMAN Transmembrane emp24 domain-containing protein 5 OS=Homo sapiens GN=TMED5 PE=1 SV=1;>tr|B1AKT3|B1AKT3_HUMAN Transmembrane emp24 domain-containing protein 5 OS=Homo sapiens GN=TMED5 PE=2 SV=1;>sp|Q9Y3A6-2|TMED5_HUMAN Isoform 2 of Trans 1.07 0.76 2.12 0.59 1.05 0.82 1.17 1.16 2.70E-22 2 10 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;establishment of localization;establishment of protein localization;Golgi organization;Golgi ribbon formation;organelle organization;protein transport;transport cell part;cis-Golgi network;cytoplasmic part;endoplasmic reticulum exit site;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus;Golgi apparatus part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part

Q9BVK6 Transmembrane emp24 domain-containing protein 9 TMED9 >sp|Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2 0.97 1.06 2.28 0.8 0.83 0.71 0.88 1.12 5.84E-40 2 8.5 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of protein localization;Golgi organization;Golgi transport vesicle coating;organelle organization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of organelle organization;protein transport;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of organelle organization;transport;vesicle coating;vesicle organization cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi-associated vesicle;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;trans-Golgi network transport vesicle;transport vesicle;vesicle

Q9BVC6 Transmembrane protein 109 TMEM109 >sp|Q9BVC6|TM109_HUMAN Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1 SV=1 NaN 0.67 1.77 NaN 1.92 NaN NaN 1.03 6.23E-06 2 5.3 "biological regulation;cellular process;cellular response to stimulus;cellular response to stress;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage" cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;nuclear membrane;nuclear outer membrane;nuclear part;organelle membrane;organelle outer membrane;organelle part;outer membrane;sarcoplasmic reticulum membrane

Q86WV6;J3QTB1 Stimulator of interferon genes protein TMEM173 >sp|Q86WV6|STING_HUMAN Stimulator of interferon genes protein OS=Homo sapiens GN=TMEM173 PE=1 SV=1;>tr|J3QTB1|J3QTB1_HUMAN Stimulator of interferon genes protein (Fragment) OS=Homo sapiens GN=TMEM173 PE=4 SV=1 NaN NaN 1.65 NaN 1.19 NaN NaN NaN 0.00015632 2 7.9 "activation of immune response;activation of innate immune response;apoptosis;biological regulation;cell death;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to dsRNA;cellular response to exogenous dsRNA;cellular response to interferon-beta;cellular response to organic substance;cellular response to stimulus;cytokine production;death;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;interferon-beta production;multicellular organismal process;multi-organism process;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of defense response to virus by host;positive regulation of gene expression;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of protein binding;positive regulation of protein import into nucleus;positive regulation of protein import into nucleus, translocation;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription factor import into nucleus;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of type I interferon production;programmed cell death;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by host;regulation of establishment of protein localization;regulation of gene expression;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein binding;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein localization;regulation of protein transport;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of type I interferon production;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to dsRNA;response to exogenous dsRNA;response to interferon-beta;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;type I interferon production" binding;cyclic nucleotide binding;cyclic-di-GMP binding;enzyme binding;guanyl nucleotide binding;guanyl ribonucleotide binding;identical protein binding;kinase binding;nucleotide binding;protein binding;protein dimerization activity;protein homodimerization activity;protein kinase binding;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding;transcription factor binding cell part;cytoplasmic part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;perinuclear region of cytoplasm;plasma membrane Cytosolic DNA-sensing pathway;RIG-I-like receptor signaling pathway

Q8NBN3-3;Q8NBN3;Q8NBN3-2 Transmembrane protein 87A TMEM87A >sp|Q8NBN3-3|TM87A_HUMAN Isoform 3 of Transmembrane protein 87A OS=Homo sapiens GN=TMEM87A;>sp|Q8NBN3|TM87A_HUMAN Transmembrane protein 87A OS=Homo sapiens GN=TMEM87A PE=1 SV=3;>sp|Q8NBN3-2|TM87A_HUMAN Isoform 2 of Transmembrane protein 87A OS=Homo sapiens 1.36 1.36 1.67 NaN 0.59 NaN 0.86 0.84 2.11E-50 2 5.3 cell part;integral to membrane;intrinsic to membrane;membrane part

Q96JJ7 Protein disulfide-isomerase TMX3 TMX3 >sp|Q96JJ7|TMX3_HUMAN Protein disulfide-isomerase TMX3 OS=Homo sapiens GN=TMX3 PE=1 SV=2 NaN NaN 1.48 NaN 1.11 NaN NaN NaN 2.26E-05 2 4.6 biological regulation;cell redox homeostasis;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycerol ether metabolic process;homeostatic process;macromolecule metabolic process;metabolic process;organic ether metabolic process;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cell surface;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part

Q9H0E2;E9PNS3;F2Z2Y8;E7EN89 Toll-interacting protein TOLLIP >sp|Q9H0E2|TOLIP_HUMAN Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=1 SV=1;>tr|E9PNS3|E9PNS3_HUMAN Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=2 SV=1;>tr|F2Z2Y8|F2Z2Y8_HUMAN Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=2 SV=1;>t 1.07 1.57 0.27 0.64 2.49 1.95 1.08 0.7 1.55E-05 2 8.4 biological regulation;cell activation;cell communication;cell-cell signaling;cellular metabolic process;cellular process;cellular response to stimulus;defense response;immune response;immune system process;inflammatory response;innate immune response;intracellular signal transduction;leukocyte activation;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein sumoylation;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein sumoylation;response to stimulus;response to stress;response to wounding;signal transduction;signaling molecular transducer activity;signal transducer activity cell part;cytoplasmic part;cytosol;interleukin-1 receptor complex;interleukin-18 receptor complex;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear body;nuclear part;nucleoplasm part;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex;receptor complex Toll-like receptor signaling pathway

Q15388 Mitochondrial import receptor subunit TOM20 homolog TOMM20 >sp|Q15388|TOM20_HUMAN Mitochondrial import receptor subunit TOM20 homolog OS=Homo sapiens GN=TOMM20 PE=1 SV=1 NaN NaN 0.21 NaN 0.28 NaN NaN NaN 4.70E-05 2 13.8 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transport active transmembrane transporter activity;binding;macromolecule transmembrane transporter activity;P-P-bond-hydrolysis-driven protein transmembrane transporter activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;unfolded protein binding cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial outer membrane translocase complex;mitochondrial part;organelle part;protein complex

B3KP96;O95361;H0Y626;K7EL43;K7ENN8;O95361-2;J3KPT5 Tripartite motif-containing protein 16 TRIM16;TRIM16L >tr|B3KP96|B3KP96_HUMAN Tripartite motif-containing protein 16 OS=Homo sapiens GN=TRIM16 PE=2 SV=1;>sp|O95361|TRI16_HUMAN Tripartite motif-containing protein 16 OS=Homo sapiens GN=TRIM16 PE=1

SV=3;>tr|H0Y626|H0Y626_HUMAN Uncharacterized protein OS=Homo sap NaN NaN 2.2 NaN 5.11 NaN NaN NaN 0.00037377 2 5.5 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;histone acetylation;histone H3 acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of cytokine secretion;positive regulation of developmental process;positive regulation of epidermal cell differentiation;positive regulation of epidermis development;positive regulation of epithelial cell differentiation;positive regulation of gene expression;positive regulation of interleukin-1 beta production;positive regulation of interleukin-1 beta secretion;positive regulation of interleukin-1 production;positive regulation of interleukin-1 secretion;positive regulation of keratinocyte differentiation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of retinoic acid receptor signaling pathway;positive regulation of RNA metabolic process;positive regulation of secretion;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription, DNA-dependent;positive regulation of transport;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of cytokine secretion;regulation of developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of establishment of protein localization;regulation of gene expression;regulation of interleukin-1 beta production;regulation of interleukin-1 beta secretion;regulation of interleukin-1 production;regulation of interleukin-1 secretion;regulation of keratinocyte differentiation;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of RNA metabolic process;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to growth hormone stimulus;response to hormone stimulus;response to insecticide;response to nutrient;response to nutrient levels;response to organic substance;response to organophosphorus;response to peptide hormone stimulus;response to retinoic acid;response to stimulus;response to toxin;response to vitamin;response to vitamin A" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear body;nuclear part;nucleoplasm part;organelle part;PML body

Q14669;Q14669-2;Q14669-3;F8W9P3;C9JLJ5;C9JSX9;C9JLD7;B4DYJ6;G5E9G6;Q14669-4 E3 ubiquitin-protein ligase TRIP12 TRIP12 >sp|Q14669|TRIPC_HUMAN E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1;>sp|Q14669-2|TRIPC_HUMAN Isoform 2 of E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12;>sp|Q14669-3|TRIPC_HUMAN Isoform 3 of E3 ubiquitin-protein liga NaN NaN 0.42 NaN 0.46 NaN NaN NaN 0.00011765 2 1.6 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;DNA repair;embryo development;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA repair;negative regulation of double-strand break repair;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of double-strand break repair;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;response to DNA damage stimulus;response to stimulus;response to stress "acid-amino acid ligase activity;binding;catalytic activity;hormone receptor binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;nuclear hormone receptor binding;protein binding;receptor binding;small conjugating protein ligase activity;thyroid hormone receptor binding;transcription factor binding;ubiquitin-protein ligase activity" cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part Ubiquitin mediated proteolysis

B1AH87;P30536 Translocator protein TSPO >tr|B1AH87|B1AH87_HUMAN Putative peripheral benzodiazepine receptor-related protein (Fragment) OS=Homo sapiens GN=TSPO PE=2 SV=1;>sp|P30536|TSPOA_HUMAN Translocator protein OS=Homo sapiens GN=TSPO PE=1 SV=3 0.99 1.16 1.13 0.56 0.47 1.37 0.88 1.05 0.00011338 2 15 adrenal gland development;aging;anatomical structure development;anatomical structure morphogenesis;anion transport;apoptosis;axon regeneration;axonogenesis;behavior;behavioral response to pain;biological regulation;biosynthetic process;cell death;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular hypotonic response;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to lipopolysaccharide;cellular response to metal ion;cellular response to molecule of bacterial origin;cellular response to osmotic stress;cellular response to stimulus;cellular response to stress;cellular response to zinc ion;cofactor biosynthetic process;cofactor metabolic process;contact inhibition;death;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;gland development;glial cell migration;heme biosynthetic process;heme metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;hypotonic response;intracellular protein transport;intracellular transport;ion transport;lipid biosynthetic process;lipid metabolic process;locomotion;metabolic process;mitochondrial transport;multicellular organismal process;multicellular organismal response to stress;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of developmental process;negative regulation of glial cell proliferation;negative regulation of gliogenesis;negative regulation of metabolic process;negative regulation of multicellular organismal process;negative regulation of neurogenesis;negative regulation of nitric oxide biosynthetic process;negative regulation of nitrogen compound metabolic process;negative regulation of tumor necrosis factor production;neuron projection morphogenesis;neuron projection regeneration;nitrogen compound metabolic process;organ development;peripheral nervous system axon regeneration;pigment biosynthetic process;pigment metabolic process;porphyrin-containing compound biosynthetic process;porphyrin-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of glial cell proliferation;positive regulation of gliogenesis;positive regulation of homeostatic process;positive regulation of ion transport;positive regulation of metabolic process;positive regulation of mitochondrial depolarization;positive regulation of necrotic cell death;positive regulation of neurogenesis;positive regulation of programmed cell death;positive regulation of reactive oxygen species metabolic process;positive regulation of transport;primary metabolic process;programmed cell death;protein import;protein targeting;protein targeting to mitochondrion;protein transport;regeneration;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of calcium ion transport;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cholesterol transport;regulation of cytokine production;regulation of developmental process;regulation of glial cell proliferation;regulation of gliogenesis;regulation of homeostatic process;regulation of ion homeostasis;regulation of ion transport;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of lipid transport;regulation of localization;regulation of membrane depolarization;regulation of metabolic process;regulation of metal ion transport;regulation of mitochondrial depolarization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of necrotic cell death;regulation of nervous system development;regulation of neurogenesis;regulation of nitric oxide biosynthetic process;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of reactive oxygen species metabolic process;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of sterol transport;regulation of transport;regulation of tumor necrosis factor production;response to abiotic stimulus;response to axon injury;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to inorganic substance;response to lipopolysaccharide;response to manganese ion;response to metal ion;response to molecule of bacterial origin;response to nutrient;response to nutrient levels;response to organic substance;response to osmotic stress;response to pain;response to progesterone stimulus;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;response to vitamin;response to vitamin B1;response to wounding;response to zinc ion;steroid biosynthetic process;steroid metabolic process;tetrapyrrole biosynthetic process;tetrapyrrole metabolic process;transport androgen binding;benzodiazepine receptor activity;binding;cholesterol binding;hormone binding;lipid binding;molecular transducer activity;neurotransmitter binding;neurotransmitter receptor activity;receptor activity;signal transducer activity;signaling receptor activity;steroid binding;sterol binding cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane Neuroactive ligand-receptor interaction

Q14157-4;Q14157-1;Q14157-3;F8W726;Q14157;Q14157-5;H0Y5H6;H7C2T8 Ubiquitin-associated protein 2-like UBAP2L >sp|Q14157-4|UBP2L_HUMAN Isoform 4 of Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L;>sp|Q14157-1|UBP2L_HUMAN Isoform 2 of Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L;>sp|Q14157-3|UBP2L_HUMAN Isoform 3 of Ubiquitin-associat 2.04 NaN NaN 0.42 NaN 0.41 2.28 NaN 2.11E-05 2 3 binding of sperm to zona pellucida;cell recognition;cell-cell recognition;cellular process;cellular process involved in reproduction;reproductive process;sperm-egg recognition

P17480-2;E9PKP7;P17480;E9PLT2 Nucleolar transcription factor 1 UBTF >sp|P17480-2|UBF1_HUMAN Isoform UBF2 of Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF;>tr|E9PKP7|E9PKP7_HUMAN Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=2 SV=1;>sp|P17480|UBF1_HUMAN Nucleolar transcription factor 1 OS=Homo sapie NaN NaN 0.94 NaN 0.56 NaN NaN NaN 0.0005594 2 4 "biological regulation;biosynthetic process;blastocyst growth;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental growth;developmental process;embryo implantation;growth;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase I promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase I promoter;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;termination of RNA polymerase I transcription;transcription elongation from RNA polymerase I promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase I promoter;transcription initiation, DNA-dependent;transcription termination, DNA-dependent" binding;DNA binding;nucleic acid binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part

Q92575;F8WB86;Q6PJ80;C9JLR4 UBX domain-containing protein 4 UBXN4 >sp|Q92575|UBXN4_HUMAN UBX domain-containing protein 4 OS=Homo sapiens GN=UBXN4 PE=1 SV=2;>tr|F8WB86|F8WB86_HUMAN UBX domain-containing protein 4 OS=Homo sapiens GN=UBXN4 PE=2 SV=1;>tr|Q6PJ80|Q6PJ80_HUMAN UBX domain-containing protein 4 OS=Homo sapiens GN= NaN NaN NaN NaN NaN NaN NaN NaN 1.95E-05 2 7.3 response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;nuclear envelope;nuclear part;nucleus;organelle;organelle envelope;organelle membrane;organelle part

F5GZ76;F5H4X1;O60763;F5GYR8;O60763-2 General vesicular transport factor p115 USO1 >tr|F5GZ76|F5GZ76_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1;>tr|F5H4X1|F5H4X1_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=2 SV=1;>sp|O60763|USO1_HUMAN General vesicular transport factor p11 NaN NaN 0.23 NaN 0.57 NaN NaN NaN 0.00078418 2 2.8 cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;M phase;M phase of mitotic cell cycle;membrane fusion;membrane organization;mitotic prophase;organelle fusion;organelle organization;prophase;protein transport;transcytosis;transport;vesicle fusion;vesicle fusion with Golgi apparatus;vesicle organization;vesicle-mediated transport protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;perinuclear region of cytoplasm

Q14694;Q14694-3;Q14694-2;H3BNS8;H3BQP1;H3BVF1;J3KT19 Ubiquitin carboxyl-terminal hydrolase 10 USP10 >sp|Q14694|UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2;>sp|Q14694-3|UBP10_HUMAN Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10;>sp|Q14694-2|UBP10_HUMAN Isoform 2 of Ubiquitin carbo 0.84 1.01 1.02 0.78 1.37 1.45 1.15 1.41 0.00023103 2 3.1 "autophagy;biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA damage response, signal transduction by p53 class mediator;DNA metabolic process;DNA repair;intracellular signal transduction;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of autophagy;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;ubiquitin-dependent protein catabolic process" "binding;catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion channel binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" cell part;cytoplasmic part;cytoskeleton;early endosome;endosome;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle

Q9Y5J1 U3 small nucleolar RNA-associated protein 18 homolog UTP18 >sp|Q9Y5J1|UTP18_HUMAN U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3 NaN NaN 1.51 NaN 0.84 NaN NaN NaN 7.16E-05 2 3.8 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part Ribosome biogenesis in eukaryotes

K7ENK9;K7EKX0;Q15836;J3QRU4;P63027;F8WCA0;L7N2F9;P23763-2;F5GZV7;P23763-3;P23763 Vesicle-associated membrane protein 3;Vesicle-associated membrane protein 2;Vesicle-associated membrane protein 1 VAMP2;VAMP3;VAMP1 >tr|K7ENK9|K7ENK9_HUMAN Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=4 SV=1;>tr|K7EKX0|K7EKX0_HUMAN Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=4 SV=1;>sp|Q15836|VAMP3_HUMAN Vesicle-associated membrane protein 3 O 1.15 1.56 0.96 0.79 1.24 1.15 1.02 0.96 2.51E-05 2 35.3 "anatomical structure morphogenesis;biological adhesion;biological regulation;calcium ion-dependent exocytosis;cell adhesion;cell morphogenesis;cell morphogenesis involved in differentiation;cell-substrate adhesion;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;endosome transport;energy derivation by oxidation of organic compounds;energy reserve metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;generation of precursor metabolites and energy;glutamate secretion;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;membrane docking;membrane fusion;membrane organization;metabolic process;neurotransmitter secretion;neurotransmitter transport;oxidation-reduction process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of receptor recycling;positive regulation of signaling;post-Golgi vesicle-mediated transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of neurotransmitter levels;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of receptor recycling;regulation of secretion;regulation of signaling;regulation of transport;retrograde transport, endosome to Golgi;secretion;secretion by cell;signal release;small molecule metabolic process;substrate adhesion-dependent cell spreading;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle-mediated transport" apical plasma membrane;cell junction;cell part;cell projection;clathrin coated vesicle membrane;clathrin sculpted gamma-aminobutyric acid transport vesicle membrane;clathrin sculpted glutamate transport vesicle membrane;clathrin sculpted monoamine transport vesicle membrane;clathrin-coated vesicle;coated vesicle;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;neuron projection;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;plasma membrane;plasma membrane part;protein complex;recycling endosome;secretory granule membrane;SNARE complex;stored secretory granule;synapse;synapse part;synaptic vesicle membrane;transport vesicle membrane;vesicle;vesicle membrane Phagosome;Salivary secretion;SNARE interactions in vesicular transport;Vasopressin-regulated water reabsorption

B8ZZT4;Q9BV40 Vesicle-associated membrane protein 8 VAMP8 >tr|B8ZZT4|B8ZZT4_HUMAN Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=2 SV=1;>sp|Q9BV40|VAMP8_HUMAN Vesicle-associated membrane protein 8 OS=Homo sapiens GN=VAMP8 PE=1 SV=1 NaN 1.02 0.59 0.91 0.39 0.76 NaN 1.08 3.89E-05 2 19.2 autophagic vacuole fusion;biological regulation;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;membrane fusion;membrane organization;organelle fusion;organelle membrane fusion;organelle organization;post-Golgi vesicle-mediated transport;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of transport;regulation of vesicle-mediated transport;transport;vesicle fusion;vesicle organization;vesicle-mediated transport cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome;endosomal part;endosome;endosome membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;late endosome membrane;lysosomal membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part;plasma membrane;protein complex;recycling endosome;secretory granule membrane;SNARE complex;vacuolar membrane;vacuolar part;vesicle membrane SNARE interactions in vesicular transport

D6RGZ6;P13611-2;P13611-5;P13611;Q86W61;P13611-4;E9PF17;P13611-3 Versican core protein VCAN >tr|D6RGZ6|D6RGZ6_HUMAN Versican core protein (Fragment) OS=Homo sapiens GN=VCAN PE=2 SV=1;>sp|P13611-2|CSPG2_HUMAN Isoform V1 of Versican core protein OS=Homo sapiens GN=VCAN;>sp|P13611-5|CSPG2_HUMAN Isoform Vint of Versican core protein OS=Homo sapiens G NaN NaN 1.08 NaN 0.27 NaN NaN NaN 0.00022535 2 1.7 amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;biological adhesion;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell adhesion;cell migration;cell motility;cell recognition;cellular biosynthetic process;cellular catabolic process;cellular component movement;cellular metabolic process;cellular process;chondroitin sulfate biosynthetic process;chondroitin sulfate catabolic process;chondroitin sulfate metabolic process;dermatan sulfate biosynthetic process;dermatan sulfate metabolic process;developmental process;glial cell migration;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;heart development;locomotion;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;nitrogen compound metabolic process;organ development;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;sulfur compound biosynthetic process;sulfur compound catabolic process;sulfur compound metabolic process binding;calcium ion binding;carbohydrate binding;cation binding;glycosaminoglycan binding;hyaluronic acid binding;ion binding;metal ion binding;pattern binding;polysaccharide binding cell part;cytoplasmic part;extracellular matrix;extracellular region part;extracellular space;Golgi apparatus part;Golgi lumen;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-enclosed lumen;organelle lumen;organelle part;proteinaceous extracellular matrix;vacuolar lumen;vacuolar part Cell adhesion molecules (CAMs)

Q709C8-4;Q709C8-2;Q709C8-3;Q709C8 Vacuolar protein sorting-associated protein 13C VPS13C >sp|Q709C8-4|VP13C_HUMAN Isoform 4 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C;>sp|Q709C8-2|VP13C_HUMAN Isoform 2 of Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C;>sp|Q709C8-3|VP13C_HUMAN Isoform 0.8 1.09 NaN NaN NaN NaN 0.43 1.09 0.00025522 2 0.5

Q86Y07-5;Q86Y07-2;Q86Y07;E9PBU1;E7ERS5;Q86Y07-4;Q86Y07-3 Serine/threonine-protein kinase VRK2 VRK2 >sp|Q86Y07-5|VRK2_HUMAN Isoform 5 of Serine/threonine-protein kinase VRK2 OS=Homo sapiens GN=VRK2;>sp|Q86Y07-2|VRK2_HUMAN Isoform 2 of Serine/threonine-protein kinase VRK2 OS=Homo sapiens GN=VRK2;>sp|Q86Y07|VRK2_HUMAN Serine/threonine-protein kinase VRK2 O NaN NaN 1.09 NaN 0.56 NaN NaN NaN 3.57E-06 2 5.6 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;macromolecule modification;metabolic process;multi-organism process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of cellular process;regulation of cytokine-mediated signaling pathway;regulation of interleukin-1-mediated signaling pathway;regulation of intracellular protein kinase cascade;regulation of MAPKKK cascade;regulation of response to cytokine stimulus;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;reproductive process;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial part;nucleus;organelle;organelle membrane;organelle part

O75083;D6RD66;O75083-3 WD repeat-containing protein 1 WDR1 >sp|O75083|WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4;>tr|D6RD66|D6RD66_HUMAN WD repeat-containing protein 1 (Fragment) OS=Homo sapiens GN=WDR1 PE=2 SV=1;>sp|O75083-3|WDR1_HUMAN Isoform 2 of WD repeat-containing protein 1 O 0.19 NaN NaN NaN NaN NaN 0.44 NaN 9.93E-05 2 4.3 cell activation;cellular process;establishment of localization;establishment of localization in cell;exocytosis;multicellular organismal process;neurological system process;platelet activation;platelet degranulation;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;system process;transport;vesicle-mediated transport cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;intracellular

non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle
Q9BV38;K7EIR0 WD repeat-containing protein 18 WDR18 >sp|Q9BV38|WDR18_HUMAN WD repeat-containing protein 18 OS=Homo sapiens GN=WDR18 PE=1 SV=2;>tr|K7EIR0|K7EIR0_HUMAN WD repeat-containing protein 18 OS=Homo sapiens GN=WDR18 PE=4 SV=1 NaN NaN 1.54 NaN 0.51 NaN NaN NaN 1.03E-22 2 4.4 developmental process;multicellular organismal development;multicellular organismal process cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part
Q15061 WD repeat-containing protein 43 WDR43 >sp|Q15061|WDR43_HUMAN WD repeat-containing protein 43 OS=Homo sapiens GN=WDR43 PE=1 SV=3 NaN NaN 0.51 NaN 0.21 NaN NaN NaN 0.00016873 2 3.4 cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes
Q5HYZ1;A2ABB6;H0Y6G3 WDR46 >tr|Q5HYZ1|Q5HYZ1_HUMAN WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=2 SV=2;>tr|A2ABB6|A2ABB6_HUMAN WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=2 SV=1;>tr|H0Y6G3|H0Y6G3_HUMAN WD repeat-containing protein NaN 1.64 1.44 1.81 0.88 0.36 NaN 0.54 4.07E-17 2 13.7
O15213 WD repeat-containing protein 46 WDR46 >sp|O15213|WDR46_HUMAN WD repeat-containing protein 46 OS=Homo sapiens GN=WDR46 PE=1 SV=3 1.01 NaN 0.55 NaN 0.3 NaN 0.56 NaN 5.68E-21 2 5.9
Q9C0B5-2;Q9C0B5;Q9ULC8-2;Q9ULC8 Palmitoyltransferase ZDHHC5;Probable palmitoyltransferase ZDHHC8 ZDHHC5;ZDHHC8 >sp|Q9C0B5-2|ZDHC5_HUMAN Isoform 2 of Palmitoyltransferase ZDHHC5 OS=Homo sapiens GN=ZDHHC5;>sp|Q9C0B5|ZDHC5_HUMAN Palmitoyltransferase ZDHHC5 OS=Homo sapiens GN=ZDHHC5 PE=1 SV=2;>sp|Q9ULC8-2|ZDHC8_HUMAN Isoform 2 of Probable palmitoyltransferase ZDHHC8 OS NaN NaN 0.94 NaN 0.37 NaN NaN NaN 1.40E-05 2 4.4 behavior;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein acylation;protein lipidation;protein metabolic process;protein modification process;protein palmitoylation;response to stimulus "binding;catalytic activity;cation binding;ion binding;metal ion binding;palmitoyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part;plasma membrane;vesicle membrane
Q96KR1 Zinc finger RNA-binding protein ZFR >sp|Q96KR1|ZFR_HUMAN Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 NaN NaN 1.47 NaN NaN NaN NaN NaN 0.00024237 2 2.8 developmental process;multicellular organismal development;multicellular organismal processbinding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;RNA binding;transition metal ion binding;zinc ion binding cell part;chromosome;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle
H7C3D3;B4DQX7;B4DQR8;H0Y2Y8;Q15942 Zyxin ZYX >tr|H7C3D3|H7C3D3_HUMAN Zyxin (Fragment) OS=Homo sapiens GN=ZYX PE=4 SV=1;>tr|B4DQX7|B4DQX7_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=2 SV=1;>tr|B4DQR8|B4DQR8_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=2 SV=1;>tr|H0Y2Y8|H0Y2Y8_HUMAN Zyxin (Fragment) OS=Homo sapiens NaN NaN 0.79 NaN 2.05 NaN NaN NaN 0.00051953 2 23.3 biological adhesion;biological regulation;cell adhesion;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;interaction with host;interspecies interaction between organisms;multi-organism process;regulation of biological process;regulation of cellular process;reproductive process;response to stimulus;signal transduction;signaling;viral reproductive process;virus-host interaction binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeletal part;focal adhesion;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part;stress fiber Focal adhesion
B5MCX3;Q15019;Q15019-2;C9J2Q4;H7C2Y0;C9IY94;C9IZU3;C9JQJ4;C9J938;H7C310;C9JB25 Septin-2 41884 >tr|B5MCX3|B5MCX3_HUMAN Septin-2 OS=Homo sapiens GN=SEPT2 PE=2 SV=1;>sp|Q15019|SEPT2_HUMAN Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1;>sp|Q15019-2|SEPT2_HUMAN Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2;>tr|C9J2Q4|C9J2Q4_HUMAN Septin-2 (Fragment) OS=Ho 1.12 0.71 0.76 0.27 1.11 0.85 1.59 1.12 1.13E-14 3 12.5 anatomical structure formation involved in morphogenesis;biological regulation;cell cycle;cell cycle phase;cell cycle process;cell division;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;cilium assembly;developmental process;mitosis;neuron projection development;nuclear division;organelle fission;organelle organization;regulation of amine transport;regulation of amino acid transport;regulation of anion transport;regulation of biological process;regulation of cellular process;regulation of ion transport;regulation of L-glutamate transport;regulation of localization;regulation of organic acid transport;regulation of protein localization;regulation of transport;response to stimulus;signal transduction;smoothened signaling pathway binding;enzyme regulator activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding actin cytoskeleton;cell cortex part;cell division site part;cell part;cell projection membrane;cell projection part;cell surface;chromosomal part;cilium membrane;cilium part;cleavage furrow;condensed chromosome kinetochore;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;exocyst;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane part;midbody;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex;septin complex;spindle;synapse
P55265-5;P55265-3;H0YCK3;P55265-2;P55265;P55265-4;E7ENU4 Double-stranded RNA-specific adenosine deaminase ADAR >sp|P55265-5|DSRAD_HUMAN Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR;>sp|P55265-3|DSRAD_HUMAN Isoform 3 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR;>tr|H0YCK3|H0YCK3_HUMAN Double-str NaN NaN 0.34 NaN 1.04 NaN NaN NaN 4.59E-07 3 4 adenosine to inosine editing;base conversion or substitution editing;biological regulation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular

response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;establishment of localization;establishment of localization in cell;establishment of protein localization;gene expression;gene silencing;gene silencing by RNA;immune effector process;immune system process;intracellular protein transport;intracellular transport;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA metabolic process;mRNA modification;mRNA processing;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;nitrogen compound metabolic process;nuclear export;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;positive regulation of biological process;positive regulation of reproductive process;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;protein export from nucleus;protein import;protein import into nucleus;protein targeting;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-alpha;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;RNA metabolic process;RNA modification;RNA processing;signal transduction;transport;type I interferon-mediated signaling pathway "adenosine deaminase activity;binding;catalytic activity;cation binding;deaminase activity;DNA binding;double-stranded RNA adenosine deaminase activity;double-stranded RNA binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;ion binding;metal ion binding;nucleic acid binding;RNA binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part Cytosolic DNA-sensing pathway;Measles

E9PC15;Q53H12;E9PG39 "Acylglycerol kinase, mitochondrial" AGK ">tr|E9PC15|E9PC15_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=2 SV=1;>sp|Q53H12|AGK_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=1 SV=2;>tr|E9PG39|E9PG39_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens"1.03 1.39 1.45 1.73 0.52 0.42 0.6 0.84 1.80E-16 3 8.6 activation of protein kinase activity;activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway;biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;ceramide biosynthetic process;ceramide metabolic process;glycerolipid metabolic process;G-protein coupled receptor protein signaling pathway;lipid biosynthetic process;lipid metabolic process;membrane lipid biosynthetic process;membrane lipid metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;signal transduction;sphingoid biosynthetic process;sphingoid metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process "acylglycerol kinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ceramide kinase activity;diacylglycerol kinase activity;kinase activity;lipid kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial membrane;mitochondrial part;organelle membrane;organelle part Glycerolipid metabolism

Q8WYP5;Q8WYP5-3;Q8WYP5-2 Protein ELYS AHCTF1 >sp|Q8WYP5|ELYS_HUMAN Protein ELYS OS=Homo sapiens GN=AHCTF1 PE=1 SV=3;>sp|Q8WYP5-3|ELYS_HUMAN Isoform 3 of Protein ELYS OS=Homo sapiens GN=AHCTF1;>sp|Q8WYP5-2|ELYS_HUMAN Isoform 2 of Protein ELYS OS=Homo sapiens GN=AHCTF1 NaN NaN 1.73 2.51 0.42 0.6 NaN NaN 2.97E-08 3 1.7 anaphase;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytokinesis;establishment of localization;establishment of protein localization;establishment of RNA localization;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;mitotic anaphase;mitotic prometaphase;mRNA transport;nuclear pore complex assembly;nuclear pore organization;nucleic acid transport;nucleobase-containing compound transport;nucleus organization;organelle organization;pore complex assembly;protein complex assembly;protein complex subunit organization;protein transport;RNA transport;transport binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;nuclear matrix;nuclear membrane;nuclear part;nuclear pore;nucleoplasm;organelle;organelle membrane;organelle part;pore complex;protein complex

F8VS02;P49419-4;P49419-2;P49419;P49419-3;H0YHM6 Alpha-aminoadipic semialdehyde dehydrogenase ALDH7A1 >tr|F8VS02|F8VS02_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=2 SV=1;>sp|P49419-4|AL7A1_HUMAN Isoform 4 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1;>sp|P49419-2|AL7A1_HUMAN Isoform 2 of Al NaN NaN 0.35 NaN 1 NaN NaN NaN 1.86E-07 3 8 alcohol metabolic process;amine biosynthetic process;amine catabolic process;amine metabolic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;betaine biosynthetic process;betaine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular aldehyde metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;choline metabolic process;ethanolamine-containing compound metabolic process;glycine betaine biosynthetic process;glycine betaine biosynthetic process from choline;glycine betaine metabolic process;lysine catabolic process;lysine metabolic process;metabolic process;multicellular organismal process;neurological system process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;system process "aldehyde dehydrogenase (NAD) activity;betaine-aldehyde dehydrogenase activity;catalytic activity;L-aminoadipate-semialdehyde dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nucleus;organelle;organelle lumen;organelle part "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Fatty acid metabolism;Glycerolipid metabolism;Glycine, serine and threonine metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Lysine biosynthesis;Lysine degradation;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation"

H3BUH7;H3BPS8;H3BQN4;P04075;J3KPS3;P04075-2;H3BMQ8;H3BR04;H3BU78 Fructose-bisphosphate aldolase;Fructose-bisphosphate aldolase A ALDOA >tr|H3BUH7|H3BUH7_HUMAN Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens GN=ALDOA PE=2 SV=1;>tr|H3BPS8|H3BPS8_HUMAN Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens GN=ALDOA PE=2 SV=1;>tr|H3BQN4|H3BQN4_HUMAN Fructose-bisphosphate aldo 0.45 2.86 0.21 1.94 0.31 0.77 0.79 1.08 1.45E-25 3 25.2 "actin cytoskeleton organization;actin filament organization;actin filament-based process;alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;anatomical structure homeostasis;ATP biosynthetic process;ATP metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell activation;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;fructose 1,6-bisphosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle biosynthetic process;heterocycle metabolic process;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multicellular organismal process;muscle cell homeostasis;muscle contraction;muscle system process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organelle organization;platelet activation;platelet degranulation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;secretion by cell;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;striated muscle contraction;system process;transport;vesicle-mediated transport" actin binding;aldehyde-lyase activity;binding;carbohydrate binding;carbon-carbon lyase activity;catalytic activity;cytoskeletal protein binding;fructose binding;fructose-bisphosphate aldolase activity;identical protein binding;lyase activity;monosaccharide binding;protein binding;sugar binding;tubulin binding actin cytoskeleton;cell part;contractile fiber part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;I band;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;non-membrane-bounded organelle;organelle;organelle lumen;organelle part;platelet alpha granule lumen;secretory granule lumen;vesicle;vesicle lumen Carbon fixation in photosynthetic organisms;Fructose and mannose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway

Q86V81;E9PB61 THO complex subunit 4 ALYREF >sp|Q86V81|THOC4_HUMAN THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3;>tr|E9PB61|E9PB61_HUMAN THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=2 SV=1 1.43 1.38 1.6 1.71 0.59 0.31 0.58 0.61 1.31E-86 3 17.1 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;intronless viral mRNA export from host nucleus;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;reproductive process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport;viral reproductive process;virus-host interaction" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;single-stranded DNA binding;structure-specific DNA binding catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex;transcription export complex mRNA surveillance pathway;RNA transport;Spliceosome

Q9BZZ5-3;Q9BZZ5-5;Q9BZZ5-2;G3V1C3;Q9BZZ5;Q9BZZ5-1;B4E283;E9PQK6 Apoptosis inhibitor 5 API5 >sp|Q9BZZ5-3|API5_HUMAN Isoform 3 of Apoptosis inhibitor 5 OS=Homo sapiens GN=API5;>sp|Q9BZZ5-5|API5_HUMAN Isoform 5 of Apoptosis inhibitor 5 OS=Homo sapiens GN=API5;>sp|Q9BZZ5-2|API5_HUMAN Isoform 2 of Apoptosis inhibitor 5 OS=Homo sapiens GN=API5;>tr|G3V 1.31 0.99 1.5 NaN 2.17 NaN 0.77 0.79 9.30E-08 3 8.8 apoptosis;biological regulation;cell death;cellular process;death;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex

P48444;B0YIW6;P48444-2 Coatomer subunit delta ARCN1 ">sp|P48444|COPD_HUMAN Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1;>tr|B0YIW6|B0YIW6_HUMAN Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=2 SV=1;>sp|P48444-2|COPD_HUMAN Isoform 2 of Coatomer subunit delta OS=Homo sapiens GN=ARCN1" NaN 1.89 0.92 NaN 1.27 NaN NaN 1.14 1.55E-06 3 5.3 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;organelle organization;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;protein complex;vesicle coat

P84077;P61204;F5H423;F5H0C7;C9J1Z8;P84085;B7ZB63 ADP-ribosylation factor 1;ADP-ribosylation factor 3;ADP-ribosylation factor 5 ARF1;ARF3;ARF5 >sp|P84077|ARF1_HUMAN ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2;>sp|P61204|ARF3_HUMAN ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2;>tr|F5H423|F5H423_HUMAN ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=2 SV=1;>tr|F5H0 0.5 3.68 0.34 2.1 0.41 1.13 0.67 1.17 4.64E-66 3 24.9 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;biosynthetic process;cation homeostasis;cellular biosynthetic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular copper ion homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chemical homeostasis;COPI coating of Golgi vesicle;copper ion homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;Golgi transport vesicle coating;Golgi vesicle transport;homeostatic process;immune system process;intracellular signal transduction;intracellular transport;ion homeostasis;lipid biosynthetic process;lipid metabolic process;metabolic process;organelle organization;organophosphate metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;post-Golgi vesicle-mediated transport;primary metabolic process;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;response to stimulus;retrograde vesicle-mediated transport, Golgi to ER;signal transduction;small GTPase mediated signal transduction;transport;vesicle coating;vesicle organization;vesicle-mediated transport;viral reproduction" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor signaling protein activity;ribonucleotide binding;signal transducer activity" cell part;contractile fiber part;cytoplasmic part;cytosol;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;sarcomere Vibrio cholerae infection

Q9NVJ2;Q96BM9;B4DI85 ADP-ribosylation factor-like protein 8B;ADP-ribosylation factor-like protein 8A ARL8B;ARL8A >sp|Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1;>sp|Q96BM9|ARL8A_HUMAN ADP-ribosylation factor-like protein 8A OS=Homo sapiens GN=ARL8A PE=1 SV=1 0.65 0.9 0.68 0.4 1.58 1.82 1.35 1.31 5.77E-39 3 17.7 biological regulation;cell cycle;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;chromosome segregation;intracellular signal transduction;mitosis;nuclear division;organelle fission;organelle organization;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction "alpha-tubulin binding;beta-tubulin binding;binding;catalytic activity;cytoskeletal protein binding;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;tubulin binding" cell part;cytoplasm;cytoplasmic part;cytoskeletal part;endosomal part;endosome membrane;intracellular;intracellular organelle part;intracellular part;late endosome membrane;lysosomal membrane;membrane;midbody;organelle membrane;organelle part;spindle midzone;vacuolar membrane;vacuolar part

Q8NBU5-2;Q8NBU5;B4E2J1 ATPase family AAA domain-containing protein 1 ATAD1 >sp|Q8NBU5-2|ATAD1_HUMAN Isoform 2 of ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1;>sp|Q8NBU5|ATAD1_HUMAN ATPase family AAA domain-containing protein 1 OS=Homo sapiens GN=ATAD1 PE=1 SV=1;>tr|B4E2J1|B4E2J1_HUMAN ATPase family AAA d 0.96 1.28 1.65 2.19 0.36 0.59 0.7 1.22 1.18E-06 3 10.1 "behavior;biological regulation;cognition;learning;learning or memory;memory;multicellular organismal process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of multicellular organismal process;negative regulation of neurological system process;negative regulation of signaling;negative regulation of synaptic transmission;negative regulation of synaptic transmission, glutamatergic;negative regulation of transmission of nerve impulse;neurological system process;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of receptor internalization;positive regulation of receptor-mediated endocytosis;positive regulation of transport;regulation of biological process;regulation of cell communication;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of receptor internalization;regulation of receptor-mediated endocytosis;regulation of signaling;regulation of synaptic transmission;regulation of synaptic transmission, glutamatergic;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;system process"	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	cell junction;cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrion;organelle;organelle membrane;organelle part;peroxisomal membrane;peroxisomal part;plasma membrane;postsynaptic membrane;synapse part;synaptic membrane

P30049	"ATP synthase subunit delta, mitochondrial"	ATP5D	">sp|P30049|ATPD_HUMAN ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2"	1.04	1.68	1.79	1.28	0.49	0.43	0.67	0.8	8.89E-46	3	22.6	"ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;response to chemical stimulus;response to copper ion;response to inorganic substance;response to metal ion;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport"	"active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity"	"cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex, catalytic core F(1);organelle lumen;organelle part;protein complex;proton-transporting ATP synthase complex, catalytic core F(1);proton-transporting two-sector ATPase complex, catalytic domain"	Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

E9PN17;O75964	"ATP synthase subunit g, mitochondrial"	ATP5L	">tr|E9PN17|E9PN17_HUMAN ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=2 SV=1;>sp|O75964|ATP5L_HUMAN ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3"	1.14	1.37	1.94	1.19	0.84	0.45	0.72	0.84	6.18E-10	3	48.7	"ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport"	cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity	"cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle part;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain" Oxidative phosphorylation

O75531;E9PJJ8 Barrier-to-autointegration factor BANF1 >sp|O75531|BAF_HUMAN Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1 0.86 1.46 1.59 2.86 0.54 0.77 0.32 0.53 8.89E-33 3 34.8 anaphase;cell cycle phase;cell cycle process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA integration;DNA metabolic process;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;membrane disassembly;membrane organization;metabolic process;mitotic anaphase;mitotic nuclear envelope disassembly;mitotic nuclear envelope reassembly;mitotic prophase;multi-organism process;nitrogen compound metabolic process;nuclear envelope disassembly;nuclear envelope organization;nuclear envelope reassembly;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;prophase;response to biotic stimulus;response to other organism;response to stimulus;response to virus binding;DNA binding;nucleic acid binding cell part;chromosome;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part

Q9NYF8-4;Q9NYF8-2;Q9NYF8;H0YF00;E9PJA7;E9PK09;E9PQN2;E9PKI6;Q9NYF8-3;E9PK91 Bcl-2-associated transcription factor 1 BCLAF1 >sp|Q9NYF8-4|BCLF1_HUMAN Isoform 4 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1;>sp|Q9NYF8-2|BCLF1_HUMAN Isoform 2 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1;>sp|Q9NYF8|BCLF1_HUMAN Bcl-2-associated transcri 1.1 0.75 0.7 1.18 0.48 0.51 1.04 0.87 2.52E-10 3 4.6 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;induction of apoptosis;induction of programmed cell death;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of protein complex assembly;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription initiation, DNA-dependent;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA-dependent transcription in response to stress;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription initiation, DNA-dependent;regulation of transcription, DNA-dependent;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part

Q8TDN6 Ribosome biogenesis protein BRX1 homolog BRIX1 >sp|Q8TDN6|BRX1_HUMAN Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens GN=BRIX1 PE=1 SV=2 1.11 1.71 0.69 2.73 0.46 0.38 0.39 0.49 4.49E-15 3 11.9 cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

Q8IVT2 Uncharacterized protein C19orf21 C19orf21 >sp|Q8IVT2|MISP_HUMAN Mitotic interactor and substrate of PLK1 OS=Homo sapiens GN=MISP PE=1 SV=1 0.82 1.23 0.68 1.85 0.52 0.62 0.62 0.89 1.09E-08 3 6.8

Q07021;I3L3Q7;I3L3B0 "Complement component 1 Q subcomponent-binding protein, mitochondrial" C1QBP ">sp|Q07021|C1QBP_HUMAN Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP PE=1 SV=1;>tr|I3L3Q7|I3L3Q7_HUMAN Complement component 1 Q subcomponent-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=C1QBP" 1.22 0.8 1.12 0.42 1.63 1.43 1.49 1.27 5.14E-64 3 15.6 "activation of immune response;apoptosis;biological regulation;biosynthetic process;blood coagulation, intrinsic pathway;cell death;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;complement activation;complement activation, classical pathway;death;defense response;humoral immune response;immune effector process;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;interaction with host;interspecies interaction between organisms;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;mature ribosome assembly;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of defense response;negative regulation of defense response to virus;negative regulation of gene expression;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of interferon-gamma production;negative regulation of interleukin-12 production;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of multicellular organismal process;negative regulation of multi-organism process;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of RNA splicing;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle assembly;phosphatidylinositol 3-kinase cascade;phosphatidylinositol-mediated signaling;positive regulation of apoptosis;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemotaxis;positive regulation of dendritic cell chemotaxis;positive regulation of immune response;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitochondrial translation;positive regulation of mitochondrion organization;positive regulation of neutrophil chemotaxis;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein activation cascade;protein metabolic process;regulation of acute inflammatory response;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of complement activation;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of dendritic cell chemotaxis;regulation of gene expression;regulation of humoral immune response;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of interferon-gamma production;regulation of interleukin-12 production;regulation of intracellular protein kinase cascade;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitochondrial translation;regulation of mitochondrion organization;regulation of mRNA processing;regulation of multicellular organismal process;regulation of multi-organism process;regulation of neutrophil chemotaxis;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein activation cascade;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein processing;regulation of response to biotic stimulus;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA splicing;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;signal transduction;transcription, DNA-dependent;viral reproductive process;virus-host interaction" adrenergic receptor binding;binding;carbohydrate binding;complement binding;complement component C1q binding;glycosaminoglycan binding;G-protein-coupled receptor binding;hyaluronic acid binding;kininogen binding;mRNA binding;nucleic acid binding;opsonin binding;pattern binding;polysaccharide binding;protein binding;protein binding transcription factor activity;receptor binding;RNA binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding;transcription factor binding transcription factor activity cell part;cell surface;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle lumen;organelle part;plasma membrane

P27482 Calmodulin-like protein 3 CALML3 >sp|P27482|CALL3_HUMAN Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2 0.26 NaN 1.24 1.43 0.8 1.09 0.83 NaN 1.40E-22 3 25.5 binding;calcium ion binding;cation binding;ion binding;metal ion binding Alzheimer's disease;Calcium signaling pathway;Gastric acid secretion;Glioma;GnRH signaling pathway;Insulin signaling pathway;ko05152;Long-term potentiation;Melanogenesis;Neurotrophin signaling pathway;Olfactory transduction;Oocyte meiosis;Phosphatidylinositol signaling system;Phototransduction;Phototransduction - fly;Plant-pathogen interaction;Salivary secretion;Vascular smooth muscle contraction

E9PP31;E9PLA9;Q14444-2;Q14444;G3V153 Caprin-1 CAPRIN1 >tr|E9PP31|E9PP31_HUMAN Uncharacterized protein OS=Homo sapiens GN=CAPRIN1 PE=2 SV=1;>tr|E9PLA9|E9PLA9_HUMAN Caprin-1 (Fragment) OS=Homo sapiens GN=CAPRIN1 PE=2 SV=1;>sp|Q14444-2|CAPR1_HUMAN Isoform 2 of Caprin-1 OS=Homo sapiens GN=CAPRIN1;>sp|Q14444|CAPR1 2.33 0.69 0.71 0.68 1.43 0.41 1.81 0.93 1.12E-11 3 16.9 biological regulation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of dendrite morphogenesis;positive regulation of dendritic spine development;positive regulation of dendritic spine morphogenesis;positive regulation of developmental process;positive regulation of neurogenesis;posttranscriptional regulation of gene expression;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biosynthetic process;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of dendritic spine development;regulation of dendritic spine morphogenesis;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation binding;nucleic acid binding;RNA binding cell part;cell projection;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;dendrite;integral to membrane;integral to plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;neuron projection;non-membrane-bounded organelle;organelle;plasma membrane part;ribonucleoprotein complex;RNA granule;stress granule

P04040 Catalase CAT >sp|P04040|CATA_HUMAN Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 NaN NaN NaN 1.19 NaN 2.33 NaN NaN 1.36E-06 3 6.5 "acylglycerol metabolic process;aerobic respiration;alcohol metabolic process;anatomical structure development;biological regulation;catabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular respiration;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to hydrogen peroxide;cellular response to organic substance;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cholesterol metabolic process;development of secondary female sexual characteristics;development of secondary sexual characteristics;developmental process;developmental process involved in reproduction;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;glycerol ether metabolic process;glycerolipid metabolic process;hemoglobin metabolic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;menopause;menstrual cycle phase;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of programmed cell death;negative regulation of sequence-specific DNA binding transcription factor activity;neutral lipid metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organic ether metabolic process;ovulation cycle process;oxidation-reduction process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell division;positive regulation of cellular process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;purine base metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell division;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphatidylinositol 3-kinase cascade;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to hydrogen peroxide;response to hyperoxia;response to hypoxia;response to inorganic substance;response to light stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to oxygen levels;response to radiation;response to reactive oxygen species;response to stimulus;response to stress;response to UV;response to vitamin;response to vitamin E;rhythmic process;small molecule metabolic process;steroid metabolic process;sterol metabolic process;system development;triglyceride metabolic process;UV protection" "aminoacylase activity;antioxidant activity;binding;catalase activity;catalytic activity;cation binding;coenzyme binding;cofactor binding;heme binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;identical protein binding;ion binding;iron ion binding;metal ion binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;protein binding;protein dimerization activity;protein homodimerization activity;tetrapyrrole binding;transition metal ion binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosome;lytic vacuole;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrial intermembrane space;mitochondrial part;organelle;organelle envelope lumen;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part;plasma membrane;vacuole Amyotrophic lateral sclerosis (ALS);Methane metabolism;Peroxisome;Tryptophan metabolism

P45973;F8VNY3 Chromobox protein homolog 5 CBX5 >sp|P45973|CBX5_HUMAN Chromobox protein homolog 5 OS=Homo sapiens GN=CBX5 PE=1 SV=1 NaN NaN 1.55 NaN NaN NaN NaN NaN 3.51E-06 3 15.7 "biological regulation;blood coagulation;coagulation;hemostasis;interaction with host;interspecies interaction between organisms;multicellular organismal process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;viral reproductive process;virus-host interaction" "binding;binding, bridging;chromatin binding;histone binding;methylated histone residue binding;protein binding;protein binding, bridging;repressing transcription factor binding;transcription factor binding" cell part;centromeric heterochromatin;chromatin;chromatin remodeling complex;chromocenter;chromosomal part;cytoplasm;envelope;heterochromatin;histone deacetylase complex;histone methyltransferase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;methyltransferase complex;non-membrane-bounded organelle;nuclear centromeric heterochromatin;nuclear chromatin;nuclear chromosome part;nuclear envelope;nuclear heterochromatin;nuclear part;nucleolus;nucleoplasm part;organelle;organelle envelope;organelle part;protein complex;transcriptional repressor complex

A6NC98-2;A6NC98-4;A6NC98;A6NC98-3 Coiled-coil domain-containing protein 88B CCDC88B >sp|A6NC98-2|CC88B_HUMAN Isoform 2 of Coiled-coil domain-containing protein 88B OS=Homo sapiens GN=CCDC88B;>sp|A6NC98-4|CC88B_HUMAN Isoform 4 of Coiled-coil domain-containing protein 88B OS=Homo sapiens GN=CCDC88B;>sp|A6NC98|CC88B_HUMAN Coiled-coil domain- 1.36 1.19 NaN NaN NaN NaN 1.36 0.87 1.19E-05 3 2.5 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;microtubule cytoskeleton organization;microtubule-based process;organelle organization cell part;cytoplasm;intracellular part

E9PMR4;P48509;E9PRJ3;E9PLZ6;K4DIB7 CD151 antigen CD151 >tr|E9PMR4|E9PMR4_HUMAN CD151 antigen OS=Homo sapiens GN=CD151 PE=2 SV=1;>sp|P48509|CD151_HUMAN CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3;>tr|E9PRJ3|E9PRJ3_HUMAN CD151 antigen (Fragment) OS=Homo sapiens GN=CD151 PE=2 SV=1 1.19 1.15 1.36 NaN 0.36 NaN 0.56 0.65 1.10E-09 3 9.6 biological adhesion;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell motility;cell proliferation;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;immune system process;leukocyte activation;leukocyte proliferation;locomotion;lymphocyte activation;lymphocyte proliferation;mononuclear cell proliferation;T cell activation;T cell proliferation cell part;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part

Q03701 CCAAT/enhancer-binding protein zeta CEBPZ >sp|Q03701|CEBPZ_HUMAN CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3 1.2 1.31 1.52 1.74 0.46 0.35 0.64 0.61 5.37E-09 3 3.9 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

P12532;P12532-2;J3KQ93;C9JSQ1;E9PCP8;F8WCN3 "Creatine kinase U-type, mitochondrial" CKMT1A ">sp|P12532|KCRU_HUMAN Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1;>sp|P12532-2|KCRU_HUMAN Isoform 2 of Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A" 1.31 0.84 1.28 0.44 1.5 1.04 1.84 1.37 8.51E-16 3 7.7 amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;creatine metabolic process;metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;phosphagen metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;creatine kinase activity;kinase activity;nucleotide binding;phosphotransferase activity, nitrogenous group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Arginine and proline metabolism

O00299 Chloride intracellular channel protein 1 CLIC1 >sp|O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 0.56 2.02 NaN 1.12 NaN 1.25 0.79 0.8 1.57E-07 3 23.7 biological regulation;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;homeostatic process;ion homeostasis;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of osteoblast differentiation;regulation of biological process;regulation of biological quality;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of membrane potential;regulation of mitochondrial membrane potential;regulation of multicellular organismal process;regulation of ossification;regulation of osteoblast differentiation;response to stimulus;signal transduction anion channel activity;anion transmembrane transporter activity;channel activity;chloride channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;passive transmembrane transporter activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated chloride channel activity;voltage-gated ion channel activity brush border;cell part;cell projection;chloride channel complex;cytoplasmic part;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrion;nuclear envelope;nuclear membrane;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex

Q5SQ17;O95833 Chloride intracellular channel protein 3 CLIC3 >tr|Q5SQ17|Q5SQ17_HUMAN Chloride intracellular channel protein 3 (Fragment) OS=Homo sapiens GN=CLIC3 PE=2 SV=1;>sp|O95833|CLIC3_HUMAN Chloride intracellular channel protein 3 OS=Homo sapiens GN=CLIC3 PE=1 SV=2 NaN NaN NaN 0.19 NaN 2.98 NaN NaN 9.66E-15 3 28.7 biological regulation;cellular process;cellular response to stimulus;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction anion channel activity;anion transmembrane transporter activity;channel activity;chloride channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;passive transmembrane transporter activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated chloride channel activity;voltage-gated ion channel activity cell part;chloride channel complex;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;protein complex

Q99715-4;D6RGG3;Q99715;Q99715-2;H0Y4P7;H0Y5N9 Collagen alpha-1(XII) chain COL12A1 >sp|Q99715-4|COCA1_HUMAN Isoform 4 of Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1;>tr|D6RGG3|D6RGG3_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=2 SV=1;>sp|Q99715|COCA1_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL1 NaN 1.09 NaN NaN NaN NaN NaN 1.77 2.40E-08 3 1.4 anatomical structure development;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen fibril organization;collagen metabolic process;developmental process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;skeletal system development;system development extracellular matrix structural constituent;extracellular matrix structural constituent conferring tensile strength;structural molecule activity anchoring collagen;cell part;collagen;collagen type XII;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;FACIT collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vesicle Protein digestion and absorption

P08123 Collagen alpha-2(I) chain COL1A2 >sp|P08123|CO1A2_HUMAN Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7 NaN NaN 0.64 NaN 36.74 NaN NaN NaN 2.26E-08 3 2.8 anatomical structure development;anatomical structure morphogenesis;biological regulation;blood vessel development;cell activation;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;collagen catabolic process;collagen fibril organization;collagen metabolic process;developmental process;enzyme linked receptor protein signaling pathway;epidermis morphogenesis;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune system process;intracellular signal transduction;leukocyte migration;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;odontogenesis;organ morphogenesis;platelet activation;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein oligomerization;protein trimerization;Ras protein signal transduction;regulation of biological process;regulation of biological quality;regulation of blood pressure;regulation of cellular process;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to organic nitrogen;response to organic substance;response to stimulus;Rho protein signal transduction;signal transduction;skeletal system development;skin morphogenesis;small GTPase mediated signal transduction;system development;tissue morphogenesis;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway "binding;binding, bridging;cation binding;extracellular matrix structural constituent;growth factor binding;identical protein binding;ion binding;metal ion binding;platelet-derived growth factor binding;protein binding;protein binding, bridging;structural molecule activity" cell part;collagen;collagen type I;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;fibrillar collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Protein digestion and absorption

Q8NBJ5;M0QX72 Procollagen galactosyltransferase 1 COLGALT1 >sp|Q8NBJ5|GT251_HUMAN Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1 NaN 0.6 0.73 0.37 2.51 0.92 NaN 1.27 6.15E-06 3 5.5 biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;extracellular matrix organization;extracellular structure organization;lipid biosynthetic process;lipid metabolic process;lipopolysaccharide biosynthetic process;lipopolysaccharide metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process "catalytic activity;galactosyltransferase activity;procollagen galactosyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;UDP-galactosyltransferase activity;UDP-glycosyltransferase activity" cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Lysine degradation;Other types of O-glycan biosynthesis

E7EU96;P68400;Q8NEV1;P68400-2 Casein kinase II subunit alpha;Casein kinase II subunit alpha 3 CSNK2A1;CSNK2A3 >tr|E7EU96|E7EU96_HUMAN Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=2 SV=1;>sp|P68400|CSK21_HUMAN Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1;>sp|Q8NEV1|CSK23_HUMAN Casein kinase II subunit alpha 3 OS=Homo sapiens G 0.57 2.18 0.31 1.53 0.64 1.39 0.66 1.02 3.27E-23 3 10.6 "axon guidance;biological regulation;biosynthetic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chaperone-mediated protein folding;chemotaxis;locomotion;M phase;M phase of mitotic cell cycle;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic cell cycle checkpoint;mitotic cell cycle spindle checkpoint;mitotic prometaphase;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cell growth;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of growth;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of Wnt receptor signaling pathway;primary metabolic process;protein autophosphorylation;protein folding;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;response to chemical stimulus;response to external stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;spindle checkpoint;taxis;transcription, DNA-dependent;Wnt receptor signaling pathway"	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme regulator activity;heat shock protein binding;Hsp90 protein binding;kinase activity;nucleotide binding;phosphatase regulator activity;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein phosphatase regulator activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups"	cell part;chromatin remodeling complex;chromosomal part;cytoplasmic part;cytosol;histone deacetylase complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;nuclear chromosome part;nuclear part;nucleoplasm part;NuRD complex;organelle part;plasma membrane;protein complex;Sin3 complex;Sin3-type complex;transcriptional repressor complex	Adherens junction;Circadian rhythm - plant;Measles;Ribosome biogenesis in eukaryotes;Tight junction;Wnt signaling pathway

P01040;C9J0E4	Cystatin-A	CSTA	>sp|P01040|CYTA_HUMAN Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1;>tr|C9J0E4|C9J0E4_HUMAN Cystatin-A OS=Homo sapiens GN=CSTA PE=2 SV=1	0.25 1.1	0.05 8.75 0.23 0.94 1.78 0.48 6.17E-14 3	42.9 biological adhesion;biological regulation;cell adhesion;cell differentiation;cell-cell adhesion;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity "binding;binding, bridging;cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;protein binding;protein binding, bridging;structural molecule activity"	cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle

Q7L576-2;Q7L576;Q7L576-3;H7C229;E7EW33;F5H583;E7EVJ5;Q96F07-2;E7EVF4;Q96F07;E7EWA4;H0YL50	Cytoplasmic FMR1-interacting protein 1;Cytoplasmic FMR1-interacting protein 2	CYFIP1;CYFIP2	>sp|Q7L576-2|CYFP1_HUMAN Isoform 2 of Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1;>sp|Q7L576|CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1;>sp|Q7L576-3|CYFP1_HUMAN Isoform 3 of Cytoplasmic FMR1-	NaN NaN 0.35 NaN 7.56 NaN NaN NaN 2.38E-06 3	3.6	apoptosis;axon extension;biological adhesion;biological regulation;cell adhesion;cell death;cell growth;cell projection assembly;cell projection organization;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;death;defense response;developmental cell growth;developmental growth;developmental growth involved in morphogenesis;developmental process;growth;immune response;immune system process;innate immune response;lamellipodium assembly;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of proteolysis;programmed cell death;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;response to stimulus;response to stress;ruffle organization actin binding;actin filament binding;binding;cytoskeletal protein binding;enzyme binding;GTPase binding;protein binding;Rac GTPase binding;Ras GTPase binding;Rho GTPase binding;small GTPase binding	cell junction;cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;intracellular part;lamellipodium;macromolecular complex;mRNA cap binding complex;neuron projection;perinuclear region of cytoplasm;protein complex;RNA cap binding complex;ruffle;synapse	Regulation of actin cytoskeleton

Q5VVL7;P11182	"Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial"	DBT	">tr|Q5VVL7|Q5VVL7_HUMAN Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DBT PE=2 SV=1;>sp|P11182|ODB2_HUMAN Lipoamide acyltransferase component of branched-chain alpha-keto acid"	NaN NaN 1.23 NaN 0.42 NaN NaN NaN 2.32E-06 3	9.7	acyl-CoA biosynthetic process;acyl-CoA metabolic process;amine catabolic process;amine metabolic process;biosynthetic process;branched chain family amino acid catabolic process;branched chain family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process "binding;catalytic activity;cofactor binding;dihydrolipoyllysine-residue (2-methylpropanoyl)transferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;cytoskeleton;dihydrolipoyl dehydrogenase complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule cytoskeleton;mitochondrial alpha-ketoglutarate dehydrogenase complex;mitochondrial nucleoid;mitochondrial part;mitochondrial tricarboxylic acid cycle enzyme complex;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle part;protein complex;tricarboxylic acid cycle enzyme complex "Valine, leucine and isoleucine degradation"

P07585;P07585-2;H0YIH3;F8VXZ8;F8VNV6;F8VUF6;F8VWU0;P07585-3 Decorin DCN >sp|P07585|PGS2_HUMAN Decorin OS=Homo sapiens GN=DCN PE=1 SV=1;>sp|P07585-2|PGS2_HUMAN Isoform B of Decorin OS=Homo sapiens GN=DCN NaN NaN 1.46 NaN 6.39 NaN NaN NaN 3.15E-07 3 9.2 aging;amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chondroitin sulfate biosynthetic process;chondroitin sulfate catabolic process;chondroitin sulfate metabolic process;dermatan sulfate biosynthetic process;dermatan sulfate metabolic process;developmental process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;kidney development;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;muscle tissue development;nitrogen compound metabolic process;organ development;organ morphogenesis;peptide cross-linking;peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan;peptidyl-amino acid modification;peptidyl-serine modification;placenta development;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;protein metabolic process;protein modification process;response to abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to external stimulus;response to lipopolysaccharide;response to mechanical stimulus;response to molecule of bacterial origin;response to organic substance;response to stimulus;response to stress;response to wounding;skeletal muscle tissue development;striated muscle tissue development;sulfur compound biosynthetic process;sulfur compound catabolic process;sulfur compound metabolic process;tissue development;wound healing binding;carbohydrate binding;extracellular matrix binding;glycosaminoglycan binding;pattern binding;polysaccharide binding anchoring collagen;cell part;collagen;collagen type VI;cytoplasmic part;extracellular matrix part;extracellular region part;extracellular space;Golgi apparatus part;Golgi lumen;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-enclosed lumen;organelle lumen;organelle part;vacuolar lumen;vacuolar part TGF-beta signaling pathway

Q96HY6-2;Q96HY6 DDRGK domain-containing protein 1 DDRGK1 >sp|Q96HY6-2|DDRGK_HUMAN Isoform 2 of DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1;>sp|Q96HY6|DDRGK_HUMAN DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1 PE=1 SV=2 NaN NaN 1.63 NaN 0.94 NaN NaN NaN 8.10E-09 3 14.7 cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle

B7Z817;Q15392;H7C4B7;F5H0H1 Delta(24)-sterol reductase DHCR24 >tr|B7Z817|B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1;>sp|Q15392|DHC24_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2 1.02 NaN 1.21 1.05 2.16 1.03 1.55 NaN 2.20E-07 3 4.2 alcohol metabolic process;amyloid precursor protein catabolic process;amyloid precursor protein metabolic process;anatomical structure development;biological regulation;biosynthetic process;catabolic process;cell cycle arrest;cell cycle process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular response to stimulus;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;developmental process involved in reproduction;epidermis development;genitalia development;glycoprotein catabolic process;glycoprotein metabolic process;intracellular signal transduction;lipid biosynthetic process;lipid metabolic process;localization;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;male genitalia development;membrane organization;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;organ development;plasminogen activation;primary metabolic process;protein localization;protein maturation;protein metabolic process;protein processing;Ras protein signal transduction;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of programmed cell death;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to oxidative stress;response to stimulus;response to stress;signal transduction;skin development;small GTPase mediated signal transduction;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;tissue development;zymogen activation"antigen binding;binding;catalytic activity;coenzyme binding;cofactor binding;delta24-sterol reductase activity;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;peptide antigen binding;peptide binding;UDP-N-acetylmuramate dehydrogenase activity" cell part;cytoplasmic part;cytoskeleton;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part Steroid biosynthesis

O60832;C9IYT0;O60832-2 H/ACA ribonucleoprotein complex subunit 4 DKC1 >sp|O60832|DKC1_HUMAN H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3 1.08 0.84 1.63 1.3 0.5 0.39 0.92 0.88 1.45E-07 3 7 anatomical structure homeostasis;biological regulation;biosynthetic process;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome organization;DNA metabolic process;DNA replication;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;pseudouridine synthesis;regulation of biological quality;RNA metabolic process;RNA modification;RNA processing;RNA-dependent DNA replication;rRNA metabolic process;rRNA processing;telomere maintenance;telomere maintenance via telomerase;telomere maintenance via telomere lengthening;telomere organization "binding;catalytic activity;DNA polymerase activity;intramolecular transferase activity;isomerase activity;nucleic acid binding;nucleotidyltransferase activity;pseudouridine synthase activity;RNA binding;RNA-directed DNA polymerase activity;telomerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" Cajal body;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleolus;nucleoplasm;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;telomerase holoenzyme complex Ribosome biogenesis in eukaryotes

Q6E0U4-4;Q6E0U4-16;Q6E0U4-2;Q6E0U4;CON__A3EZ82;Q6E0U4-7;Q6E0U4-3;Q6E0U4-5;E7EUS0;Q6E0U4-6;Q6E0U4-13;Q6E0U4-11;Q6E0U4-14;Q6E0U4-12;Q6E0U4-10;Q6E0U4-9;C9J186;M0QZV2;M0R265;Q6E0U4-8;H7C145;M0R0A5;H7BZ95;C9JCN1;C9IYI1 Dermokine DMKN >sp|Q6E0U4-4|DMKN_HUMAN Isoform 4 of Dermokine OS=Homo sapiens GN=DMKN;>sp|Q6E0U4-16|DMKN_HUMAN Isoform 16 of Dermokine OS=Homo sapiens GN=DMKN;>sp|Q6E0U4-2|DMKN_HUMAN Isoform 2 of Dermokine OS=Homo sapiens GN=DMKN;>sp|Q6E0U4|DMKN_HUMAN Dermokine OS=Homo s NaN NaN NaN NaN NaN NaN NaN NaN 1.08E-09 3 8.9 extracellular region part;extracellular space

C9J2C4;O75190-2;O75190-3;O75190;C9JB42;C9JDR7;C9JDX6;F8WCZ4;C9J2P2;E9PH18;C9JN01;Q8WWF6;C9JRD2;Q8NHS0;C9JXB9;P25686-2;B4DN73;P25686 DnaJ homolog subfamily B member 6 DNAJB6 >tr|C9J2C4|C9J2C4_HUMAN DnaJ homolog subfamily B member 6 (Fragment) OS=Homo sapiens GN=DNAJB6 PE=2 SV=1;>sp|O75190-2|DNJB6_HUMAN Isoform B of DnaJ homolog subfamily B member 6 OS=Homo sapiens GN=DNAJB6;>sp|O75190-3|DNJB6_HUMAN Isoform C of DnaJ homolog su 1.2 1.16 1.01 0.95 1.86 0.87 0.72 1.01 8.87E-08 3 14.9 biological regulation;catabolic process;cell death;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cytoskeleton organization;death;ER-associated protein catabolic process;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of growth;negative regulation of hydrolase activity;negative regulation of inclusion body assembly;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of protein deubiquitination;negative regulation of protein metabolic process;negative regulation of protein modification process;organelle organization;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of proteolysis;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein folding;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell growth;regulation of cell proliferation;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of growth;regulation of hydrolase activity;regulation of inclusion body assembly;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein deubiquitination;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of proteolysis;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;ubiquitin-dependent protein catabolic process ATPase activator activity;ATPase regulator activity;binding;chaperone binding;enzyme activator activity;enzyme regulator activity;heat shock protein binding;nucleoside-triphosphatase regulator activity;polyubiquitin binding;proteasome binding;protein binding;protein complex binding;small conjugating protein binding;ubiquitin binding;unfolded protein binding cell part;contractile fiber part;cytoplasm;cytoplasmic part;inclusion body;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;Z disc Protein processing in endoplasmic reticulum

E7EQU2;E7ESD3;E7EMU4;E7EV09;E7EQL5;Q13409-6;Q13409-3;B7ZA04;Q13409-2;Q13409-5;Q13409;F8W8S0;E9PGG1;E7EUM4;E7ERR6;E7ERH4;E7ET01;E7ETL8;E7EU01 Cytoplasmic dynein 1 intermediate chain 2 DYNC1I2 >tr|E7EQU2|E7EQU2_HUMAN Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1;>tr|E7ESD3|E7ESD3_HUMAN Cytoplasmic dynein 1 intermediate chain 2 (Fragment) OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1;>tr|E7EMU4|E7EMU4_HUMAN Cyto 1.25 0.85 0.39 NaN 1.4 NaN 2.29 1.47 8.29E-11 3 30.8 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cell cycle process;cellular component movement;cellular process;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;interaction with host;interspecies interaction between organisms;microtubule-based movement;microtubule-based process;multi-organism process;reproductive process;transport;viral reproductive process;virus-host interaction "catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;pyrophosphatase activity" cell part;centrosome;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle Phagosome;Vasopressin-regulated water reabsorption

P24534;C9JZW3;F8WF65;F2Z2G2 Elongation factor 1-beta EEF1B2 >sp|P24534|EF1B_HUMAN Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1

SV=3;>tr|C9JZW3|C9JZW3_HUMAN Elongation factor 1-beta (Fragment) OS=Homo sapiens GN=EEF1B2 PE=2 SV=1 1.3 0.49 1.34 0.35 1.09 0.6 2.34 1.52 2.50E-31 3 18.2 "binding;nucleic acid binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular part;macromolecular complex;protein complex

Q9NZN4;B4DNU6 EH domain-containing protein 2 EHD2 >sp|Q9NZN4|EHD2_HUMAN EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2;>tr|B4DNU6|B4DNU6_HUMAN EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=2 SV=1 0.66 1.87 NaN 1.48 NaN 0.65 0.66 0.73 8.19E-08 3 6.3 actin cytoskeleton organization;actin filament-based process;biological regulation;blood coagulation;catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;coagulation;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;endocytic recycling;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;GTP catabolic process;GTP metabolic process;hemostasis;heterocycle catabolic process;heterocycle metabolic process;intracellular transport;membrane invagination;membrane organization;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological quality;regulation of body fluid levels;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;recycling endosome membrane Endocytosis

O00303;B3KSH1;B4DEW9;H0YDT6 Eukaryotic translation initiation factor 3 subunit F EIF3F >sp|O00303|EIF3F_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1;>tr|B3KSH1|B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1;>tr|B4DEW9|B4DEW9_HUMAN Eukaryoti 0.85 NaN 0.38 NaN 0.7 NaN 1.41 NaN 8.69E-11 3 11.2 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "binding;catalytic activity;cysteine-type peptidase activity;hydrolase activity;nucleic acid binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport

B0QY90;Q9Y262-2;Q9Y262;B0QY89 Eukaryotic translation initiation factor 3 subunit L EIF3L >tr|B0QY90|B0QY90_HUMAN Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=2 SV=1;>sp|Q9Y262-2|EIF3L_HUMAN Isoform 2 of Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L;>sp|Q9Y262|EIF3L_HUMAN Eukar 1.03 1.92 0.33 0.86 0.77 0.69 1.16 1.2 1.53E-13 3 10.5 cellular process;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;eukaryotic translation initiation factor 3 complex;fibrillar center;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleolar part;nucleoplasm;organelle part;protein complex

O60841 Eukaryotic translation initiation factor 5B EIF5B >sp|O60841|IF2P_HUMAN Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 NaN NaN 0.51 NaN 9.23 NaN NaN NaN 1.88E-12 3 5.8 biological regulation;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;intracellular part RNA transport

Q15717;B4DVB8;M0QZR9;M0R055 ELAV-like protein 1 ELAVL1 >sp|Q15717|ELAV1_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2;>tr|B4DVB8|B4DVB8_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1;>tr|M0QZR9|M0QZR9_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=4 SV=1 1.59 0.92 1.23 1.7 0.98 0.38 1.45 0.81 1.65E-15 3 10.7 3'-UTR-mediated mRNA stabilization;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;gene expression;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA stabilization;multicellular organismal development;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of translation;RNA metabolic process;RNA stabilizationAU-rich element binding;binding;mRNA 3'-UTR AU-rich region binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part

Q15006;E5RGJ2;H0YAS9 ER membrane protein complex subunit 2 EMC2 >sp|Q15006|EMC2_HUMAN ER membrane protein complex subunit 2 OS=Homo sapiens GN=EMC2 PE=1 SV=1 1.53 1.52 1.66 1.04 0.54 0.57 0.79 0.85 8.28E-08 3 14.1 cell part;cytoplasmic part;ER membrane protein complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nucleus;organelle;protein complex

O75477;B0QZ43;O94905-2;O94905-3 Erlin-1 ERLIN1 >sp|O75477|ERLN1_HUMAN Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1;>tr|B0QZ43|B0QZ43_HUMAN Erlin-1 (Fragment) OS=Homo sapiens GN=ERLIN1 PE=2 SV=1 0.96 1.26 1.59 NaN 0.54 NaN 0.7 0.77 7.21E-41 3 11 catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;ER-associated protein catabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;protein complex

H0YL12;P13804-2;H0YKF0;H0YLU7;P13804;H0YK49;H0YNX6 "Electron transfer flavoprotein subunit alpha, mitochondrial" ETFA ">tr|H0YL12|H0YL12_HUMAN Electron transfer flavoprotein subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=ETFA PE=4 SV=1;>sp|P13804-2|ETFA_HUMAN Isoform 2 of Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA;>tr|H0" 0.66 0.58 0.19 0.57 3.15 2.74 0.93 1.15 1.90E-08 3 16.2 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process binding;catalytic activity;coenzyme binding;cofactor binding;electron carrier activity;flavin adenine dinucleotide binding;oxidoreductase activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part

P38117;P38117-2;M0QY67 Electron transfer flavoprotein subunit beta ETFB >sp|P38117|ETFB_HUMAN Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3;>sp|P38117-2|ETFB_HUMAN Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB;>tr|M0QY67|M0QY67_HUMAN Electron transfer flavoprot 0.58 0.83 0.2 0.81 2.16 2.43 1.14 0.95 1.08E-06 3 12.9 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process electron carrier activity cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part

F8W7Q4;Q96A26;E9PH05 Protein FAM162A FAM162A >tr|F8W7Q4|F8W7Q4_HUMAN Protein FAM162A OS=Homo sapiens GN=FAM162A PE=2 SV=1;>sp|Q96A26|F162A_HUMAN Protein FAM162A OS=Homo sapiens GN=FAM162A PE=1 SV=2;>tr|E9PH05|E9PH05_HUMAN Protein FAM162A OS=Homo sapiens GN=FAM162A PE=2 SV=1 0.95 1.46 1.25 1.33 0.77 0.61 0.73 0.94 4.48E-19 3 26.4 activation of caspase activity;apoptosis;biological regulation;cell death;cellular process;cellular response to chemical stimulus;cellular response to hypoxia;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;death;neuron apoptosis;neuron death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of mitochondrion organization;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of release of cytochrome c from mitochondria;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular component organization;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of mitochondrion organization;regulation of molecular function;regulation of organelle organization;regulation of peptidase activity;regulation of programmed cell death;regulation of release of cytochrome c from mitochondria;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;transformed cell apoptosis cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle

Q92520;C9JP35;C9JMN4 Protein FAM3C FAM3C >sp|Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1;>tr|C9JP35|C9JP35_HUMAN Protein FAM3C (Fragment) OS=Homo sapiens GN=FAM3C PE=2 SV=1;>tr|C9JMN4|C9JMN4_HUMAN Protein FAM3C (Fragment) OS=Homo sapiens GN=FAM3C PE=2 SV=1 NaN NaN 1.53 NaN 0.3 NaN NaN NaN 1.38E-13 3 15.9 developmental process;multicellular organismal development;multicellular organismal processbinding;cytokine activity;protein binding;receptor binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular region;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;organelle;vesicle

Q14512 Fibroblast growth factor-binding protein 1 FGFBP1 >sp|Q14512|FGFP1_HUMAN Fibroblast growth factor-binding protein 1 OS=Homo sapiens GN=FGFBP1 PE=1 SV=1 1.32 1.06 1.56 0.97 0.19 0.07 0.37 0.21 2.08E-136 3 14.1 biological regulation;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of fibroblast growth factor receptor signaling pathway;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cell proliferation;regulation of cellular process;regulation of fibroblast growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;signaling binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding cell part;cell surface;extracellular region part;extracellular space;membrane;plasma membrane

Q13045-2;Q13045-3;Q13045 Protein flightless-1 homolog FLII >sp|Q13045-2|FLII_HUMAN Isoform 2 of Protein flightless-1 homolog OS=Homo sapiens GN=FLII;>sp|Q13045-3|FLII_HUMAN Isoform 3 of Protein flightless-1 homolog OS=Homo sapiens GN=FLII;>sp|Q13045|FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII P NaN NaN 0.73 NaN 8.92 NaN NaN NaN 2.75E-06 3 2.9 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;muscle contraction;muscle system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;system process;transcription, DNA-dependent" actin binding;binding;cytoskeletal protein binding;protein binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part

P35637-2;P35637;H3BPE7;K7EPT6;Q92804-2;Q92804 RNA-binding protein FUS;TATA-binding protein-associated factor 2N FUS;TAF15 >sp|P35637-2|FUS_HUMAN Isoform Short of RNA-binding protein FUS OS=Homo sapiens GN=FUS;>sp|P35637|FUS_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1;>tr|H3BPE7|H3BPE7_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=2 SV=1;>tr|K7EPT6 1.46 0.85 0.87 1.35 0.55 0.45 1.11 0.86 2.19E-14 3 4.8 "biological regulation;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part Basal transcription factors

P06241-3;Q5R3A8;P06241-2;P06241;P07947;J3QRU1;P07948-2;P08631-3;P08631-2;A8K4G3;P06239;P07948;Q573B4;P08631-4;H0Y3C5;P08631;J3KPD6;P12931;P06239-3;P12931-2;F8VXD2;H0YE20;K7ELV5;F8VYH9;B4DNF9;F8VZZ0;E5RIU6;F8VTV8;F8VWX7;F8VZ51;K7EJ83;E7ESI2;Q8IZL9-2;Q00535-2;H0YAZ9;P24941-2;Q8IZL9-3;H0Y9P2;B3KUS6;Q9UPZ9-2;Q00535;P06493;P24941;P11802;Q00526;Q8IZL9-5;Q00534;Q8IZL9-4;E7EUK8;Q8IZL9;G3V5T9;Q96Q40-2;H7C265;P50750;Q96Q40-4;E5RGN0;Q96Q40-3;O94921-3;Q96Q40-5;E9PJX5;Q96Q40;O94921-2;Q8IXN4;F5H3M4;O94921;F5H6Z0;Q07002;Q07002-2;P50750-2;Q00536;Q00536-3;Q07002-3;P51451;Q00537-2;Q00537;P09769;Q00536-2;P20794-3;P20794;Q9UPZ9;P20794-2;P11362-6;P11362-5;H7BXU9;P21802-22;P21802-4;P22607-3;P21802-20;P21802-15;P21802-21;E7EVR7;P21802-23;P11362-4;P11362-14;P11362-3;E7EU09;J3KPQ0;P22455-2;P21802-8;P21802-2;P21802-13;P21802-17;P21802-12;P21802-6;P22455;P22607-2;P11362-20;P21802-7;P21802-5;P21802-10;P21802-18;P11362-7;P11362-2;P21802;P21802-3;P21802-16;P11362-19;P11362;J3KNT4;P21802-11;P11362-21;J3QSD7;Q9NYV4-3;Q14004-2;Q9NYV4-2;Q9NYV4;Q14004 Tyrosine-protein kinase Fyn;Tyrosine-protein kinase Yes;Tyrosine-protein kinase Lck;Tyrosine-protein kinase Lyn;Tyrosine-protein kinase HCK;Proto-oncogene tyrosine-protein kinase Src FYN;YES1;HCK;LCK;LYN;SRC >sp|P06241-3|FYN_HUMAN Isoform 3 of Tyrosine-protein kinase Fyn OS=Homo sapiens GN=FYN;>tr|Q5R3A8|Q5R3A8_HUMAN Tyrosine-protein kinase Fyn OS=Homo sapiens GN=FYN PE=2 SV=1;>sp|P06241-2|FYN_HUMAN Isoform 2 of Tyrosine-protein kinase Fyn OS=Homo sapiens GN=F 1.37 1.46 1.04 1.37 0.73 0.49 0.65 0.74 2.26E-07 3 5.4 "actin cytoskeleton organization;actin filament-based process;activated T cell proliferation;activation of caspase activity;activation of immune response;activation of innate immune response;activation of MAPK activity;activation of MAPKK activity;activation of protein kinase activity;adult behavior;aging;alternative nuclear mRNA splicing, via spliceosome;alveolar secondary septum development;amine transport;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;anatomical structure morphogenesis;angiogenesis;anion homeostasis;antigen receptor-mediated signaling pathway;apoptosis;appendage morphogenesis;associative learning;astrocyte development;auditory receptor cell development;axis elongation;axon extension;axon guidance;axonogenesis;B cell homeostasis;B cell receptor signaling pathway;behavior;behavioral response to cocaine;biological adhesion;biological regulation;biomineral tissue development;biosynthetic process;blood coagulation;bone mineralization;bone morphogenesis;bone resorption;branch elongation involved in salivary gland morphogenesis;branch elongation of an epithelium;branching involved in embryonic placenta morphogenesis;branching involved in mammary gland duct morphogenesis;branching involved in prostate gland morphogenesis;branching involved in salivary gland morphogenesis;branching morphogenesis of a nerve;branching morphogenesis of a tube;bud elongation involved in lung branching;calcium ion homeostasis;calcium ion import;calcium ion transmembrane transport;calcium ion transport;calcium ion transport into cytosol;carbohydrate homeostasis;carbohydrate transport;cardiac cell development;cardiac muscle cell development;cardiac muscle tissue morphogenesis;cardiac septum morphogenesis;catabolic process;cation homeostasis;cation transport;cell activation;cell adhesion;cell aging;cell communication;cell cycle;cell cycle arrest;cell cycle checkpoint;cell cycle phase;cell cycle process;cell death;cell dedifferentiation;cell development;cell differentiation;cell division;cell fate commitment;cell growth;cell maturation;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cell-cell signaling involved in cell fate commitment;cell-matrix adhesion;cell-substrate adhesion;cellular biosynthetic process;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component maintenance;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex assembly;cellular protein localization;cellular protein metabolic process;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to heat;cellular response to hormone stimulus;cellular response to hydrogen peroxide;cellular response to inorganic substance;cellular response to insulin stimulus;cellular response to interferon-gamma;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to nitric oxide;cellular response to nutrient;cellular response to nutrient levels;cellular response to organic substance;cellular response to oxidative stress;cellular response to peptide hormone stimulus;cellular response to progesterone stimulus;cellular response to reactive oxygen species;cellular response to retinoic acid;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to stress;cellular response to vitamin;cellular response to vitamin A;cellular zinc ion homeostasis;central nervous system neuron development;centrosome cycle;centrosome duplication;centrosome organization;cerebellar cortex formation;chemical homeostasis;chemotaxis;chondrocyte differentiation;chordate embryonic development;chromatin modification;chromatin organization;chromosome condensation;chromosome organization;circadian rhythm;circulatory system process;coagulation;cognition;columnar/cuboidal epithelial cell differentiation;coronal suture morphogenesis;corpus callosum development;cortical actin cytoskeleton organization;cortical cytoskeleton organization;covalent chromatin modification;cranial suture morphogenesis;craniofacial suture morphogenesis;cytokine secretion;cytokine-mediated signaling pathway;cytoskeleton organization;cytosolic calcium ion homeostasis;cytosolic calcium ion transport;death;dedifferentiation;defense response;defense response to bacterium;defense response to Gram-positive bacterium;dendrite morphogenesis;dendritic cell differentiation;dentate gyrus development;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection of mechanical stimulus involved in sensory perception;detection of mechanical stimulus involved in sensory perception of pain;detection of stimulus;detection of stimulus involved in sensory perception;developmental cell growth;developmental growth;developmental growth involved in morphogenesis;developmental induction;developmental maturation;developmental process;developmental process involved in reproduction;digestive tract morphogenesis;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;DNA conformation change;DNA damage checkpoint;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA integrity checkpoint;DNA metabolic process;DNA packaging;DNA repair;DNA replication;elevation of cytosolic calcium ion concentration;embryo development;embryo development ending in birth or egg hatching;embryonic appendage morphogenesis;embryonic cranial skeleton morphogenesis;embryonic digestive tract morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;embryonic pattern specification;embryonic skeletal system morphogenesis;endocytosis;endodermal digestive tract morphogenesis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epithelial cell differentiation;epithelial cell differentiation involved in prostate gland development;epithelial cell proliferation;epithelial cell proliferation involved in salivary gland morphogenesis;epithelium development;erythrocyte differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;Fc receptor mediated inhibitory signaling pathway;feeding behavior;female gamete generation;fibroblast growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway involved in hemopoiesis;fibroblast growth factor receptor signaling pathway involved in mammary gland specification;fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptosis in bone marrow;fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development;fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow;forebrain development;forebrain neuroblast division;forebrain neuron development;forebrain ventricular zone progenitor cell division;G0 to G1 transition;G1 phase;G1 phase of mitotic cell cycle;G1/S transition of mitotic cell cycle;G2 phase;G2 phase of mitotic cell cycle;G2/M transition checkpoint;G2/M transition DNA damage checkpoint;G2/M transition of mitotic cell cycle;gamete generation;generation of neurons;gland development;glandular epithelial cell differentiation;glial cell development;glial cell differentiation;glucose homeostasis;glucose transport;growth;growth hormone secretion;hair cycle process;hair follicle morphogenesis;hemopoiesis;hemopoietic or lymphoid organ development;hemopoietic progenitor cell differentiation;hemopoietic stem cell differentiation;hemostasis;hexose transport;hippocampus development;histamine secretion;histamine secretion by mast cell;histamine secretion involved in inflammatory response;histamine transport;histone modification;histone phosphorylation;homeostasis of number of cells;homeostatic process;hormone secretion;hormone transport;immune effector process;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-inhibiting cell surface receptor signaling pathway;immune response-inhibiting signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;in utero embryonic development;induction of apoptosis;induction of programmed cell death;inflammatory response;innate immune response;innate immune response-activating signal transduction;inner ear morphogenesis;inner ear receptor cell development;inositol lipid-mediated signaling;insulin receptor signaling pathway;integrin-mediated signaling pathway;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;karyogamy;lacrimal gland development;lateral sprouting from an epithelium;lateral ventricle development;layer formation in cerebral cortex;learning;learning or memory;lens fiber cell development;leukocyte activation;leukocyte degranulation;leukocyte differentiation;leukocyte homeostasis;leukocyte migration;leukocyte migration involved in immune response;leukocyte proliferation;limb bud formation;limb morphogenesis;lipopolysaccharide-mediated signaling pathway;localization;locomotion;lung alveolus development;lung epithelium development;lung lobe morphogenesis;lung-associated mesenchyme development;lymphocyte activation;lymphocyte costimulation;lymphocyte differentiation;lymphocyte homeostasis;lymphocyte proliferation;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;macromolecule modification;maintenance of fidelity involved in DNA-dependent DNA replication;male gamete generation;mammary gland bud formation;MAPKKK cascade;meiosis;membrane depolarization;membrane disassembly;membrane invagination;membrane organization;membranous septum morphogenesis;mesenchymal cell differentiation;mesenchymal cell differentiation involved in lung development;mesenchymal cell proliferation;mesenchymal cell proliferation involved in lung development;mesenchymal-epithelial cell signaling;mesenchyme development;mesoderm development;metabolic process;metal ion homeostasis;metal ion transport;microtubule organizing center organization;midbrain development;middle ear morphogenesis;mitosis;mitotic cell cycle checkpoint;mitotic cell cycle G2/M transition checkpoint;mitotic cell cycle G2/M transition DNA damage checkpoint;mitotic nuclear envelope disassembly;mitotic prometaphase;mitotic prophase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;molting cycle;molting cycle process;mononuclear cell proliferation;monosaccharide transport;monovalent inorganic cation transport;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;motor axon guidance;mRNA metabolic process;mRNA processing;multicellular organism growth;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell development;muscle tissue development;muscle tissue morphogenesis;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;myeloid cell differentiation;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of B cell activation;negative regulation of B cell proliferation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase activity;negative regulation of catabolic process;negative regulation of catalytic activity;negative regulation of cell activation;negative regulation of cell adhesion;negative regulation of cell aging;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell cycle arrest;negative regulation of cell cycle process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cell-matrix adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cellular senescence;negative regulation of developmental process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of epithelial cell proliferation;negative regulation of ERK1 and ERK2 cascade;negative regulation of focal adhesion assembly;negative regulation of gene expression;negative regulation of hydrolase activity;negative regulation of immune response;negative regulation of immune system process;negative regulation of intracellular protein kinase cascade;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of kinase activity;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of MAPKKK cascade;negative regulation of mast cell proliferation;negative regulation of metabolic process;negative regulation of mitosis;negative regulation of molecular function;negative regulation of mononuclear cell proliferation;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear division;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of organelle organization;negative regulation of osteoblast differentiation;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of protein catabolic process;negative regulation of protein complex assembly;negative regulation of protein export from nucleus;negative regulation of protein homooligomerization;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein oligomerization;negative regulation of protein serine/threonine kinase activity;negative regulation of protein transport;negative regulation of protein ubiquitination;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequestering of calcium ion;negative regulation of signal transduction;negative regulation of signaling;negative regulation of synaptic plasticity;negative regulation of toll-like receptor 2 signaling pathway;negative regulation of toll-like receptor 4 signaling pathway;negative regulation of toll-like receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of transport;nerve growth factor receptor signaling pathway;neuroblast division;neurogenesis;neurological system process;neuromuscular junction development;neuron apoptosis;neuron death;neuron development;neuron migration;neuron projection development;neuron projection morphogenesis;neuron-neuron synaptic transmission;nitrogen compound metabolic process;nitrogen compound transport;Notch signaling pathway;nuclear division;nuclear envelope disassembly;nuclear envelope organization;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;odontogenesis;oligodendrocyte development;oligodendrocyte differentiation;oogenesis;organ development;organ growth;organ induction;organ morphogenesis;organ regeneration;organelle fission;organelle fusion;organelle organization;organic substance transport;otic vesicle formation;outer ear morphogenesis;outflow tract septum morphogenesis;paraxial mesoderm development;pattern recognition receptor signaling pathway;pattern specification process;peptide hormone secretion;peptide secretion;peptide transport;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;peptidyl-threonine modification;peptidyl-threonine phosphorylation;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phagocytosis;phosphate ion homeostasis;phosphate-containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;phosphorylation of RNA polymerase II C-terminal domain;photoreceptor cell maintenance;platelet activation;platelet degranulation;positive regulation of actin cytoskeleton reorganization;positive regulation of actin filament polymerization;positive regulation of antigen receptor-mediated signaling pathway;positive regulation of apoptosis;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of calcium ion-dependent exocytosis;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cardiac muscle cell proliferation;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell cycle;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cell size;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokine secretion;positive regulation of cytoskeleton organization;positive regulation of defense response;positive regulation of dendritic cell apoptosis;positive regulation of developmental process;positive regulation of DNA biosynthetic process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of DNA-dependent DNA replication initiation;positive regulation of epithelial cell proliferation;positive regulation of epithelial cell proliferation involved in lung morphogenesis;positive regulation of ERK1 and ERK2 cascade;positive regulation of exocytosis;positive regulation of Fc receptor mediated stimulatory signaling pathway;positive regulation of fibroblast proliferation;positive regulation of gamma-delta T cell activation;positive regulation of gamma-delta T cell differentiation;positive regulation of gene expression;positive regulation of glial cell proliferation;positive regulation of gliogenesis;positive regulation of hormone secretion;positive regulation of hydrolase activity;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of insulin secretion;positive regulation of integrin activation;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JAK-STAT cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of leukocyte apoptosis;positive regulation of leukocyte degranulation;positive regulation of leukocyte proliferation;positive regulation of ligase activity;positive regulation of lipase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway;positive regulation of mast cell activation;positive regulation of mast cell activation involved in immune response;positive regulation of mast cell degranulation;positive regulation of mast cell proliferation;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of metalloenzyme activity;positive regulation of mitotic cell cycle;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of neural precursor cell proliferation;positive regulation of neurogenesis;positive regulation of neuron apoptosis;positive regulation of neuron differentiation;positive regulation of neuron projection development;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of oligodendrocyte progenitor proliferation;positive regulation of organelle organization;positive regulation of peptidase activity;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of podosome assembly;positive regulation of programmed cell death;positive regulation of protein binding;positive regulation of protein complex assembly;positive regulation of protein import into nucleus, translocation;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein polymerization;positive regulation of protein secretion;positive regulation of protein serine/threonine kinase activity;positive regulation of protein targeting to membrane;positive regulation of protein transport;positive regulation of protein ubiquitination;positive regulation of proteolysis;positive regulation of reproductive process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of secretion;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smooth muscle contraction;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of T cell activation;positive regulation of T cell differentiation;positive regulation of T cell receptor signaling pathway;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of translation;positive regulation of transport;positive regulation of tyrosine phosphorylation of STAT protein;positive regulation of tyrosine phosphorylation of Stat5 protein;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;positive regulation of uterine smooth muscle contraction;positive regulation of viral reproduction;positive regulation of viral transcription;positive regulation of Wnt receptor signaling pathway;post-embryonic development;posttranscriptional regulation of gene expression;potassium ion transport;primary metabolic process;progesterone receptor signaling pathway;programmed cell death;pronuclear fusion;prophase;prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis;prostate epithelial cord elongation;prostate gland epithelium morphogenesis;prostate gland growth;prostate gland morphogenetic growth;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein autophosphorylation;protein complex assembly;protein complex subunit organization;protein localization;protein localization in membrane;protein localization to chromosome;protein localization to kinetochore;protein localization to organelle;protein localization to synapse;protein metabolic process;protein modification process;protein phosphorylation;protein secretion;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;pyramidal neuron development;Ras protein signal transduction;receptor catabolic process;receptor clustering;receptor metabolic process;re-entry into mitotic cell cycle;regeneration;regulated secretory pathway;regulation of actin cytoskeleton organization;regulation of actin cytoskeleton reorganization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of anoikis;regulation of antigen receptor-mediated signaling pathway;regulation of apoptosis;regulation of B cell activation;regulation of B cell apoptosis;regulation of B cell proliferation;regulation of B cell receptor signaling pathway;regulation of behavior;regulation of bile acid biosynthetic process;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood coagulation;regulation of body fluid levels;regulation of bone remodeling;regulation of bone resorption;regulation of branching involved in prostate gland morphogenesis;regulation of branching involved in salivary gland morphogenesis;regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of calcium ion-dependent exocytosis;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac muscle cell proliferation;regulation of cardiac muscle tissue development;regulation of cardiac muscle tissue growth;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation of cell aging;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell division;regulation of cell fate commi"	"acetylcholine receptor activator activity;acetylcholine receptor regulator activity;adenyl nucleotide binding;adenyl ribonucleotide binding;antigen binding;ATP binding;binding;binding, bridging;carbohydrate binding;catalytic activity;cation binding;cyclin binding;cyclin-dependent protein kinase activity;DNA binding;enzyme binding;ErbB-2 class receptor binding;ErbB-3 class receptor binding;Fc-gamma receptor I complex binding;fibroblast growth factor binding;fibroblast growth factor-activated receptor activity;glycolipid binding;glycosaminoglycan binding;glycosphingolipid binding;growth factor binding;heme binding;heparin binding;histone kinase activity;hydrolase activity;hydrolase activity, acting on ester bonds;immunoglobulin receptor binding;integrin binding;ion binding;iron ion binding;kinase activity;kinase binding;lipid binding;magnesium ion binding;metal ion binding;molecular transducer activity;non-membrane spanning protein tyrosine kinase activity;nucleic acid binding;nucleotide binding;pattern binding;phosphatase activity;phosphoprotein binding;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;phosphotransferase activity, alcohol group as acceptor;phosphotyrosine binding;polysaccharide binding;protein binding;protein binding transcription factor activity;protein binding, bridging;protein complex binding;protein domain specific binding;protein kinase activity;protein kinase binding;protein phosphorylated amino acid binding;protein serine/threonine kinase activity;protein serine/threonine phosphatase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activator activity;receptor activity;receptor binding;receptor regulator activity;receptor signaling protein activity;receptor signaling protein tyrosine kinase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA binding;RNA polymerase II carboxy-terminal domain kinase activity;SH2 domain binding;SH3/SH2 adaptor activity;signal transducer activity;signaling adaptor activity;signaling receptor activity;snRNA binding;sphingolipid binding;tau-protein kinase activity;tetrapyrrole binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity" "actin cytoskeleton;adherens junction;alpha2-beta1 integrin complex;anchoring junction;axon;Cajal body;carboxy-terminal domain protein kinase complex;caveola;cell body;cell cortex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell surface;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;chromatin;chromosomal part;chromosome;chromosome, telomeric region;cilium;condensed chromosome;cyclin-dependent protein kinase 5 holoenzyme complex;cyclin-dependent protein kinase holoenzyme complex;cytoplasm;cytoplasmic cyclin-dependent protein kinase holoenzyme complex;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;cytosol;endocytic vesicle;endoplasmic reticulum;endosome;excitatory synapse;extracellular region;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;filopodium;focal adhesion;Golgi apparatus;growth cone;immunological synapse;integral to membrane;integral to plasma membrane;integrin complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium;late endosome;leading edge membrane;lysosome;lytic vacuole;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microtubule;microtubule organizing center;microtubule organizing center part;midbody;mitochondrial crista;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrion;mitotic spindle;neuromuscular junction;neuron projection;neuronal cell body;non-membrane-bounded organelle;nonmotile primary cilium;nuclear body;nuclear cyclin-dependent protein kinase holoenzyme complex;nuclear membrane;nuclear part;nuclear speck;nucleolus;nucleoplasm;nucleoplasm part;nucleus;occluding junction;organelle;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part;pericentriolar material;perikaryon;perinuclear region of cytoplasm;photoreceptor inner segment;photoreceptor outer segment;plasma membrane;plasma membrane part;PML body;positive transcription elongation factor complex b;postsynaptic density;postsynaptic membrane;primary cilium;protein complex;receptor complex;ruffle;ruffle membrane;sex chromosome;site of polarized growth;spindle;spindle microtubule;synapse;synapse part;synaptic membrane;tight junction;transcription elongation factor complex;transcription factor complex;transport vesicle;vacuole;vesicle;X chromosome;Y chromosome" Adherens junction;Alzheimer's disease;Axon guidance;B cell receptor signaling pathway;Bacterial invasion of epithelial cells;Bladder cancer;Cell cycle;Chemokine signaling pathway;Chronic myeloid leukemia;Endocytosis;Epithelial cell signaling in Helicobacter pylori infection;ErbB signaling pathway;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;ko05152;Long-term depression;MAPK signaling pathway;Measles;Melanoma;Natural killer cell mediated cytotoxicity;Non-small cell lung cancer;Oocyte meiosis;Osteoclast differentiation;p53 signaling pathway;Pancreatic cancer;Pathogenic Escherichia coli infection;Pathways in cancer;Primary immunodeficiency;Prion diseases;Progesterone-mediated oocyte maturation;Prostate cancer;Regulation of actin cytoskeleton;Small cell lung cancer;T cell receptor signaling pathway;Tight junction;VEGF signaling pathway;Viral myocarditis

G3V1S6;Q10471;B7Z8V8;Q8N4A0-2;F8VUJ3;Q8N4A0 Polypeptide N-acetylgalactosaminyltransferase 2;Polypeptide N-acetylgalactosaminyltransferase 2 soluble form GALNT2 >tr|G3V1S6|G3V1S6_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 soluble form OS=Homo sapiens GN=GALNT2 PE=2 SV=1;>sp|Q10471|GALT2_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1 0.96 1.07 1.38 1.08 0.53 0.58 0.95 1.45 2.83E-59 3 7.5 biosynthetic process;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;immunoglobulin biosynthetic process;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;O-glycan processing;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-threonine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein O-linked glycosylation;protein O-linked glycosylation via serine;protein O-linked glycosylation via threonine "acetylgalactosaminyltransferase activity;binding;catalytic activity;cation binding;ion binding;manganese ion binding;metal ion binding;polypeptide N-acetylgalactosaminyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;transition metal ion binding;UDP-glycosyltransferase activity" cell part;cytoplasmic part;extracellular region;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi stack;integral to Golgi membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to Golgi membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm Mucin type O-Glycan biosynthesis

Q14435;Q14435-2;C9J2C3;E7EUL0 Polypeptide N-acetylgalactosaminyltransferase 3 GALNT3 >sp|Q14435|GALT3_HUMAN Polypeptide N-acetylgalactosaminyltransferase 3 OS=Homo sapiens GN=GALNT3 PE=1 SV=2;>sp|Q14435-2|GALT3_HUMAN Isoform 2 of Polypeptide N-acetylgalactosaminyltransferase 3 OS=Homo sapiens GN=GALNT3;>tr|C9J2C3|C9J2C3_HUMAN Polypeptide N NaN NaN 2.72 NaN 0.78 NaN NaN NaN 3.54E-18 3 6.5 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;O-glycan processing;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-threonine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein O-linked glycosylation;protein O-linked glycosylation via serine;protein O-linked glycosylation via threonine "acetylgalactosaminyltransferase activity;binding;calcium ion binding;catalytic activity;cation binding;ion binding;manganese ion binding;metal ion binding;polypeptide N-acetylgalactosaminyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;transition metal ion binding;UDP-glycosyltransferase activity" cell part;cytoplasmic part;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm Mucin type O-Glycan biosynthesis

Q06210-2;Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 GFPT1 >sp|Q06210-2|GFPT1_HUMAN Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1;>sp|Q06210|GFPT1_HUMAN Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 NaN NaN 0.47 NaN 1.21 NaN NaN NaN 6.89E-06 3 6.5 activation of signaling protein activity involved in unfolded protein response;alcohol biosynthetic process;alcohol metabolic process;amine metabolic process;amino sugar biosynthetic process;amino sugar metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;dolichol-linked oligosaccharide biosynthetic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;fructose 6-phosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;glucosamine biosynthetic process;glucosamine metabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;glycosylation;hexose metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;N-acetylglucosamine biosynthetic process;N-acetylglucosamine metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of carbohydrate metabolic process;negative regulation of cellular biosynthetic process;negative regulation of cellular carbohydrate metabolic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of glycogen biosynthetic process;negative regulation of glycogen metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;post-translational protein modification;primary metabolic process;protein complex assembly;protein complex subunit organization;protein glycosylation;protein homooligomerization;protein homotetramerization;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein oligomerization;protein tetramerization;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular carbohydrate metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen biosynthetic process;regulation of glycogen metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to carbohydrate stimulus;response to chemical stimulus;response to disaccharide stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to sucrose stimulus;small molecule biosynthetic process;small molecule metabolic process;UDP-N-acetylglucosamine biosynthetic process;UDP-N-acetylglucosamine metabolic process "amine binding;amino acid binding;binding;carbohydrate binding;carboxylic acid binding;catalytic activity;glutamine-fructose-6-phosphate transaminase (isomerizing) activity;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups" cell part;cytoplasmic part;cytosol;intracellular part "Alanine, aspartate and glutamate metabolism;Amino sugar and nucleotide sugar metabolism"

Q92896;Q92896-3;Q92896-2;H3BM42 Golgi apparatus protein 1 GLG1 >sp|Q92896|GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2;>sp|Q92896-3|GSLG1_HUMAN Isoform 3 of Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1;>sp|Q92896-2|GSLG1_HUMAN Isoform 2 of Golgi apparatus protein 1 OS=Homo sapiens GN=GL 1.21 1.41 1.74 0.75 1.05 0.51 0.97 0.87 3.08E-08 3 3 anatomical structure morphogenesis;biological regulation;bone morphogenesis;developmental process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of protein processing;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of biological process;regulation of cartilage development;regulation of cell communication;regulation of cell differentiation;regulation of cellular process;regulation of chondrocyte differentiation;regulation of developmental process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein processing;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway binding;protein binding;receptor binding cell part;cytoplasmic part;extracellular matrix;extracellular region part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Cell adhesion molecules (CAMs)

Q08379-2;Q08379;B7ZC06;Q9NVV4-2 Golgin subfamily A member 2 GOLGA2>sp|Q08379-2|GOGA2_HUMAN Isoform 2 of Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2;>sp|Q08379|GOGA2_HUMAN Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3 NaN NaN 0.98 NaN 12.42 NaN NaN NaN 1.60E-07 3 5.5 cell cycle phase;cell cycle process;cellular process;M phase;M phase of mitotic cell cycle;mitotic prophase;prophase cell part;cis-Golgi network;cytoplasmic part;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part

P09211;A8MX94 Glutathione S-transferase P GSTP1 >sp|P09211|GSTP1_HUMAN Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 0.76 0.66 NaN 0.29 NaN 1.86 1.66 0.88 2.06E-17 3 17.6 amine metabolic process;anatomical structure development;biological regulation;carboxylic acid metabolic process;cell proliferation;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to biotic stimulus;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to stimulus;central nervous system development;common myeloid progenitor cell proliferation;developmental process;glutathione metabolic process;localization;metabolic process;negative regulation of acute inflammatory response;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of chemokine production;negative regulation of cytokine production;negative regulation of cytokine-mediated signaling pathway;negative regulation of defense response;negative regulation of ERK1 and ERK2 cascade;negative regulation of fibroblast proliferation;negative regulation of I-kappaB kinase/NF-kappaB cascade;negative regulation of inflammatory response;negative regulation of interleukin-1 beta production;negative regulation of interleukin-1 production;negative regulation of intracellular protein kinase cascade;negative regulation of JUN kinase activity;negative regulation of kinase activity;negative regulation of leukocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of MAPKKK cascade;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of monocyte chemotactic protein-1 production;negative regulation of multicellular organismal process;negative regulation of necrotic cell death;negative regulation of nitric-oxide synthase biosynthetic process;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of response to cytokine stimulus;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of stress-activated MAPK cascade;negative regulation of stress-activated protein kinase signaling cascade;negative regulation of transferase activity;negative regulation of tumor necrosis factor production;negative regulation of tumor necrosis factor-mediated signaling pathway;nitric oxide storage;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;peptide metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;positive regulation of reactive oxygen species metabolic process;positive regulation of superoxide anion generation;primary metabolic process;regulation of acute inflammatory response;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chemokine production;regulation of cytokine production;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of ERK1 and ERK2 cascade;regulation of fibroblast proliferation;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of inflammatory response;regulation of interleukin-1 beta production;regulation of interleukin-1 production;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of leukocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of monocyte chemotactic protein-1 production;regulation of multicellular organismal process;regulation of necrotic cell death;regulation of nitric-oxide synthase biosynthetic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of reactive oxygen species metabolic process;regulation of response to cytokine stimulus;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of superoxide anion generation;regulation of superoxide metabolic process;regulation of transferase activity;regulation of tumor necrosis factor production;regulation of tumor necrosis factor-mediated signaling pathway;response to biotic stimulus;response to chemical stimulus;response to inorganic substance;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;small molecule metabolic process;sulfur compound metabolic process;system development;xenobiotic metabolic process "binding;catalytic activity;dinitrosyl-iron complex binding;enzyme binding;enzyme regulator activity;glutathione transferase activity;JUN kinase binding;kinase binding;kinase regulator activity;nitric oxide binding;protein binding;protein kinase binding;S-nitrosoglutathione binding;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nucleus;organelle;protein complex;TRAF2-GSTP1 complex Drug metabolism - cytochrome P450;Glutathione metabolism;Metabolism of xenobiotics by cytochrome P450

Q92522 Histone H1x H1FX >sp|Q92522|H1X_HUMAN Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1 1.05 1.6 0.91 2.94 0.21 0.3 0.36 0.33 1.60E-15 3 17.4 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex

K7EMV3;K7EP01;B4DEB1;K7EK07;Q6NXT2;Q71DI3;Q16695;P84243;P68431;K7ES00 Histone H3;Histone H3.3C;Histone H3.2;Histone H3.1t;Histone H3.3;Histone H3.1 H3F3B;H3F3A;H3F3C;HIST2H3A;HIST3H3;HIST1H3A >tr|K7EMV3|K7EMV3_HUMAN Histone H3 OS=Homo sapiens GN=H3F3B PE=3 SV=1;>tr|K7EP01|K7EP01_HUMAN Histone H3.3 OS=Homo sapiens GN=H3F3B PE=4 SV=1;>tr|B4DEB1|B4DEB1_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1;>tr|K7EK07|K7EK07_HUMAN Histone H3 (Fragment 1.14 1.48 1.09 3.13 0.34 0.37 0.36 0.32 2.83E-07 3 17.4 anatomical structure homeostasis;biological regulation;blood coagulation;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;coagulation;DNA metabolic process;hemostasis;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;regulation of gene silencing;S phase;telomere maintenance;telomere organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleosome;nucleus;organelle;organelle

part;protein-DNA complex Systemic lupus erythematosus
B3KRS5;Q92769;J3KPW7;E5RK19;E5RFI6;E5RJ04;E5RGV4;E5RHE7;E5RH52;E5RG37;E5RFP9;H3BM24 Histone deacetylase;Histone deacetylase 2 HDAC2 >tr|B3KRS5|B3KRS5_HUMAN Histone deacetylase OS=Homo sapiens GN=HDAC2 PE=2 SV=1;>sp|Q92769|HDAC2_HUMAN Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=1 SV=2;>tr|J3KPW7|J3KPW7_HUMAN Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=4 SV=1 1.34 1.43 1.31 2.29 0.55 0.53 0.61 0.65 5.54E-26 3 8.3 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;biosynthetic process;blood coagulation;cell differentiation;cell projection organization;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;coagulation;covalent chromatin modification;dendrite development;developmental process;ectodermal placode formation;embryonic digit morphogenesis;embryonic morphogenesis;enzyme linked receptor protein signaling pathway;epidermal cell differentiation;eyelid development in camera-type eye;fungiform papilla formation;hair follicle placode formation;hemostasis;hippocampus development;histone deacetylation;histone H3 deacetylation;histone H4 deacetylation;histone modification;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;maintenance of chromatin silencing;metabolic process;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell projection organization;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of MHC class II biosynthetic process;negative regulation of molecular function;negative regulation of neuron projection development;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of Wnt receptor signaling pathway;nerve growth factor receptor signaling pathway;neuron projection development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of collagen biosynthetic process;positive regulation of collagen metabolic process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of glial cell differentiation;positive regulation of gliogenesis;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal metabolic process;positive regulation of multicellular organismal process;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of oligodendrocyte differentiation;positive regulation of protein metabolic process;positive regulation of proteolysis;positive regulation of receptor biosynthetic process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein deacetylation;protein deacylation;protein metabolic process;protein modification process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of collagen biosynthetic process;regulation of collagen metabolic process;regulation of developmental process;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of MHC class II biosynthetic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal metabolic process;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oligodendrocyte differentiation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein deacetylation;regulation of protein metabolic process;regulation of protein modification process;regulation of proteolysis;regulation of receptor biosynthetic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway" "binding;catalytic activity;chromatin binding;chromatin DNA binding;deacetylase activity;DNA binding;histone deacetylase activity;histone deacetylase activity (H3-K14 specific);histone deacetylase activity (H3-K9 specific);hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;NAD-dependent histone deacetylase activity;NAD-dependent histone deacetylase activity (H3-K14 specific);NAD-dependent histone deacetylase activity (H3-K9 specific);NAD-dependent histone deacetylase activity (H4-K16 specific);NAD-dependent protein deacetylase activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein deacetylase activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;structure-specific DNA binding" cell part;chromatin;chromatin remodeling complex;chromosomal part;cytoplasm;ESC/E(Z) complex;heterochromatin;histone deacetylase complex;histone methyltransferase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;methyltransferase complex;nuclear chromatin;nuclear chromosome part;nuclear part;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;PcG protein complex;protein complex;replication fork;Sin3 complex;Sin3-type complex;transcription factor complex;transcriptional repressor complex Cell cycle;Chronic myeloid leukemia;Huntington's disease;Notch signaling pathway;Pathways in cancer

F5H2U8;P52926;F5H2A4;Q1M185;Q1M188;Q1M186;Q1M187;P52926-2;F5H6H0 High mobility group protein HMGI-C HMGA2 >tr|F5H2U8|F5H2U8_HUMAN High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=2 SV=1;>sp|P52926|HMGA2_HUMAN High mobility group protein HMGI-C OS=Homo sapiens GN=HMGA2 PE=1 SV=1;>tr|F5H2A4|F5H2A4_HUMAN High mobility group protein HMGI-C OS=Homo sa 0.99 1.69 1.14 2.66 0.36 0.29 0.46 0.84 3.99E-24 3 42.4 "adipose tissue development;adrenal gland development;aging;anatomical structure development;anatomical structure morphogenesis;base-excision repair;biological regulation;cell aging;cell communication;cell cycle checkpoint;cell cycle phase;cell cycle process;cell differentiation;cell division;cell morphogenesis;cell morphogenesis involved in differentiation;cell proliferation;cell proliferation in forebrain;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cellular senescence;chondrocyte differentiation;chondrocyte proliferation;chromatin assembly;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromosome breakage;chromosome condensation;chromosome organization;covalent chromatin modification;detection of stimulus;developmental process;developmental process involved in reproduction;DNA conformation change;DNA damage checkpoint;DNA damage response, detection of DNA damage;DNA integrity checkpoint;DNA metabolic process;DNA packaging;DNA repair;endodermal cell differentiation;epithelial to mesenchymal transition;fat cell differentiation;fat pad development;G2/M transition checkpoint;G2/M transition DNA damage checkpoint;G2/M transition of mitotic cell cycle;gamete generation;gland development;gonad development;heterochromatin formation;heterochromatin organization;histone H2A-S139 phosphorylation;histone modification;histone phosphorylation;histone-serine phosphorylation;interaction with symbiont;interspecies interaction between organisms;macromolecule metabolic process;macromolecule modification;male gamete generation;male gonad development;mesodermal cell differentiation;mesodermal-endodermal cell signaling;metabolic process;mitosis;mitotic cell cycle checkpoint;mitotic cell cycle G2/M transition checkpoint;mitotic cell cycle G2/M transition DNA damage checkpoint;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;negative regulation by host of viral transcription;negative regulation of apoptosis;negative regulation of astrocyte differentiation;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA binding;negative regulation of DNA metabolic process;negative regulation of DNA repair;negative regulation of double-strand break repair;negative regulation of double-strand break repair via nonhomologous end joining;negative regulation of glial cell differentiation;negative regulation of gliogenesis;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of neurogenesis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of reproductive process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of retroviral genome replication;negative regulation of RNA metabolic process;negative regulation of viral genome replication;negative regulation of viral reproduction;negative regulation of viral transcription;neural precursor cell proliferation;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oncogene-induced senescence;organ development;organelle fission;organelle organization;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;pituitary gland development;positive regulation of apoptosis;positive regulation of binding;positive regulation of biological process;positive regulation of cell aging;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of cellular response to X-ray;positive regulation of cellular senescence;positive regulation of developmental process;positive regulation of DNA binding;positive regulation of growth;positive regulation of molecular function;positive regulation of multicellular organism growth;positive regulation of multicellular organismal process;positive regulation of programmed cell death;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of stem cell proliferation;positive regulation of transcription regulatory region DNA binding;positive regulation of viral reproduction;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of apoptosis;regulation of astrocyte differentiation;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell aging;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to drug;regulation of cellular response to stress;regulation of cellular response to X-ray;regulation of cellular senescence;regulation of developmental process;regulation of DNA binding;regulation of DNA metabolic process;regulation of DNA repair;regulation of double-strand break repair;regulation of double-strand break repair via nonhomologous end joining;regulation of G2/M transition of mitotic cell cycle;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of growth;regulation of growth hormone secretion;regulation of hormone secretion;regulation of interphase of mitotic cell cycle;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organism growth;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of response to DNA damage stimulus;regulation of response to drug;regulation of response to stimulus;regulation of response to stress;regulation of retroviral genome replication;regulation of RNA metabolic process;regulation of secretion;regulation of signaling;regulation of stem cell differentiation;regulation of stem cell maintenance;regulation of stem cell proliferation;regulation of transcription regulatory region DNA binding;regulation of transcription, DNA-dependent;regulation of transport;regulation of viral genome replication;regulation of viral reproduction;regulation of viral transcription;reproductive process;reproductive structure development;response to biotic stimulus;response to DNA damage stimulus;response to other organism;response to stimulus;response to stress;response to virus;senescence-associated heterochromatin focus formation;signaling;somatic stem cell maintenance;spermatogenesis;stem cell differentiation;stem cell maintenance;tissue development" "5'-deoxyribose-5-phosphate lyase activity;AT DNA binding;binding;C2H2 zinc finger domain binding;cAMP response element binding;carbon-oxygen lyase activity;catalytic activity;chromatin binding;chromatin DNA binding;core promoter binding;DNA bending activity;DNA binding;DNA-(apurinic or apyrimidinic site) lyase activity;DNA-dependent protein kinase activity;kinase activity;lyase activity;MH1 domain binding;MH2 domain binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleosomal DNA binding;nucleosome binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein domain specific binding;protein kinase activity;protein serine/threonine kinase activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;structure-specific DNA binding;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;chromatin;chromosomal part;chromosome;heterochromatin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleus;organelle;organelle part;protein complex;protein-DNA complex;senescence-associated heterochromatin focus;SMAD protein complex

I3L159;I3L1F5;I3L430;P30519;I3L276;I3L4P8;I3L463 Heme oxygenase 2 HMOX2 >tr|I3L159|I3L159_HUMAN Heme oxygenase 2 (Fragment) OS=Homo sapiens GN=HMOX2 PE=2 SV=1;>tr|I3L1F5|I3L1F5_HUMAN Heme oxygenase 2 (Fragment) OS=Homo sapiens GN=HMOX2 PE=2 SV=1;>tr|I3L430|I3L430_HUMAN Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=2 SV=1;>sp|P3 0.92 0.69 1.23 0.32 1.27 0.89 0.9 1.02 1.89E-10 3 18.8 biological regulation;catabolic process;cation homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;cofactor catabolic process;cofactor metabolic process;establishment of localization;heme catabolic process;heme metabolic process;heme oxidation;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;ion homeostasis;iron ion homeostasis;metabolic process;metal ion homeostasis;nitrogen compound metabolic process;oxidation-reduction process;pigment catabolic process;pigment metabolic process;porphyrin-containing compound catabolic process;porphyrin-containing compound metabolic process;regulation of biological quality;response to chemical stimulus;response to hypoxia;response to oxidative stress;response to oxygen levels;response to stimulus;response to stress;small molecule metabolic process;tetrapyrrole catabolic process;tetrapyrrole metabolic process;transmembrane transport;transport "binding;catalytic activity;cation binding;heme oxygenase (decyclizing) activity;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;membrane;membrane part;organelle membrane;organelle part;plasma membrane Mineral absorption;Porphyrin and chlorophyll metabolism

Q99729-3;D6R9P3;D6RD18;Q99729-4;D6RBZ0;Q99729-2;Q99729 HNRNPAB >sp|Q99729-3|ROAA_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB;>tr|D6R9P3|D6R9P3_HUMAN Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1;>tr|D6RD18|D6RD18_HUMAN Heterogeneous nucle 1.23 0.8 1.28 1.71 0.25 0.16 1.02 0.76 1.85E-46 3 15.8 "anatomical structure morphogenesis;biological regulation;cell morphogenesis;cell morphogenesis involved in differentiation;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;developmental process;epithelial to mesenchymal transition;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent" binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex

M0R3F1;Q9BUJ2-3;Q9BUJ2-4;B7Z4B8;Q9BUJ2-2;Q9BUJ2;M0QYZ0;Q9BUJ2-5 Heterogeneous nuclear ribonucleoprotein U-like protein 1 HNRNPUL1 >tr|M0R3F1|M0R3F1_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Fragment) OS=Homo sapiens GN=HNRNPUL1 PE=4 SV=1;>sp|Q9BUJ2-3|HNRL1_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1;>sp NaN NaN 0.88 NaN 1.36 NaN NaN NaN 2.90E-19 3 9 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to biotic stimulus;response to other organism;response to stimulus;response to virus;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;nucleic acid binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex

O14979-3;O14979-2;O14979 Heterogeneous nuclear ribonucleoprotein D-like HNRPDL >sp|O14979-3|HNRDL_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL;>sp|O14979-2|HNRDL_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL;>sp|O14979|HNRDL_HUMAN Heterogeneo 1.22 0.96 1.08 1.78 0.41 0.34 0.85 0.79 1.99E-44 3 13.1 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;transcription, DNA-dependent" binding;DNA binding;double-stranded DNA binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly(G) RNA binding;poly-purine tract binding;RNA binding;single-stranded DNA binding;single-stranded RNA binding;structure-specific DNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex

Q53GQ0;E9PI21 Estradiol 17-beta-dehydrogenase 12 HSD17B12 >sp|Q53GQ0|DHB12_HUMAN Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 0.6 0.55 0.98 0.19 2.47 1.65 1.45 0.94 2.47E-17 3 12.2 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;estrogen biosynthetic process;estrogen metabolic process;extracellular matrix organization;extracellular structure organization;fatty acid biosynthetic process;fatty acid metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;hormone biosynthetic process;hormone metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular process;regulation of hormone levels;small molecule biosynthetic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;thioester biosynthetic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process "binding;carbohydrate binding;catalytic activity;estradiol 17-beta-dehydrogenase activity;glycosaminoglycan binding;heparin binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;pattern binding;polysaccharide binding;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular matrix;extracellular region part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Biosynthesis of unsaturated fatty acids;Steroid hormone biosynthesis

B8ZZL8;P61604;B8ZZ54 "10 kDa heat shock protein, mitochondrial" HSPE1 ">tr|B8ZZL8|B8ZZL8_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=2 SV=1;>sp|P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2" 0.85 0.79 NaN 0.21 NaN 0.52 2 1.29 4.76E-20 3 31.7 activation of caspase activity;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;chaperone binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part

P05161 Ubiquitin-like protein ISG15 ISG15 >sp|P05161|ISG15_HUMAN Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5 NaN NaN 1.73 1.63 0.49 0.68 NaN NaN 1.06E-14 3 28.5 biological regulation;catabolic process;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;immune effector process;immune system process;interaction with host;interspecies interaction between organisms;ISG15-protein conjugation;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of type I interferon production;primary metabolic process;protein metabolic process;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cellular process;regulation of cytokine production;regulation of multicellular organismal process;regulation of type I interferon production;reproductive process;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;signal transduction;signaling;type I interferon-mediated signaling pathway;viral reproductive process;virus-host interaction protein tag cell part;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular part RIG-I-like receptor signaling pathway

E7EMF1;E7ESP4;P17301;E9PB77 Integrin alpha-2 ITGA2 >tr|E7EMF1|E7EMF1_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=2 SV=1;>tr|E7ESP4|E7ESP4_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=2 SV=1;>sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1;>tr|E9PB77|E9PB77_HUMAN Integr NaN NaN 1.38 NaN 0.96 NaN NaN NaN 1.27E-07 3 5.6 anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular process;cellular response to stimulus;chemotaxis;coagulation;developmental process;hemostasis;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;locomotion;multicellular organismal process;multi-organism process;organ morphogenesis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis;viral reproductive process;virus-host interaction binding;cation binding;collagen binding;ion binding;metal ion binding;protein binding basal part of cell;cell part;cell surface;external side of plasma membrane;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Small cell lung cancer

P26006;P26006-1;H0YA49;D6R9X8 Integrin alpha-3;Integrin alpha-3 heavy chain;Integrin alpha-3 light chain ITGA3 >sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5;>sp|P26006-1|ITA3_HUMAN Isoform 2 of Integrin alpha-3 OS=Homo sapiens GN=ITGA3;>tr|H0YA49|H0YA49_HUMAN Integrin alpha-3 (Fragment) OS=Homo sapiens GN=ITGA3 PE=4 SV=1 0.94 1.04 1.28 NaN 0.64 NaN 0.9 0.96 1.39E-07 3 2.8 behavior;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular process;cellular response to stimulus;coagulation;cognition;hemostasis;immune system process;integrin-mediated signaling pathway;learning or memory;leukocyte migration;locomotion;memory;multicellular organismal process;neurological system process;neuron migration;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;response to stimulus;signal transduction;system process binding;cation binding;ion binding;metal ion binding basolateral plasma membrane;cell part;cell surface;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex;synapse Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer

Q9NSB4;CON__Q9NSB4 "Keratin, type II cuticular Hb2" KRT82 ">sp|Q9NSB4|KRT82_HUMAN Keratin, type II cuticular Hb2 OS=Homo sapiens GN=KRT82 PE=1 SV=3;>Q9NSB4 SWISS-PROT:Q9NSB4 Keratin, type II cuticular Hb2 (Hair keratin, type II Hb2) - Homo sapiens (Human)." 1.24 1.07 0.87 NaN 1.21 NaN 0.68 1.05 1.57E-09 3 5.1 structural constituent of epidermis;structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P78386;CON__P78386 "Keratin, type II cuticular Hb5" KRT85 ">sp|P78386|KRT85_HUMAN Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1;>P78386 SWISS-PROT:P78386 Keratin, type II cuticular Hb5 (Hair keratin, type II Hb5) - Homo sapiens (Human)." 0.88 0.83 NaN NaN NaN NaN 1 1.16 4.37E-17 3 5.7 anatomical structure development;developmental process;epidermis development;tissue development structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P11047 Laminin subunit gamma-1 LAMC1 >sp|P11047|LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=31.8 1.18 1.21 0.97 0.45 0.24 0.65 0.61 1.43E-08 3 2.6 anatomical structure development;anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;chemotaxis;developmental process;endoderm development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of epithelial cell proliferation;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of epithelial cell proliferation;response to chemical stimulus;response to external stimulus;response to stimulus;substrate adhesion-dependent cell spreading;taxis;tissue development binding;extracellular matrix structural constituent;glycolipid binding;glycosphingolipid binding;lipid binding;sphingolipid binding;structural molecule activity extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;laminin complex;laminin-1 complex;laminin-10 complex;laminin-11 complex;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;organelle;protein complex;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Prion diseases;Small cell lung cancer;Toxoplasmosis

Q14739;C9JXK0 Lamin-B receptor LBR >sp|Q14739|LBR_HUMAN Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2 NaN NaN 1.75 NaN 0.7 NaN NaN NaN 1.05E-13 3 6.2 alcohol metabolic process;biosynthetic process;cholesterol biosynthetic process;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "binding;catalytic activity;DNA binding;lamin binding;nucleic acid binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;protein binding" cell part;cytoplasmic part;integral to membrane;integral to nuclear inner membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to nuclear inner membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;nuclear membrane;nuclear membrane part;nuclear part;organelle;organelle membrane;organelle part

P00338;P00338-3;F5GXH2;F5GYU2;F5GXY2;P00338-5;P00338-4;P00338-2;F5GZQ4;F5H5J4;F5H6W8 L-lactate dehydrogenase A chain LDHA >sp|P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2;>sp|P00338-3|LDHA_HUMAN Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA;>tr|F5GXH2|F5GXH2_HUMAN L-lactate dehydrogenase A chain (Fragment) OS=Homo 1.18 NaN 0.97 0.24 2.02 0.97 1.93 NaN 3.36E-29 3 10.2 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cell communication;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to stimulus;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;response to external stimulus;response to extracellular stimulus;response to stimulus;small molecule catabolic process;small molecule metabolic process "catalytic activity;lactate dehydrogenase activity;L-lactate dehydrogenase

activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Cysteine and methionine metabolism;Glycolysis / Gluconeogenesis;Propanoate metabolism;Pyruvate metabolism
P07195;F5H793;C9J7H8;A8MW50 L-lactate dehydrogenase B chain;L-lactate dehydrogenase LDHB >sp|P07195|LDHB_HUMAN L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2;>tr|F5H793|F5H793_HUMAN L-lactate dehydrogenase B chain (Fragment) OS=Homo sapiens GN=LDHB PE=2 SV=1;>tr|C9J7H8|C9J7H8_HUMAN L-lactate dehydrogenase B chain (Fragment) 1.48 0.45 1.21 0.25 1.36 0.68 1.94 0.89 1.59E-14 3 12 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;lactate metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;NAD metabolic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;pyruvate metabolic process;small molecule catabolic process;small molecule metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;lactate dehydrogenase activity;L-lactate dehydrogenase activity;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor"cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Cysteine and methionine metabolism;Glycolysis / Gluconeogenesis;Propanoate metabolism;Pyruvate metabolism
Q8NC56;D6RBV0;D6R958;Q8NC56-2;H7C2Z0 LEM domain-containing protein 2 LEMD2 >sp|Q8NC56|LEMD2_HUMAN LEM domain-containing protein 2 OS=Homo sapiens GN=LEMD2 PE=1 SV=1;>tr|D6RBV0|D6RBV0_HUMAN LEM domain-containing protein 2 OS=Homo sapiens GN=LEMD2 PE=2 SV=1 NaN 0.96 0.49 NaN 0.4 NaN NaN 0.74 1.25E-09 3 7.8 biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;muscle cell differentiation;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of intracellular protein kinase cascade;negative regulation of MAPKKK cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of intracellular protein kinase cascade;regulation of MAPKKK cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;skeletal muscle cell differentiation;striated muscle cell differentiation cell part;integral to membrane;integral to nuclear inner membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to nuclear inner membrane;intrinsic to organelle membrane;membrane;membrane part;nuclear membrane;nuclear membrane part;nuclear part;organelle membrane;organelle part
P49257 Protein ERGIC-53 LMAN1 >sp|P49257|LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2 1.04 0.87 1.46 0.58 0.99 0.82 0.91 0.95 9.57E-08 3 5.9 biological regulation;blood coagulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;coagulation;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi organization;Golgi vesicle transport;hemostasis;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of organelle organization;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular process;regulation of organelle organization;transport;vesicle-mediated transport binding;carbohydrate binding;cation binding;ion binding;mannose binding;metal ion binding;monosaccharide binding;protein binding;sugar binding;unfolded protein binding cell part;coated vesicle membrane;contractile fiber part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;ER to Golgi transport vesicle membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;sarcomere;transport vesicle membrane;vesicle membrane Protein processing in endoplasmic reticulum
O95274 Ly6/PLAUR domain-containing protein 3 LYPD3 >sp|O95274|LYPD3_HUMAN Ly6/PLAUR domain-containing protein 3 OS=Homo sapiens GN=LYPD3 PE=1 SV=2 1.46 0.7 1.34 0.54 1.69 1.25 1.43 0.65 4.10E-10 3 9.8 biological adhesion;cell adhesion;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular process anchored to membrane;anchored to plasma membrane;cell part;integral to membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part
Q9H0U3 Magnesium transporter protein 1 MAGT1 >sp|Q9H0U3|MAGT1_HUMAN Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1 NaN NaN 1.99 NaN 0.76 NaN NaN NaN 2.70E-07 3 8.4 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cognition;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;neurological system process;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;system process cation transmembrane transporter activity;divalent inorganic cation transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;magnesium ion transmembrane transporter activity;metal ion transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;oligosaccharyltransferase complex;organelle part;plasma membrane part;protein complex
P46821;D6RA40;D6RA32 Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1 MAP1B >sp|P46821|MAP1B_HUMAN Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2;>tr|D6RA40|D6RA40_HUMAN Microtubule-associated protein 1B (Fragment) OS=Homo sapiens GN=MAP1B PE=2

SV=1;>tr|D6RA32|D6RA32_HUMAN Microtubule-associated protein 1B (F NaN 2.38 0.13 0.29 0.48 2.06 NaN 1.07 3.78E-13 3 1.9 "anatomical structure development;anatomical structure morphogenesis;axonogenesis;biological regulation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;dendrite development;developmental process;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of mitochondrion localization;establishment of mitochondrion localization, microtubule-mediated;establishment of monopolar cell polarity;establishment of organelle localization;establishment or maintenance of cell polarity;establishment or maintenance of monopolar cell polarity;intracellular transport;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrion transport along microtubule;negative regulation of biological process;negative regulation of intracellular transport;negative regulation of transport;neuron projection development;neuron projection morphogenesis;organelle organization;organelle transport along microtubule;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of neurogenesis;regulation of anatomical structure morphogenesis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of intracellular transport;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of transport;transport" catalytic activity;hydrolase activity;structural molecule activity cell junction;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;dendritic spine;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule associated complex;neuron projection;neuron spine;organelle part;plasma membrane;protein complex;synapse

Q14244-5;Q14244-3;Q14244-6;Q14244;Q14244-7;Q14244-2;Q14244-4 Ensconsin MAP7 >sp|Q14244-5|MAP7_HUMAN Isoform 5 of Ensconsin OS=Homo sapiens GN=MAP7;>sp|Q14244-3|MAP7_HUMAN Isoform 3 of Ensconsin OS=Homo sapiens GN=MAP7;>sp|Q14244-6|MAP7_HUMAN Isoform 6 of Ensconsin OS=Homo sapiens GN=MAP7;>sp|Q14244|MAP7_HUMAN Ensconsin OS=Homo sap NaN NaN 0.66 NaN 1.92 NaN NaN NaN 1.52E-06 3 6.3 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cytoskeleton organization;establishment or maintenance of cell polarity;localization;macromolecule localization;membrane organization;microtubule cytoskeleton organization;microtubule-based process;organelle organization;plasma membrane organization;protein localization;protein localization in membrane;protein localization in plasma membrane;response to abiotic stimulus;response to osmotic stress;response to stimulus;response to stress binding;protein binding;receptor binding;structural molecule activity basolateral plasma membrane;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;microtubule;microtubule associated complex;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex

Q9UBB5;Q9UBB5-3 Methyl-CpG-binding domain protein 2 MBD2 >sp|Q9UBB5|MBD2_HUMAN Methyl-CpG-binding domain protein 2 OS=Homo sapiens GN=MBD2 PE=1 SV=1 1.26 0.89 1.77 1.72 0.36 0.47 0.82 0.63 7.99E-09 3 9.5 "behavior;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;maternal behavior;metabolic process;multicellular organismal process;multicellular organismal reproductive behavior;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;parental behavior;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of Wnt receptor signaling pathway;primary metabolic process;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;reproductive behavior;reproductive process;response to stimulus;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;chromatin binding;DNA binding;methyl-CpG binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;satellite DNA binding;sequence-specific DNA binding;siRNA binding cell part;chromatin;chromatin remodeling complex;chromosomal part;cytoplasm;heterochromatin;histone deacetylase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex

P40926;G3XAL0;E9PDB2 "Malate dehydrogenase, mitochondrial;Malate dehydrogenase" MDH2 ">sp|P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3;>tr|G3XAL0|G3XAL0_HUMAN Malate dehydrogenase OS=Homo sapiens GN=MDH2 PE=2 SV=1;>tr|E9PDB2|E9PDB2_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 P" 0.24 4.74 0.3 2.84 0.27 1.65 0.54 1.17 3.58E-20 3 11.8 acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;gluconeogenesis;glucose metabolic process;heterocycle metabolic process;hexose biosynthetic process;hexose metabolic process;internal protein amino acid acetylation;macromolecule metabolic process;macromolecule modification;malate metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;NAD metabolic process;NADH metabolic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxaloacetate metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule biosynthetic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;L-malate dehydrogenase activity;malate dehydrogenase (NADP+) activity;malate dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane Carbon fixation in photosynthetic organisms;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism;Pyruvate metabolism

C9JHF5;Q9GZY8-4;Q9GZY8-5;Q9GZY8-3;Q9GZY8-2;Q9GZY8 Mitochondrial fission factor MFF >tr|C9JHF5|C9JHF5_HUMAN Mitochondrial fission factor (Fragment) OS=Homo sapiens GN=MFF PE=2 SV=1;>sp|Q9GZY8-4|MFF_HUMAN Isoform 4 of Mitochondrial fission factor OS=Homo sapiens GN=MFF;>sp|Q9GZY8-5|MFF_HUMAN Isoform 5 of Mitochondrial fission factor OS=Hom 1.29 1.2 2.4 0.89 1.06 0.66 1.35 1 5.85E-13 3 34.1 anatomical structure morphogenesis;apoptotic mitochondrial changes;biological regulation;cell part morphogenesis;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;mitochondrial fission;mitochondrial fragmentation involved in apoptosis;mitochondrial transport;mitochondrion morphogenesis;mitochondrion organization;organelle fission;organelle organization;peroxisome fission;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of mitochondrion organization;positive regulation of organelle organization;positive regulation of release of cytochrome c from mitochondria;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein import;protein oligomerization;protein targeting;protein targeting to mitochondrion;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component organization;regulation of cellular process;regulation of mitochondrion organization;regulation of organelle organization;regulation of programmed cell death;regulation of release of cytochrome c from mitochondria;release of cytochrome c from mitochondria;transport cell part;cytoplasmic part;integral to membrane;integral to mitochondrial membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;microbody;mitochondrial membrane;mitochondrial membrane part;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;peroxisome

C9JX83;O00566 U3 small nucleolar ribonucleoprotein protein MPP10 MPHOSPH10 >tr|C9JX83|C9JX83_HUMAN U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=2 SV=1;>sp|O00566|MPP10_HUMAN U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=1 SV=2 NaN NaN 1.16 0.85 0.88 0.53 NaN NaN 4.11E-07 3 10.7 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;rRNA metabolic process;rRNA processing" cell part;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes

P52815;B4DLN1 "39S ribosomal protein L12, mitochondrial" MRPL12;SLC25A10 ">sp|P52815|RM12_HUMAN 39S ribosomal protein L12, mitochondrial OS=Homo sapiens GN=MRPL12 PE=1 SV=2;>tr|B4DLN1|B4DLN1_HUMAN Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=2 SV=1" 0.96 1.37 1.86 1.21 0.35 0.34 0.73 0.82 5.84E-44 3 17.7 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrial RNA metabolic process;mitochondrial transport;mitochondrion organization;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from mitochondrial promoter;transcription, DNA-dependent;translation;transport" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;large ribosomal subunit;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial large ribosomal subunit;mitochondrial membrane;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleus;organellar large ribosomal subunit;organelle;organelle membrane;organelle part;ribonucleoprotein complex;ribosome

J3QLR8;Q9Y3D9 "28S ribosomal protein S23, mitochondrial" MRPS23 ">tr|J3QLR8|J3QLR8_HUMAN 28S ribosomal protein S23, mitochondrial OS=Homo sapiens GN=MRPS23 PE=4 SV=1;>sp|Q9Y3D9|RT23_HUMAN 28S ribosomal protein S23, mitochondrial OS=Homo sapiens GN=MRPS23 PE=1 SV=2" 1.11 NaN 2.34 NaN 0.39 NaN 0.77 NaN 4.00E-08 3 19.7 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytoskeleton;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear membrane;nuclear part;organelle;organelle membrane;organelle part;ribonucleoprotein complex;ribosome

P00403 Cytochrome c oxidase subunit 2 MT-CO2 >sp|P00403|COX2_HUMAN Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1 1.21 1.39 1.05 1.78 0.46 0.69 0.57 1.05 1.81E-69 3 14.5 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, cytochrome c to oxygen;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "binding;catalytic activity;cation binding;cation transmembrane transporter activity;copper ion binding;cytochrome-c oxidase activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transition metal ion binding;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;respiratory chainAlzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q9Y4I1-2;F8WE88;G3V394;Q9Y4I1;Q9Y4I1-3;F8W6H6;Q9UES5;O95317;Q9H6Y6;K7EIJ6;Q9ULV0 Unconventional myosin-Va MYO5A >sp|Q9Y4I1-2|MYO5A_HUMAN Isoform 2 of Unconventional myosin-Va OS=Homo sapiens GN=MYO5A;>tr|F8WE88|F8WE88_HUMAN Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=2 SV=1;>tr|G3V394|G3V394_HUMAN Unconventional myosin-Va OS=Homo sapiens GN=MYO5A PE=2 SV=1; NaN 1.89 0.89 1.29 1.02 1.51 NaN 1.26 1.10E-05 3 1.8 "actin filament-based movement;actin filament-based process;anagen;anatomical structure morphogenesis;axon ensheathment;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cell communication;cell differentiation;cell-cell signaling;cellular biosynthetic process;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular ketone metabolic process;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;developmental growth;developmental process;endoplasmic reticulum localization;ensheathment of neurons;establishment of localization;establishment of localization in cell;establishment of melanosome localization;establishment of organelle localization;establishment of pigment granule localization;establishment of protein localization;establishment of vesicle localization;exocytosis;fatty acid biosynthetic process;fatty acid metabolic process;fluid transport;growth;hair cycle process;hormone secretion;hormone transport;insulin secretion;lipid biosynthetic process;lipid metabolic process;localization;locomotion;locomotion involved in locomotory behavior;long-chain fatty acid biosynthetic process;long-chain fatty acid metabolic process;macromolecule localization;macromolecule metabolic process;melanin biosynthetic process;melanin metabolic process;melanocyte differentiation;melanosome transport;membrane organization;metabolic process;molting cycle;molting cycle process;monocarboxylic acid metabolic process;multicellular organismal process;myelination;neurological system process;odontogenesis;organ morphogenesis;organelle localization;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptide hormone secretion;peptide secretion;peptide transport;pigment biosynthetic process;pigment cell differentiation;pigment granule transport;pigment metabolic process;plasma membrane organization;primary metabolic process;protein localization;protein localization in membrane;protein localization in plasma membrane;protein metabolic process;protein transport;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of cellular process;regulation of hormone levels;regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of molecular function;regulation of receptor activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;secondary metabolic process;secretion;secretion by cell;secretory granule localization;sensory perception;sensory perception of light stimulus;signal release;signaling;small molecule biosynthetic process;small molecule metabolic process;synapse organization;synaptic transmission;system process;transmembrane transport;transport;vesicle localization;vesicle-mediated transport;visual perception;water transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actomyosin;cell body;cell part;cell projection;cell projection part;cilium;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;Golgi apparatus;growth cone;insulin-responsive compartment;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule plus end;myosin complex;neuronal cell body;nonmotile primary cilium;organelle;organelle membrane;organelle part;photoreceptor outer segment;pigment granule;primary cilium;protein complex;ruffle;site of polarized growth;stored secretory granule;vesicle;vesicle membrane

F8VRJ2;H0YHC3;F8W020;F8W118;F8VXI6;F8VUX1;F8VY35;B3KV44;F8VV59;B7Z9C2;B3KNT8;F8W0J6;F5H4R6;H0YIV4;P55209;F8VVB5;H0YH88;F8W543 Nucleosome assembly protein 1-like 1 NAP1L1 >tr|F8VRJ2|F8VRJ2_HUMAN Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1;>tr|H0YHC3|H0YHC3_HUMAN Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1;>tr|F8W020|F8W020_HUMAN Nucleosome assem 0.61 1.82 0.23 1.35 0.67 1.64 0.88 1.03 1.26E-10 3 33.3 biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;DNA metabolic process;DNA replication;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;pigment granule;vesicle

H7BYD0;Q5H9R2;Q16718;F8WAS3;C9IZN5 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 NDUFA5;DKFZp781K1356 >tr|H7BYD0|H7BYD0_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 (Fragment) OS=Homo sapiens GN=NDUFA5 PE=4 SV=1;>tr|Q5H9R2|Q5H9R2_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=DKFZp781K1356 PE=2 S 0.94 1.42 1.49 1.74 0.47 0.36 0.63 0.85 3.46E-24 3 30.4 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle inner membrane;organelle membrane;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

O95168-2;O95168;F2Z3P9;C9JXQ9 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 NDUFB4 >sp|O95168-2|NDUB4_HUMAN Isoform 2 of NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Homo sapiens GN=NDUFB4;>sp|O95168|NDUB4_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Homo sapiens GN=NDUFB4 PE=1 SV=3;>tr|F2Z3P9|F2 1.11 1.86 0.84 1.95 0.32 0.48 0.53 0.84 3.20E-22 3 32.5 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;mitochondrion;NADH dehydrogenase complex;organelle;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P49821-2;G3V0I5;P49821;E9PPS5;E9PQP1;E9PPR0;E9PMX3;B4DE93 "NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial" NDUFV1">sp|P49821-2|NDUV1_HUMAN Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Homo sapiens GN=NDUFV1;>tr|G3V0I5|G3V0I5_HUMAN NADH dehydrogenase (Ubiquinone) flavoprotein 1, 51kDa, isoform CRA_c OS=Homo sapiens GN=NDUFV1 PE=2 SV=1;>"1.08 1.42 1.33 2.06 0.79 0.67 0.55 0.94 4.45E-10 3 6.6 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "4 iron, 4 sulfur cluster binding;binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;FMN binding;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;NAD binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle inner membrane;organelle membrane;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P55769;B1AHD1 NHP2-like protein 1 NHP2L1 >sp|P55769|NH2L1_HUMAN NHP2-like protein 1 OS=Homo sapiens GN=NHP2L1 PE=1 SV=3;>tr|B1AHD1|B1AHD1_HUMAN NHP2-like protein 1 OS=Homo sapiens GN=NHP2L1 PE=2 SV=1 1.32 1.61 NaN 2.16 NaN 0.31 0.75 0.66 8.13E-07 3 24.2 "cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;RNA binding box C/D snoRNP complex;cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolar part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex;spliceosomal complex Ribosome biogenesis in eukaryotes;Spliceosome

Q9H6R4-4;Q9H6R4;Q9H6R4-3;Q9H6R4-2;G8JLK7 Nucleolar protein 6 NOL6 >sp|Q9H6R4-4|NOL6_HUMAN Isoform 4 of Nucleolar protein 6 OS=Homo sapiens GN=NOL6;>sp|Q9H6R4|NOL6_HUMAN Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2;>sp|Q9H6R4-3|NOL6_HUMAN Isoform 3 of Nucleolar protein 6 OS=Homo sapiens GN=NOL6;>sp|Q9H6R4-2|NOL6_ NaN NaN 2.02 NaN 1.7 NaN NaN NaN 6.66E-12 3 4.5 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing binding;nucleic acid binding;RNA binding cell part;chromosome;condensed chromosome;condensed nuclear chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes

F5H5C2;Q8WUM0;Q5T8N1;Q5TDI3 Nuclear pore complex protein Nup133 NUP133 >tr|F5H5C2|F5H5C2_HUMAN Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=2 SV=1;>sp|Q8WUM0|NU133_HUMAN Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=1 SV=2;>tr|Q5T8N1|Q5T8N1_HUMAN Nuclear pore complex protein Nup133 OS=Ho NaN NaN 0.54 NaN 2.86 NaN NaN NaN 2.69E-09 3 4.2 anaphase;anatomical structure development;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular transport;M phase;M phase of mitotic cell cycle;macromolecular complex subunit organization;mesoderm development;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear export;nuclear pore organization;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;nucleus organization;organelle organization;organic substance transport;paraxial mesoderm development;primary metabolic process;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;tissue development;transmembrane transport;transport;viral reproductive process nucleocytoplasmic transporter activity;transporter activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane part;non-membrane-bounded organelle;nuclear part;Nup107-160 complex;organelle;organelle part;protein complex RNA transport

E9PF10;O75694-2;O75694 Nuclear pore complex protein Nup155 NUP155 >tr|E9PF10|E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1;>sp|O75694-2|NU155_HUMAN Isoform 2 of Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155;>sp|O75694|NU155_HUMAN Nuclear pore complex protein Nup155 O NaN NaN 0.65 NaN 10.48 NaN NaN NaN 9.24E-06 3 2.9 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular protein transport;intracellular transport;membrane organization;metabolic process;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear envelope organization;nuclear export;nuclear import;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;organic substance transport;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process structural constituent of nuclear pore;structural molecule activity;transporter activity cell part;envelope;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear envelope;nuclear membrane;nuclear part;nuclear pore;organelle envelope;organelle membrane;organelle part;pore complex;protein complex RNA transport

Q8N1F7;H3BVG0;H3BRD9;Q8N1F7-2;H3BV15;H3BVE2;H3BNN5;H3BV11;H3BRI8;H3BM93 Nuclear pore complex protein Nup93 NUP93 >sp|Q8N1F7|NUP93_HUMAN Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2;>tr|H3BVG0|H3BVG0_HUMAN Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=2 SV=1;>tr|H3BRD9|H3BRD9_HUMAN Nuclear pore complex protein Nup93 (Fragment) NaN NaN 0.51 NaN 2.56 NaN NaN NaN 3.32E-05 3 6.6 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide transport;mRNA transport;nuclear pore complex assembly;nuclear pore organization;nucleic acid transport;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process structural constituent of nuclear pore;structural molecule activity cell part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;organelle membrane;organelle part;pore complex;protein complex RNA transport

O95747;C9JIG9 Serine/threonine-protein kinase OSR1 OXSR1 >sp|O95747|OXSR1_HUMAN Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1

NaN NaN NaN 0.4 NaN 2.04 NaN NaN 1.02E-17 3 9.1 biological regulation;cellular process;cellular response to stimulus;intracellular protein kinase cascade;intracellular signal transduction;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;intracellular part

P08559-3;P08559;P08559-2;P08559-4;Q5JPU0;Q5JPT9;Q5JPU1;Q5JPU3;Q5JPU2 "Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial" PDHA1 ">sp|P08559-3|ODPA_HUMAN Isoform 3 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1;>sp|P08559|ODPA_HUMAN Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapien" 0.67 1.54 0.97 0.92 0.69 0.95 1.11 1.41 2.55E-08 3 8.6 acetyl-CoA biosynthetic process;acetyl-CoA biosynthetic process from pyruvate;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol catabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor catabolic process;cofactor metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of metabolic process;small molecule catabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor;pyruvate dehydrogenase (acetyl-transferring) activity;pyruvate dehydrogenase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part;protein complex;pyruvate dehydrogenase complex "Butanoate metabolism;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Pyruvate metabolism;Valine, leucine and isoleucine biosynthesis"

H7BZJ3 Thioredoxin PDIA3 >tr|H7BZJ3|H7BZJ3_HUMAN Thioredoxin (Fragment) OS=Homo sapiens GN=PDIA3 PE=2 SV=1 1.69 1.23 0.68 0.85 0.79 0.69 1.34 0.99 1.47E-111 3 28.5 biological regulation;cell redox homeostasis;cellular homeostasis;cellular process;glycerol ether metabolic process;homeostatic process;metabolic process;organic ether metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide oxidoreductase activity"

Q9NR12;Q9NR12-3;D6RF83;Q9NR12-5;H7BYK4;Q9NR12-6;Q9NR12-4;D6RH06;Q9NR12-2;D6RAN1 PDZ and LIM domain protein 7 PDLIM7 >sp|Q9NR12|PDLI7_HUMAN PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1;>sp|Q9NR12-3|PDLI7_HUMAN Isoform 3 of PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7;>tr|D6RF83|D6RF83_HUMAN PDZ and LIM domain protein 7 (Fragment) OS=Homo sap 1.04 0.55 1.28 0.82 0.95 0.92 1.73 1.85 1.26E-06 3 7 actin cytoskeleton organization;actin filament-based process;biological regulation;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cytoskeleton organization;developmental process;endocytosis;establishment of localization;membrane invagination;membrane organization;multicellular organismal development;multicellular organismal process;organelle organization;ossification;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of osteoblast differentiation;receptor-mediated endocytosis;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal process;regulation of ossification;regulation of osteoblast differentiation;transport;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding actin cytoskeleton;actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeletal part;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;ruffle;stress fiber

O75381-2;O75381;K7EK59;F5H4J2 Peroxisomal membrane protein PEX14 PEX14 >sp|O75381-2|PEX14_HUMAN Isoform 2 of Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14;>sp|O75381|PEX14_HUMAN Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=1 SV=1 NaN NaN 1.85 NaN 0.85 NaN NaN NaN 2.29E-05 3 12.6 "biological regulation;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to peroxisome;intracellular protein transmembrane transport;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;microtubule anchoring;microtubule cytoskeleton organization;microtubule-based process;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein binding;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of transcription, DNA-dependent;organelle organization;peroxisomal transport;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein import;protein import into peroxisome matrix;protein import into peroxisome matrix, translocation;protein oligomerization;protein targeting;protein targeting to peroxisome;protein transmembrane transport;protein

transport;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein binding;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;transmembrane transport;transport" binding;cytoskeletal protein binding;microtubule binding;protein binding;protein binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;tubulin binding cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;nucleus;organelle;organelle membrane;organelle part;peroxisomal membrane;peroxisomal part;protein complex Peroxisome
P17858;P17858-2;P08237;P08237-3 "6-phosphofructokinase, liver type" PFKL ">sp|P17858|K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6;>sp|P17858-2|K6PL_HUMAN Isoform 2 of 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL" NaN NaN 0.18 NaN 0.64 NaN NaN NaN 2.05E-14 3 5.9 "alcohol catabolic process;alcohol metabolic process;anatomical structure homeostasis;biological regulation;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular metabolic process;cellular process;fructose 1,6-bisphosphate metabolic process;fructose 6-phosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;muscle cell homeostasis;negative regulation of biological process;negative regulation of cellular process;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of secretion;negative regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;response to carbohydrate stimulus;response to chemical stimulus;response to glucose stimulus;response to hexose stimulus;response to monosaccharide stimulus;response to organic substance;response to stimulus;small molecule catabolic process;small molecule metabolic process" "6-phosphofructokinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate binding;carbohydrate kinase activity;catalytic activity;cation binding;fructose binding;fructose-6-phosphate binding;ion binding;kinase activity;metal ion binding;monosaccharide binding;nucleotide binding;phosphofructokinase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;sugar binding;transferase activity;transferase activity, transferring phosphorus-containing groups" 6-phosphofructokinase complex;apical plasma membrane;cell part;cytoplasmic part;cytosolic part;intracellular part;macromolecular complex;membrane part;plasma membrane part;protein complex Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Methane metabolism;Pentose phosphate pathway
P07737;I3L3D5;K7EJ44 Profilin-1 PFN1 >sp|P07737|PROF1_HUMAN Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2;>tr|I3L3D5|I3L3D5_HUMAN Profilin-1 (Fragment) OS=Homo sapiens GN=PFN1 PE=2 SV=1 0.94 0.47 0.94 0.51 1.8 1.61 1.57 0.83 1.11E-21 3 30 "actin cytoskeleton organization;actin filament-based process;anatomical structure formation involved in morphogenesis;biological regulation;cell activation;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;death;developmental process;establishment of localization;establishment of localization in cell;exocytosis;neural tube closure;organelle organization;platelet activation;platelet degranulation;positive regulation of actin filament bundle assembly;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of DNA metabolic process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of stress fiber assembly;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of DNA metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of stress fiber assembly;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;secretion;secretion by cell;transport;tube closure;tube formation;vesicle-mediated transport" "binding;lipid binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding" cell part;cell projection;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nucleus;organelle;synapse Regulation of actin cytoskeleton;Shigellosis
P18669;P15259 Phosphoglycerate mutase 1;Phosphoglycerate mutase 2 PGAM1;PGAM2 >sp|P18669|PGAM1_HUMAN Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2;>sp|P15259|PGAM2_HUMAN Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3 NaN NaN 0.03 8.43 0.24 1.8 NaN NaN 3.58E-15 3 17.3 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;gamete generation;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic

process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;male gamete generation;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multicellular organismal process;multicellular organismal reproductive process;muscle contraction;muscle system process;primary metabolic process;regulation of biological process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of cellular amide metabolic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of generation of precursor metabolites and energy;regulation of glucose metabolic process;regulation of glycolysis;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide metabolic process;regulation of pentose-phosphate shunt;regulation of primary metabolic process;regulation of secondary metabolic process;reproductive process;respiratory burst;response to chemical stimulus;response to inorganic substance;response to mercury ion;response to metal ion;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;spermatogenesis;striated muscle contraction;system process "2,3-bisphosphoglycerate-dependent phosphoglycerate mutase activity;binding;bisphosphoglycerate 2-phosphatase activity;bisphosphoglycerate mutase activity;bisphosphoglycerate phosphatase activity;catalytic activity;cofactor binding;hydrolase activity;hydrolase activity, acting on ester bonds;intramolecular transferase activity;intramolecular transferase activity, phosphotransferases;isomerase activity;phosphatase activity;phosphoglycerate mutase activity;phosphoric ester hydrolase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Glycolysis / Gluconeogenesis;Methane metabolism

F5H7U0;B4DQJ8;P52209;K7EMN2;K7EM49;K7EPF6;K7ELN9 "6-phosphogluconate dehydrogenase, decarboxylating" PGD ">tr|F5H7U0|F5H7U0_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1;>tr|B4DQJ8|B4DQJ8_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1;>sp|P52209|6PGD_HUMAN 6-phosphogluconate d" 0.18 NaN NaN NaN NaN NaN 0.21 NaN 7.55E-07 3 6.1 "alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;aldonic acid metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;D-gluconate metabolic process;glucose catabolic process;glucose metabolic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;NADP metabolic process;NADPH regeneration;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;pentose biosynthetic process;pentose metabolic process;pentose-phosphate shunt;pentose-phosphate shunt, oxidative branch;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process" "binding;catalytic activity;coenzyme binding;cofactor binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;phosphogluconate dehydrogenase (decarboxylating) activity" cell part;cytoplasmic part;cytosol;intracellular part Glutathione metabolism;Pentose phosphate pathway

O00264;B7Z1L3 Membrane-associated progesterone receptor component 1 PGRMC1 >sp|O00264|PGRC1_HUMAN Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3;>tr|B7Z1L3|B7Z1L3_HUMAN Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=2 SV=1 NaN 1.27 2.07 0.77 0.94 0.99 NaN 0.93 2.11E-21 3 25.1 axon guidance;chemotaxis;locomotion;response to chemical stimulus;response to external stimulus;response to stimulus;taxis binding;cation binding;heme binding;ion binding;iron ion binding;lipid binding;metal ion binding;steroid binding;tetrapyrrole binding;transition metal ion binding cell part;cell surface;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle membrane;organelle part

Q5JRX3-3;Q5JRX3;Q5JRX3-2;C9JSL2;B1APQ0;H0Y7L7 "Presequence protease, mitochondrial" PITRM1 ">sp|Q5JRX3-3|PREP_HUMAN Isoform 3 of Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1;>sp|Q5JRX3|PREP_HUMAN Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3;>sp|Q5JRX3-2|PREP_HUMAN Isoform 2 of Presequence protease, mito" NaN NaN 0.68 NaN 3.64 NaN NaN NaN 1.80E-08 3 4.6 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "binding;catalytic activity;cation binding;endopeptidase activity;enzyme activator activity;enzyme regulator activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part

O60664-4;O60664-3;O60664;K7EL96;K7ERZ3;K7ER39;O60664-2 Perilipin-3 PLIN3 >sp|O60664-4|PLIN3_HUMAN Isoform 4 of Perilipin-3 OS=Homo sapiens GN=PLIN3;>sp|O60664-3|PLIN3_HUMAN Isoform 3 of Perilipin-3 OS=Homo sapiens GN=PLIN3;>sp|O60664|PLIN3_HUMAN Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3;>tr|K7EL96|K7EL96_HUMAN Perilipin-3 NaN NaN 3.92 0.23 1.2 1.57 NaN NaN 4.12E-17 3 11.4 cellular process;establishment of localization;transport;vesicle-mediated transport cell part;cytoplasmic part;endosomal part;endosome;endosome membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part

P29590-4;P29590-2;P29590-5;P29590-9;P29590-3;P29590-8;P29590;H3BT29;P29590-14;P29590-10;H3BT57;P29590-12;P29590-13;P29590-11;H3BVD2;H3BUJ5 Protein PML PML >sp|P29590-4|PML_HUMAN Isoform PML-6 of Protein PML OS=Homo sapiens GN=PML;>sp|P29590-2|PML_HUMAN Isoform PML-5 of Protein PML OS=Homo sapiens GN=PML;>sp|P29590-5|PML_HUMAN Isoform PML-4 of Protein PML OS=Homo sapiens GN=PML;>sp|P29590-9|PML_HUMAN Isoform 0.81 0.6 0.8 0.35 1.14 0.62 1.73 1.93 2.15E-14 3 6.1 "activation of caspase activity;aging;anatomical structure morphogenesis;biological regulation;biosynthetic process;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a tube;calcium ion homeostasis;catabolic process;cation homeostasis;cell aging;cell cycle arrest;cell cycle process;cell differentiation;cell fate commitment;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;cellular senescence;chemical homeostasis;common-partner SMAD protein phosphorylation;cytokine-mediated signaling pathway;defense response;defense response to virus;developmental process;divalent inorganic cation homeostasis;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;endoplasmic reticulum calcium ion homeostasis;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;homeostatic process;immune effector process;immune system process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;ion homeostasis;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;maintenance of location;maintenance of location in cell;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;maintenance of protein location in nucleus;metabolic process;metal ion homeostasis;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;multi-organism process;myeloid cell differentiation;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of gene expression;negative regulation of growth;negative regulation of homeostatic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitotic cell cycle;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;negative regulation of RNA metabolic process;negative regulation of telomerase activity;negative regulation of telomere maintenance;negative regulation of telomere maintenance via telomerase;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of translation;negative regulation of translation in response to oxidative stress;negative regulation of translation in response to stress;nitrogen compound metabolic process;nuclear body organization;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;nucleus organization;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;PML body organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of defense response to virus by host;positive regulation of histone deacetylation;positive regulation of histone modification;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of protein deacetylation;positive regulation of protein metabolic process;positive regulation of protein modification process;posttranscriptional regulation of gene expression;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex assembly;protein complex subunit organization;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein phosphorylation;protein stabilization;protein targeting;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome organization;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by host;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA repair;regulation of DNA replication;regulation of double-strand break repair;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of histone deacetylation;regulation of histone modification;regulation of homeostatic process;regulation of hydrolase activity;regulation of immune effector process;regulation of immune system process;regulation of ion homeostasis;regulation of ion transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of MHC class I biosynthetic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein deacetylation;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein ubiquitination;regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of proteolysis;regulation of response to biotic stimulus;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of telomerase activity;regulation of telomere maintenance;regulation of telomere maintenance via telomerase;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of translation in response to oxidative stress;regulation of translation in response to stress;regulation of transport;reproductive process;response to abiotic stimulus;response to biotic

stimulus;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to gamma radiation;response to hypoxia;response to interferon-gamma;response to ionizing radiation;response to light stimulus;response to organic substance;response to other organism;response to oxidative stress;response to oxygen levels;response to radiation;response to stimulus;response to stress;response to UV;response to virus;retinoic acid receptor signaling pathway;RNA biosynthetic process;RNA metabolic process;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;SMAD protein import into nucleus;tissue morphogenesis;transcription, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;transport;tube morphogenesis;ubiquitin-dependent protein catabolic process;viral reproductive process;virus-host interaction" binding;cation binding;cobalt ion binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein heterodimerization activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding   cell part;cytoplasm;cytoplasmic part;cytosol;early endosome membrane;endoplasmic reticulum part;endosomal part;endosome membrane;extrinsic to endoplasmic reticulum membrane;extrinsic to membrane;extrinsic to organelle membrane;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear membrane;nuclear part;nucleolus;nucleoplasm part;nucleus;organelle;organelle membrane;organelle part;PML body
Acute myeloid leukemia;Endocytosis;Pathways in cancer;Ubiquitin mediated proteolysis

F8WE65;C9J5S7;P62937;Q567Q0   Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase A   PPIA   >tr|F8WE65|F8WE65_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=2 SV=1;>tr|C9J5S7|C9J5S7_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=2 SV=1;>sp|P62937|PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo 0.47 0.83 0.63 1.21 0.99 1.82 0.73 0.84 3.01E-16 3   17.5 biological regulation;biosynthetic process;cell activation;cell migration;cell motility;cellular biosynthetic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;DNA metabolic process;DNA replication;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;establishment of localization;establishment of localization in cell;exocytosis;immune system process;interaction with host;interspecies interaction between organisms;leukocyte migration;lipid particle organization;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-proline modification;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cellular process;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of reproductive process;positive regulation of secretion;positive regulation of transport;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;protein folding;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of localization;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of reproductive process;regulation of secretion;regulation of transport;regulation of viral genome replication;regulation of viral reproduction;release of virus from host;reproductive process;RNA-dependent DNA replication;secretion;secretion by cell;transport;uncoating of virus;vesicle-mediated transport;viral reproductive process   binding;catalytic activity;cis-trans isomerase activity;isomerase activity;peptide binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;unfolded protein binding;virion binding   cell part;cytoplasmic part;cytosol;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q8WUF5 RelA-associated inhibitor   PPP1R13L   >sp|Q8WUF5|IASPP_HUMAN RelA-associated inhibitor OS=Homo sapiens GN=PPP1R13L PE=1 SV=4   NaN NaN 0.92 NaN 1.47 NaN NaN NaN 9.87E-11 3   5.9   "anatomical structure development;anatomical structure morphogenesis;apoptosis;biological regulation;biosynthetic process;camera-type eye development;cardiac chamber morphogenesis;cardiac muscle contraction;cardiac muscle tissue development;cardiac right ventricle morphogenesis;cardiac ventricle morphogenesis;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;developmental process;embryonic camera-type eye development;embryonic organ development;eye development;growth;hair cycle;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;molting cycle;multicellular organism growth;multicellular organismal homeostasis;multicellular organismal process;muscle contraction;muscle system process;muscle tissue development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;post-embryonic development;primary metabolic process;programmed cell death;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;sensory organ development;striated muscle contraction;striated muscle tissue development;system process;tissue development;transcription, DNA-dependent;ventricular cardiac muscle tissue development"   binding;protein binding;protein binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding;transcription factor binding transcription factor activity   cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q6NYC8;Q6NYC8-2 Phostensin PPP1R18 >sp|Q6NYC8|PPR18_HUMAN Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1 0.92 0.9 1.15 1.7 0.49 0.85 0.79 0.97 1.47E-13 3 9.1 cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

Q96SB3;Q9ULJ8;Q9ULJ8-4;F8W7J9;Q9ULJ8-3 Neurabin-2 PPP1R9B >sp|Q96SB3|NEB2_HUMAN Neurabin-2 OS=Homo sapiens GN=PPP1R9B PE=1 SV=2 NaN 1.63 1.35 2.07 NaN 0.65 NaN 1.24 3.63E-10 3 5.3 anatomical structure development;biological regulation;cell cycle arrest;cell cycle process;cell differentiation;cell migration;cell motility;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to alkaloid;cellular response to chemical stimulus;cellular response to isoquinoline alkaloid;cellular response to morphine;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;developmental process;filopodium assembly;locomotion;macromolecule metabolic process;metabolic process;microspike assembly;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell growth;negative regulation of cellular process;negative regulation of growth;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cell cycle process;regulation of cell growth;regulation of cell growth by extracellular stimulus;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular process;regulation of exit from mitosis;regulation of G-protein coupled receptor protein signaling pathway;regulation of growth;regulation of mitotic cell cycle;regulation of opioid receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to alkaloid;response to chemical stimulus;response to isoquinoline alkaloid;response to morphine;response to organic cyclic compound;response to organic substance;response to stimulus;RNA metabolic process;RNA processing;RNA splicing;system development binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;phosphatase binding;phosphatase inhibitor activity;phosphatase regulator activity;protein binding;protein phosphatase 1 binding;protein phosphatase binding;protein phosphatase inhibitor activity;protein phosphatase regulator activity adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoplasmic part;cytoskeleton;dendritic spine;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;leading edge membrane;macromolecular complex;membrane part;neuron projection;neuron spine;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;plasma membrane part;protein complex;protein phosphatase type 1 complex;protein serine/threonine phosphatase complex;ruffle membrane;synapse

P30044-2;P30044;P30044-3;P30044-4 "Peroxiredoxin-5, mitochondrial" PRDX5 ">sp|P30044-2|PRDX5_HUMAN Isoform Cytoplasmic+peroxisomal of Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5;>sp|P30044|PRDX5_HUMAN Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4;>sp|P30044-3|PRDX5_HUMAN Isoform 3 of Peroxiredoxin" 0.93 2.45 0.21 0.95 2.23 2.52 1.38 1.26 3.48E-07 3 20.4 "biological regulation;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;coenzyme metabolic process;cofactor metabolic process;defense response;heterocycle metabolic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;inflammatory response;metabolic process;NADP metabolic process;NADPH oxidation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of oxidoreductase activity;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase III promoter;negative regulation of transcription, DNA-dependent;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of collagen biosynthetic process;positive regulation of collagen metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal metabolic process;positive regulation of multicellular organismal process;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;reactive nitrogen species metabolic process;reactive oxygen species metabolic process;regulation of apoptosis;regulation of apoptosis involved in tissue homeostasis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of collagen biosynthetic process;regulation of collagen metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal metabolic process;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oxidoreductase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription from RNA polymerase III promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;response to wounding;small molecule metabolic process" "antioxidant activity;binding;caspase inhibitor activity;caspase regulator activity;catalytic activity;cysteine-type endopeptidase inhibitor activity;DNA binding;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;nucleic acid binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peptidase inhibitor activity;peptidase regulator activity;peroxidase activity;peroxiredoxin activity;peroxynitrite reductase activity;protein binding;protein dimerization activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase III regulatory region DNA binding;transcription regulatory region DNA binding" cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody part;mitochondrion;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;peroxisomal matrix;peroxisomal part;peroxisome;vesicle Peroxisome

O14818-2;O14818;H0Y586;Q8TAA3-2;Q8TAA3-5;Q8TAA3;O14818-4 Proteasome subunit alpha type-7;Proteasome subunit alpha type-7-like PSMA7;PSMA8 >sp|O14818-2|PSA7_HUMAN Isoform 2 of Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7;>sp|O14818|PSA7_HUMAN Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1;>tr|H0Y586|H0Y586_HUMAN Proteasome subunit alpha type-7 (Fragment) OS=Hom 0.78 1.02 0.46 0.84 0.48 0.61 1.6 1.35 3.89E-09 3 22.5 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex" Proteasome

P62195-2;P62195;J3QQM1;J3QRW1;J3QSE0;J3QLH6;J3KRP2;J3QSA9 26S protease regulatory subunit 8 PSMC5 >sp|P62195-2|PRS8_HUMAN Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5;>sp|P62195|PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1;>tr|J3QQM1|J3QQM1_HUMAN 26S protease regulatory subunit 8 (Fragment) 0.91 1.12 0.66 1.21 0.78 1.29 1.25 1.29 1.13E-13 3 10.1 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;biosynthetic process;catabolic process;cell cycle phase;cell cycle process;cell death;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of ligase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of ligase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of ligase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;transcription from RNA polymerase II promoter;transcription, DNA-dependent;ubiquitin-dependent protein catabolic process;viral reproduction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nuclear proteasome complex;nucleoplasm;organelle;organelle part;proteasome accessory complex;proteasome complex;protein complex;vesicle Proteasome

P62333;H0YJC0;H0YJE9;H0YJT1;H0YJS826S protease regulatory subunit 10B PSMC6 >sp|P62333|PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1;>tr|H0YJC0|H0YJC0_HUMAN 26S protease regulatory subunit 10B (Fragment) OS=Homo sapiens GN=PSMC6 PE=4 SV=1 0.81 1.26 0.52 0.95 0.66 1.52 1.03 1.39 3.29E-24 3 10.3 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal

transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction""adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;binding, bridging;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane;proteasome accessory complex;protein complex
Proteasome

O00231;O00231-2;J3QRY4 26S proteasome non-ATPase regulatory subunit 11 PSMD11 >sp|O00231|PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3;>sp|O00231-2|PSD11_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11;>tr|J3QRY4|J3QRY4_HUMAN 26S proteasom 0.63 1.44 0.5 1.5 0.67 1.35 1.1 1.21 9.21E-11 3 8.3 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cell differentiation;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;proteasome assembly;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;stem cell differentiation;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;protein complex Proteasome

H3BPZ1;Q9P035;H3BS72;H3BMZ1;H3BRL8;B4DRF4 Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 PTPLAD1 >tr|H3BPZ1|H3BPZ1_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 PE=2 SV=1;>sp|Q9P035|HACD3_HUMAN Very-long-chain (3R)-3-hydroxyacyl-[acyl-carrier protein] dehydratase 3 OS=Homo sapiens GN=PTPLAD1 P 1.24 1.4 2.08 1.58 0.66 0.57 0.6 0.86 8.84E-11 3 9.5 activation of JUN kinase activity;activation of MAPK activity;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;fatty acid biosynthetic process;fatty acid metabolic process;I-kappaB kinase/NF-kappaB cascade;intracellular protein kinase cascade;intracellular signal transduction;JNK cascade;lipid biosynthetic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of JUN kinase activity;positive regulation of kinase activity;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;Rac protein signal transduction;Ras protein signal transduction;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;response to stimulus;response to stress;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction;small molecule biosynthetic process;small molecule metabolic process;stress-activated protein kinase signaling cascade catalytic activity;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;lyase activity;nucleoside-triphosphatase regulator activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part

B4DSN5;P18031 Tyrosine-protein phosphatase non-receptor type;Tyrosine-protein phosphatase non-receptor type 1 PTPN1 >tr|B4DSN5|B4DSN5_HUMAN Tyrosine-protein phosphatase non-receptor type OS=Homo sapiens GN=PTPN1 PE=2 SV=1;>sp|P18031|PTN1_HUMAN Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 1.03 1.68 1.78 0.61 0.91 0.65 1.66 0.92 1.30E-64 3 8.8 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;biological regulation;cell activation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;cellular response to topologically incorrect protein;cellular response to type I interferon;cellular response to unfolded protein;cytokine-mediated signaling pathway;cytoskeleton organization;dephosphorylation;endoplasmic reticulum unfolded protein response;enzyme linked receptor protein signaling pathway;ER-nucleus signaling pathway;insulin receptor signaling pathway;interferon-gamma-mediated signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of insulin receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle organization;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;platelet activation;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of cell communication;regulation of cellular component organization;regulation of cellular process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of endocytosis;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of insulin receptor signaling pathway;regulation of interferon-gamma-mediated signaling pathway;regulation of localization;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of type I interferon-mediated signaling pathway;regulation of vesicle-mediated transport;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to endoplasmic reticulum stress;response to hormone stimulus;response to insulin stimulus;response to interferon-gamma;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;response to topologically incorrect protein;response to type I interferon;response to unfolded protein;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;type I interferon-mediated signaling pathway "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein tyrosine phosphatase activity;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;early endosome;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;vesicle Adherens junction;Insulin signaling pathway

Q9Y3E5;J3KQ48 "Peptidyl-tRNA hydrolase 2, mitochondrial" PTRH2 ">sp|Q9Y3E5|PTH2_HUMAN Peptidyl-tRNA hydrolase 2, mitochondrial OS=Homo sapiens GN=PTRH2 PE=1 SV=1;>tr|J3KQ48|J3KQ48_HUMAN Peptidyl-tRNA hydrolase 2, mitochondrial OS=Homo sapiens GN=PTRH2 PE=4 SV=1" 1.03 0.86 1.53 0.41 1.05 1.1 1.21 1.4 2.05E-63 3 31.8 apoptosis;biological regulation;cell death;cellular process;death;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;positive regulation of anoikis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;programmed cell death;regulation of anoikis;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of programmed cell death "aminoacyl-tRNA hydrolase activity;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle

Q6IQ22 Ras-related protein Rab-12 RAB12 >sp|Q6IQ22|RAB12_HUMAN Ras-related protein Rab-12 OS=Homo sapiens GN=RAB12 PE=1 SV=3 NaN NaN 0.94 0.91 1.24 1.22 NaN NaN 1.15E-30 3 14.8 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein catabolic process;cellular protein metabolic process;cellular response to stimulus;endosome to lysosome transport;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular signal transduction;intracellular transport;lysosomal transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein catabolic process;protein metabolic process;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vacuolar transport;vesicle-mediated transport binding;GDP binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic part;endosomal part;endosome membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lysosomal membrane;lysosome;lytic vacuole;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;recycling endosome membrane;vacuolar membrane;vacuolar part;vacuole

P57735 Ras-related protein Rab-25 RAB25 >sp|P57735|RAB25_HUMAN Ras-related protein Rab-25 OS=Homo sapiens GN=RAB25 PE=1 SV=2 0.8 0.83 0.49 0.25 2.81 2.45 1.31 1.01 2.67E-20 3 19.7 biological regulation;cell projection organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;establishment of localization;establishment of protein localization;intracellular signal transduction;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;protein transport;pseudopodium organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane part;pseudopodium;pseudopodium membrane;vesicle

P20337;O95716;P20336;Q96E17;M0R257 Ras-related protein Rab-3B;Ras-related protein Rab-3D;Ras-related protein Rab-3A;Ras-related protein Rab-3C RAB3B;RAB3D;RAB3A;RAB3C >sp|P20337|RAB3B_HUMAN Ras-related protein Rab-3B OS=Homo sapiens GN=RAB3B PE=1 SV=2;>sp|O95716|RAB3D_HUMAN Ras-related protein Rab-3D OS=Homo sapiens GN=RAB3D PE=1 SV=1;>sp|P20336|RAB3A_HUMAN Ras-related protein Rab-3A OS=Homo sapiens GN=RAB3A PE=1 SV=1;>1 1.44 1.23 0.84 1.39 1.27 1.18 0.8 2.24E-34 3 16.9 anatomical structure development;anatomical structure morphogenesis;axonogenesis;biological regulation;cell communication;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell signaling;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;developmental maturation;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;glutamate secretion;intracellular signal transduction;lung development;macromolecule metabolic process;macromolecule methylation;macromolecule modification;maintenance of presynaptic active zone structure;metabolic process;methylation;mitochondrion organization;multicellular organismal process;neurological system process;neuromuscular synaptic transmission;neuron projection morphogenesis;neurotransmitter secretion;neurotransmitter transport;one-carbon metabolic process;organ development;organelle organization;peptidyl-amino acid modification;peptidyl-cysteine methylation;peptidyl-cysteine modification;post-embryonic development;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of localization;regulation of multicellular organismal process;regulation of neurological system process;regulation of neurotransmitter levels;regulation of neurotransmitter secretion;regulation of neurotransmitter transport;regulation of organelle organization;regulation of secretion;regulation of signaling;regulation of synaptic transmission;regulation of synaptic vesicle exocytosis;regulation of synaptic vesicle fusion to presynaptic membrane;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;regulation of vesicle fusion;regulation of vesicle-mediated transport;respiratory gaseous exchange;respiratory system process;response to abiotic stimulus;response to electrical stimulus;response to stimulus;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of touch;signal release;signal transduction;signaling;small GTPase mediated signal transduction;small molecule metabolic process;synaptic transmission;synaptic vesicle exocytosis;synaptic vesicle maturation;synaptic vesicle transport;system process;transport;vesicle organization;vesicle-mediated transport "ATPase activator activity;ATPase regulator activity;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleoside-triphosphatase regulator activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" acrosomal vesicle;cell part;clathrin coated vesicle membrane;clathrin sculpted acetylcholine transport vesicle membrane;clathrin sculpted gamma-aminobutyric acid transport vesicle membrane;clathrin sculpted glutamate transport vesicle membrane;clathrin sculpted monoamine transport vesicle membrane;clathrin-coated vesicle;coated vesicle;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;organelle membrane;organelle part;plasma membrane;protein complex;stored secretory granule;synapse part;synaptic vesicle;transport vesicle;transport vesicle membrane;vesicle;vesicle membrane;zymogen granule Pancreatic secretion;Tight junction

P11234;Q6ZS74;B4E040;C9J6B1 Ras-related protein Ral-B RALB >sp|P11234|RALB_HUMAN Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=1 SV=1;>tr|Q6ZS74|Q6ZS74_HUMAN Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=2 SV=1;>tr|B4E040|B4E040_HUMAN Ras-related protein Ral-B OS=Homo sapiens GN=RALB PE=2 SV=1;>tr|C9 NaN NaN NaN NaN NaN NaN NaN NaN 4.75E-09 3 18 apoptosis;biological regulation;cell cycle;cell death;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cytokinesis;death;enzyme linked receptor protein signaling pathway;intracellular signal transduction;nerve growth factor receptor signaling pathway;programmed cell death;Ras protein signal transduction;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of exocyst assembly;regulation of exocyst localization;regulation of exocytosis;regulation of localization;regulation of protein complex assembly;regulation of protein localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;membrane;midbody;plasma membrane Pancreatic cancer;Pathways in cancer

P49792;P0DJD0;J3QTV4;P0DJD1;F8VYC4;Q7Z3J3;A6NKT7;J3KNY6;J3KNE0 E3 SUMO-protein ligase RanBP2;Putative peptidyl-prolyl cis-trans isomerase RANBP2 >sp|P49792|RBP2_HUMAN E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 NaN NaN 0.9 0.79 1.26 1.08 NaN NaN 4.96E-05 3 1.2 "anaphase;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular

macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;establishment of RNA localization;glucose transport;Golgi vesicle transport;hexose transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA transport;nuclear import;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;organic substance transport;peptidyl-amino acid modification;peptidyl-proline modification;primary metabolic process;protein folding;protein import;protein import into nucleus;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein peptidyl-prolyl isomerization;protein sumoylation;protein targeting;protein targeting to Golgi;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;retrograde transport, vesicle recycling within Golgi;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;vesicle-mediated transport;viral reproductive process"   binding;catalytic activity;cation binding;cis-trans isomerase activity;enzyme binding;GTPase binding;ion binding;isomerase activity;ligase activity;metal ion binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;Ran GTPase binding;Ras GTPase binding;small GTPase binding;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;cytosol;inclusion body;intracellular organelle part;intracellular part;membrane;nuclear inclusion body;nuclear membrane;nuclear part;organelle membrane;organelle part   RNA transport
P61225;F6U784;P10114 Ras-related protein Rap-2b;Ras-related protein Rap-2a RAP2B;RAP2A   >sp|P61225|RAP2B_HUMAN Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1;>tr|F6U784|F6U784_HUMAN Ras-related protein Rap-2a OS=Homo sapiens GN=RAP2A PE=2 SV=1;>sp|P10114|RAP2A_HUMAN Ras-related protein Rap-2a OS=Homo sapiens GN=RAP2A PE=1 SV=1   1.06 1.51 1.53 0.76 1.11 0.76 0.75 0.81 1.06E-23 3   18   actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to stimulus;cytoskeleton organization;establishment of localization;establishment of protein localization;intracellular signal transduction;localization;macromolecule localization;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;organelle organization;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein autophosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;protein localization;Rap protein signal transduction;Ras protein signal transduction;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of catalytic activity;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein autophosphorylation;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein tyrosine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;response to stimulus;signal transduction;small GTPase mediated signal transduction   "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"   cell part;cytoplasmic part;cytosol;endosomal part;endosome membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;recycling endosome membrane
Q8TC12;G3V2G6;G3V234;Q8TC12-3;Q8TC12-2;H0YJ10;H0YIZ8;H0YJ46   Retinol dehydrogenase 11   RDH11   >sp|Q8TC12|RDH11_HUMAN Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2;>tr|G3V2G6|G3V2G6_HUMAN Retinol dehydrogenase 11 (Fragment) OS=Homo sapiens GN=RDH11 PE=2 SV=1;>tr|G3V234|G3V234_HUMAN Retinol dehydrogenase 11 (Fragment) OS=Homo sapiens GN   0.9   0.6   1.3   0.22 2.47 1.32 1.44 1.15 2.62E-20 3   12.3 "adaptation of rhodopsin mediated signaling;adaptation of signaling pathway;apocarotenoid metabolic process;biological regulation;cellular aldehyde metabolic process;cellular hormone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;diterpenoid metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;fat-soluble vitamin metabolic process;hormone metabolic process;intracellular protein transport;intracellular transport;isoprenoid metabolic process;lipid metabolic process;metabolic process;oxidation-reduction process;phototransduction;phototransduction, visible light;primary metabolic process;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of hormone levels;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinal metabolic process;retinoid metabolic process;retinol metabolic process;signal transduction;small molecule metabolic process;terpenoid metabolic process;transport;vesicle-mediated transport;vitamin A metabolic process;vitamin metabolic process"   "alcohol dehydrogenase (NADP+) activity;aldo-keto reductase (NADP) activity;catalytic activity;NADP-retinol dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;retinol dehydrogenase activity"   cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part;photoreceptor inner segment   Retinol metabolism

Q5T093;Q5T092;Q5T091;O15258 Protein RER1 RER1 >tr|Q5T093|Q5T093_HUMAN Protein RER1 OS=Homo sapiens GN=RER1 PE=2 SV=1;>tr|Q5T092|Q5T092_HUMAN Protein RER1 (Fragment) OS=Homo sapiens GN=RER1 PE=2 SV=1;>tr|Q5T091|Q5T091_HUMAN Protein RER1 OS=Homo sapiens GN=RER1 PE=2 SV=1;>sp|O15258|RER1_HUMAN Protein RE 1.44 0.94 1.56 0.82 0.82 0.85 1.27 1.04 1.28E-09 3 25.6 "cellular process;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle-mediated transport" cell part;cytoplasmic part;Golgi apparatus part;integral to Golgi membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to Golgi membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane part;organelle part

P13489;E9PMJ3;E9PLZ3;E9PIM9;E9PMA9;E9PMN0;E9PIK5;H0YCR7 Ribonuclease inhibitor RNH1 >sp|P13489|RINI_HUMAN Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2;>tr|E9PMJ3|E9PMJ3_HUMAN Ribonuclease H1 (Fragment) OS=Homo sapiens GN=RNH1 PE=2 SV=1;>tr|E9PLZ3|E9PLZ3_HUMAN Ribonuclease H1 (Fragment) OS=Homo sapiens GN=RNH1 PE=2 SV=1;>tr|E9P 0.86 NaN 1.11 0.26 2.72 2.05 1.4 NaN 1.78E-11 3 8.9 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;RNA catabolic process;RNA metabolic process enzyme inhibitor activity;enzyme regulator activity;ribonuclease inhibitor activity angiogenin-PRI complex;cell part;cytoplasm;extracellular region part;intracellular part;macromolecular complex;protein complex

P62913-2;P62913;Q5VVC9;Q5VVC8 60S ribosomal protein L11 RPL11 >sp|P62913-2|RL11_HUMAN Isoform 2 of 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11;>sp|P62913|RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2;>tr|Q5VVC9|Q5VVC9_HUMAN 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 1.3 0.87 1.45 0.74 1.31 0.82 1.16 0.78 1.36E-71 3 16.9 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein localization;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;localization;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein localization;protein localization to nucleus;protein localization to organelle;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

M0R3D6;M0R1A7;M0R117;Q02543;M0R0P7 60S ribosomal protein L18a RPL18A >tr|M0R3D6|M0R3D6_HUMAN 60S ribosomal protein L18a (Fragment) OS=Homo sapiens GN=RPL18A PE=4 SV=1;>tr|M0R1A7|M0R1A7_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=3 SV=1;>tr|M0R117|M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=R 1.33 0.61 0.52 0.6 1.06 0.87 1.46 0.95 9.97E-09 3 18.4 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

K7ERI7;P35268;K7EJT5;K7EP65;K7EKS7;K7ELC4;K7EMH160S ribosomal protein L22 RPL22 >tr|K7ERI7|K7ERI7_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=4 SV=1;>sp|P35268|RL22_HUMAN 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2;>tr|K7EJT5|K7EJT5_HUMAN 60S ribosomal protein L22 (Fragment) OS=Homo sapiens GN=RPL22 PE 1.49 0.85 1.06 0.7 1.15 0.7 1.35 0.69 2.09E-09 3 41.1 "alpha-beta T cell activation;alpha-beta T cell differentiation;biosynthetic process;catabolic process;cell activation;cell differentiation;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;immune system process;intracellular protein transport;intracellular transport;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;T cell activation;T cell differentiation;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;nucleic acid binding;pattern binding;polysaccharide binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P62829;J3KTJ3;C9JD32;J3KT29;J3QQT9;B9ZVP7 60S ribosomal protein L23 RPL23 >sp|P62829|RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1;>tr|J3KTJ3|J3KTJ3_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=3 SV=1;>tr|C9JD32|C9JD32_HUMAN 60S ribosomal protein L23 (Fragment) OS=Homo sapiens GN=RPL23 PE 1.75 0.93 0.74 0.57 0.8 0.54 1.05 0.72 6.72E-07 3 18.6 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear import;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein import;protein import into nucleus;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribosomal protein import into nucleus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P46779;P46779-2;P46779-3;H0YKD8;P46779-4;P46779-5;H0YLP6;H0YMF460S ribosomal protein L28 RPL28 >sp|P46779|RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3;>sp|P46779-2|RL28_HUMAN Isoform 2 of 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28;>sp|P46779-3|RL28_HUMAN Isoform 3 of 60S ribosomal protein L28 OS=Homo sapiens GN=RPL 1.15 0.76 0.3 0.57 1.26 0.75 1.41 0.95 2.30E-12 3 21.9 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P47914 60S ribosomal protein L29 RPL29 >sp|P47914|RL29_HUMAN 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 1.36 0.62 0.44 0.86 1.04 0.58 1.5 1.09 1.01E-15 3 18.9 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;embryo implantation;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;nucleic acid binding;pattern binding;polysaccharide binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

P49207 60S ribosomal protein L34 RPL34 >sp|P49207|RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 1.25 0.68 0.33 0.62 1.18 0.94 1.47 0.98 7.81E-08 3 20.5 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

J3KT73;J3QL01;P63173;J3KSP2;M0QYY5;E0CX11;Q9Y2S6;A8MXR1;Q9Y2C4-3;Q9H7B4-2;Q9Y2C4-4;Q9Y2C4;Q9H7B4-3;Q9H7B4;Q15172-2;Q15172;A2A3P3;Q5SZL2;Q5SZL2-4;REV__B8ZZW2 60S ribosomal protein L38 RPL38 >tr|J3KT73|J3KT73_HUMAN 60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=3 SV=1;>tr|J3QL01|J3QL01_HUMAN 60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=3 SV=1;>sp|P63173|RL38_HUMAN 60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2;>tr 1.5 0.81 0.83 0.46 1.19 0.92 1.1 0.76 2.20E-08 3 35.9 "anatomical structure morphogenesis;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;cotranslational protein targeting to membrane;covalent chromatin modification;developmental process;embryonic morphogenesis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;histone lysine methylation;histone methylation;histone modification;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;middle ear morphogenesis;mRNA catabolic process;mRNA metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of establishment of protein localization in plasma membrane;negative regulation of kinase activity;negative regulation of lipid kinase activity;negative regulation of lipid metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of transferase activity;neurological system process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;ossification;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of dephosphorylation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;primary metabolic process;protein alkylation;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein methylation;protein modification process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of kinase activity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of transferase activity;reproductive process;response to stimulus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal transduction;small molecule metabolic process;SRP-dependent cotranslational protein targeting to membrane;system process;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" "binding;catalytic activity;cation binding;endonuclease activity;enzyme regulator activity;histone methyltransferase activity;histone-lysine N-methyltransferase activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lysine N-methyltransferase activity;metal ion binding;methyltransferase activity;N-methyltransferase activity;nuclease activity;nucleic acid binding;phosphatase regulator activity;protein methyltransferase activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein-lysine N-methyltransferase activity;RNA binding;S-adenosylmethionine-dependent methyltransferase activity;structural constituent of ribosome;structural molecule activity;transferase activity;transferase activity, transferring one-carbon groups;transition metal ion binding;zinc ion binding" "cell part;centrosome;chromosomal part;chromosome, centromeric region;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosolic large ribosomal subunit;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;M band;macromolecular complex;membrane;membrane-bounded organelle;microtubule organizing center;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex;ribonucleoprotein complex;ribosome;Z disc" Apoptosis;Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;Ribosome;Wnt signaling pathway

P46777;Q5T7N0 60S ribosomal protein L5 RPL5 >sp|P46777|RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 1.17 0.54 0.37 0.38 1.23 0.7 2.25 1.05 1.81E-10 3 11.1 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" 5S rRNA binding;binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P25398 40S ribosomal protein S12 RPS12 >sp|P25398|RS12_HUMAN 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 1.22 0.69 1.22 0.51 0.98 0.7 1.87 1.11 2.22E-06 3 30.3 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytosolic small ribosomal subunit;intracellular organelle part;intracellular part;macromolecular complex;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome

P62263;H0YB22;E5RH77 40S ribosomal protein S14 RPS14 >sp|P62263|RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3;>tr|H0YB22|H0YB22_HUMAN 40S ribosomal protein S14 (Fragment) OS=Homo sapiens GN=RPS14 PE=4 SV=1;>tr|E5RH77|E5RH77_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE1.82 1.11 0.78 0.64 0.9 0.67 0.96 0.7 1.73E-22 3 22.5 "biological regulation;biosynthetic process;catabolic process;cell differentiation;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;erythrocyte differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maturation of SSU-rRNA;metabolic process;mRNA catabolic process;mRNA metabolic process;myeloid cell differentiation;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity;translation regulator activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

I3L3P7;P62244;I3L246;H3BN98;H3BVC7 40S ribosomal protein S15a RPS15A >tr|I3L3P7|I3L3P7_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=2 SV=1;>sp|P62244|RS15A_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2;>tr|I3L246|I3L246_HUMAN 40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=2 S1.48 0.87 1.11 0.58 1.48 0.89 1.16 0.86 4.69E-21 3 31 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell cycle;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cell cycle;regulation of cell proliferation;regulation of cellular process;reproductive process;response to biotic stimulus;response to other organism;response to stimulus;response to virus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

Q86WX3;F8WFE7 Active regulator of SIRT1 RPS19BP1 >sp|Q86WX3|AROS_HUMAN Active regulator of SIRT1 OS=Homo sapiens GN=RPS19BP1 PE=1 SV=1 NaN NaN 1.58 2.05 0.42 0.34 NaN NaN 1.53E-09 3 27.9 cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part

P62266;D6RDJ2;D6RIX0;D6R9I7;D6RD47 40S ribosomal protein S23 RPS23 >sp|P62266|RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3;>tr|D6RDJ2|D6RDJ2_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=2 SV=1;>tr|D6RIX0|D6RIX0_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=2 SV=1;>tr 1.86 0.94 0.27 0.58 0.71 0.57 1.09 0.71 5.05E-11 3 21 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

P62851 40S ribosomal protein S25 RPS25 >sp|P62851|RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 1.66 1.01 0.82 0.57 0.74 0.7 1.14 0.73 2.24E-24 3 22.4 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome

M0QZN2;M0R0F0;P46782;M0R0R2 "40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed" RPS5 >tr|M0QZN2|M0QZN2_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=4 SV=1;>tr|M0R0F0|M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=3 SV=1;>sp|P46782|RS5_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 1.22 0.95 1.06 0.68 1.08 0.88 1.14 0.79 8.18E-08 3 26.1 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic small ribosomal subunit;intracellular organelle part;intracellular part;macromolecular complex;organelle part;ribonucleoprotein complex;small ribosomal subunitRibosome

P56182;D6RE82 Ribosomal RNA processing protein 1 homolog A RRP1 >sp|P56182|RRP1_HUMAN Ribosomal RNA processing protein 1 homolog A OS=Homo sapiens GN=RRP1 PE=1 SV=1 1.13 1.33 0.88 2.16 0.57 0.48 0.56 0.6 5.96E-10 3 8.5 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing "cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;preribosome, small subunit precursor;ribonucleoprotein complex"

Q14684-2;Q14684 Ribosomal RNA processing protein 1 homolog B RRP1B >sp|Q14684-2|RRP1B_HUMAN Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B;>sp|Q14684|RRP1B_HUMAN Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 1.28 1.32 1.32 1.93 0.39 0.44 0.63 0.54 1.55E-12 3 5.9 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing "cell part;chromatin;chromosomal part;cytoplasmic part;cytosol;euchromatin;heterochromatin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;preribosome, small subunit precursor;ribonucleoprotein complex"

Q9Y265;Q9Y265-2;J3QLR1;H7C4G5;E7ETR0 RuvB-like 1 RUVBL1>sp|Q9Y265|RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1;>sp|Q9Y265-2|RUVB1_HUMAN Isoform 2 of RuvB-like 1 OS=Homo sapiens GN=RUVBL1 1.01 0.9 1.04 0.81 0.99 0.85 1.17 0.84 9.10E-07 3 9.6 "ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell division;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;covalent chromatin modification;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA recombination;DNA repair;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;gamete generation;histone acetylation;histone exchange;histone H2A acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;mitosis;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle fission;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;spermatogenesis;transcription, DNA-dependent" "5'-3' DNA helicase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent 5'-3' DNA helicase activity;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromatin remodeling complex;chromosomal part;cytoplasmic part;cytoskeletal part;DNA helicase complex;Golgi apparatus;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;histone methyltransferase complex;Ino80 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;methyltransferase complex;microtubule organizing center;MLL1 complex;NuA4 histone acetyltransferase complex;nuclear chromosome part;nuclear matrix;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex Wnt signaling pathway

Q9Y512;A8MZI2 Sorting and assembly machinery component 50 homolog SAMM50 >sp|Q9Y512|SAM50_HUMAN Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3;>tr|A8MZI2|A8MZI2_HUMAN Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=2 SV=2 0.6 1.72 0.08 0.23 0.06 0.1 0.51 1.53 4.16E-14 3 11.7 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;organelle organization;outer mitochondrial membrane organization;primary metabolic process;protein import;protein import into mitochondrial outer membrane;protein metabolic process;protein targeting;protein targeting to membrane;protein targeting to mitochondrion;protein transport;transport cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial sorting and assembly machinery complex;organelle inner membrane;organelle membrane;organelle part;outer membrane;protein complex

P49591;Q5T5C7 "Serine--tRNA ligase, cytoplasmic" SARS ">sp|P49591|SYSC_HUMAN Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3;>tr|Q5T5C7|Q5T5C7_HUMAN Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=2 SV=1" 0.42 NaN NaN NaN NaN NaN 0.52 NaN 4.63E-06 3 5.3 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;RNA processing;selenocysteinyl-tRNA(Sec) biosynthetic process;seryl-tRNA aminoacylation;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tRNA processing "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;serine-tRNA ligase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Aminoacyl-tRNA biosynthesis

O00767 Acyl-CoA desaturase SCD>sp|O00767|ACOD_HUMAN Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2 1.34 1.9 1.73 1.11 0.66 0.28 0.75 0.54 4.70E-42 3 10.9 biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid biosynthetic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process"binding;catalytic activity;cation binding;CoA desaturase activity;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water;stearoyl-CoA 9-desaturase activity;transition metal ion binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Biosynthesis of unsaturated fatty acids;PPAR signaling pathway

Q8WVM8;B7Z5N7;Q8WVM8-2;Q8WVM8-3;B7Z738;G3V4I1;G3V363;H0YJS6;G3V5F3;J3KNG4;G3V2M8 Sec1 family domain-containing protein 1 SCFD1 >sp|Q8WVM8|SCFD1_HUMAN Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4;>tr|B7Z5N7|B7Z5N7_HUMAN Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=2 SV=1;>sp|Q8WVM8-2|SCFD1_HUMAN Isoform 2 of Sec1 family domain-co NaN 2.85 NaN 2 NaN 0.75 NaN 1.01 1.96E-06 3 6.9 "biological regulation;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;membrane docking;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of ER to Golgi vesicle-mediated transport;regulation of intracellular transport;regulation of localization;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;response to toxin;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle-mediated transport" binding;protein binding;SNARE binding;syntaxin binding cell part;cis-Golgi network;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi transport complex;Golgi-associated vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane;protein complex;vesicle

P18827;E9PHH3;H7C1K4 Syndecan-1 SDC1 >sp|P18827|SDC1_HUMAN Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3 1.58 1.16 1.38 0.67 0.84 0.51 1.22 1.03 1.68E-16 3 15.2 "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;canonical Wnt receptor signaling pathway;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell development;cell surface receptor linked signaling pathway;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;developmental process involved in reproduction;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;lipoprotein metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;muscle cell development;myoblast development;nitrogen compound metabolic process;odontogenesis;organ morphogenesis;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to abiotic stimulus;response to calcium ion;response to cAMP;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to light stimulus;response to metal ion;response to organic substance;response to oxidative stress;response to radiation;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;response to toxin;response to wounding;retinoid metabolic process;Sertoli cell development;signal transduction;striated muscle cell development;sulfur compound metabolic process;terpenoid metabolic process;tube development;ureteric bud development;Wnt receptor signaling pathway;wound healing" adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;external side of plasma membrane;extracellular region;focal adhesion;Golgi apparatus part;Golgi lumen;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane part;protein complex;vacuolar lumen;vacuolar part Cell adhesion molecules (CAMs);ECM-receptor interaction;Malaria

H0YNX5;B4DUL4;H0YNG3;H0YK72;P67812;H0YK83;H0YNA5;H0YKT4;P0C7V7 Signal peptidase complex catalytic subunit SEC11A SEC11A;SEC11L1 ">tr|H0YNX5|H0YNX5_HUMAN Signal peptidase complex catalytic subunit SEC11A (Fragment) OS=Homo sapiens GN=SEC11A PE=2 SV=1;>tr|B4DUL4|B4DUL4_HUMAN SEC11-like 1 (S. cerevisiae), isoform CRA_d OS=Homo sapiens GN=SEC11A PE=2 SV=1;>tr|H0YNG3|H0YNG3_HUMAN Signal" 1.11 1.19 1.69 1.23 0.56 0.61 0.76 0.89 7.75E-08 3 24.5 biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;peptide metabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;proteolysis;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;signal peptide processing;SRP-dependent cotranslational protein targeting to membrane;translation;transport "catalytic activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type peptidase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Protein export

O75396 Vesicle-trafficking protein SEC22b SEC22B >sp|O75396|SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 0.89 0.93 1.41 0.52 1.6 1.04 1.16 1.24 2.74E-29 3 14 cellular process;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;vesicle Phagosome;SNARE interactions in vesicular transport

P60468 Protein transport protein Sec61 subunit beta SEC61B >sp|P60468|SC61B_HUMAN Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2 1.36 1.34 2.45 0.86 0.8 0.44 0.97 1.09 4.47E-13 3 37.5 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;ER-associated protein catabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;immune system process;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein import into nucleus, translocation;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;retrograde protein transport, ER to cytosol;SRP-dependent cotranslational protein targeting to membrane;translation;transport;ubiquitin-dependent protein catabolic process" cell part;cytoplasmic part;endoplasmic reticulum part;endoplasmic reticulum Sec complex;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;organelle part;protein complex Phagosome;Protein export;Protein processing in endoplasmic reticulum;Vibrio cholerae infection

Q9UBV2;Q9UBV2-2 Protein sel-1 homolog 1 SEL1L >sp|Q9UBV2|SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3;>sp|Q9UBV2-2|SE1L1_HUMAN Isoform 2 of Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L NaN NaN 1.5 NaN 2.58 NaN NaN NaN 6.00E-08 3 7.9 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cellular response to stress;Notch signaling pathway;regulation of biological process;regulation of cellular process;response to endoplasmic reticulum stress;response to stimulus;response to stress;signal transduction cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Protein processing in endoplasmic reticulum

Q01105-3;Q01105-4;Q01105-2;Q01105 Protein SET SET >sp|Q01105-3|SET_HUMAN Isoform 3 of Protein SET OS=Homo sapiens GN=SET;>sp|Q01105-4|SET_HUMAN Isoform 4 of Protein SET OS=Homo sapiens GN=SET;>sp|Q01105-2|SET_HUMAN Isoform 2 of Protein SET OS=Homo sapiens GN=SET;>sp|Q01105|SET_HUMAN Protein SET OS=Homo sa 0.68 0.88 0.42 0.77 0.36 0.4 2.86 1.52 2.27E-11 3 13.2 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;DNA metabolic process;DNA replication;establishment of localization;establishment of localization in cell;gene expression;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of histone acetylation;negative regulation of histone modification;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron apoptosis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of peptidyl-lysine acetylation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;nucleosome assembly;nucleosome disassembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of gene expression;regulation of histone acetylation;regulation of histone modification;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-lysine acetylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA metabolic process;transport" binding;DNA binding;enzyme inhibitor activity;enzyme regulator activity;histone binding;nucleic acid binding;phosphatase inhibitor activity;phosphatase regulator activity;protein binding;protein phosphatase inhibitor activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity cell part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;perinuclear region of cytoplasm;protein complex

P53007;B4DP62 "Tricarboxylate transport protein, mitochondrial" SLC25A1 ">sp|P53007|TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2;>tr|B4DP62|B4DP62_HUMAN Solute carrier family 25 (Mitochondrial carrier;citrate transporter), member 1, isoform CRA_b OS=Homo sapiens GN=SLC25A1 PE=" 0.96 1.16 1.71 1.74 0.61 0.61 0.66 1.02 1.84E-10 3 11.3 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;alcohol biosynthetic process;alcohol metabolic process;anion transport;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid transport;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;citrate transport;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;establishment of localization;establishment of localization in cell;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;gluconeogenesis;glucose metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;hexose biosynthetic process;hexose metabolic process;intracellular transport;ion transport;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;mitochondrial citrate transport;mitochondrial transport;monosaccharide biosynthetic process;monosaccharide metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid transport;organic anion transport;organic ether metabolic process;organic substance transport;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;transport;tricarboxylic acid transport;triglyceride biosynthetic process;triglyceride metabolic process carboxylic acid transmembrane transporter activity;citrate transmembrane transporter activity;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;tricarboxylic acid transmembrane transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

E9PS95;E9PJH7;Q9H936;Q9H1K4;K4DIA8;K4DIA2;K4DIB0;K4DIB2;E9PQ36;K4DIB8;E9PI74;K4DIB3 Mitochondrial glutamate carrier 1;Mitochondrial glutamate carrier 2 SLC25A22;SLC25A18 >tr|E9PS95|E9PS95_HUMAN Mitochondrial glutamate carrier 1 (Fragment) OS=Homo sapiens GN=SLC25A22 PE=2 SV=1;>tr|E9PJH7|E9PJH7_HUMAN Mitochondrial glutamate carrier 1 (Fragment) OS=Homo sapiens GN=SLC25A22 PE=2 SV=1;>sp|Q9H936|GHC1_HUMAN Mitochondrial glutam 0.97 NaN 0.96 NaN 0.51 NaN 0.78 NaN 1.69E-05 3 12.2 cellular process;establishment of localization;transmembrane transport;transport acidic amino acid transmembrane transporter activity;active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;carboxylic acid transmembrane transporter activity;L-amino acid transmembrane transporter activity;L-glutamate transmembrane transporter activity;organic acid transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part

F8VVM2;Q00325-2;Q00325;F8VZL5;F8VWR4;F8VWQ0 "Phosphate carrier protein, mitochondrial" SLC25A3 ">tr|F8VVM2|F8VVM2_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=2 SV=1;>sp|Q00325-2|MPCP_HUMAN Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3;>sp|Q00325|MPCP_HUMAN Phosphate carrier protein," 0.66 1.26 1.74 1.67 0.71 0.43 0.57 1 5.67E-09 3 10.5 cellular metabolic process;cellular process;establishment of localization;generation of precursor metabolites and energy;metabolic process;transport active transmembrane transporter activity;anion transmembrane transporter activity;inorganic anion transmembrane transporter activity;ion transmembrane transporter activity;phosphate ion carrier activity;phosphate ion transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane part

Q14683;G8JLG1 Structural maintenance of chromosomes protein 1A SMC1A >sp|Q14683|SMC1A_HUMAN Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2 NaN NaN NaN 0.49 NaN 0.29 NaN NaN 2.30E-05 3 2 "anaphase;biological regulation;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome condensation;chromosome organization;cytokinesis;cytoskeleton organization;developmental process;DNA conformation change;DNA metabolic process;DNA packaging;DNA recombination;DNA repair;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;meiosis;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;mitotic sister chromatid cohesion;mitotic spindle organization;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA endoreduplication;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA endoreduplication;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to abiotic stimulus;response to DNA damage stimulus;response to radiation;response to stimulus;response to stress;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction in response to DNA damage;sister chromatid cohesion;spindle organization;stem cell maintenance" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;chromatin binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromosomal part;chromosome;cohesin complex;cohesin core heterodimer;condensed chromosome;condensed chromosome kinetochore;condensed nuclear chromosome;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;meiotic cohesin complex;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleoplasm;organelle;organelle part;protein complex Cell cycle;Cell cycle - yeast;Meiosis - yeast;Oocyte meiosis

Q96Q15-4;Q96Q15-3;Q96Q15-2;J3KRA9;Q96Q15;I3L0C1;H3BQN7 Serine/threonine-protein kinase SMG1 SMG1 >sp|Q96Q15-4|SMG1_HUMAN Isoform 4 of Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1;>sp|Q96Q15-3|SMG1_HUMAN Isoform 3 of Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1;>sp|Q96Q15-2|SMG1_HUMAN Isoform 2 of Serine/threonine-protei NaN NaN 0.63 NaN 1.98 NaN NaN NaN 4.98E-05 3 1.6 "catabolic process;cellular catabolic process;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;establishment of localization;establishment of localization in cell;establishment of RNA localization;gene expression;glycerolipid metabolic process;glycerophospholipid metabolic process;intracellular transport;lipid metabolic process;lipid modification;lipid phosphorylation;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;organophosphate metabolic process;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphatidylinositol metabolic process;phosphatidylinositol phosphorylation;phospholipid metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;response to DNA damage stimulus;response to stimulus;response to stress;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA transport;transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle mRNA surveillance pathway

P62316;K7ERG4;P62316-2;K7EJB5 Small nuclear ribonucleoprotein Sm D2 SNRPD2 >sp|P62316|SMD2_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1;>tr|K7ERG4|K7ERG4_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=4 SV=1;>sp|P62316-2|SMD2_HUMAN Isoform 2 of Small nuclear ribonucleop 1.12 1.14 1.29 1.61 0.4 0.42 0.94 0.93 3.21E-08 3 32.2 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA processing;RNA splicing;spliceosomal snRNP assembly;spliceosome assembly catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome

P61009 Signal peptidase complex subunit 3 SPCS3 >sp|P61009|SPCS3_HUMAN Signal peptidase complex subunit 3 OS=Homo sapiens GN=SPCS3 PE=1 SV=1 1.12 0.62 1.71 1 0.69 0.54 1 0.36 2.69E-14 3 17.8 biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;peptide metabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;proteolysis;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;signal peptide processing;SRP-dependent cotranslational protein targeting to membrane;translation;transport catalytic activity;hydrolase activity;peptidase activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;protein complex;signal peptidase complex Protein export

O76094-2;O76094;P15514;D6RFX5;D6RDY6;REV__A6NIV6 Signal recognition particle subunit SRP72 SRP72 >sp|O76094-2|SRP72_HUMAN Isoform 2 of Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72;>sp|O76094|SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3 NaN NaN 0.45 NaN 1.7 NaN NaN NaN 6.63E-08 3 7 biological regulation;biosynthetic process;cell communication;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cotranslational protein targeting to membrane;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;G-protein coupled receptor protein signaling pathway;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to chemical stimulus;response to drug;response to stimulus;signal transduction;signaling;SRP-dependent cotranslational protein targeting to membrane;translation;transmembrane receptor protein tyrosine kinase signaling pathway;transport 7S RNA binding;binding;growth factor activity;nucleic acid binding;protein binding;receptor binding;ribonucleoprotein binding;RNA binding;signal recognition particle binding "cell part;cell surface;cytoplasmic part;cytosol;endoplasmic reticulum;extracellular region part;extracellular space;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;ribonucleoprotein complex;signal recognition particle;signal recognition particle, endoplasmic reticulum targeting" ErbB signaling pathway;Protein export

O75494-5;Q5JRI1;O75494-4;O75494-6;O75494-3;O75494-2;O75494;Q8WXF0 Serine/arginine-rich splicing factor 10;Serine/arginine-rich splicing factor 12 SRSF10;SRSF12 >sp|O75494-5|SRS10_HUMAN Isoform 5 of Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10;>tr|Q5JRI1|Q5JRI1_HUMAN Serine/arginine-rich-splicing factor 10 OS=Homo sapiens GN=SRSF10 PE=2 SV=1;>sp|O75494-4|SRS10_HUMAN Isoform 4 of Serine/arginin 1.38 0.96 1.23 1.57 0.51 0.45 0.98 0.85 2.78E-10 3 20 "assembly of spliceosomal tri-snRNP;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cytoplasmic transport;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;mRNA export from nucleus;mRNA splice site selection;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nuclear export;nuclear mRNA 5'-splice site recognition;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of transcription, DNA-dependent;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA export from nucleus;RNA transport;transport" binding;nucleic acid binding;nucleotide binding;protein binding;protein domain specific binding;RNA binding;RS domain binding;unfolded protein binding cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle partSpliceosome

B4E241;P84103 Serine/arginine-rich splicing factor 3 SRSF3 >tr|B4E241|B4E241_HUMAN Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1;>sp|P84103|SRSF3_HUMAN Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 1.31 0.94 1.28 NaN 0.6 NaN 1.21 0.58 2.81E-54 3 28.2 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part Spliceosome

C9JA28;Q9UNL2;B4E2P2;C9J365 Translocon-associated protein subunit gamma SSR3 >tr|C9JA28|C9JA28_HUMAN Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=2 SV=1;>sp|Q9UNL2|SSRG_HUMAN Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=1 SV=1;>tr|B4E2P2|B4E2P2_HUMAN Translocon-associated protein 1.15 1.24 1.66 1.17 0.63 0.58 0.82 1.01 6.30E-20 3 16.1 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;SRP-dependent cotranslational protein targeting to membrane;translation;transport cell part;cytoplasmic part;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane part;organelle part;protein complex;Sec61 translocon complex;translocon complex Protein processing in endoplasmic reticulum

P42224;P42224-2;J3KPM9;E7EPD2;D2KFR9 Signal transducer and activator of transcription 1-alpha/betaSTAT1 >sp|P42224|STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2;>sp|P42224-2|STAT1_HUMAN Isoform Beta of Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1;>tr|J3KP NaN 1.73 0.92 1.41 2.34 1.51 NaN 0.97 1.02E-05 3 4.9 "anatomical structure development;biological regulation;biosynthetic process;blood circulation;cell differentiation;cell differentiation involved in kidney development;cell differentiation involved in metanephros development;cell proliferation;cell proliferation involved in kidney development;cell proliferation involved in metanephros development;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-beta;cellular response to interferon-gamma;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to organic substance;cellular response to stimulus;cellular response to tumor necrosis factor;cellular response to type I interferon;circulatory system process;cytokine-mediated signaling pathway;defense response;defense response to virus;developmental process;immune effector process;immune system process;induction of apoptosis;induction of programmed cell death;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;kidney mesenchymal cell proliferation;lipopolysaccharide-mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;mesenchymal cell differentiation;mesenchymal cell differentiation involved in kidney development;mesenchymal cell differentiation involved in renal system development;mesenchymal cell proliferation;metabolic process;metanephric mesenchymal cell differentiation;metanephric mesenchymal cell proliferation involved in metanephros development;multicellular organismal process;multi-organism process;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell morphogenesis involved in differentiation;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell differentiation;negative regulation of epithelial cell differentiation involved in kidney development;negative regulation of epithelial cell proliferation;negative regulation of gene expression;negative regulation of I-kappaB kinase/NF-kappaB cascade;negative regulation of intracellular protein kinase cascade;negative regulation of kidney development;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis;negative regulation of metabolic process;negative regulation of metanephric nephron tubule epithelial cell differentiation;negative regulation of multicellular organismal process;negative regulation of nephron tubule epithelial cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of smooth muscle cell proliferation;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of developmental process;regulation of endothelial cell proliferation;regulation of epithelial cell differentiation;regulation of epithelial cell differentiation involved in kidney development;regulation of epithelial cell proliferation;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-gamma-mediated signaling pathway;regulation of intracellular protein kinase cascade;regulation of kidney development;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of mesenchymal cell proliferation;regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis;regulation of metabolic process;regulation of metanephric nephron tubule epithelial cell differentiation;regulation of metanephros development;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nephron tubule epithelial cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of smooth muscle cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of type I interferon-mediated signaling pathway;renal tubule development;reproductive process;response to biotic stimulus;response to cAMP;response to chemical stimulus;response to cytokine stimulus;response to dsRNA;response to exogenous dsRNA;response to interferon-beta;response to interferon-gamma;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;response to tumor necrosis factor;response to type I interferon;response to virus;RNA biosynthetic process;RNA metabolic process;signal transduction;system process;transcription, DNA-dependent;tube development;tumor necrosis factor-mediated signaling pathway;type I interferon-mediated signaling pathway;viral reproductive process;virus-host interaction"	binding;calcium ion binding;cation binding;core promoter binding;core promoter proximal region DNA binding;core promoter proximal region sequence-specific DNA binding;core promoter sequence-specific DNA binding;DNA binding;double-stranded DNA binding;identical protein binding;ion binding;metal ion binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein dimerization activity;protein homodimerization activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding;RNA polymerase II core promoter sequence-specific DNA binding;RNA polymerase II core promoter sequence-specific DNA binding transcription factor activity;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;signal transducer activity;structure-specific DNA binding;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding	axon;cell part;cell projection;chromatin;chromosomal part;cytoplasm;cytoplasmic part;cytosol;dendrite;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part	Chemokine signaling pathway;Hepatitis C;Jak-STAT signaling pathway;ko05152;Leishmaniasis;Measles;Osteoclast differentiation;Pancreatic cancer;Pathways in cancer;Toll-like receptor signaling pathway;Toxoplasmosis

E9PNJ4;Q13586;H0YDB2;E9PQJ4;E9PIQ8	Stromal interaction molecule 1	STIM1	>tr|E9PNJ4|E9PNJ4_HUMAN Stromal interaction molecule 1 OS=Homo sapiens GN=STIM1 PE=2 SV=1;>sp|Q13586|STIM1_HUMAN Stromal interaction molecule 1 OS=Homo sapiens GN=STIM1 PE=1 SV=3;>tr|H0YDB2|H0YDB2_HUMAN Stromal interaction molecule 1 (Fragment) OS=Homo sap	NaN	NaN	1.32	NaN	0.84	NaN	NaN	NaN	4.97E-10	3	8.4	activation of store-operated calcium channel activity;biological regulation;blood coagulation;calcium ion transport;cation transport;coagulation;detection of calcium ion;detection of chemical stimulus;detection of stimulus;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;hemostasis;ion transport;metal ion transport;multicellular organismal process;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of calcium ion transport via store-operated calcium channel activity;positive regulation of ion transmembrane transporter activity;positive regulation of ion transport;positive regulation of molecular function;positive regulation of transport;positive regulation of transporter activity;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of calcium ion transport;regulation of calcium ion transport via store-operated calcium channel activity;regulation of cellular process;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of molecular function;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;transport binding;calcium ion binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;microtubule binding;microtubule plus-end binding;protein binding;tubulin binding cell cortex part;cell part;cortical endoplasmic reticulum;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;membrane-bounded organelle;microtubule;organelle;organelle part;plasma membrane part;protein complex

O94901-6;O94901-8;O94901;E9PHI4;O94901-9;A4D2Q0;E7EP45;H0Y6N5;O94901-5;H0Y742;C9JR15;O94901-4;C9JS54;C9JJU6;C9K051;H7C019;C9JK55;O94901-2;O94901-7;O94901-3;H7C2K3 SUN domain-containing protein 1 SUN1;UNC84A >sp|O94901-6|SUN1_HUMAN Isoform 6 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1;>sp|O94901-8|SUN1_HUMAN Isoform 8 of SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1;>sp|O94901|SUN1_HUMAN SUN domain-containing protein 1 OS=Homo sapiens NaN 1.54 1.82 NaN 0.39 NaN NaN 0.62 2.60E-07 3 4.4 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cytoskeletal anchoring at nuclear membrane;cytoskeleton organization;maintenance of location;maintenance of location in cell;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;maintenance of protein location in nucleus;membrane organization;nuclear envelope organization;nuclear matrix anchoring at nuclear membrane;nuclear matrix organization;nucleus organization;organelle organization;regulation of biological quality acrosomal membrane;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;integral to membrane;integral to nuclear inner membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to nuclear inner membrane;intrinsic to organelle membrane;macromolecular complex;membrane;membrane part;nuclear inner membrane;nuclear membrane;nuclear membrane part;nuclear part;organelle inner membrane;organelle membrane;organelle part;protein complex;secretory granule membrane;SUN-KASH complex;vesicle membrane

Q16563-2;C9JYN0;Q16563 Synaptophysin-like protein 1 SYPL1 >sp|Q16563-2|SYPL1_HUMAN Isoform 2 of Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1;>tr|C9JYN0|C9JYN0_HUMAN Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=2 SV=1;>sp|Q16563|SYPL1_HUMAN Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 0.75 0.99 1.62 0.63 0.56 0.85 1.09 1.18 3.56E-10 3 19.5 cell communication;cell-cell signaling;cellular process;signaling;synaptic transmission transporter activity cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;stored secretory granule;synapse part;synaptic vesicle;vesicle;vesicle membrane

P02786;G3V0E5;F8WBE5;F5H6B1 "Transferrin receptor protein 1;Transferrin receptor protein 1, serum form" TFRC ">sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2;>tr|G3V0E5|G3V0E5_HUMAN Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=2 SV=1" NaN NaN 0.4 NaN 1.29 NaN NaN NaN 1.07E-07 3 5.7 biological regulation;cation homeostasis;cation transport;cell differentiation;cellular cation homeostasis;cellular chemical homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;chemical homeostasis;developmental process;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;leukocyte differentiation;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;multi-organism process;myeloid cell differentiation;myeloid leukocyte differentiation;osteoclast differentiation;positive regulation of biological process;positive regulation of bone remodeling;positive regulation of bone resorption;positive regulation of homeostatic process;positive regulation of multicellular organismal process;positive regulation of tissue remodeling;primary metabolic process;protein metabolic process;protein transport;proteolysis;regulation of biological process;regulation of biological quality;regulation of bone remodeling;regulation of bone resorption;regulation of homeostatic process;regulation of multicellular organismal process;regulation of tissue remodeling;reproductive process;transferrin transport;transition metal ion transport;transmembrane transport;transport;viral reproductive process;virus-host interaction cargo receptor activity;catalytic activity;hydrolase activity;peptidase activity;receptor activity;transferrin receptor activity cell part;coated pit;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endosome;external side of plasma membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region;extracellular region part;extracellular vesicular exosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;perinuclear region of cytoplasm;pigment granule;plasma membrane part;vesicle Endocytosis;Hematopoietic cell lineage;Phagosome

Q3ZCQ8;Q3ZCQ8-2;M0R0C3;M0R2F8;Q330K1;M0R047 Mitochondrial import inner membrane translocase subunit TIM50 TIMM50 >sp|Q3ZCQ8|TIM50_HUMAN Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2;>sp|Q3ZCQ8-2|TIM50_HUMAN Isoform 2 of Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50;>tr|M0R0C 1.54 1.4 2.26 0.9 1.05 0.53 0.94 1.2 8.05E-35 3 9.9 apoptotic mitochondrial changes;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;membrane organization;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;organelle organization;protein import;protein targeting;protein targeting to mitochondrion;protein transport;release of cytochrome c from mitochondria;transport "binding;catalytic activity;cytokine receptor binding;growth factor receptor binding;hydrolase activity;hydrolase activity, acting on ester bonds;interleukin-2 receptor binding;nucleic acid binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein binding;protein serine/threonine phosphatase activity;protein tyrosine phosphatase activity;receptor binding;ribonucleoprotein binding;RNA binding" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;mitochondrial inner membrane presequence translocase complex;mitochondrial membrane part;mitochondrial part;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex

Q9UDY2-6;Q9UDY2-3;Q9UDY2;Q9UDY2-7;Q9UDY2-5;Q9UDY2-4;Q9UDY2-2 Tight junction protein ZO-2 TJP2 >sp|Q9UDY2-6|ZO2_HUMAN Isoform 6 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2;>sp|Q9UDY2-3|ZO2_HUMAN Isoform C1 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2;>sp|Q9UDY2|ZO2_HUMAN Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 S NaN NaN NaN NaN NaN NaN NaN NaN 1.48E-07 3 3.5 biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;hippo signaling cascade;intracellular signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction "catalytic activity;guanylate kinase activity;kinase activity;nucleobase-containing compound kinase activity;nucleotide kinase activity;phosphotransferase activity, phosphate group as acceptor;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;membrane;nuclear part;nucleoplasm;occluding junction;organelle part;plasma membrane;tight junction Tight junction;Vibrio cholerae infection

Q99805 Transmembrane 9 superfamily member 2 TM9SF2 >sp|Q99805|TM9S2_HUMAN Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1 1.42 1.26 2.01 0.51 0.79 0.48 0.92 0.99 4.32E-11 3 4.7 establishment of localization;transport cell part;cytoplasmic part;endosomal part;endosome;endosome membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part

F5GX39;Q15363;E7EQ72 Transmembrane emp24 domain-containing protein 2 TMED2 >tr|F5GX39|F5GX39_HUMAN Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=2 SV=1;>sp|Q15363|TMED2_HUMAN Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=1 SV=1 1.14 0.9 2.03 0.78 0.93 0.55 1.15 2.17 5.12E-25 3 25.9 anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;anterior/posterior axis specification;axis specification;biological regulation;cargo loading into vesicle;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;COPI coating of Golgi vesicle;COPII vesicle coating;developmental process;embryonic axis specification;embryonic organ development;embryonic pattern specification;embryonic placenta development;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;Golgi organization;Golgi transport vesicle coating;growth;heart looping;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;maternal placenta development;multicellular organism growth;multicellular organismal process;negative regulation of catalytic activity;negative regulation of GTPase activity;negative regulation of hydrolase activity;negative regulation of molecular function;neural tube closure;organ development;organelle organization;pattern specification process;positive regulation of biological process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;protein complex assembly;protein complex subunit organization;protein targeting;protein targeting to plasma membrane;protein transport;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;somite rostral/caudal axis specification;transport;tube closure;tube formation;tube morphogenesis;vesicle coating;vesicle organization cell part;coated vesicle;coated vesicle membrane;COPI coated vesicle membrane;COPI-coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi-associated vesicle;Golgi-associated vesicle membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;secretory granule membrane;vesicle;vesicle membrane;zymogen granule membrane

Q9H061;E9PI90;E9PIH8;Q9H061-2 Transmembrane protein 126A TMEM126A >sp|Q9H061|T126A_HUMAN Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=1 SV=1;>tr|E9PI90|E9PI90_HUMAN Transmembrane protein 126A OS=Homo sapiens GN=TMEM126A PE=2 SV=1 NaN 0.73 1.93 0.77 1.4 0.6 NaN 1.11 2.69E-06 3 14.4 anatomical structure development;cranial nerve development;developmental process;nerve development;optic nerve development cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle

Q9HC07;B4DHW1;D6RBL0;D6RD79 Transmembrane protein 165 TMEM165 >sp|Q9HC07|TM165_HUMAN Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=1 SV=1;>tr|B4DHW1|B4DHW1_HUMAN Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=2 SV=1 1.3 1.43 2.02 1.09 0.93 0.42 0.85 0.93 2.88E-23 3 16.4 cell part;cytoplasmic part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle

Q9NYL9;H0YKU1;H0YNJ8;H0YNU8 Tropomodulin-3 TMOD3 >sp|Q9NYL9|TMOD3_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1;>tr|H0YKU1|H0YKU1_HUMAN Tropomodulin-3 (Fragment) OS=Homo sapiens GN=TMOD3 PE=4 SV=1;>tr|H0YNJ8|H0YNJ8_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=2 SV=1 0.88 0.77 0.71 0.68 0.81 1.22 1.28 1.44 3.43E-96 3 13.4 binding;cytoskeletal protein binding;protein binding;tropomyosin binding cell part;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;striated muscle thin filament

C9JE12;C9JCW7;Q9BVT8 Transmembrane and ubiquitin-like domain-containing protein 1 TMUB1 >tr|C9JE12|C9JE12_HUMAN Transmembrane and ubiquitin-like domain-containing protein 1 (Fragment) OS=Homo sapiens GN=TMUB1 PE=2 SV=1;>tr|C9JCW7|C9JCW7_HUMAN Transmembrane and ubiquitin-like domain-containing protein 1 (Fragment) OS=Homo sapiens GN=TMUB1 PE=2 NaN NaN 1.94 NaN 1.57 NaN NaN NaN 7.21E-06 3 33.6 cell part;cytoplasm;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;nucleus;organelle

Q9H3N1;G3V448 Thioredoxin-related transmembrane protein 1 TMX1 >sp|Q9H3N1|TMX1_HUMAN Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1 0.76 NaN 1.57 0.22 1.81 1.39 1.24 NaN 7.48E-07 3 11.1 "biological regulation;biosynthetic process;cell activation;cell proliferation;cell redox homeostasis;cellular biosynthetic process;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;DNA metabolic process;DNA replication;electron transport chain;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;Golgi vesicle transport;homeostatic process;immune system process;intracellular transport;leukocyte activation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oxidation-reduction process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of growth;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;response to stress;signal transduction;transport;vesicle-mediated transport" "arsenate reductase (thioredoxin) activity;arsenate reductase activity;catalytic activity;disulfide oxidoreductase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part

Q92973-3;Q92973-2;Q92973;B4DSC0;E7EW37;O14787-2 Transportin-1 TNPO1 >sp|Q92973-3|TNPO1_HUMAN Isoform 3 of Transportin-1 OS=Homo sapiens GN=TNPO1;>sp|Q92973-2|TNPO1_HUMAN Isoform 2 of Transportin-1 OS=Homo sapiens GN=TNPO1;>sp|Q92973|TNPO1_HUMAN Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2 0.85 1.55 0.65 1.46 1.27 0.95 1.03 1.16 4.10E-06 3 5 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;gene expression;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mRNA metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein import into nucleus, translocation;protein transport;reproductive process;RNA metabolic process;transport;viral reproductive process;virus-host interaction" binding;nuclear localization sequence binding;peptide binding;protein transporter activity;signal sequence binding;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;nuclear part;nuclear pore;nucleus;organelle;organelle part;pore complex;protein complex

Q9NS69 Mitochondrial import receptor subunit TOM22 homolog TOMM22 >sp|Q9NS69|TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3 1.01 1.72 1.48 1.94 0.44 0.56 0.5 0.98 7.38E-25 3 40.8 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;organelle organization;outer mitochondrial membrane organization;primary metabolic process;protein import;protein import into mitochondrial outer membrane;protein metabolic process;protein targeting;protein targeting to membrane;protein targeting to mitochondrion;protein transport;transport macromolecule transmembrane transporter activity;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial outer membrane translocase complex;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex

P62995-3;P62995;H7BXF3;H7C2L4 Transformer-2 protein homolog beta TRA2B >sp|P62995-3|TRA2B_HUMAN Isoform 3 of Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B;>sp|P62995|TRA2B_HUMAN Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1;>tr|H7BXF3|H7BXF3_HUMAN Transformer-2 protein homolog beta (Fragm 1.27 0.94 1.11 2.01 0.5 0.61 0.81 0.74 6.05E-14 3 19.7 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Spliceosome

Q14258 E3 ubiquitin/ISG15 ligase TRIM25 TRIM25 >sp|Q14258|TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 1.02 NaN 0.93 0.42 2.07 1.09 1.58 NaN 1.31E-08 3 5.6 biological regulation;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of type I interferon production;regulation of biological process;regulation of cytokine production;regulation of multicellular organismal process;regulation of type I interferon production;reproductive process;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus;viral reproductive process;virus-host interaction "acid-amino acid ligase activity;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell junction;cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle RIG-I-like receptor signaling pathway

K7ENG2;P26368-2;P26368 Splicing factor U2AF 65 kDa subunit U2AF2 >tr|K7ENG2|K7ENG2_HUMAN Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=4 SV=1;>sp|P26368-2|U2AF2_HUMAN Isoform 2 of Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2;>sp|P26368|U2AF2_HUMAN Splicing factor U2AF 65 kDa subunit OS= 1.27 0.92 1.12 1.05 0.74 0.86 1.23 1.11 1.65E-17 3 15.3 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

Q9NQZ2 Something about silencing protein 10 UTP3 >sp|Q9NQZ2|SAS10_HUMAN Something about silencing protein 10 OS=Homo sapiens GN=UTP3 PE=1 SV=1 NaN NaN 0.86 2.8 0.68 0.4 NaN NaN 1.23E-11 3 10.6 anatomical structure development;brain development;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chromatin modification;chromatin organization;chromosome organization;developmental process;organ development;organelle organization cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

Q9GZL7 Ribosome biogenesis protein WDR12 WDR12 >sp|Q9GZL7|WDR12_HUMAN Ribosome biogenesis protein WDR12 OS=Homo sapiens GN=WDR12 PE=1 SV=2 NaN NaN 1.84 NaN 0.79 NaN NaN NaN 3.02E-13 3 11.1 "biological regulation;cell proliferation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;macromolecule metabolic process;maturation of 5.8S rRNA;maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);maturation of LSU-rRNA;maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;Notch signaling pathway;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;signal transduction" "cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleolar part;nucleoplasm;organelle part;PeBoW complex;preribosome;preribosome, large subunit precursor;protein complex;ribonucleoprotein complex"

Q7Z2W4-2;Q7Z2W4;Q7Z2W4-3;C9J6P4 Zinc finger CCCH-type antiviral protein 1 ZC3HAV1 >sp|Q7Z2W4-2|ZCCHV_HUMAN Isoform 2 of Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1;>sp|Q7Z2W4|ZCCHV_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3;>sp|Q7Z2W4-3|ZCCHV_HUMAN Isoform 3 of Zinc fing 1.52 0.91 1.13 0.66 0.75 0.61 1.21 0.82 2.59E-09 3 6.6 biological regulation;cellular process;cellular response to chemical stimulus;cellular response to dsRNA;cellular response to exogenous dsRNA;cellular response to organic substance;cellular response to stimulus;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;multi-organism process;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of interferon-alpha production;positive regulation of interferon-beta production;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA catabolic process;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of type I interferon production;regulation of biological process;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of interferon-alpha production;regulation of interferon-beta production;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA catabolic process;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of type I interferon production;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus "binding;catalytic activity;cation binding;ion binding;metal ion binding;NAD+ ADP-ribosyltransferase activity;nucleic acid binding;RNA binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane

O75844 CAAX prenyl protease 1 homolog ZMPSTE24 >sp|O75844|FACE1_HUMAN CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2 1.13 1.06 1.52 0.92 0.75 0.71 0.83 0.91 1.50E-34 3 6.3 CAAX-box protein processing;catabolic process;cellular catabolic process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;membrane organization;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nuclear envelope organization;prenylated protein catabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;proteolysis involved in cellular protein catabolic process "binding;catalytic activity;cation binding;endopeptidase activity;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part

Q9UHI8 A disintegrin and metalloproteinase with thrombospondin motifs 1 ADAMTS1 >sp|Q9UHI8|ATS1_HUMAN A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Homo sapiens GN=ADAMTS1 PE=1 SV=4 1.92 1.47 0.84 NaN 0.47 NaN 0.79 2.22 1.02E-13 4 6.6 anatomical structure development;anatomical structure formation involved in morphogenesis;biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;developmental process;heart trabecula formation;integrin-mediated signaling pathway;kidney development;macromolecule metabolic process;metabolic process;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;organ development;ovulation;ovulation cycle process;ovulation from ovarian follicle;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of cell proliferation;regulation of cellular process;reproductive process;response to stimulus;rhythmic process;signal transduction;trabecula formation "binding;carbohydrate binding;catalytic activity;cation binding;endopeptidase activity;glycosaminoglycan binding;heparin binding;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;pattern binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;polysaccharide binding;transition metal ion binding;zinc ion binding" basement membrane;cell part;cytoplasmic part;cytoplasmic vesicle;extracellular matrix part;extracellular region part;intracellular organelle;intracellular part;organelle;vesicle

Q04828;P52895;H0Y804;B4DK69;P52895-2;A6NHU4;P42330;B4DL37;P17516 Aldo-keto reductase family 1 member C1;Aldo-keto reductase family 1 member C2;Aldo-keto reductase family 1 member C3 AKR1C1;AKR1C2;AKR1C3 >sp|Q04828|AK1C1_HUMAN Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1;>sp|P52895|AK1C2_HUMAN Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3;>tr|H0Y804|H0Y804_HUMAN Aldo-keto reductase family 1 member 0.99 0.2 0.84 NaN 3.24 NaN 1.49 0.78 5.55E-12 4 14.6 "alcohol catabolic process;alcohol metabolic process;anatomical structure development;androgen biosynthetic process;androgen metabolic process;apocarotenoid metabolic process;arachidonic acid metabolic process;bile acid and bile salt transport;bile acid biosynthetic process;bile acid metabolic process;biological regulation;biosynthetic process;C21-steroid hormone metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;catabolic process;cell communication;cell differentiation;cellular aldehyde metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to cadmium ion;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to corticosteroid stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to hormone stimulus;cellular response to inorganic substance;cellular response to jasmonic acid stimulus;cellular response to lipid;cellular response to metal ion;cellular response to nutrient levels;cellular response to organic substance;cellular response to oxidative stress;cellular response to prostaglandin stimulus;cellular response to reactive oxygen species;cellular response to starvation;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to stress;chemical homeostasis;cholesterol homeostasis;cholesterol transport;cyclooxygenase pathway;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;developmental process involved in reproduction;digestion;digestive system process;diterpenoid metabolic process;epidermal cell differentiation;epithelial cell differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;farnesol catabolic process;farnesol metabolic process;fat-soluble vitamin metabolic process;fatty acid metabolic process;gonad development;homeostatic process;hormone biosynthetic process;hormone metabolic process;icosanoid metabolic process;intestinal absorption;intestinal cholesterol absorption;intracellular protein transport;intracellular transport;isoprenoid catabolic process;isoprenoid metabolic process;keratinocyte differentiation;lipid biosynthetic process;lipid catabolic process;lipid homeostasis;lipid metabolic process;lipid transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;male gonad development;metabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;organ development;organic acid biosynthetic process;organic acid metabolic process;organic acid transport;organic substance transport;oxoacid metabolic process;phototransduction;phototransduction, visible light;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of endothelial cell apoptosis;positive regulation of intracellular protein kinase cascade;positive regulation of metabolic process;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of reactive oxygen species metabolic process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary alcohol catabolic process;primary alcohol metabolic process;primary metabolic process;progesterone metabolic process;prostaglandin metabolic process;prostanoid metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein import into nucleus, translocation;protein oligomerization;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of endothelial cell apoptosis;regulation of hormone biosynthetic process;regulation of hormone levels;regulation of hormone metabolic process;regulation of intracellular protein kinase cascade;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of reactive oxygen species metabolic process;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of signal transduction;regulation of signaling;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of testosterone biosynthetic process;renal absorption;renal system process;reproductive process;reproductive structure development;response to abiotic stimulus;response to cadmium ion;response to calcium ion;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to inorganic substance;response to insecticide;response to jasmonic acid stimulus;response to light stimulus;response to lipid;response to metal ion;response to nutrient;response to nutrient levels;response to organic substance;response to organophosphorus;response to oxidative stress;response to prostaglandin stimulus;response to radiation;response to reactive oxygen species;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;response to toxin;retinal metabolic process;retinoid metabolic process;sesquiterpene catabolic process;sesquiterpene metabolic process;sesquiterpenoid catabolic process;sesquiterpenoid metabolic process;signal transduction;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol homeostasis;sterol transport;system process;terpene catabolic process;terpene metabolic process;terpenoid catabolic process;terpenoid metabolic process;testosterone biosynthetic process;transport;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process;vitamin A metabolic process;vitamin metabolic process;xenobiotic metabolic process" "15-hydroxyprostaglandin-D dehydrogenase (NADP+) activity;17-alpha,20-alpha-dihydroxypregn-4-en-3-one dehydrogenase activity;alcohol dehydrogenase (NADP+) activity;alditol:NADP+ 1-oxidoreductase activity;aldo-keto reductase (NADP) activity;androsterone dehydrogenase (A-specific) activity;androsterone dehydrogenase (B-specific) activity;androsterone dehydrogenase activity;bile acid binding;bile acid transmembrane transporter activity;binding;carboxylic acid binding;carboxylic acid transmembrane transporter activity;catalytic activity;chlordecone reductase activity;delta4-3-oxosteroid 5beta-reductase activity;dihydrotestosterone 17-beta-dehydrogenase activity;electron carrier activity;enone reductase activity;geranylgeranyl reductase activity;G-protein coupled receptor activity;icosanoid receptor activity;indanol dehydrogenase activity;ketoreductase activity;ketosteroid monooxygenase activity;lipid binding;molecular transducer activity;monocarboxylic acid binding;monocarboxylic acid transmembrane transporter activity;monooxygenase activity;organic acid transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;phenanthrene 9,10-monooxygenase activity;prostaglandin F receptor activity;prostaglandin receptor activity;prostaglandin-F synthase activity;prostanoid receptor activity;receptor activity;retinal dehydrogenase activity;retinol dehydrogenase activity;signal transducer activity;signaling receptor activity;steroid binding;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;testosterone 17-beta-dehydrogenase (NADP+) activity;testosterone dehydrogenase (NAD+) activity;trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity;transmembrane signaling receptor activity;transmembrane transporter activity;transporter activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Arachidonic acid metabolism;Metabolism of xenobiotics by cytochrome P450;Primary bile acid biosynthesis;Steroid hormone biosynthesis

P30038-2;D2D4A3;P30038 "Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial" ALDH4A1 ">sp|P30038-2|AL4A1_HUMAN Isoform 2 of Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1;>tr|D2D4A3|D2D4A3_HUMAN Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=2 SV=1;>sp|P300" NaN NaN 2.2 NaN 3.11 NaN NaN NaN 6.19E-16 4 9.7 4-hydroxyproline catabolic process;4-hydroxyproline metabolic process;amine biosynthetic process;amine catabolic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid catabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutamate metabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;proline biosynthetic process;proline catabolic process;proline catabolic process to glutamate;proline metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "1-pyrroline-5-carboxylate dehydrogenase activity;aldehyde dehydrogenase (NAD) activity;catalytic activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-NH group of donors;oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism"

O75342 "Arachidonate 12-lipoxygenase, 12R-type" ALOX12B ">sp|O75342|LX12B_HUMAN Arachidonate 12-lipoxygenase, 12R-type OS=Homo sapiens GN=ALOX12B PE=1 SV=1" 1.19 1.01 1.19 0.52 3.82 3.77 1.14 1.14 8.14E-14 4 6.7 alkene biosynthetic process;anatomical structure development;arachidonic acid metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular alkene metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;developmental process;epidermis development;fatty acid biosynthetic process;fatty acid metabolic process;icosanoid biosynthetic process;icosanoid metabolic process;leukotriene biosynthetic process;leukotriene metabolic process;lipid biosynthetic process;lipid metabolic process;lipoxygenase pathway;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;tissue development;unsaturated fatty acid biosynthetic process;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process "arachidonate 12-lipoxygenase activity;binding;catalytic activity;cation binding;dioxygenase activity;ion binding;iron ion binding;lipoxygenase activity;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;transition metal ion binding" cell part;cytoplasmic part;cytosol;intracellular part Arachidonic acid metabolism

O95782-2;O95782;O94973-3;M0R2D9;E9PR62 AP-2 complex subunit alpha-1 AP2A1 >sp|O95782-2|AP2A1_HUMAN Isoform B of AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1;>sp|O95782|AP2A1_HUMAN AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3;>sp|O94973-3|AP2A2_HUMAN Isoform 3 of AP-2 complex subunit alpha-2 OS=Homo sa NaN NaN 0.46 NaN 1.29 NaN NaN NaN 2.98E-10 4 5 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;endocytosis;endosome transport;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi to endosome transport;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;locomotion;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of epidermal growth factor receptor signaling pathway;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;synaptic transmission;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport;viral reproduction protein transporter activity;substrate-specific transporter activity;transporter activity AP-2 adaptor complex;apical plasma membrane;AP-type membrane coat adaptor complex;basolateral plasma membrane;cell part;clathrin adaptor complex;clathrin coat;clathrin coat of trans-Golgi network vesicle;clathrin vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;plasma membrane part;protein complex;vesicle coat Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease

Q07960;H0YE29 Rho GTPase-activating protein 1 ARHGAP1 >sp|Q07960|RHG01_HUMAN Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1;>tr|H0YE29|H0YE29_HUMAN Rho GTPase-activating protein 1 (Fragment) OS=Homo sapiens GN=ARHGAP1 PE=4 SV=1 0.82 0.78 NaN 0.19 NaN 2.17 1.36 0.66 3.14E-13 4 13.2 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;Ras protein signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction "binding;binding, bridging;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;protein binding, bridging;Rac GTPase activator activity;Ras GTPase activator activity;Rho GTPase activator activity;SH3/SH2 adaptor activity;signaling adaptor activity;small GTPase regulator activity"cell part;cell projection;cytoplasmic part;cytosol;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle;plasma membrane;ruffle

Q9BPX5 Actin-related protein 2/3 complex subunit 5-like protein ARPC5L >sp|Q9BPX5|ARP5L_HUMAN Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens GN=ARPC5L PE=1 SV=1 0.89 1.6 1.3 2.32 0.41 0.59 0.52 1.04 1.31E-50 4 41.2 biological regulation;cellular component organization;cellular component organization or biogenesis;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis

E9PBU3;P31939;F5GWY2;C9JLK0;F8WEF0;H7C084 Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimidazolecarboxamide formyltransferase;IMP cyclohydrolase ATIC >tr|E9PBU3|E9PBU3_HUMAN Phosphoribosylaminoimidazolecarboxamide formyltransferase OS=Homo sapiens GN=ATIC PE=2 SV=1;>sp|P31939|PUR9_HUMAN Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3;>tr|F5GWY2|F5GWY2_HUMAN Phosphoribosyl NaN NaN 0.41 NaN 0.95 NaN NaN NaN 6.36E-23 4 10.3 anatomical structure development;anatomical structure morphogenesis;aromatic compound biosynthetic process;biosynthetic process;brainstem development;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cerebellum development;cerebral cortex development;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;'de novo' IMP biosynthetic process;developmental process;dihydrofolate metabolic process;folic acid-containing compound biosynthetic process;folic acid-containing compound metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organ morphogenesis;organ regeneration;primary metabolic process;pteridine-containing compound biosynthetic process;pteridine-containing compound metabolic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regeneration;response to chemical stimulus;response to inorganic substance;response to stimulus;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;tetrahydrofolate biosynthetic process;tetrahydrofolate metabolic process "catalytic activity;cyclohydrolase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;hydroxymethyl-, formyl- and related transferase activity;IMP cyclohydrolase activity;phosphoribosylaminoimidazolecarboxamide formyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle One carbon pool by folate;Purine metabolism

F5H6I7;Q6DD88;C9JUU1;F5GWF8 Atlastin-3ATL3 >tr|F5H6I7|F5H6I7_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=2 SV=1;>sp|Q6DD88|ATLA3_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1;>tr|C9JUU1|C9JUU1_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=2 SV=1 0.49 0.56 0.88 0.23 2.48 2.33 1.26 1.71 5.04E-16 4 9.2 catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;endoplasmic reticulum organization;Golgi organization;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part

P18859;P18859-2;A8MUH2 "ATP synthase-coupling factor 6, mitochondrial" ATP5J ">sp|P18859|ATP5J_HUMAN ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1;>sp|P18859-2|ATP5J_HUMAN Isoform 2 of ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J;>tr|A8MUH2|A8MUH2_HUMAN ATP synthase-coupli" 1.3 1.68 2.19 1.37 0.5 0.38 0.73 0.89 1.28E-139 4 30.6 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity "cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);mitochondrion;organelle;organelle part;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain"Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

J3QL14;R4GN72;P61421;F5GYQ1 V-type proton ATPase subunit d 1 ATP6V0D1 >tr|J3QL14|J3QL14_HUMAN V-type proton ATPase subunit d 1 (Fragment) OS=Homo sapiens GN=ATP6V0D1 PE=4 SV=1;>tr|R4GN72|R4GN72_HUMAN V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=4 SV=1;>sp|P61421|VA0D1_HUMAN V-type proton ATPase subunit d 1 1.14 NaN 1.13 1.22 1.04 1.41 0.99 NaN 1.19E-18 4 17.7 "activation of signaling protein activity involved in unfolded protein response;anatomical structure development;ATP hydrolysis coupled proton transport;biological regulation;brain development;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;developmental process;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organ development;organelle organization;phagosome maturation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;hydrogen-exporting ATPase activity, phosphorylative mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "apical plasma membrane;axon part;axon terminus;cell part;cell projection part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuron projection terminus;organelle;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain;proton-transporting V-type ATPase complex;proton-transporting V-type ATPase, V0 domain;synapse part;synaptic vesicle;vacuolar part;vacuolar proton-transporting V-type ATPase complex;vesicle;vesicle membrane" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

P36543;C9J8H1;P36543-2;P36543-3;Q96A05 V-type proton ATPase subunit E 1;V-type proton ATPase subunit E 2ATP6V1E1;ATP6V1E2 >sp|P36543|VATE1_HUMAN V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1;>tr|C9J8H1|C9J8H1_HUMAN V-type proton ATPase subunit E 1 (Fragment) OS=Homo sapiens GN=ATP6V1E1 PE=2 SV=1;>sp|P36543-2|VATE1_HUMAN Isoform 2 of V-type proton ATPa 0.34 4.07 0.32 2.63 0.32 1.38 0.5 1.27 1.24E-52 4 13.7 "ATP hydrolysis coupled proton transport;biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organelle organization;phagosome maturation;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrogen-exporting ATPase activity, phosphorylative mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "acrosomal vesicle;apical plasma membrane;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microvillus;mitochondrion;organelle;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain;stored secretory granule;vesicle"Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

Q9UI12-2;Q9UI12;G3V126;E5RK31;E5RJG1;E5RG49;E5RHH0 V-type proton ATPase subunit H ATP6V1H ">sp|Q9UI12-2|VATH_HUMAN Isoform 2 of V-type proton

ATPase subunit H OS=Homo sapiens GN=ATP6V1H;>sp|Q9UI12|VATH_HUMAN V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1;>tr|G3V126|G3V126_HUMAN ATPase, H+ transporting, lysosomal 50/57kDa, V1" NaN 2.87 0.52 1.76 0.57 2.14 NaN 1.16 2.15E-10 4 12.5 "ATP catabolic process;ATP hydrolysis coupled proton transport;ATP metabolic process;biological regulation;catabolic process;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular monovalent inorganic cation homeostasis;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;endocytosis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;intracellular pH reduction;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;pH reduction;phagosome maturation;primary metabolic process;protein transport;proton transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular pH;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune system process;regulation of intracellular pH;regulation of multi-organism process;regulation of pH;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport;vacuolar acidification;vesicle-mediated transport;viral reproduction;viral reproductive process;virus-host interaction" "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;enzyme regulator activity;hydrogen ion transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;organelle part;plasma membrane;protein complex;proton-transporting two-sector ATPase complex, catalytic domain;proton-transporting V-type ATPase, V1 domain;vacuolar part;vacuolar proton-transporting V-type ATPase, V1 domain" Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

Q9Y3I0;E7EQS9 tRNA-splicing ligase RtcB homolog C22orf28 >sp|Q9Y3I0|RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=C22orf28 PE=1 SV=1;>tr|E7EQS9|E7EQS9_HUMAN Protein RTCB OS=Homo sapiens GN=RTCB PE=2 SV=2 0.85 1.04 0.59 0.88 0.99 1.19 0.93 0.93 6.79E-26 4 8.7 "anatomical structure development;anatomical structure morphogenesis;biological adhesion;cell adhesion;cell morphogenesis;cell morphogenesis involved in differentiation;cell-matrix adhesion;cell-substrate adhesion;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;in utero embryonic development;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;placenta development;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via endonucleolytic cleavage and ligation;substrate adhesion-dependent cell spreading;tRNA metabolic process;tRNA processing;tRNA splicing, via endonucleolytic cleavage and ligation""adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming phosphoric ester bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA ligase (ATP) activity;RNA ligase activity" cell part;cytoplasm;intracellular part;macromolecular complex;protein complex;tRNA-splicing ligase complex

Q96A33-2;Q96A33Coiled-coil domain-containing protein 47 CCDC47 >sp|Q96A33-2|CCD47_HUMAN Isoform 2 of Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47;>sp|Q96A33|CCD47_HUMAN Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1 0.99 1.32 2.07 0.96 0.76 0.63 0.78 1.05 1.82E-12 4 12.1 biological regulation;calcium ion homeostasis;cation homeostasis;cellular process;cellular response to biotic stimulus;cellular response to stimulus;cellular response to stress;chemical homeostasis;developmental process;divalent inorganic cation homeostasis;embryo development;ER overload response;ER-nucleus signaling pathway;homeostatic process;ion homeostasis;metal ion homeostasis;post-embryonic development;regulation of biological process;regulation of biological quality;regulation of cellular process;response to biotic stimulus;response to endoplasmic reticulum stress;response to stimulus;response to stress;signal transduction binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;organelle

Q8TD31;B0S7V6;Q8TD31-3;Q8TD31-

2;E7EPK4;B0V090;B0S7V7;A2ABH1;D6RDI7;B0V092;D6RAE7;E7EQE8;E7EQC5;A2ABH4;E9PGB6;E9PHV1;A2ABH0;B0V091;A2ABH3;A2ABH5 Coiled-coil alpha-helical rod protein 1 CCHCR1 >sp|Q8TD31|CCHCR_HUMAN Coiled-coil alpha-helical rod protein 1 OS=Homo sapiens GN=CCHCR1 PE=2 SV=2;>tr|B0S7V6|B0S7V6_HUMAN Coiled-coil alpha-helical rod protein 1 OS=Homo sapiens GN=CCHCR1 PE=2 SV=1;>sp|Q8TD31-3|CCHCR_HUMAN Isoform 3 of Coiled-coil alpha-h NaN NaN NaN NaN NaN NaN NaN NaN 1.72E-06 4 4.1 cell differentiation;cellular developmental process;cellular process;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;multicellular organismal development;multicellular organismal process;nuclear export;nuclear transport;nucleocytoplasmic transport;protein export from nucleus;protein targeting;protein transport;transport cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

J3KTE9;P22223;P22223-2;J3QR60 Cadherin-3 CDH3 >tr|J3KTE9|J3KTE9_HUMAN Cadherin-3 OS=Homo sapiens GN=CDH3 PE=3 SV=1;>sp|P22223|CADH3_HUMAN Cadherin-3 OS=Homo sapiens GN=CDH3 PE=1 SV=2;>sp|P22223-2|CADH3_HUMAN Isoform 2 of Cadherin-3 OS=Homo sapiens GN=CDH3 0.86 1.41 1.24 1.45 0.29 0.15 0.69 1.05 4.79E-16 4 8.7 adherens junction organization;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion;multicellular organismal process;neurological system process;response to stimulus;sensory perception;sensory perception of light stimulus;system process;visual perception binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Cell adhesion molecules (CAMs)

P23528;G3V1A4;E9PP50;E9PK25;E9PLJ3;E9PS23;E9PQB7;Q9Y281-3;Q9Y281 Cofilin-1 CFL1 ">sp|P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3;>tr|G3V1A4|G3V1A4_HUMAN Cofilin 1 (Non-muscle), isoform CRA_a OS=Homo sapiens GN=CFL1 PE=2 SV=1;>tr|E9PP50|E9PP50_HUMAN Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=2 SV=1;>tr|E9PK25|E9PK" 0.44 1.71 0.18 1.28 0.89 1.87 0.89 1.04 2.18E-258 4 33.1 actin cytoskeleton organization;actin filament depolymerization;actin filament organization;actin filament-based process;actin polymerization or depolymerization;ameboidal cell migration;anatomical structure morphogenesis;axon guidance;biological regulation;cell activation;cell migration;cell motility;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;chemotaxis;cytokinesis;cytoskeleton organization;defense response;developmental process;embryonic morphogenesis;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment or maintenance of cell polarity;exocytosis;immune response;immune system process;innate immune response;intracellular signal transduction;locomotion;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of an epithelial fold;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;neural crest cell migration;neural fold formation;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;platelet degranulation;positive regulation of actin filament depolymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex disassembly;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein depolymerization;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cell morphogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of organelle organization;regulation of programmed cell death;regulation of protein complex disassembly;response to acid;response to amine stimulus;response to amino acid stimulus;response to biotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to organic nitrogen;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;Rho protein signal transduction;secretion;secretion by cell;signal transduction;small GTPase mediated signal transduction;taxis;tissue morphogenesis;transport;vesicle-mediated transport actin cytoskeleton;cell cortex part;cell part;cell projection membrane;cell projection part;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium membrane;leading edge membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear matrix;nuclear part;nucleus;organelle;organelle part;plasma membrane part;ruffle membrane Axon guidance;Fc gamma R-mediated phagocytosis;Regulation of actin cytoskeleton

G3V1K1;Q9NX63;C9JRZ6;F8WAR4;F8WD73 "Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial" CHCHD3 ">tr|G3V1K1|G3V1K1_HUMAN Coiled-coil-helix-coiled-coil-helix domain containing 3, isoform CRA_b OS=Homo sapiens GN=CHCHD3 PE=2 SV=1;>sp|Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCH" 0.95 1.4 1.45 1.74 0.7 0.71 0.6 1.03 5.61E-18 4 31.2 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;inner mitochondrial membrane organization;membrane fusion;membrane organization;mitochondrial fusion;mitochondrial membrane organization;mitochondrion organization;organelle fusion;organelle organization binding;enzyme binding;phosphatase binding;protein binding;protein complex scaffold;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part

Q969X6;H3BSH7;Q969X6-2;Q969X6-3;J3KSI1;J3KSE6;J3KTR0;H3BPD7;I3L4T9;H3BRM8 Cirhin CIRH1A >sp|Q969X6|CIR1A_HUMAN Cirhin OS=Homo sapiens GN=CIRH1A PE=1 SV=1;>tr|H3BSH7|H3BSH7_HUMAN Cirhin (Fragment) OS=Homo sapiens GN=CIRH1A PE=2 SV=1;>sp|Q969X6-2|CIR1A_HUMAN Isoform 2 of Cirhin OS=Homo sapiens GN=CIRH1A;>sp|Q969X6-3|CIR1A_HUMAN Isoform 3 of Cir 1.19 1.55 1.29 2.04 0.6 0.38 0.46 0.58 1.93E-19 4 7.4 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes

P39060-2;H7BXV5;P39060-1;P39060;H7C457 Collagen alpha-1(XVIII) chain;Endostatin COL18A1 >sp|P39060-2|COIA1_HUMAN Isoform 3 of Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1;>tr|H7BXV5|H7BXV5_HUMAN Endostatin (Fragment) OS=Homo sapiens GN=COL18A1 PE=2 SV=1;>sp|P39060-1|COIA1_HUMAN Isoform 2 of Collagen alpha-1(XVIII) chain OS=Homo sa NaN NaN 1.53 NaN 0.26 NaN NaN NaN 2.56E-06 4 4 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological adhesion;biological regulation;cell adhesion;cell morphogenesis;cell morphogenesis involved in differentiation;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;collagen catabolic process;collagen metabolic process;developmental process;endothelial cell morphogenesis;epithelial cell morphogenesis;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;neurological system process;organ morphogenesis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;positive regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of locomotion;regulation of programmed cell death;sensory perception;sensory perception of light stimulus;system process;visual perception binding;cation binding;ion binding;metal ion binding;structural molecule activity basement membrane;cell part;collagen;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix;extracellular matrix part;extracellular region part;extracellular space;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Protein digestion and absorption

Q10570 Cleavage and polyadenylation specificity factor subunit 1 CPSF1 >sp|Q10570|CPSF1_HUMAN Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2 NaN NaN 1.62 NaN 0.72 NaN NaN NaN 3.03E-09 4 3.7 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA cleavage;mRNA export from nucleus;mRNA metabolic process;mRNA polyadenylation;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA polyadenylation;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;mRNA cleavage and polyadenylation specificity factor complex;mRNA cleavage factor complex;nuclear part;nucleoplasm part;organelle part;protein complex mRNA surveillance pathway

Q5TZA2-2;Q5TZA2;B1AKD8;REV__Q9NRC6 Rootletin CROCC >sp|Q5TZA2-2|CROCC_HUMAN Isoform 2 of Rootletin OS=Homo sapiens GN=CROCC;>sp|Q5TZA2|CROCC_HUMAN Rootletin OS=Homo sapiens GN=CROCC PE=1 SV=1;>tr|B1AKD8|B1AKD8_HUMAN Rootletin (Fragment) OS=Homo sapiens GN=CROCC PE=2 SV=2 1.02 0.98 NaN 0.36 NaN 0.65 0.56 0.77 1.06E-05 4 2.4 cell cycle;cell projection organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;centrosome organization;localization;macromolecule localization;microtubule organizing center organization;organelle organization;protein localization binding;cytoskeletal protein binding;kinesin binding;protein binding;structural molecule activity actin cytoskeleton;cell part;cell projection part;centriole;centrosome;ciliary rootlet;cilium part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;microtubule organizing center;microtubule organizing center part;non-membrane-bounded organelle;organelle;organelle part;plasma membrane

P26232-3;P26232-2;P26232-5;P26232;C9IZ88;C9J144 Catenin alpha-2 CTNNA2>sp|P26232-3|CTNA2_HUMAN Isoform 3 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232-2|CTNA2_HUMAN Isoform 2 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232-5|CTNA2_HUMAN Isoform 5 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232|CTNA2 NaN NaN 0.95 NaN 0.58 NaN NaN NaN 3.69E-22 4 6.9 anatomical structure morphogenesis;axonogenesis;biological adhesion;biological regulation;brain morphogenesis;cell adhesion;cell differentiation;cell migration;cell migration in hindbrain;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;dendrite morphogenesis;developmental process;hindbrain radial glia guided cell migration;locomotion;muscle cell differentiation;negative regulation of biological process;negative regulation of response to external stimulus;negative regulation of response to stimulus;neuron projection morphogenesis;organ morphogenesis;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle cell differentiation;prepulse inhibition;radial glia guided migration of Purkinje cell;regulation of biological process;regulation of cell differentiation;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of muscle cell differentiation;regulation of response to external stimulus;regulation of response to stimulus;regulation of synapse organization;regulation of synapse structural plasticity structural constituent of cytoskeleton;structural molecule activity actin cytoskeleton;adherens junction;anchoring junction;axon;basolateral plasma membrane;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane part;neuron projection;non-membrane-bounded organelle;organelle;plasma membrane part Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Endometrial cancer;Leukocyte transendothelial migration;Pathways in cancer;Tight junction

O00622 Protein CYR61 CYR61 >sp|O00622|CYR61_HUMAN Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 1.38 0.63 0.61 0.5 1.35 0.62 0.7 1.42 1.06E-39 4 10.2 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;apoptosis;apoptosis involved in heart morphogenesis;apoptosis involved in morphogenesis;atrial septum morphogenesis;atrioventricular valve morphogenesis;biological adhesion;biological regulation;blood vessel development;cardiac septum development;cardiac septum morphogenesis;cell adhesion;cell death;cell differentiation;cell migration;cell motility;cell proliferation;cell-cell adhesion;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular metabolic process;cellular process;chemotaxis;chondroblast differentiation;chorio-allantoic fusion;death;developmental process;developmental programmed cell death;embryonic organ development;extracellular matrix organization;extracellular structure organization;heart valve morphogenesis;intussusceptive angiogenesis;labyrinthine layer blood vessel development;locomotion;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organ development;osteoblast differentiation;placenta blood vessel development;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of BMP signaling pathway;positive regulation of cartilage development;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of ceramide biosynthetic process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of lipase activity;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of osteoblast differentiation;positive regulation of osteoblast proliferation;positive regulation of peptidase activity;positive regulation of phospholipase activity;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of sphingolipid biosynthetic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;programmed cell death;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of BMP signaling pathway;regulation of cartilage development;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cell-substrate adhesion;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ceramide biosynthetic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of ERK1 and ERK2 cascade;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of lipase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoblast proliferation;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of sphingolipid biosynthetic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to chemical stimulus;response to external stimulus;response to stimulus;taxis;ventricular septum development;wound healing, spreading of cells" binding;carbohydrate binding;extracellular matrix binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding extracellular region

B7Z6B8;Q16698;E5RJD2;E5RJG7;E5RFV2;H0YAW3;E5RID6 "2,4-dienoyl-CoA reductase, mitochondrial" DECR1 ">tr|B7Z6B8|B7Z6B8_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=2 SV=1;>sp|Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1;>tr|E5RJD2|E5RJD2_HUMAN 2,4-dienoyl-CoA reductase, mitocho" 0.63 0.61 0.41 0.55 2.14 1.7 1.42 1.36 1.90E-20 4 14.4 carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;small molecule catabolic process;small molecule metabolic process "2,4-dienoyl-CoA reductase (NADPH) activity;binding;catalytic activity;coenzyme binding;cofactor binding;NADP binding;NADPH binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded

organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part
P23743;G3V327;C9JM35;P23743-2;F8W1M3;F8W1H7;Q3ZE25;G3V4E1;F8VWX8;G3V4I3;F8VNZ9;G3V312;H0YJH4 Diacylglycerol kinase alpha DGKA >sp|P23743|DGKA_HUMAN Diacylglycerol kinase alpha OS=Homo sapiens GN=DGKA PE=1 SV=3;>tr|G3V327|G3V327_HUMAN Diacylglycerol kinase alpha (Fragment) OS=Homo sapiens GN=DGKA PE=2 SV=1;>tr|C9JM35|C9JM35_HUMAN Diacylglycerol kinase alpha (Fragment) OS=Homo sapi NaN NaN 0.93 0.18 1.81 2.37 NaN NaN 7.83E-12 4 8.6 activation of protein kinase activity;activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway;biological regulation;cell activation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;G-protein coupled receptor protein signaling pathway;intracellular signal transduction;platelet activation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;diacylglycerol kinase activity;ion binding;kinase activity;lipid binding;metal ion binding;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Glycerolipid metabolism;Glycerophospholipid metabolism;Phosphatidylinositol signaling system
Q9UBM7;E9PJ54;E9PMT8;E9PM00;E9PRL8;E9PQ71;E9PIP9 7-dehydrocholesterol reductase DHCR7 >sp|Q9UBM7|DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1;>tr|E9PJ54|E9PJ54_HUMAN 7-dehydrocholesterol reductase (Fragment) OS=Homo sapiens GN=DHCR7 PE=2 SV=1;>tr|E9PMT8|E9PMT8_HUMAN 7-dehydrocholesterol reductase (Fragment) 1.09 1.29 1.28 0.91 1.33 1.02 0.94 1.26 2.47E-46 4 10.1 alcohol metabolic process;anatomical structure development;biological regulation;biosynthetic process;blood vessel development;cell differentiation;cellular developmental process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;growth;lipid biosynthetic process;lipid metabolic process;lung development;metabolic process;multicellular organism growth;multicellular organismal process;organ development;post-embryonic development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular process;regulation of cholesterol biosynthetic process;regulation of cholesterol metabolic process;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of steroid biosynthetic process;regulation of steroid metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "7-dehydrocholesterol reductase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nuclear membrane;nuclear outer membrane;nuclear part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane Steroid biosynthesis
O00429-4;O00429-5;O00429-3;G8JLD5;O00429-2;O00429;J3KPI2;O00429-6;F8VZ52;B4DGC9;H0YHY4;F8VR28;F8VYL3;B4DPZ9;F8W1W3;F8VUJ9;B4DDQ3 Dynamin-1-like protein DNM1L >sp|O00429-4|DNM1L_HUMAN Isoform 3 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L;>sp|O00429-5|DNM1L_HUMAN Isoform 5 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L;>sp|O00429-3|DNM1L_HUMAN Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1 NaN NaN 0.23 NaN 0.81 NaN NaN NaN 1.33E-08 4 6 anatomical structure morphogenesis;apoptotic mitochondrial changes;biological regulation;catabolic process;cell part morphogenesis;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;developmental process;dynamin polymerization involved in membrane fission;dynamin polymerization involved in mitochondrial fission;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;membrane fission;membrane fission involved in mitochondrial fission;membrane organization;metabolic process;mitochondrial fission;mitochondrial fragmentation involved in apoptosis;mitochondrion morphogenesis;mitochondrion organization;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle fission;organelle organization;peroxisome fission;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of mitochondrial fission;positive regulation of mitochondrion organization;positive regulation of organelle organization;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of release of cytochrome c from mitochondria;positive regulation of secretion;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein polymerization;protein tetramerization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of developmental process;regulation of establishment of protein localization;regulation of localization;regulation of mitochondrial fission;regulation of mitochondrion organization;regulation of organelle organization;regulation of programmed cell death;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of release of cytochrome c from mitochondria;regulation of secretion;regulation of transport;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine

nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytoskeletal part;cytosol;endomembrane system;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microbody;microtubule;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;perinuclear region of cytoplasm;peroxisome;protein complex Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Fc gamma R-mediated phagocytosis

P50570-3;P50570-2;P50570-5;P50570-4;P50570;F5H4R9;E5RIK2;K7ELR1;Q6P2G1;E5RHK8;Q05193-5;Q05193-3;Q05193-4;Q9UQ16-2;Q9UQ16-3;Q05193-2;Q05193;Q9UQ16;Q9UQ16-4 Dynamin-2 DNM2 >sp|P50570-3|DYN2_HUMAN Isoform 3 of Dynamin-2 OS=Homo sapiens GN=DNM2;>sp|P50570-2|DYN2_HUMAN Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2;>sp|P50570-5|DYN2_HUMAN Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2;>sp|P50570-4|DYN2_HUMAN Isoform 4 of Dynami NaN NaN 0.62 NaN 2.94 NaN NaN NaN 6.33E-08 4 6.2 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;catabolic process;cation transport;cell cycle process;cell projection assembly;cell projection organization;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;endocytosis;endosome organization;establishment of localization;establishment of localization in cell;establishment of protein localization;ferric iron transport;filopodium assembly;G2/M transition of mitotic cell cycle;Golgi vesicle transport;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;immune system process;intracellular transport;ion transport;iron ion transport;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;metal ion transport;microspike assembly;nitric oxide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;post-Golgi vesicle-mediated transport;primary metabolic process;protein transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oxidoreductase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;synapse assembly;synapse organization;synaptic vesicle transport;transferrin transport;transition metal ion transport;transport;vesicle-mediated transport" "binding;catalytic activity;cytoskeletal protein binding;enzyme binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;microtubule binding;nucleoside-triphosphatase activity;nucleotide binding;phospholipid binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;tubulin binding" cell junction;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endocytic vesicle membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;microtubule;midbody;mitochondrion;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;postsynaptic density;postsynaptic membrane;protein complex;synapse part;synaptic membrane;vesicle membrane Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Fc gamma R-mediated phagocytosis

C9JC03;Q9H4M9;C9J2Z4;C9JDQ8;C9JIJ3;C9IZH1 EH domain-containing protein 1 EHD1 >tr|C9JC03|C9JC03_HUMAN EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=2 SV=1;>sp|Q9H4M9|EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2;>tr|C9J2Z4|C9J2Z4_HUMAN EH domain-containing protein 1 (Fragment) OS= 0.76 2.06 0.23 0.94 1.19 1.97 0.7 0.93 1.31E-10 4 11.8 biological regulation;blood coagulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;cholesterol homeostasis;coagulation;endocytic recycling;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;GTP catabolic process;GTP metabolic process;hemostasis;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;intracellular protein transport;intracellular transport;lipid homeostasis;low-density lipoprotein particle clearance;macromolecular complex assembly;macromolecular complex subunit organization;membrane invagination;membrane organization;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;plasma lipoprotein particle clearance;positive regulation of biological process;positive regulation of cholesterol storage;positive regulation of lipid storage;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;protein transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cholesterol storage;regulation of lipid storage;regulation of localization;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;sterol homeostasis;transport;vesicle-mediated transport"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome;early endosome membrane;endocytic vesicle;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;platelet dense tubular network membrane;recycling endosome membrane;vesicle Endocytosis

Q9H223 EH domain-containing protein 4 EHD4 >sp|Q9H223|EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 NaN 1.06 0.59 0.75 1.61 1.75 NaN 0.78 2.83E-10 4 9.2 biological regulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;endocytic recycling;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;membrane invagination;membrane organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;pinocytosis;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of endocytosis;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;early endosome membrane;endoplasmic reticulum;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;recycling endosome membrane Endocytosis

P20042 Eukaryotic translation initiation factor 2 subunit 2EIF2S2 >sp|P20042|IF2B_HUMAN Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2 1.46 0.66 1.05 0.72 1.64 1.03 1.52 0.99 3.12E-24 4 14.1 "binding;cation binding;ion binding;metal ion binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 2 complex;intracellular part;macromolecular complex;protein complex RNA transport

E5RHW4;O94905;E5RJ09 Erlin-2 ERLIN2 >tr|E5RHW4|E5RHW4_HUMAN Erlin-2 (Fragment) OS=Homo sapiens GN=ERLIN2 PE=2 SV=1;>sp|O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 0.89 1.23 1.48 1.61 0.63 0.56 0.7 0.75 4.60E-108 4 15.1 catabolic process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;death;ER-associated protein catabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;protein complex

O95864-3;O95864;B7Z634;O95864-2;F5GZ92;F5H622 Fatty acid desaturase 2 FADS2 >sp|O95864-3|FADS2_HUMAN Isoform 3 of Fatty acid desaturase 2 OS=Homo sapiens GN=FADS2;>sp|O95864|FADS2_HUMAN Fatty acid desaturase 2 OS=Homo sapiens GN=FADS2 PE=1 SV=1;>tr|B7Z634|B7Z634_HUMAN Fatty acid desaturase 2 OS=Homo sapiens GN=FADS2 PE=2 SV=1;>sp| 1.28 1.3 2.06 0.39 0.55 0.76 0.95 0.95 5.18E-13 4 20.7 biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;electron transport chain;fatty acid biosynthetic process;fatty acid metabolic process;generation of precursor metabolites and energy;linoleic acid metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty acid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;unsaturated fatty acid biosynthetic process;unsaturated fatty acid metabolic process "binding;catalytic activity;cation binding;CoA desaturase activity;heme binding;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water;stearoyl-CoA 9-desaturase activity;tetrapyrrole binding;transition metal ion binding" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;organelle membrane;organelle part;plasma membrane part alpha-Linolenic acid metabolism;Biosynthesis of unsaturated fatty acids;PPAR signaling pathway

Q96CS3 FAS-associated factor 2 FAF2 >sp|Q96CS3|FAF2_HUMAN FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2 NaN 1.08 1.51 0.77 0.93 1.12 NaN 0.83 2.23E-08 4 8.1 response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein binding;enzyme binding;protein binding;small conjugating protein binding;ubiquitin binding;ubiquitin protein ligase binding Cdc48p-Npl4p-Ufd1p AAA ATPase complex;cell part;cytoplasmic part;endoplasmic reticulum part;intracellular organelle part;intracellular part;lipid particle;macromolecular complex;membrane part;organelle part;protein complex

P51114-2;B4DXZ6;P51114;E7EU85;E9PFF5;P51114-3;C9JAJ4;F8W871;A8MQB8;Q06787-8;Q06787-6;G3V0J0;Q06787-2;Q06787-4;Q06787-5;G8JL90;Q06787-7;Q06787-3;Q06787;P51116 Fragile X mental retardation syndrome-related protein 1 FXR1 >sp|P51114-2|FXR1_HUMAN Isoform 2 of Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1;>tr|B4DXZ6|B4DXZ6_HUMAN Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=2 SV=1;>sp|P51114|FXR1_HUMAN Fra 1.57 0.57 1.16 0.23 1.32 0.24 1.7 1.01 1.00E-10 4 11.7 anatomical structure development;apoptosis;biological regulation;cell death;cell differentiation;cellular developmental process;cellular process;central nervous system development;death;developmental process;establishment of localization;establishment of RNA localization;mRNA transport;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;negative regulation of translational initiation;nucleic acid transport;nucleobase-containing compound transport;organ development;posttranscriptional regulation of gene expression;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;RNA transport;system development;transport binding;G-quadruplex RNA binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;RNA binding cell part;cell projection;cell projection part;contractile fiber part;costamere;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;dendritic shaft;dendritic spine;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;mRNA cap binding complex;neuron projection;neuron spine;neuronal RNA granule;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;polysome;protein complex;ribonucleoprotein complex;RNA cap binding complex;RNA granule;stress granule;synapse

P41250 Glycine--tRNA ligase GARS >sp|P41250|SYG_HUMAN Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 NaN NaN 0.67 NaN 4.23 NaN NaN NaN 2.39E-09 4 7.7 amine metabolic process;amino acid activation;biosynthetic process;bis(5'-nucleosidyl) oligophosphate biosynthetic process;bis(5'-nucleosidyl) oligophosphate metabolic process;carboxylic acid metabolic process;cell death;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;death;diadenosine polyphosphate biosynthetic process;diadenosine polyphosphate metabolic process;diadenosine tetraphosphate biosynthetic process;diadenosine tetraphosphate metabolic process;glycyl-tRNA aminoacylation;heterocycle biosynthetic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside biosynthetic process;ribonucleoside metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;glycine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;protein binding;protein dimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle;organelle lumen;organelle part;stored secretory granule;vesicle Aminoacyl-tRNA biosynthesis

Q8IWJ2;B8ZZW2;B3KR21;H7BYJ9 GRIP and coiled-coil domain-containing protein 2 GCC2 >sp|Q8IWJ2|GCC2_HUMAN GRIP and coiled-coil domain-containing protein 2 OS=Homo sapiens GN=GCC2 PE=1 SV=4;>tr|B8ZZW2|B8ZZW2_HUMAN GRIP and coiled-coil domain-containing protein 2 (Fragment) OS=Homo sapiens GN=GCC2 PE=2 SV=1;>tr|B3KR21|B3KR21_HUMAN GRIP and 0.8 1.09 NaN 0.97 NaN 1.27 0.91 0.84 6.90E-08 4 2.1 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cytoskeleton organization;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;establishment of protein localization to vacuole;Golgi organization;Golgi ribbon formation;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;late endosome to Golgi transport;localization;lysosomal transport;macromolecule localization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;microtubule anchoring;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based process;organelle organization;protein localization;protein localization in Golgi apparatus;protein localization to organelle;protein targeting;protein targeting to Golgi;protein targeting to lysosome;protein targeting to vacuole;protein transport;recycling endosome to Golgi transport;regulation of biological process;regulation of biological quality;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of protein exit from endoplasmic reticulum;regulation of protein localization;regulation of protein transport;regulation of transport;retrograde transport, endosome to Golgi;retrograde transport, vesicle recycling within Golgi;transport;vacuolar transport;vesicle-mediated transport" cell part;cytoplasmic part;Golgi apparatus;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;trans-Golgi network

P63096;P63096-2;C9JPP4 Guanine nucleotide-binding protein G(i) subunit alpha-1 GNAI1 >sp|P63096|GNAI1_HUMAN Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2;>sp|P63096-2|GNAI1_HUMAN Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1;>tr|C9JPP4|C9JPP4_HUMAN NaN NaN NaN 0.95 NaN 0.54 NaN NaN 1.94E-15 4 13.6 "biological regulation;cAMP-mediated signaling;cell activation;cell communication;cell cycle;cell division;cell surface receptor linked signaling pathway;cell-cell signaling;cellular process;cellular response to stimulus;cyclic-nucleotide-mediated signaling;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;negative regulation of adenylate cyclase activity;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of molecular function;platelet activation;regulation of adenylate cyclase activity;regulation of biological process;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;second-messenger-mediated signaling;signal transduction;signaling;synaptic transmission" "binding;catalytic activity;cation binding;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metabotropic serotonin receptor binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity" cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;microtubule organizing center;midbody;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part;protein complex Axon guidance;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Gap junction;Gastric acid secretion;Leukocyte transendothelial migration;Long-term depression;Melanogenesis;Progesterone-mediated oocyte maturation;Tight junction;Toxoplasmosis

Q9BVP2-2;Q9BVP2 Guanine nucleotide-binding protein-like 3 GNL3 >sp|Q9BVP2-2|GNL3_HUMAN Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3;>sp|Q9BVP2|GNL3_HUMAN Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=21.16 0.86 1.45 1.84 0.68 0.42 0.73 0.63 5.32E-14 4 9.5 biological regulation;cell proliferation;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part Ribosome biogenesis in eukaryotes

P78347-2;P78347-4;P78347-3;P78347;Q86U51 General transcription factor II-I GTF2I >sp|P78347-2|GTF2I_HUMAN Isoform 2 of General transcription factor II-I OS=Homo sapiens GN=GTF2I;>sp|P78347-4|GTF2I_HUMAN Isoform 4 of General transcription factor II-I OS=Homo sapiens GN=GTF2I;>sp|P78347-3|GTF2I_HUMAN Isoform 3 of General transcription fa NaN NaN 1.43 NaN 2.59 NaN NaN NaN 1.73E-09 4 6.9 "biological regulation;biosynthetic process;calcium ion homeostasis;cation homeostasis;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chemical homeostasis;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;embryo development;homeostatic process;ion homeostasis;macromolecule metabolic process;metabolic process;metal ion homeostasis;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of developmental process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;reduction of cytosolic calcium ion concentration;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent"binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity cell body;cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;neuronal cell body;nucleus;organelle Basal transcription factors

Q71UI9;P0C0S5;Q71UI9-3;Q71UI9-4;Q71UI9-2;C9J0D1;C9J386 Histone H2A.V;Histone H2A.Z;Histone H2A H2AFV;H2AFZ >sp|Q71UI9|H2AV_HUMAN Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3;>sp|P0C0S5|H2AZ_HUMAN Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2;>sp|Q71UI9-3|H2AV_HUMAN Isoform 3 of

Histone H2A.V OS=Homo sapiens GN=H2AFV;>sp|Q71UI9-4|H2AV_HUMAN Isoform 4 of H 1.42 2.02 1.23 3.06 0.4 0.46 0.27 0.23 2.39E-15 4 31.2 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus

Q9P0M6;Q5SQT3 Core histone macro-H2A.2 H2AFY2 >sp|Q9P0M6|H2AW_HUMAN Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3;>tr|Q5SQT3|Q5SQT3_HUMAN Core histone macro-H2A.2 (Fragment) OS=Homo sapiens GN=H2AFY2 PE=2 SV=1 0.75 1.3 0.62 2.88 0.37 0.66 0.55 0.56 1.11E-19 4 15.6 "biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin modification;chromatin organization;chromosome organization;dosage compensation;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule metabolic process;regulation of metabolic process" binding;DNA binding;nucleic acid binding Barr body;cell part;chromosomal part;chromosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleosome;nucleus;organelle;organelle part;protein-DNA complex;sex chromosome;X chromosome Systemic lupus erythematosus

P69905 Hemoglobin subunit alpha HBA1 >sp|P69905|HBA_HUMAN Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 NaN NaN NaN NaN NaN NaN NaN NaN 9.95E-13 4 34.5 anion transport;bicarbonate transport;biological regulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;establishment of localization;gas transport;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;inorganic anion transport;ion transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;organic anion transport;oxygen transport;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;reactive oxygen species metabolic process;regulation of biological process;regulation of cell death;regulation of cellular process;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;small molecule metabolic process;transport binding;cation binding;heme binding;ion binding;iron ion binding;metal ion binding;oxygen binding;oxygen transporter activity;substrate-specific transporter activity;tetrapyrrole binding;transition metal ion binding;transporter activity cell part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytosolic part;cytosolic small ribosomal subunit;endocytic vesicle lumen;extracellular region;haptoglobin-hemoglobin complex;hemoglobin complex;intracellular organelle part;intracellular part;macromolecular complex;membrane-enclosed lumen;organelle lumen;organelle part;protein complex;ribonucleoprotein complex;small ribosomal subunit;vesicle lumen African trypanosomiasis;Malaria

A6NL93;P05114;A6NEL0;F2Z2W6;F2Z2Y5;H7BXJ5 Non-histone chromosomal protein HMG-14 HMGN1 >tr|A6NL93|A6NL93_HUMAN Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=2 SV=1;>sp|P05114|HMGN1_HUMAN Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=3;>tr|A6NEL0|A6NEL0_HUMAN Non-histone chromosomal protein HMG-1 1.07 1.46 1.02 2.64 0.33 0.15 0.45 0.42 4.01E-47 4 47.8 "anatomical structure morphogenesis;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromatin organization;chromosome organization;developmental process;DNA metabolic process;DNA repair;eye morphogenesis;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;organ morphogenesis;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription elongation, DNA-dependent;post-embryonic camera-type eye morphogenesis;post-embryonic eye morphogenesis;post-embryonic morphogenesis;post-embryonic organ morphogenesis;primary metabolic process;pyrimidine dimer repair;pyrimidine dimer repair by nucleotide-excision repair;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of development, heterochronic;regulation of developmental process;regulation of epithelial cell proliferation;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription elongation, DNA-dependent;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;response to UV-B;response to UV-C;transcription-coupled nucleotide-excision repair" binding;chromatin binding;chromatin DNA binding;DNA binding;nucleic acid binding;nucleosomal DNA binding;nucleosome binding;structure-specific DNA binding cell part;chromatin;chromosomal part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nucleus;organelle;organelle part

P52597 "Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-terminally processed" HNRNPF>sp|P52597|HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 NaN NaN 1.16 NaN 0.36 NaN NaN NaN 2.28E-131 4 14.5 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding;single-stranded RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex

P31942-2;P31942;B4DHY1;P31942-3;P31942-4;P31942-6;P31942-5 Heterogeneous nuclear ribonucleoprotein H3 HNRNPH3 >sp|P31942-2|HNRH3_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3;>sp|P31942|HNRH3_HUMAN Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2;>tr|B4DHY1|B4DHY1_HUMAN Heterogeneous nuclear 1.19 5.28 1.02 2.15 0.3 0.4 0.59 0.64 5.39E-28 4 16.9 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex

P11717 Cation-independent mannose-6-phosphate receptor IGF2R >sp|P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3 0.95 0.76 0.65 0.48 0.84 0.72 2.13 1.58 1.05E-06 4 1.8 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;membrane invagination;membrane organization;receptor-mediated endocytosis;transport;vesicle-mediated transport "binding;carbohydrate binding;catalytic activity;glycoprotein binding;insulin-like growth factor-activated receptor activity;kinase activity;mannose binding;molecular transducer activity;monosaccharide binding;phosphoprotein binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein tyrosine kinase activity;receptor activity;signal transducer activity;signaling receptor activity;sugar binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity;transporter activity" cell part;cell surface;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;endosome;Golgi apparatus part;Golgi-associated vesicle;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;nuclear envelope lumen;nuclear part;organelle;organelle envelope lumen;organelle membrane;organelle part;plasma membrane part;trans-Golgi network transport vesicle;transport vesicle;vacuolar membrane;vacuolar part;vesicle Lysosome

O00410-2;O00410;H0Y8C6;O00410-3;B4E0R6;C9JMV5;E7ETV3;H0Y3V4;O60518 Importin-5 IPO5 >sp|O00410-2|IPO5_HUMAN Isoform 2 of Importin-5 OS=Homo sapiens GN=IPO5;>sp|O00410|IPO5_HUMAN Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4;>tr|H0Y8C6|H0Y8C6_HUMAN Importin-5 (Fragment) OS=Homo sapiens GN=IPO5 PE=4 SV=1;>sp|O00410-3|IPO5_HUMAN Isoform 3 of 0.69 2.95 0.5 NaN 0.37 NaN 0.78 1.85 1.31E-29 4 5.5 establishment of localization;establishment of localization in cell;establishment of protein localization;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;multi-organism process;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleocytoplasmic transport;protein import;protein import into nucleus;protein targeting;protein transport;reproductive process;ribosomal protein import into nucleus;transport;viral reproductive process;virus-host interaction binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;GTPase binding;GTPase inhibitor activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;protein transporter activity;Ran GTPase binding;Ras GTPase binding;small GTPase binding;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleolus;nucleus;organelle;organelle part;pore complex;protein complex

Q96Q25;Q14137;E9PIF8;E9PRN9 Ribosome biogenesis protein BOP1 KM-PA-2;BOP1 >tr|Q96Q25|Q96Q25_HUMAN KM-PA-2 protein OS=Homo sapiens GN=KM-PA-2 PE=2 SV=1;>sp|Q14137|BOP1_HUMAN Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP1 PE=1 SV=2;>tr|E9PIF8|E9PIF8_HUMAN Ribosome biogenesis protein BOP1 (Fragment) OS=Homo sapiens GN=BOP 1.14 1.28 1.32 2.21 0.58 0.37 0.64 0.57 4.32E-11 4 10.9 "biological regulation;cell proliferation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;maturation of LSU-rRNA;maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cellular process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleolar part;nucleoplasm;nucleus;organelle;organelle part;PeBoW complex;protein complex

P01130-2;P01130-3;P01130-6;P01130-4;P01130-5;P01130;J3KMZ9;H0YM92;H0YMD1;H0YMQ3 Low-density lipoprotein receptor LDLR >sp|P01130-2|LDLR_HUMAN Isoform 2 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR;>sp|P01130-3|LDLR_HUMAN Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR;>sp|P01130-6|LDLR_HUMAN Isoform 6 of Low-density lipoprotein recepto 1.32 1.19 0.88 0.68 5.51 0.99 0.92 1.42 1.16E-28 4 6.9 "alcohol metabolic process;biological regulation;catabolic process;cellular catabolic process;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chemical homeostasis;cholesterol homeostasis;cholesterol import;cholesterol metabolic process;cholesterol transport;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;digestive system process;diterpenoid metabolic process;establishment of localization;homeostatic process;interaction with host;interspecies interaction between organisms;intestinal absorption;intestinal cholesterol absorption;isoprenoid metabolic process;lipid homeostasis;lipid metabolic process;lipid transport;lipoprotein catabolic process;lipoprotein metabolic process;low-density lipoprotein particle clearance;macromolecule catabolic process;macromolecule metabolic process;metabolic process;multicellular organismal process;multi-organism process;organic substance transport;phospholipid transport;phototransduction;phototransduction, visible light;plasma lipoprotein particle clearance;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of triglyceride biosynthetic process;positive regulation of triglyceride metabolic process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catabolic process;regulation of cellular amine metabolic process;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of lipid biosynthetic process;regulation of lipid catabolic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of phosphatidylcholine catabolic process;regulation of phospholipid catabolic process;regulation of primary metabolic process;regulation of triglyceride biosynthetic process;regulation of triglyceride metabolic process;reproductive process;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;small molecule metabolic process;steroid metabolic process;sterol homeostasis;sterol import;sterol metabolic process;sterol transmembrane transport;sterol transport;system process;terpenoid metabolic process;transmembrane transport;transport;viral reproductive process;virus-host interaction" binding;calcium ion binding;cargo receptor activity;cation binding;ion binding;lipoprotein particle binding;lipoprotein particle receptor activity;low-density lipoprotein particle binding;low-density lipoprotein receptor activity;metal ion binding;protein-lipid complex binding;receptor activity;very-low-density lipoprotein particle binding;very-low-density lipoprotein particle receptor activity cell part;clathrin coated vesicle membrane;clathrin-coated endocytic vesicle membrane;coated pit;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;external side of plasma membrane;extracellular region part;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome;low-density lipoprotein particle;lysosome;lytic vacuole;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma lipoprotein particle;plasma membrane part;protein-lipid complex;vacuole;vesicle membrane Bile secretion;Endocytosis;Hepatitis C;Toxoplasmosis

E9PLY5 MACF1 ">tr|E9PLY5|E9PLY5_HUMAN Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Fragment) OS=Homo sapiens GN=MACF1 PE=2 SV=1" NaN NaN 0.98 NaN 1.02 NaN NaN NaN 7.67E-13 4 4.1

Q96A72;F5H6P7;A6NEC0;P61326;F5H6N1;B1ARP8;F5H3U9;F5H124 Protein mago nashi homolog 2;Protein mago nashi homolog MAGOHB;MAGOH >sp|Q96A72|MGN2_HUMAN Protein mago nashi homolog 2 OS=Homo sapiens GN=MAGOHB PE=1 SV=1;>tr|F5H6P7|F5H6P7_HUMAN Protein mago nashi homolog 2 OS=Homo sapiens GN=MAGOHB PE=2 SV=1;>tr|A6NEC0|A6NEC0_HUMAN Protein mago nashi homolog 2 OS=Homo sapiens GN=MAGOHB P 1.1 1.96 NaN 2.64 NaN 0.26 0.39 0.44 2.01E-10 4 26.4 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;exon-exon junction complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport;Spliceosome

P11137-3;P11137;P11137-2;P11137-4 Microtubule-associated protein 2 MAP2 >sp|P11137-3|MTAP2_HUMAN Isoform 3 of Microtubule-associated protein 2 OS=Homo sapiens GN=MAP2;>sp|P11137|MTAP2_HUMAN Microtubule-associated protein 2 OS=Homo sapiens GN=MAP2 PE=1 SV=4;>sp|P11137-2|MTAP2_HUMAN Isoform 2 of Microtubule-associated protein 2 0.66 0.65 0.4 0.13 4.26 3.32 1.64 1.01 2.02E-08 4 3.8 anatomical structure development;anatomical structure morphogenesis;axonogenesis;cell development;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;central nervous system neuron development;cytoskeleton organization;dendrite morphogenesis;developmental process;macromolecule metabolic process;macromolecule modification;metabolic process;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based process;neuron development;neuron projection morphogenesis;organelle organization;peptidyl-amino acid modification;peptidyl-threonine modification;peptidyl-threonine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;response to chemical stimulus;response to organic substance;response to stimulus structural molecule activity cell body;cell part;cell projection part;cytoplasm;cytoskeletal part;dendritic shaft;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule associated complex;neuronal cell body;nuclear part;nuclear periphery;organelle part;protein complex

Q7Z434-4;Q7Z434 Mitochondrial antiviral-signaling protein MAVS >sp|Q7Z434-4|MAVS_HUMAN Isoform 4 of Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS;>sp|Q7Z434|MAVS_HUMAN Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2 NaN 1.2 1.34 0.84 0.83 0.68 NaN 1.25 9.05E-12 4 19.5 "activation of immune response;activation of innate immune response;biological regulation;cellular process;cellular response to chemical stimulus;cellular response to dsRNA;cellular response to exogenous dsRNA;cellular response to organic substance;cellular response to stimulus;defense response;defense response to bacterium;defense response to virus;immune effector process;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of reproductive process;negative regulation of type I interferon production;negative regulation of viral genome replication;negative regulation of viral reproduction;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemokine (C-C motif) ligand 5 production;positive regulation of chemokine production;positive regulation of cytokine production;positive regulation of cytokine-mediated signaling pathway;positive regulation of defense response;positive regulation of defense response to virus by host;positive regulation of gene expression;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of interferon-alpha production;positive regulation of interferon-beta production;positive regulation of interleukin-8 production;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of IP-10 production;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein import into nucleus;positive regulation of protein import into nucleus, translocation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein transport;positive regulation of response to cytokine stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription factor import into nucleus;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of tumor necrosis factor production;positive regulation of type I interferon production;positive regulation of type I interferon-mediated signaling pathway;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemokine (C-C motif) ligand 5 production;regulation of chemokine production;regulation of cytokine production;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by host;regulation of establishment of protein localization;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-alpha production;regulation of interferon-beta production;regulation of interleukin-8 production;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of IP-10 production;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein transport;regulation of reproductive process;regulation of response to biotic stimulus;regulation of response to cytokine stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of tumor necrosis factor production;regulation of type I interferon production;regulation of type I interferon-mediated signaling pathway;regulation of viral genome replication;regulation of viral reproduction;reproductive process;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;viral reproductive process;virus-host interaction" molecular transducer activity;signal transducer activitycell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;peroxisomal membrane;peroxisomal part Cytosolic DNA-sensing pathway;Hepatitis C;Measles;RIG-I-like receptor signaling pathway

Q13405;H0YDP7;E9PI78;E9PNF1 "39S ribosomal protein L49, mitochondrial" MRPL49 ">sp|Q13405|RM49_HUMAN 39S ribosomal protein L49, mitochondrial OS=Homo sapiens GN=MRPL49 PE=1 SV=1;>tr|H0YDP7|H0YDP7_HUMAN 39S ribosomal protein L49, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL49 PE=4 SV=1" 1.14 1.56 2.13 1.1 0.58 0.33 0.79 0.89 8.61E-11 4 28.3 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial ribosome;non-membrane-bounded organelle;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome

G5E9W7;G5E9V5;P82650;H7C5F2;Q9H3I1;H7C5H3;H7C5L9 "28S ribosomal protein S22, mitochondrial" MRPS22 ">tr|G5E9W7|G5E9W7_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1;>tr|G5E9V5|G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1;>sp|P82650|RT22_HUMAN 28S ribosomal protein S22, mitoc" NaN NaN 2.15 NaN 1.22 NaN NaN NaN 2.16E-12 4 13.5 structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial part;mitochondrial small ribosomal subunit;mitochondrion;non-membrane-bounded organelle;organellar small ribosomal subunit;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit

G5EA06;Q92552;B4DRT2;D6RH20;D6RJC7;E5RJ73 "28S ribosomal protein S27, mitochondrial" MRPS27 ">tr|G5EA06|G5EA06_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=2 SV=1;>sp|Q92552|RT27_HUMAN 28S ribosomal protein S27, mitochondrial OS=Homo sapiens GN=MRPS27 PE=1 SV=3;>tr|B4DRT2|B4DRT2_HUMAN 28S ribosomal protein S27, mitoc" NaN NaN 1.98 NaN 0.72 NaN NaN NaN 4.03E-21 4 16.5 cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome

Q92614-3;Q92614-4;Q92614;J3KNX9;Q92614-5;Q92614-2 Unconventional myosin-XVIIIa MYO18A >sp|Q92614-3|MY18A_HUMAN Isoform 3 of Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A;>sp|Q92614-4|MY18A_HUMAN Isoform 4 of Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A;>sp|Q92614|MY18A_HUMAN Unconventional myosin-XVIIIa OS=Homo sapiens GN NaN NaN 1.17 0.81 1.43 1.14 NaN NaN 1.61E-13 4 3 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;biological regulation;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoskeleton organization;DNA metabolic process;locomotion;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;DNA binding;DNA-dependent ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actomyosin;cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;myosin complex;organelle;organelle part;protein complex

Q12965;H0YN00;H0YLE5;O00160 Unconventional myosin-Ie MYO1E >sp|Q12965|MYO1E_HUMAN Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2 0.94 0.86 0.55 0.78 7.97 1.37 0.83 0.63 1.73E-16 4 4.6 actin filament-based movement;actin filament-based process;anatomical structure development;biological regulation;cell activation;cell activation involved in immune response;cell development;cell differentiation;cell surface receptor linked signaling pathway;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to stimulus;chordate embryonic development;defense response;defense response to bacterium;defense response to Gram-positive bacterium;developmental process;embryo development;embryo development ending in birth or egg hatching;endocytosis;enzyme linked receptor protein signaling pathway;epithelial cell development;establishment of localization;establishment of localization in cell;exocytosis;extracellular matrix organization;extracellular structure organization;glomerular basement membrane development;glomerular epithelial cell development;glomerular filtration;glomerular visceral epithelial cell development;hemopoiesis;hemopoietic or lymphoid organ development;immune effector process;immune system process;in utero embryonic development;leukocyte activation;leukocyte activation involved in immune response;leukocyte degranulation;membrane invagination;membrane organization;multicellular organismal process;multi-organism process;myeloid cell activation involved in immune response;myeloid leukocyte activation;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;neutrophil activation;neutrophil activation involved in immune response;neutrophil degranulation;organ development;platelet-derived growth factor receptor signaling pathway;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;post-embryonic hemopoiesis;post-embryonic organ development;regulated secretory pathway;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of localization;regulation of locomotion;regulation of organelle organization;regulation of response to stimulus;regulation of response to stress;renal system process;response to bacterium;response to biotic stimulus;response to other organism;response to stimulus;response to stress;secretion;secretion by cell;signal transduction;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vasculogenesis;vesicle-mediated transport "actin binding;actin filament binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;calmodulin binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;phosphatidylinositol binding;phospholipid binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" adherens junction;anchoring junction;cell cortex part;cell junction;cell part;cell-cell junction;clathrin-coated vesicle;coated vesicle;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;filamentous actin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;myosin complex;non-membrane-bounded organelle;organelle;organelle part;protein complex;unconventional myosin complex;vesicle

Q9P0J0;B4DF76;J3KN00;B4DEZ3;K7EJE1;E7ENQ6NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 NDUFA13;YJEFN3 >sp|Q9P0J0|NDUAD_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Homo sapiens GN=NDUFA13 PE=1 SV=3;>tr|B4DF76|B4DF76_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Homo sapiens GN=NDUFA13 PE=2 SV=1;>tr|J3KN00| 1.14 1.5 1.61 1.93 0.36 0.34 0.63 0.88 4.32E-20 4 29.9 "apoptotic nuclear change;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular process;electron transport chain;establishment of localization;establishment of localization in cell;establishment of protein localization;generation of precursor metabolites and energy;induction of apoptosis;induction of programmed cell death;intracellular protein transport;intracellular transport;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;negative regulation of translation;nuclear import;nuclear transport;nucleocytoplasmic transport;oxidation-reduction process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;posttranscriptional regulation of gene expression;protein import;protein import into nucleus;protein targeting;protein transport;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;respiratory electron transport chain;small molecule metabolic process;transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;nuclear part;nucleoplasm;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P51970;F5H7V7 NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 NDUFA8>sp|P51970|NDUA8_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Homo sapiens GN=NDUFA8 PE=1 SV=3;>tr|F5H7V7|F5H7V7_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Homo sapiens GN=NDUFA8 PE=2 SV=1 1.05 1.49 1.7 1.77 0.38 0.41 0.59 0.9 5.52E-24 4 34.9 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial intermembrane space;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;mitochondrion;NADH dehydrogenase complex;organelle;organelle envelope lumen;organelle part;protein complex;respiratory chain complex IAlzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q16795;F5H0J3;H3BRM9 "NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial" NDUFA9">sp|Q16795|NDUA9_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=NDUFA9 PE=1 SV=2;>tr|F5H0J3|F5H0J3_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=ND" 0.91 1.15 1.44 2.25 0.44 0.41 0.69 0.85 1.27E-12 4 14.1 "cation transport;cellular metabolic process;cellular process;electron transport chain;establishment of localization;generation of precursor metabolites and energy;ion transport;metabolic process;metal ion transport;mitochondrial electron transport, NADH to ubiquinone;monovalent inorganic cation transport;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process;sodium ion transport;transport" "binding;catalytic activity;coenzyme binding;cofactor binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle lumen;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

H3BPJ9;O96000;Q96II6;H3BV16 NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 NDUFB10 >tr|H3BPJ9|H3BPJ9_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=2 SV=1;>sp|O96000|NDUBA_HUMAN NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=3;>tr|Q96II6|Q9 1.29 1.32 1.48 1.63 1 0.51 0.69 0.93 4.09E-31 4 29.2 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P19404;E7EPT4 "NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial" NDUFV2">sp|P19404|NDUV2_HUMAN NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2;>tr|E7EPT4|E7EPT4_HUMAN NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=2 SV=1" 1.08 1.51 1.56 2.05 0.57 0.38 0.54 0.77 1.71E-37 4 21.3 "anatomical structure development;cardiac muscle tissue development;cellular metabolic process;cellular process;developmental process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;muscle tissue development;nervous system development;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process;striated muscle tissue development;system development;tissue development" "2 iron, 2 sulfur cluster binding;binding;catalytic activity;cation binding;electron carrier activity;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q9H8H0;J3QLQ6;J3QKS9;J3QR28;B7Z5V9 Nucleolar protein 11 NOL11 >sp|Q9H8H0|NOL11_HUMAN Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=1 SV=1;>tr|J3QLQ6|J3QLQ6_HUMAN Nucleolar protein 11 (Fragment) OS=Homo sapiens GN=NOL11 PE=4 SV=1;>tr|J3QKS9|J3QKS9_HUMAN Nucleolar protein 11 OS=Homo sapiens GN=NOL11 PE=4 SV=1;>tr|J3 1.09 NaN 1.65 NaN 0.51 NaN 0.47 NaN 2.30E-10 4 6.8 cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part

Q15738;C9JDR0 "Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating" NSDHL ">sp|Q15738|NSDHL_HUMAN Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2;>tr|C9JDR0|C9JDR0_HUMAN Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating (Fragment) OS=Homo sapiens GN=NSDHL PE=2 SV=1" 0.76 0.62 2.32 0.3 2.16 2.07 1.25 1.26 3.32E-61 4 13.9 alcohol metabolic process;anatomical structure development;biological regulation;biosynthetic process;blood vessel development;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;embryonic organ development;epidermis development;hair cycle process;hair follicle development;labyrinthine layer blood vessel development;lipid biosynthetic process;lipid metabolic process;metabolic process;molting cycle;molting cycle process;multicellular organismal process;organ development;placenta blood vessel development;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small molecule metabolic process;smoothened signaling pathway;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;tissue development "3-beta-hydroxy-delta5-steroid dehydrogenase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) activity" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lipid particle;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Steroid biosynthesis

J3KP29;P52948-6;P52948-2;P52948-5;P52948;H7C3P6;P52948-4;P52948-3 Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;Nuclear pore complex protein Nup96 NUP98 >tr|J3KP29|J3KP29_HUMAN Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98 PE=4 SV=1;>sp|P52948-6|NUP98_HUMAN Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98;>sp|P52948-2|NUP98_HUMAN Isoform 2 of Nuclear pore c NaN NaN 1.17 NaN 1.36 NaN NaN NaN 1.14E-08 4 3.2 "anaphase;biological regulation;biosynthetic process;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;DNA metabolic process;DNA replication;establishment of localization;establishment of RNA localization;glucose transport;hexose transport;interaction with host;interspecies interaction between organisms;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear pore complex assembly;nuclear pore organization;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein import into nucleus, docking;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process;virus-host interaction" binding;peptide binding;structural constituent of nuclear pore;structural molecule activity;transporter activity cell part;cytoplasmic part;cytosol;inclusion body;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear inclusion body;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;nucleoplasm;Nup107-160 complex;organelle membrane;organelle part;pore complex;protein complex RNA transport

Q15646;Q15646-2;Q15646-3;H0YGP3;H0YHL3;H0YI20;F8VXY3;P00973-2;P00973-4;P00973;P00973-3;Q9Y6K5 2-5-oligoadenylate synthase-like protein OASL >sp|Q15646|OASL_HUMAN 2-5-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL PE=1 SV=2;>sp|Q15646-2|OASL_HUMAN Isoform p30 of 2-5-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL;>sp|Q15646-3|OASL_HUMAN Isoform 3 of 2-5-oligoade NaN NaN 1 0.28 4.54 2.52 NaN NaN 2.96E-17 4 11.5 biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-alpha;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;heterocycle biosynthetic process;heterocycle metabolic process;immune effector process;immune response;immune system process;interferon-gamma-mediated signaling pathway;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multi-organism process;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular process;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of reproductive process;regulation of ribonuclease activity;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-alpha;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;signal transduction;small molecule metabolic process;type I interferon-mediated signaling pathway "2'-5'-oligoadenylate synthetase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;adenylyltransferase activity;ATP binding;binding;catalytic activity;cation binding;DNA binding;double-stranded RNA binding;hormone receptor binding;ion binding;metal ion binding;nuclear hormone receptor binding;nucleic acid binding;nucleotide binding;nucleotidyltransferase activity;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;RNA binding;thyroid hormone receptor binding;transcription factor binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part Hepatitis C;Measles

P04181;P04181-2 "Ornithine aminotransferase, mitochondrial;Ornithine aminotransferase, hepatic form;Ornithine aminotransferase, renal form" OAT ">sp|P04181|OAT_HUMAN Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1" NaN 0.69 0.69 NaN 1.01 NaN NaN 2.36 5.30E-39 4 13.7 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutamine family amino acid biosynthetic process;glutamine family amino acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;L-proline biosynthetic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multicellular organismal process;neurological system process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;proline biosynthetic process;proline metabolic process;protein complex assembly;protein complex subunit organization;protein hexamerization;protein oligomerization;sensory perception;sensory perception of light stimulus;small molecule biosynthetic process;small molecule metabolic process;system process;visual perception "binding;catalytic activity;cofactor binding;ornithine-oxo-acid transaminase activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part Arginine and proline metabolism

D6RDK6;D6RBN5;Q9NX40;D6RI08;D6RDK1;D6RIV2;D6R9T5;D6RG39;D6RIT9;Q9NX40-3;Q9NX40-2;Q9NX40-4;D6R918;D6RBC5;D6RDI5;D6RA54;D6RC55 OCIA domain-containing protein 1 OCIAD1 >tr|D6RDK6|D6RDK6_HUMAN OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=2 SV=1;>tr|D6RBN5|D6RBN5_HUMAN OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=2 SV=1;>sp|Q9NX40|OCAD1_HUMAN OCIA domain-containing protein 1 OS= 0.84 1.57 1.34 1.71 0.67 0.39 0.57 0.79 6.44E-08 4 21.2 cell part;cytoplasmic part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle

Q8WX93-4;Q8WX93-8;Q8WX93-3;Q8WX93-5;Q8WX93;Q8WX93-2;Q8WX93-9;Q8WX93-7;D6R9F5;H0YA05;F8WA26 Palladin PALLD >sp|Q8WX93-4|PALLD_HUMAN Isoform 4 of Palladin OS=Homo sapiens GN=PALLD;>sp|Q8WX93-8|PALLD_HUMAN Isoform 8 of Palladin OS=Homo sapiens GN=PALLD;>sp|Q8WX93-3|PALLD_HUMAN Isoform 3 of Palladin OS=Homo sapiens GN=PALLD;>sp|Q8WX93-5|PALLD_HUMAN Isoform 5 of Pa 0.92 0.42 0.62 NaN 1.67 NaN 2.08 1.15 3.29E-10 4 6.2 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization actinin binding;alpha-actinin binding;binding;cytoskeletal protein binding;muscle alpha-actinin binding;protein binding actin filament;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasmic part;cytoskeletal part;focal adhesion;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;ruffle;Z disc

Q96HS1-2;Q96HS1;F5GXG4 "Serine/threonine-protein phosphatase PGAM5, mitochondrial" PGAM5 ">sp|Q96HS1-2|PGAM5_HUMAN Isoform 2 of Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5;>sp|Q96HS1|PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2" 1.1 1.56 1.67 1.72 0.42 0.51 0.62 0.88 1.51E-17 4 16.5 "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane

P24928;Q6NX41 DNA-directed RNA polymerase II subunit RPB1 POLR2A >sp|P24928|RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 NaN NaN NaN NaN NaN NaN NaN NaN 6.03E-12 4 2.5 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA capping;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA capping;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent;transcription-coupled nucleotide-excision repair;viral reproductive process" "binding;catalytic activity;cation binding;DNA binding;DNA-directed RNA polymerase activity;ion binding;metal ion binding;nucleic acid binding;nucleotidyltransferase activity;RNA polymerase activity;RNA-directed RNA polymerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" "cell part;DNA-directed RNA polymerase complex;DNA-directed RNA polymerase II, core complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear DNA-directed RNA polymerase complex;nuclear part;nucleoplasm part;organelle part;protein complex;RNA polymerase complex" Huntington's disease;Purine metabolism;Pyrimidine metabolism;RNA polymerase

Q15063-4;Q15063-2;Q15063-3;B1ALD9;B1ALD8;Q15063;F5H628;CON__Q2KJC7 Periostin POSTN >sp|Q15063-4|POSTN_HUMAN Isoform 4 of Periostin OS=Homo sapiens GN=POSTN;>sp|Q15063-2|POSTN_HUMAN Isoform 2 of Periostin OS=Homo sapiens GN=POSTN;>sp|Q15063-3|POSTN_HUMAN Isoform 3 of Periostin OS=Homo sapiens GN=POSTN;>tr|B1ALD9|B1ALD9_HUMAN Periostin OS= NaN 1.44 NaN NaN NaN NaN NaN 3.53 1.13E-11 4 8.3 anatomical structure development;biological adhesion;biological regulation;cell adhesion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;extracellular matrix organization;extracellular structure organization;regulation of biological process;regulation of cellular process;regulation of Notch signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;skeletal system development;system development;tissue development binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding cell part;cytoplasmic part;extracellular matrix;extracellular region part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle;proteinaceous extracellular matrix

P30153;B3KQV6;F5H3X9;E9PH38;P30154-5;P30154-4;P30154;P30154-2;E9PPI5;E9PNM7;E9PHZ6;H0YDG7;C9J9C1;J3KR29;P30154-3 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform PPP2R1A;PPP2R1B >sp|P30153|2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4;>tr|B3KQV6|B3KQV6_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo s 0.48 3.52 0.5 1.48 0.75 1.08 0.73 1.46 8.42E-76 4 9.3 "anaphase;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;ceramide metabolic process;chromosome segregation;dephosphorylation;enzyme linked receptor protein signaling pathway;fibroblast growth factor receptor signaling pathway;G2/M transition of mitotic cell cycle;inactivation of MAPK activity;induction of apoptosis;induction of programmed cell death;intracellular signal transduction;lipid metabolic process;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane lipid metabolic process;membrane organization;metabolic process;mitotic anaphase;mitotic nuclear envelope reassembly;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell growth;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of growth;negative regulation of intracellular protein kinase cascade;negative regulation of JAK-STAT cascade;negative regulation of kinase activity;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidyl-tyrosine phosphorylation;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of protein serine/threonine kinase activity;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transferase activity;negative regulation of tyrosine phosphorylation of STAT protein;negative regulation of tyrosine phosphorylation of Stat3 protein;nitrogen compound metabolic process;nuclear envelope organization;nuclear envelope reassembly;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;peptidyl-serine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex assembly;protein complex subunit organization;protein dephosphorylation;protein metabolic process;protein modification process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of gene expression;regulation of growth;regulation of intracellular protein kinase cascade;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat3 protein;regulation of Wnt receptor signaling pathway;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;second-messenger-mediated signaling;signal transduction;sphingoid metabolic process;sphingolipid metabolic process;transmembrane receptor protein tyrosine kinase signaling pathway" "antigen binding;binding;catalytic activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphatase regulator activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein serine/threonine phosphatase activity" "cell part;chromosomal part;chromosome, centromeric region;cytoplasmic part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule cytoskeleton;mitochondrion;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex" Cell cycle - yeast;Chagas disease (American trypanosomiasis);Hepatitis C;Long-term depression;Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;TGF-beta signaling pathway;Tight junction;Wnt signaling pathway

E9PH29;P30048 "Thioredoxin-dependent peroxide reductase, mitochondrial" PRDX3 ">tr|E9PH29|E9PH29_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=2 SV=1;>sp|P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3" 0.87 0.67 1.78 0.19 1.68 1.02 1.78 1.68 4.68E-32 4 18.9 "anatomical structure development;biological regulation;catabolic process;cell differentiation;cellular catabolic process;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;chemical homeostasis;developmental process;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;ion homeostasis;maternal placenta development;metabolic process;mitochondrion organization;myeloid cell differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of kinase activity;negative regulation of molecular function;negative regulation of programmed cell death;negative regulation of transferase activity;organelle organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of mitochondrial membrane potential;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;regulation of transferase activity;response to biotic stimulus;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress" "alkyl hydroperoxide reductase activity;antioxidant activity;caspase inhibitor activity;caspase regulator activity;catalytic activity;cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peptidase inhibitor activity;peptidase regulator activity;peroxidase activity;peroxiredoxin activity" cell part;cytoplasmic part;early endosome;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle

Q9UMS4;F5GY56;H0YGF3;F5H2I0 Pre-mRNA-processing factor 19 PRPF19 >sp|Q9UMS4|PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1;>tr|F5GY56|F5GY56_HUMAN Pre-mRNA-processing factor 19 (Fragment) OS=Homo sapiens GN=PRPF19 PE=2 SV=1 0.76 NaN 1.08 1.88 0.3 0.42 0.5 NaN 1.67E-08 4 10.5 "biological regulation;biosynthetic process;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;inner cell mass cell proliferation;lipid biosynthetic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neuron differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of astrocyte differentiation;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of glial cell differentiation;positive regulation of gliogenesis;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;regulation of astrocyte differentiation;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;response to DNA damage stimulus;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;spliceosome assembly" "acid-amino acid ligase activity;binding;catalytic activity;DNA binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleic acid binding;small conjugating protein ligase activity;ubiquitin-protein ligase activity;ubiquitin-ubiquitin ligase activity" catalytic step 2 spliceosome;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part;protein complex;Prp19 complex;ribonucleoprotein complex;spindle;spliceosomal complex;ubiquitin ligase complex Spliceosome;Ubiquitin mediated proteolysis

P35998;C9JLS9;B7Z5E2 26S protease regulatory subunit 7 PSMC2 >sp|P35998|PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3;>tr|C9JLS9|C9JLS9_HUMAN 26S protease regulatory subunit 7 (Fragment) OS=Homo sapiens GN=PSMC2 PE=2 SV=1;>tr|B7Z5E2|B7Z5E2_HUMAN 26S protease regulatory subunit 7 OS= 0.83 1.27 0.39 0.69 0.92 1 1.25 1.18 3.87E-15 4 11.5 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome accessory complex;protein complex;ribonucleoprotein complex;RNA granule Proteasome

F5H157;Q15286 Ras-related protein Rab-35 RAB35 >tr|F5H157|F5H157_HUMAN Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=2 SV=1;>sp|Q15286|RAB35_HUMAN Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 NaN 1.45 1.2 NaN 0.58 NaN NaN 0.79 5.20E-36 4 22.7 biological regulation;cellular process;cellular response to stimulus;cytokinesis;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular signal transduction;intracellular transport;localization;macromolecule localization;protein localization;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport"binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;nucleoside-triphosphatase activity;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cell projection membrane;cell projection part;clathrin-coated endocytic vesicle;clathrin-coated vesicle;coated pit;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;endosome;extracellular region part;intercellular bridge;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;pigment granule;plasma membrane part;vesicle

B4DJA5;P20339 Ras-related protein Rab-5A RAB5A >tr|B4DJA5|B4DJA5_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=2 SV=1;>sp|P20339|RAB5A_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2 0.5 3.04 0.39 1.15 1 1.4 0.68 1.09 1.41E-50 4 23.9 anatomical structure development;biological regulation;blood coagulation;cell differentiation;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular response to stimulus;coagulation;developmental process;endocytosis;establishment of localization;establishment of protein localization;hemostasis;intracellular signal transduction;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;multicellular organismal process;nervous system development;positive regulation of biological process;positive regulation of cellular process;positive regulation of exocytosis;positive regulation of secretion;positive regulation of transport;protein transport;receptor internalization;receptor internalization involved in canonical Wnt receptor signaling pathway;receptor metabolic process;receptor-mediated endocytosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of filopodium assembly;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;system development;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin cytoskeleton;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;early endosome;early endosome membrane;endocytic vesicle;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;ruffle;vesicle Amoebiasis;Amyotrophic lateral sclerosis (ALS);Endocytosis;ko05152;Phagosome;Vasopressin-regulated water reabsorption

P61020-2;P61020 Ras-related protein Rab-5B RAB5B >sp|P61020-2|RAB5B_HUMAN Isoform 2 of Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B;>sp|P61020|RAB5B_HUMAN Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1 NaN NaN 0.44 NaN 0.93 NaN NaN NaN 3.83E-46 4 27.6 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;endosome organization;establishment of localization;establishment of protein localization;intracellular signal transduction;organelle organization;protein transport;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;GTP-dependent protein binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome membrane;endocytic vesicle;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;vesicle Amoebiasis;Endocytosis;ko05152;Phagosome;Vasopressin-regulated water reabsorption

P61224-2;P61224-3;P62834;P61224;F5GX62;P61224-4;E7ESV4;F5H7Y6;A6NIZ1;F5H4H0;F5GYH7;F5H077;F5GWU8;F5H491;F5H0B7;F5H500;F5H823;B7ZB78;F5H6R7;F5GZG1;F5H004;F5GYB5;F8WBC0 Ras-related protein Rap-1A;Ras-related protein Rap-1b;Ras-related protein Rap-1b-like protein RAP1A;RAP1B >sp|P61224-2|RAP1B_HUMAN Isoform 2 of Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B;>sp|P61224-3|RAP1B_HUMAN Isoform 3 of Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B;>sp|P62834|RAP1A_HUMAN Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A P 0.99 1.57 1.44 1.11 0.7 0.67 0.71 0.88 3.32E-47 4 29.9 activation of MAPKK activity;activation of protein kinase activity;biological regulation;cell activation;cell proliferation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;generation of precursor metabolites and energy;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;metabolic process;nerve growth factor receptor signaling pathway;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of catalytic activity;regulation of cell communication;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of establishment of cell polarity;regulation of establishment or maintenance of cell polarity;regulation of hormone secretion;regulation of insulin secretion;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of secretion;regulation of signaling;regulation of transferase activity;regulation of transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;guanyl-nucleotide exchange factor complex;intracellular part;lipid particle;macromolecular complex;membrane;plasma membrane;protein complex Chemokine signaling pathway;Focal adhesion;Leukocyte transendothelial migration;Long-term potentiation;MAPK signaling pathway;Neurotrophin signaling pathway;Pancreatic secretion;Renal cell carcinoma

Q9Y5S9;Q9Y5S9-2 RNA-binding protein 8A RBM8A >sp|Q9Y5S9|RBM8A_HUMAN RNA-binding protein 8A OS=Homo sapiens GN=RBM8A PE=1 SV=1;>sp|Q9Y5S9-2|RBM8A_HUMAN Isoform 2 of RNA-binding protein 8A OS=Homo sapiens GN=RBM8A 1.29 1.32 2.11 2.1 0.32 0.28 0.54 0.5 1.13E-37 4 20.7 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;exon-exon junction complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport;Spliceosome

P40429;M0QYS1;Q6NVV1;M0QZU1 60S ribosomal protein L13a;Putative 60S ribosomal protein L13a-like MGC87657 RPL13A >sp|P40429|RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2;>tr|M0QYS1|M0QYS1_HUMAN 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=4 SV=1;>sp|Q6NVV1|R13AX_HUMAN Putative 60S ribosomal protein L13a-like MGC87657 1.25 0.67 1.13 0.53 1.5 0.8 1.49 0.93 1.01E-33 4 20.2 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P50914;E7EPB3 60S ribosomal protein L14 RPL14 >sp|P50914|RL14_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4;>tr|E7EPB3|E7EPB3_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=2 SV=1 1.34 0.73 0.74 0.57 0.94 1.04 1.32 0.96 8.14E-35 4 22.3 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

J3QR09;J3KTE4;P84098;J3QL15 Ribosomal protein L19;60S ribosomal protein L19 RPL19 >tr|J3QR09|J3QR09_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=3 SV=1;>tr|J3KTE4|J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=3 SV=1;>sp|P84098|RL19_HUMAN 60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1;>tr|J3QL15| 1.54 0.73 0.85 0.64 0.81 0.66 1.5 0.97 5.67E-52 4 20.2 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P46778;G3V1B3;M0R181 60S ribosomal protein L21 RPL21 >sp|P46778|RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2;>tr|G3V1B3|G3V1B3_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=2 SV=1;>tr|M0R181|M0R181_HUMAN 60S ribosomal protein L21 (Fragment) OS=Homo sapiens GN=RPL21 PE 1.18 0.69 0.4 0.64 1.06 0.74 1.34 0.85 1.49E-07 4 23.1 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P62750;H7BY10;K7EJV9;K7ERT8;A8MUS3;K7EMA7 60S ribosomal protein L23a RPL23A >sp|P62750|RL23A_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1;>tr|H7BY10|H7BY10_HUMAN 60S ribosomal protein L23a (Fragment) OS=Homo sapiens GN=RPL23A PE=3 SV=1;>tr|K7EJV9|K7EJV9_HUMAN 60S ribosomal protein L23a (Fragment) OS=Homo sa 1.31 0.76 0.55 0.81 0.83 0.56 1.32 0.83 4.31E-49 4 25.6 "biosynthetic process;catabolic process;cell proliferation;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;nucleotide binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

C9JXB8;C9JNW5;P83731 60S ribosomal protein L24 RPL24 >tr|C9JXB8|C9JXB8_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1;>tr|C9JNW5|C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1;>sp|P83731|RL24_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 1.31 0.74 0.24 0.67 1.09 0.85 1.37 0.99 1.05E-23 4 31.4 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

J3KTJ8;J3QRI7;J3QQQ9;J3QQV1;J3QRC4;P61254;E5RIT6;Q9UNX3;J3KSS0;E5RHH1 60S ribosomal protein L26;60S ribosomal protein L26-like 1 RPL26;KRBA2;RPL26L1 >tr|J3KTJ8|J3KTJ8_HUMAN 60S ribosomal protein L26 (Fragment) OS=Homo sapiens GN=RPL26 PE=4 SV=1;>tr|J3QRI7|J3QRI7_HUMAN 60S ribosomal protein L26 (Fragment) OS=Homo sapiens GN=RPL26 PE=4 SV=1;>tr|J3QQQ9|J3QQQ9_HUMAN KRAB-A domain-containing protein 2 OS=Ho1.55 0.8 0.39 0.67 0.89 0.68 1.44 1 2.84E-12 4 27.8 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosol;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

D6RAN4;P32969;E7ESE0;H0Y9V9;H0Y9R4 60S ribosomal protein L9 RPL9 >tr|D6RAN4|D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1;>sp|P32969|RL9_HUMAN 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1;>tr|E7ESE0|E7ESE0_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL 1.44 0.8 0.67 0.64 1.16 0.87 1.19 0.85 1.96E-43 4 27.5 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

G3V210;F8VU65;Q3B7A4;F8VWS0;P05388;F8VS58;F8VQY6;F8VPE8;F8VRK7;F8VW21;F8VZS0;Q8NHW5;F8VWV4 60S acidic ribosomal protein P0;60S acidic ribosomal protein P0-likeRPLP0;RPLP0P6 >tr|G3V210|G3V210_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=2 SV=1;>tr|F8VU65|F8VU65_HUMAN 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens GN=RPLP0 PE=2 SV=1;>tr|Q3B7A4|Q3B7A4_HUMAN 60S acidic ribosomal protein P0 OS=Homo 1.2 0.78 0.96 0.53 0.98 0.85 1.71 1.15 3.06E-34 4 25.3 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular

transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral reproductive process;viral transcription;virus-host interaction" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosomeRibosome
P0CW22;P08708;H0YN88;H0YK46;H0YN73;H3BNC9 40S ribosomal protein S17-like;40S ribosomal protein S17 RPS17L;RPS17 >sp|P0CW22|RS17L_HUMAN 40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1;>sp|P08708|RS17_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2;>tr|H0YN88|H0YN88_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17L PE=2 SV 1.56 1.05 1.13 0.57 1.58 0.68 1.2 0.84 1.49E-16 4 31.1 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;erythrocyte homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;homeostasis of number of cells;homeostatic process;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological quality;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;nucleotide binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome
P39019;M0R2L9;M0QXK4;M0QYF7;M0R140 40S ribosomal protein S19 RPS19 >sp|P39019|RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2;>tr|M0R2L9|M0R2L9_HUMAN 40S ribosomal protein S19 (Fragment) OS=Homo sapiens GN=RPS19 PE=4 SV=1;>tr|M0QXK4|M0QXK4_HUMAN 40S ribosomal protein S19 (Fragment) OS=Homo sapiens 1.78 0.82 15.59 0.55 1.13 0.61 1.16 0.72 8.25E-31 4 27.6 "biological regulation;biosynthetic process;catabolic process;cell chemotaxis;cell differentiation;cell migration;cell motility;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to stimulus;chemotaxis;cotranslational protein targeting to membrane;developmental process;erythrocyte differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;immune system process;intracellular protein transport;intracellular transport;leukocyte chemotaxis;leukocyte migration;locomotion;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maturation of SSU-rRNA;maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;monocyte chemotaxis;mRNA catabolic process;mRNA metabolic process;myeloid cell differentiation;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of defense response;negative regulation of immune effector process;negative regulation of immune response;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of innate immune response;negative regulation of metabolic process;negative regulation of multicellular organismal process;negative regulation of respiratory burst;negative regulation of respiratory burst involved in inflammatory response;negative regulation of response to external stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleolus organization;nucleus organization;organelle organization;positive regulation of biological process;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of defense response;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune system process;positive regulation of inflammatory response;positive regulation of innate immune response;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of respiratory burst;positive regulation of respiratory burst involved in inflammatory response;positive regulation of response to external stimulus;positive regulation of response to stimulus;primary metabolic process;protein complex assembly;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein oligomerization;protein targeting;protein targeting to ER;protein targeting to membrane;protein tetramerization;protein transport;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cellular component movement;regulation of cellular process;regulation of defense response;regulation of developmental

process;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of innate immune response;regulation of localization;regulation of metabolic process;regulation of multicellular organismal process;regulation of respiratory burst;regulation of respiratory burst involved in inflammatory response;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;reproductive process;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;taxis;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

P10301 Ras-related protein R-Ras RRAS >sp|P10301|RRAS_HUMAN Ras-related protein R-Ras OS=Homo sapiens GN=RRAS PE=1 SV=1 0.92 1.71 1.07 0.95 0.67 0.64 0.64 0.95 1.46E-113 4 23.9 axon guidance;biological regulation;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;chemotaxis;intracellular signal transduction;locomotion;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;positive regulation of angiogenesis;positive regulation of biological process;positive regulation of developmental process;Ras protein signal transduction;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of developmental process;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;small GTPase mediated signal transduction;synaptic transmission;taxis "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;membrane;plasma membrane MAPK signaling pathway;Regulation of actin cytoskeleton;Tight junction

P62070;B7Z5Z2;E9PK85;P62070-3;P62070-2;E9PQK5;E9PQC5;E9PQ87 Ras-related protein R-Ras2 RRAS2 >sp|P62070|RRAS2_HUMAN Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=1 SV=1;>tr|B7Z5Z2|B7Z5Z2_HUMAN Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=2 SV=1;>tr|E9PK85|E9PK85_HUMAN Ras-related protein R-Ras2 (Fragment) OS=Homo sapiens GN=RRAS 1.34 1.69 1.69 0.92 0.6 0.44 0.63 0.76 1.05E-21 4 23 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;Ras protein signal transduction;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of locomotion;response to stimulus;signal transduction;small GTPase mediated signal transduction "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle;plasma membrane MAPK signaling pathway;Regulation of actin cytoskeleton;Tight junction

P06702 Protein S100-A9 S100A9 >sp|P06702|S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 0.22 0.36 0.03 0.13 4.76 3.42 1.59 1.63 2.72E-115 4 43.9 "actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;activation of caspase activity;autophagy;biological adhesion;biological regulation;catabolic process;cell adhesion;cell chemotaxis;cell communication;cell migration;cell motility;cell-cell adhesion;cell-cell signaling;cellular catabolic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemokine production;chemotaxis;chronic inflammatory response;cytokine production;cytoskeleton organization;defense response;defense response to bacterium;defense response to fungus;homotypic cell-cell adhesion;immune response;immune system process;induction of apoptosis;induction of programmed cell death;inflammatory response;innate immune response;leukocyte aggregation;leukocyte cell-cell adhesion;leukocyte chemotaxis;leukocyte migration;leukocyte migration involved in inflammatory response;locomotion;maintenance of location;metabolic process;multicellular organismal process;multi-organism process;neutrophil aggregation;neutrophil chemotaxis;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular process;positive regulation of defense response;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of inflammatory response;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytoskeleton organization;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of inflammatory response;regulation of integrin biosynthetic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to ethanol;response to external stimulus;response to fungus;response to inorganic substance;response to lipopolysaccharide;response to metal ion;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;response to wounding;response to zinc ion;sequestering of metal ion;sequestering of zinc ion;signaling;taxis"antioxidant activity;arachidonic acid binding;binding;calcium ion binding;carboxylic acid binding;cation binding;cytoskeletal protein binding;fatty acid binding;icosanoid binding;icosatetraenoic acid binding;ion binding;lipid binding;metal ion binding;microtubule binding;molecular transducer activity;monocarboxylic acid binding;protein binding;RAGE receptor binding;receptor binding;signal transducer activity;Toll-like receptor 4 binding;Toll-like receptor binding;transition metal ion binding;tubulin binding;zinc ion binding cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;plasma membrane

Q14108;Q14108-2;D6RDG0 Lysosome membrane protein 2 SCARB2 >sp|Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2;>sp|Q14108-2|SCRB2_HUMAN Isoform 2 of Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 NaN NaN 1.51 NaN 1.17 NaN NaN NaN 1.46E-09 4 6.7 biological adhesion;cell adhesion;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;intracellular protein transport;intracellular transport;lysosomal transport;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;transport;vacuolar transport receptor activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;lysosomal membrane;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part;plasma membrane part;vacuolar lumen;vacuolar membrane;vacuolar part;vacuole Lysosome

D6RFM5;E9PBJ5;P31040 "Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial" SDHA ">tr|D6RFM5|D6RFM5_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=2 SV=1;>tr|E9PBJ5|E9PBJ5_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=2" 1.08 1.3 1.41 0.87 1.43 0.79 1.05 0.97 1.82E-16 4 11.7 acetyl-CoA catabolic process;acetyl-CoA metabolic process;anatomical structure development;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental process;dicarboxylic acid metabolic process;electron transport chain;generation of precursor metabolites and energy;metabolic process;nervous system development;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;respiratory electron transport chain;small molecule metabolic process;succinate metabolic process;system development;tricarboxylic acid cycle "binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor;succinate dehydrogenase (ubiquinone) activity;succinate dehydrogenase activity" cell part;cytoplasmic part;fumarate reductase complex;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex II;organelle part;protein complex;succinate dehydrogenase complex;succinate dehydrogenase complex (ubiquinone) Alzheimer's disease;Citrate cycle (TCA cycle);Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P61619;B4DR61;P61619-3;F8W776;Q8TC24;Q9H9S3-2;Q9H9S3-3;Q9H9S3;H7C1Q9;C9JXC6;H7C069;A6NK38;F2Z2C7;A6NIF9;C9JJV4 Protein transport protein Sec61 subunit alpha isoform 1;Protein transport protein Sec61 subunit alpha isoform 2 SEC61A1;SEC61A2 >sp|P61619|S61A1_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2;>tr|B4DR61|B4DR61_HUMAN Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=2 SV=1;>sp|P61619-3|S61A1_HUMA 1.07 1.2 2.33 0.81 0.73 0.54 0.95 1.06 5.73E-11 4 8.4 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;immune system process;intracellular protein transport;intracellular transport;protein targeting;protein targeting to ER;protein transport;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;transport" binding;ribonucleoprotein binding;ribosome binding cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;rough endoplasmic reticulumPhagosome;Protein export;Protein processing in endoplasmic reticulum;Vibrio cholerae infection

P50454;E9PQ34;E9PJH8;E9PIG2;E9PRS3;E9PKH2;E9PNX1;E9PK86;E9PMI5;E9PR70;E9PPV6;H0YEP8;E9PLA6 Serpin H1 SERPINH1 >sp|P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2;>tr|E9PQ34|E9PQ34_HUMAN Serpin H1 (Fragment) OS=Homo sapiens GN=SERPINH1 PE=2 SV=1;>tr|E9PJH8|E9PJH8_HUMAN Serpin H1 (Fragment) OS=Homo sapiens GN=SERPINH1 PE=2 SV=1;>tr|E9PIG2|E9PIG2_H 0.55 0.68 0.93 0.97 0.66 0.48 1.26 1.03 3.41E-20 4 10.8 biological regulation;biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen biosynthetic process;collagen fibril organization;collagen metabolic process;extracellular matrix organization;extracellular structure organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;primary metabolic process;protein maturation;protein metabolic process;regulation of biological process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein binding;collagen binding;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;protein binding;serine-type endopeptidase inhibitor activity cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part

E7EUT8;Q12874 Splicing factor 3A subunit 3 SF3A3 >tr|E7EUT8|E7EUT8_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=2 SV=1;>sp|Q12874|SF3A3_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1 1.18 1.04 1.24 1.57 0.45 0.33 0.72 0.95 4.37E-34 4 14.1 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;mRNA splice site selection;nuclear mRNA 3'-splice site recognition;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

Q9BWM7 Sideroflexin-3 SFXN3 >sp|Q9BWM7|SFXN3_HUMAN Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=2 0.81 0.7 1.09 0.99 3.06 0.67 1.37 1.34 2.01E-11 4 16 biological regulation;cation homeostasis;chemical homeostasis;homeostatic process;ion homeostasis;iron ion homeostasis;regulation of biological quality cation transmembrane transporter activity;ion transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle part

B4DLV4;P34897-3;P34897;H0YIZ0;P34897-2;G3V5L0;G3V2Y4 "Serine hydroxymethyltransferase;Serine hydroxymethyltransferase, mitochondrial" SHMT2 ">tr|B4DLV4|B4DLV4_HUMAN Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT2 PE=2 SV=1;>sp|P34897-3|GLYM_HUMAN Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2;>sp|P34897|GLYM_HUMAN Serine hydroxymethyltransferase, m" 0.81 0.93 1.02 0.65 1.29 0.83 1.49 0.99 5.75E-15 4 11 amine biosynthetic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;folic acid-containing compound metabolic process;glycine biosynthetic process;glycine biosynthetic process from serine;glycine metabolic process;heterocycle metabolic process;L-serine biosynthetic process;L-serine metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;one-carbon metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;pteridine-containing compound metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;serine family amino acid biosynthetic process;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule metabolic process;tetrahydrofolate interconversion;tetrahydrofolate metabolic process "aldehyde-lyase activity;amine binding;amino acid binding;binding;carbon-carbon lyase activity;carboxylic acid binding;catalytic activity;chromatin binding;cofactor binding;glycine hydroxymethyltransferase activity;hydroxymethyl-, formyl- and related transferase activity;L-allo-threonine aldolase activity;lyase activity;methyltransferase activity;pyridoxal phosphate binding;threonine aldolase activity;transferase activity;transferase activity, transferring one-carbon groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microtubule cytoskeleton;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial matrix;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle envelope lumen;organelle inner membrane;organelle lumen;organelle membrane;organelle part "Cyanoamino acid metabolism;Glycine, serine and threonine metabolism;Methane metabolism;One carbon pool by folate"

P53985;Q5T8R3;Q49A45;Q5T8R5 Monocarboxylate transporter 1 SLC16A1 >sp|P53985|MOT1_HUMAN Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 0.78 1.31 1.63 1.16 0.6 0.3 0.64 0.88 4.29E-13 4 7.4 biological regulation;blood coagulation;carboxylic acid metabolic process;cell migration;cell motility;cellular component movement;cellular ketone metabolic process;cellular metabolic process;cellular process;coagulation;establishment of localization;hemostasis;immune system process;leukocyte migration;locomotion;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;organic acid metabolic process;oxoacid metabolic process;pyruvate metabolic process;regulation of biological quality;regulation of body fluid levels;small molecule metabolic process;transmembrane transport;transport active transmembrane transporter activity;carboxylic acid transmembrane transporter activity;mevalonate transmembrane transporter activity;monocarboxylic acid transmembrane transporter activity;organic acid transmembrane transporter activity;secondary active monocarboxylate transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;plasma membrane

P30825;Q5JR49;P52569;P52569-3 High affinity cationic amino acid transporter 1 SLC7A1 >sp|P30825|CTR1_HUMAN High affinity cationic amino acid transporter 1 OS=Homo sapiens GN=SLC7A1 PE=1 SV=1 NaN NaN 1.02 NaN 0.66 NaN NaN NaN 2.38E-09 4 7 amine metabolic process;amine transport;amino acid transport;biological regulation;biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;cell activation;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;immune system process;leukocyte activation;macrophage activation;metabolic process;multicellular organismal process;myeloid leukocyte activation;nitric oxide biosynthetic process;nitric oxide metabolic process;nitric oxide production involved in inflammatory response;nitrogen compound metabolic process;nitrogen compound transport;organic acid metabolic process;organic acid transport;organic substance transport;oxoacid metabolic process;primary metabolic process;production of molecular mediator involved in inflammatory response;regulation of biological process;regulation of cell activation;regulation of cellular process;regulation of defense response;regulation of immune system process;regulation of inflammatory response;regulation of leukocyte activation;regulation of macrophage activation;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;small molecule metabolic process;transmembrane transport;transport active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;arginine transmembrane transporter activity;basic amino acid transmembrane transporter activity;carboxylic acid transmembrane transporter activity;high affinity arginine transmembrane transporter activity;high affinity basic amino acid transmembrane transporter activity;L-amino acid transmembrane transporter activity;L-lysine transmembrane transporter activity;L-ornithine transmembrane transporter activity;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasm;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane part

Q01650;H0YJ95;G3V4Z6;Q9UM01;Q92536 Large neutral amino acids transporter small subunit 1 SLC7A5 >sp|Q01650|LAT1_HUMAN Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2 0.68 1.46 1.49 1.09 0.22 0.11 0.62 0.76 3.77E-31 4 10.1 amine metabolic process;amine transport;amino acid transport;anatomical structure development;biological regulation;blood coagulation;carboxylic acid metabolic process;carboxylic acid transport;cell differentiation;cell migration;cell motility;cellular amine metabolic process;cellular amino acid metabolic process;cellular component assembly;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coagulation;developmental process;establishment of localization;hemostasis;immune system process;leukocyte migration;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multicellular organismal process;nervous system development;nitrogen compound metabolic process;nitrogen compound transport;organic acid metabolic process;organic acid transport;organic substance transport;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;regulation of biological quality;regulation of body fluid levels;small molecule metabolic process;system development;transmembrane transport;transport active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;antigen binding;antiporter activity;binding;carboxylic acid transmembrane transporter activity;L-amino acid transmembrane transporter activity;neutral amino acid transmembrane transporter activity;organic acid transmembrane transporter activity;peptide antigen binding;peptide binding;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity apical plasma membrane;basolateral plasma membrane;cell part;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane;plasma membrane part Protein digestion and absorption

Q9NWH9;H0YLE6;H0YMW8;H0YNF3;H0YMR6;H0YL55;H7BXE3;H0YLW7;H0YMM0;H0YKU6;H7C3F4;A8K5V8 SAFB-like transcription modulatorSLTM >sp|Q9NWH9|SLTM_HUMAN SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2;>tr|H0YLE6|H0YLE6_HUMAN SAFB-like transcription modulator (Fragment) OS=Homo sapiens GN=SLTM PE=2 SV=1;>tr|H0YMW8|H0YMW8_HUMAN SAFB-like transcription modulator OS=Ho NaN NaN 0.51 NaN 0.33 NaN NaN NaN 2.22E-10 4 6.3 "apoptosis;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

H0YMA0;P09661;H0YLR3;H0YKK0 U2 small nuclear ribonucleoprotein A SNRPA1 >tr|H0YMA0|H0YMA0_HUMAN U2 small nuclear ribonucleoprotein A (Fragment) OS=Homo sapiens GN=SNRPA1 PE=2 SV=1;>sp|P09661|RU2A_HUMAN U2 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA1 PE=1 SV=2;>tr|H0YLR3|H0YLR3_HUMAN U2 small nuclear ribonucleo 1.18 0.96 2.09 1.44 0.79 0.35 0.8 0.67 1.41E-09 4 32.4 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U2 snRNP Spliceosome

P35321 Cornifin-A SPRR1A >sp|P35321|SPR1A_HUMAN Cornifin-A OS=Homo sapiens GN=SPRR1A PE=1 SV=2 0.62 0.89 0.39 0.25 2.75 2.59 1.42 0.52 5.45E-43 4 61.8 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity" cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P22528;E7ETD7 Cornifin-B SPRR1B >sp|P22528|SPR1B_HUMAN Cornifin-B OS=Homo sapiens GN=SPRR1B PE=1 SV=2;>tr|E7ETD7|E7ETD7_HUMAN Cornifin-B OS=Homo sapiens GN=SPRR1B PE=2 SV=1 0.41 0.51 0.27 0.11 3.24 3.73 1.38 1.05 3.16E-15 4 61.8 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity" cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

C9J3L8;C9J5W0;P43307;E9PAL7;C9IZQ1;P43307-2;F5H5Y2;C9JBX5 Translocon-associated protein subunit alpha SSR1 >tr|C9J3L8|C9J3L8_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1;>tr|C9J5W0|C9J5W0_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1;>sp|P43307|SSRA_HUMAN Translocon-associated protein 1.06 1.28 1.42 1.09 0.79 0.68 0.83 0.96 1.05E-195 4 21.5 activation of signaling protein activity involved in unfolded protein response;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;SRP-dependent cotranslational protein targeting to membrane;translation;transport cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Protein processing in endoplasmic reticulum

P51571;H7C1C6;A6NLM8 Translocon-associated protein subunit delta SSR4 >sp|P51571|SSRD_HUMAN Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1;>tr|H7C1C6|H7C1C6_HUMAN Translocon-associated protein subunit delta (Fragment) OS=Homo sapiens GN=SSR4 PE=4 SV=1;>tr|A6NLM8|A6NLM8_HUMAN Translocon-associat1.13 1.28 1.43 1.11 1.12 0.68 0.86 1.01 4.38E-41 4 28.9 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;SRP-dependent cotranslational protein targeting to membrane;translation;transport binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;membrane-bounded organelle;organelle;organelle part;protein complex;Sec61 translocon complex;translocon complex Protein processing in endoplasmic reticulum

Q5T9Q5;F5GXC8;Q9P2R7-2;Q9P2R7;Q5T9Q8;F5H5G8 "Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial" SUCLA2 ">tr|Q5T9Q5|Q5T9Q5_HUMAN Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=SUCLA2 PE=2 SV=1;>tr|F5GXC8|F5GXC8_HUMAN Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=2 SV=1;>"0.41 1.24 NaN 0.48 NaN 2.31 0.95 1.2 3.02E-08 4 13.8 acetyl-CoA catabolic process;acetyl-CoA metabolic process;biosynthetic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;porphyrin-containing compound biosynthetic process;porphyrin-containing compound metabolic process;small molecule metabolic process;succinate metabolic process;succinyl-CoA metabolic process;succinyl-CoA pathway;tetrapyrrole biosynthetic process;tetrapyrrole metabolic process;tricarboxylic acid cycle "acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;CoA-ligase activity;ion binding;ligase activity;ligase activity, forming carbon-sulfur bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;succinate-CoA ligase (ADP-forming) activity;succinate-CoA ligase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle partCitrate cycle (TCA cycle);Propanoate metabolism

Q9NZ01;B3KSQ1;M0R3C3;M0QXM3;Q9NZ01-2 Very-long-chain enoyl-CoA reductase TECR >sp|Q9NZ01|TECR_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1;>tr|B3KSQ1|B3KSQ1_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=2 SV=1;>tr|M0R3C3|M0R3C3_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sa 0.82 1.18 1.05 1.25 0.89 0.92 0.78 0.82 4.26E-16 4 13 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;fatty acid biosynthetic process;fatty acid elongation;fatty acid metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic ether metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process;very long-chain fatty acid biosynthetic process;very long-chain fatty acid metabolic process "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors" cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane part;organelle part Biosynthesis of unsaturated fatty acids

D6RAA6;P57088;H0Y8N0 Transmembrane protein 33 TMEM33 >tr|D6RAA6|D6RAA6_HUMAN Transmembrane protein 33 (Fragment) OS=Homo sapiens GN=TMEM33 PE=2 SV=1;>sp|P57088|TMM33_HUMAN Transmembrane protein 33 OS=Homo sapiens GN=TMEM33 PE=1 SV=2;>tr|H0Y8N0|H0Y8N0_HUMAN Transmembrane protein 33 (Fragment) OS=Homo sapiens 1.24 1.29 2.67 1.07 0.69 0.72 0.88 0.85 7.55E-15 4 17.1 cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;vesicle

Q8WWA1-2;Q8WWA1;B4DXI0;C9JID5 Transmembrane protein 40 TMEM40 >sp|Q8WWA1-2|TMM40_HUMAN Isoform 2 of Transmembrane protein 40 OS=Homo sapiens GN=TMEM40;>sp|Q8WWA1|TMM40_HUMAN Transmembrane protein 40 OS=Homo sapiens GN=TMEM40 PE=1 SV=2;>tr|B4DXI0|B4DXI0_HUMAN Transmembrane protein 40 OS=Homo sapiens GN=TMEM40 PE=2 SV= 0.75 0.75 0.53 0.22 2.12 1.79 1.26 1.35 8.31E-24 4 30.5 cell part;integral to membrane;intrinsic to membrane;membrane part

H0YF27 TRIM29 >tr|H0YF27|H0YF27_HUMAN Tripartite motif-containing protein 29 (Fragment) OS=Homo sapiens GN=TRIM29 PE=2 SV=1 NaN NaN NaN NaN NaN NaN NaN NaN 3.11E-12 4 28.4

P14927;E5RHG9;P14927-2;B7Z2R2 Cytochrome b-c1 complex subunit 7 UQCRB >sp|P14927|QCR7_HUMAN Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=1 SV=2;>tr|E5RHG9|E5RHG9_HUMAN Cytochrome b-c1 complex subunit 7 OS=Homo sapiens GN=UQCRB PE=2 SV=1;>sp|P14927-2|QCR7_HUMAN Isoform 2 of Cytochrome b-c1 complex subunit 7 O 1.08 1.61 1.68 1.81 0.46 0.35 0.54 0.91 8.01E-76 4 36 "aerobic respiration;cellular metabolic process;cellular process;cellular respiration;electron transport chain;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, ubiquinol to cytochrome c;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;respiratory electron transport chain;small molecule metabolic process" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain;mitochondrial respiratory chain complex III;organelle part;protein complex;respiratory chain;respiratory chain complex III Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P47985;P0C7P4 "Cytochrome b-c1 complex subunit Rieske, mitochondrial;Cytochrome b-c1 complex subunit 11;Putative cytochrome b-c1 complex subunit Rieske-like protein 1" UQCRFS1;UQCRFS1P1 ">sp|P47985|UCRI_HUMAN Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 PE=1 SV=2;>sp|P0C7P4|UCRIL_HUMAN Putative cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo sapiens GN=UQCRFS1P1 PE=5 SV=1" 1.29 1.42 1.5 1.6 0.52 0.36 0.79 0.88 2.66E-37 4 16.1 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;response to antibiotic;response to chemical stimulus;response to drug;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;small molecule metabolic process "2 iron, 2 sulfur cluster binding;binding;catalytic activity;cation binding;cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;iron-sulfur cluster binding;metal cluster binding;metal ion binding;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on diphenols and related substances as donors;oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;ubiquinol-cytochrome-c reductase activity" cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex III;mitochondrion;organelle;organelle part;protein complex;respiratory chain complex III Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

O95292;E5RK64;O95292-2 Vesicle-associated membrane protein-associated protein B/C VAPB >sp|O95292|VAPB_HUMAN Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3;>tr|E5RK64|E5RK64_HUMAN Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=2 SV=1;>sp|O95292-2|VAPB_HUMAN 1.08 1.25 1.85 0.88 0.82 0.79 0.83 0.91 1.76E-25 4 22.2 activation of signaling protein activity involved in unfolded protein response;biological regulation;biosynthetic process;calcium ion homeostasis;cation homeostasis;cell death;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;chemical homeostasis;death;divalent inorganic cation homeostasis;homeostatic process;interaction with host;interspecies interaction between organisms;ion homeostasis;lipid biosynthetic process;lipid metabolic process;membrane lipid biosynthetic process;membrane lipid metabolic process;metabolic process;metal ion homeostasis;multi-organism process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of reproductive process;positive regulation of transferase activity;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of reproductive process;regulation of transferase activity;regulation of viral genome replication;regulation of viral reproduction;reproductive process;small molecule metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process;viral reproductive process;virus-host interaction beta-tubulin binding;binding;cytoskeletal protein binding;protein binding;structural molecule activity;tubulin binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part

B0AZP7;B4DPX4;Q99536;K7EJM4;K7ESA3;K7ENX2;K7EM19 Synaptic vesicle membrane protein VAT-1 homolog VAT1 >tr|B0AZP7|B0AZP7_HUMAN Chromaffin granule amine transporter OS=Homo sapiens GN=VAT1 PE=2 SV=1;>tr|B4DPX4|B4DPX4_HUMAN Chromaffin granule amine transporter OS=Homo sapiens GN=VAT1 PE=2 SV=1;>sp|Q99536|VAT1_HUMAN Synaptic vesicle membrane protein VAT-1 homo NaN NaN 0.04 NaN 0.19 NaN NaN NaN 8.60E-21 4 15.8 biological regulation;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of mitochondrial fusion;negative regulation of mitochondrion organization;negative regulation of organelle organization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of mitochondrial fusion;regulation of mitochondrion organization;regulation of organelle organization binding;catalytic activity;cation binding;ion binding;metal ion binding;oxidoreductase activity;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane

Q9UNX4 WD repeat-containing protein 3 WDR3 >sp|Q9UNX4|WDR3_HUMAN WD repeat-containing protein 3 OS=Homo sapiens GN=WDR3 PE=1 SV=1 NaN NaN 1.44 NaN 0.89 NaN NaN NaN 1.09E-10 4 7 cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;organelle;organelle membrane;organelle part Ribosome biogenesis in eukaryotes

Q9H0D6-2;B4DZC3;Q9H0D6 5-3 exoribonuclease 2 XRN2 >sp|Q9H0D6-2|XRN2_HUMAN Isoform 2 of 5-3 exoribonuclease 2 OS=Homo sapiens GN=XRN2;>tr|B4DZC3|B4DZC3_HUMAN 5-3 exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=2 SV=1;>sp|Q9H0D6|XRN2_HUMAN 5-3 exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1 1.29 0.96 1.07 1.84 0.75 0.67 1.06 0.96 4.43E-10 4 5.8 "biological regulation;biosynthetic process;catabolic process;cell growth;cellular biosynthetic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA catabolic process;DNA catabolic process, exonucleolytic;DNA metabolic process;gamete generation;growth;macromolecule catabolic process;macromolecule metabolic process;male gamete generation;metabolic process;mRNA metabolic process;mRNA processing;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;spermatogenesis;transcription termination, DNA-dependent" "5'-3' exonuclease activity;5'-3' exoribonuclease activity;binding;catalytic activity;cation binding;exonuclease activity;exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;exoribonuclease activity;exoribonuclease activity, producing 5'-phosphomonoesters;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nuclease activity;nucleic acid binding;ribonuclease activity;transition metal ion binding;zinc ion binding" aggresome;cell part;inclusion body;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes;RNA degradation

P56181-2 ">sp|P56181-2|NDUV3_HUMAN Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial OS=Homo sapiens GN=NDUFV3" 1.04 1.57 1.03 1.97 0.42 0.4 0.69 0.87 1.63E-31 4 14.8

H0Y3Y4;H0YFF6;G3V1Q4;Q16181-2;E7ES33;E7EPK1;Q16181;F5GZE5;C9JV02;Q14141-3;Q92599-3;B4E049;D6RDU5;D6RGI3;Q14141-2;Q9NVA2;Q92599-2;Q14141-4;A6NMH6;B1AMS2;Q6ZU15;D6RER5;Q14141;Q9NVA2-2;A6NFQ9;F6W7K9;F5H1J5;F8W8I8;Q92599 Septin-7 41889 ">tr|H0Y3Y4|H0Y3Y4_HUMAN Septin-7 (Fragment) OS=Homo sapiens GN=SEPT7 PE=2 SV=1;>tr|H0YFF6|H0YFF6_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=2 SV=1;>tr|G3V1Q4|G3V1Q4_HUMAN Septin 7, isoform CRA_a OS=Homo sapiens GN=SEPT7 PE=2 SV=1;>sp|Q16181-2|SEPT7_HUMAN I" 0.69 2.42 0.28 1.48 0.42 1.14 0.84 1.11 1.28E-24 5 13.1 anatomical structure morphogenesis;biological regulation;cell cycle;cell cycle phase;cell cycle process;cell division;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cilium morphogenesis;cytokinesis;developmental process;interaction with host;interspecies interaction between organisms;macromolecular complex assembly;macromolecular complex subunit organization;mitosis;multi-organism process;nuclear division;organelle fission;organelle organization;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of embryonic cell shape;regulation of embryonic development;regulation of multicellular organismal development;regulation of multicellular organismal process;reproductive process;viral reproductive process;virus-host interaction binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural molecule activity actin cytoskeleton;actin filament bundle;actomyosin;axon;axon part;axon terminus;axoneme;cell cortex part;cell division site part;cell junction;cell part;cell projection;cell projection part;chromosomal part;cilium axoneme;cilium part;clathrin-coated vesicle;cleavage furrow;coated vesicle;condensed chromosome kinetochore;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;dendritic spine;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule cytoskeleton;midbody;neuron projection;neuron projection terminus;neuron spine;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;protein complex;septin complex;spindle;stress fiber;synapse;synapse part;synaptic vesicle;vesicle

Q9H845;H0Y8Z9 "Acyl-CoA dehydrogenase family member 9, mitochondrial" ACAD9 ">sp|Q9H845|ACAD9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1;>tr|H0Y8Z9|H0Y8Z9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial (Fragment) OS=Homo sapiens GN=ACAD9 PE=2 SV=1" 0.9 1 1.04 1.1 1.18 1.24 0.99 0.87 1.79E-10 5 8.1 "acyl-CoA dehydrogenase activity;binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors" cell part;cell projection;cytoplasmic part;dendrite;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;nucleus;organelle Geraniol degradation;Naphthalene degradation

B7Z3Z9;E7EPM6;P33121-2;P33121;B7Z452;D6RER0;H0Y9Z9;H0Y9U7 Long-chain-fatty-acid--CoA ligase 1 ACSL1 >tr|B7Z3Z9|B7Z3Z9_HUMAN Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=2 SV=1;>tr|E7EPM6|E7EPM6_HUMAN Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=2 SV=1;>sp|P33121-2|ACSL1_HUMAN Isoform 2 of Long-chain-fatty-acid--CoA l 0.85 0.6 0.81 0.15 4.09 2.49 1.46 0.96 7.80E-11 5 10.1 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;adiponectin-mediated signaling pathway;biological regulation;biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;cytokine-mediated signaling pathway;establishment of localization;fatty acid metabolic process;fatty acid transport;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;linoleic acid metabolic process;lipid biosynthetic process;lipid metabolic process;lipid transport;long-chain fatty acid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid metabolic process;organic acid transport;organic ether metabolic process;organic substance transport;oxoacid metabolic process;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of transferase activity;response to chemical stimulus;response to cytokine stimulus;response to drug;response to external stimulus;response to extracellular stimulus;response to fatty acid;response to lipid;response to nutrient;response to nutrient levels;response to oleic acid;response to organic cyclic compound;response to organic substance;response to stimulus;signal transduction;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;transport;triglyceride biosynthetic process;triglyceride metabolic process;unsaturated fatty acid metabolic process;xenobiotic catabolic process;xenobiotic metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;fatty acid ligase activity;ligase activity;ligase activity, forming carbon-sulfur bonds;long-chain fatty acid-CoA ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;peroxisomal membrane;peroxisomal part;plasma membrane Adipocytokine signaling pathway;Fatty acid metabolism;Peroxisome;PPAR signaling pathway

P02649;E9PEV4;E7ERP7;H0Y7L5 Apolipoprotein E APOE >sp|P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1;>tr|E9PEV4|E9PEV4_HUMAN Apolipoprotein E (Fragment) OS=Homo sapiens GN=APOE PE=2 SV=1;>tr|E7ERP7|E7ERP7_HUMAN Apolipoprotein E (Fragment) OS=Homo sapiens GN=APOE PE=2 SV=1;>tr|H0Y7L5| 0.53 1.29 1.02 0.7 0.37 0.4 0.94 1.35 8.38E-96 5 20.2 "acylglycerol metabolic process;aging;alcohol metabolic process;anatomical structure morphogenesis;artery morphogenesis;axon regeneration;axonogenesis;biological regulation;biosynthetic process;blood vessel morphogenesis;calcium ion homeostasis;catabolic process;cation homeostasis;cell communication;cell death;cell differentiation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cell-cell signaling;cellular biosynthetic process;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to cholesterol;cellular response to cytokine stimulus;cellular response to growth factor stimulus;cellular response to interleukin-1;cellular response to lipid;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cGMP-mediated signaling;chemical homeostasis;cholesterol catabolic process;cholesterol efflux;cholesterol homeostasis;cholesterol metabolic process;cholesterol transport;chylomicron remnant clearance;circulatory system process;cyclic-nucleotide-mediated signaling;cytoskeleton organization;death;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;divalent inorganic cation homeostasis;endocytosis;establishment of localization;establishment of localization in cell;glial cell differentiation;glycerol ether metabolic process;glycerolipid metabolic process;G-protein coupled receptor protein signaling pathway;high-density lipoprotein particle assembly;high-density lipoprotein particle clearance;high-density lipoprotein particle remodeling;homeostatic process;induction of apoptosis;induction of programmed cell death;intracellular signal transduction;intracellular transport;ion homeostasis;isoprenoid metabolic process;lipid catabolic process;lipid homeostasis;lipid metabolic process;lipid transport;lipoprotein biosynthetic process;lipoprotein catabolic process;lipoprotein metabolic process;low-density lipoprotein particle remodeling;macromolecular complex assembly;macromolecular complex remodeling;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maintenance of location;maintenance of location in cell;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of blood coagulation;negative regulation of blood vessel endothelial cell migration;negative regulation of catalytic activity;negative regulation of cell activation;negative regulation of cell death;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of cholesterol biosynthetic process;negative regulation of cholesterol metabolic process;negative regulation of coagulation;negative regulation of defense response;negative regulation of endothelial cell migration;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;negative regulation of inflammatory response;negative regulation of kinase activity;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of locomotion;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of neuron apoptosis;negative regulation of platelet activation;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of steroid biosynthetic process;negative regulation of steroid metabolic process;negative regulation of transferase activity;neuron projection morphogenesis;neuron projection regeneration;neutral lipid metabolic process;nitric oxide mediated signal transduction;oligodendrocyte differentiation;organelle organization;organic ether metabolic process;organic substance transport;peripheral nervous system axon regeneration;phospholipid efflux;phospholipid transport;phototransduction;phototransduction, visible light;plasma lipoprotein particle assembly;plasma lipoprotein particle clearance;plasma lipoprotein particle organization;plasma lipoprotein particle remodeling;positive regulation of apoptosis;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular biosynthetic process;positive regulation of cellular catabolic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cGMP biosynthetic process;positive regulation of cGMP metabolic process;positive regulation of cholesterol efflux;positive regulation of cholesterol esterification;positive regulation of cholesterol transport;positive regulation of cyclic nucleotide biosynthetic process;positive regulation of cyclic nucleotide metabolic process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of lipid metabolic process;positive regulation of lipid transport;positive regulation of low-density lipoprotein particle receptor catabolic process;positive regulation of macromolecule metabolic process;positive regulation of membrane protein ectodomain proteolysis;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of monooxygenase activity;positive regulation of neurogenesis;positive regulation of nitric-oxide synthase activity;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleotide biosynthetic process;positive regulation of nucleotide metabolic process;positive regulation of oxidoreductase activity;positive regulation of programmed cell death;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of proteolysis;positive regulation of receptor catabolic process;positive regulation of steroid metabolic process;positive regulation of sterol transport;positive regulation of transport;primary metabolic process;protein-lipid complex assembly;protein-lipid complex remodeling;protein-lipid complex subunit organization;receptor-mediated endocytosis;regeneration;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of apoptosis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood coagulation;regulation of blood vessel endothelial cell migration;regulation of blood vessel size;regulation of catabolic process;regulation of catalytic activity;regulation of Cdc42 protein signal transduction;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cGMP biosynthetic process;regulation of cGMP metabolic process;regulation of cholesterol biosynthetic process;regulation of cholesterol efflux;regulation of cholesterol esterification;regulation of cholesterol metabolic process;regulation of cholesterol transport;regulation of coagulation;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of defense response;regulation of developmental growth;regulation of developmental process;regulation of endothelial cell migration;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of extent of cell growth;regulation of gene expression;regulation of growth;regulation of inflammatory response;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of lipid transport;regulation of localization;regulation of locomotion;regulation of low-density lipoprotein particle receptor catabolic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of membrane protein ectodomain proteolysis;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron apoptosis;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of oxidoreductase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of platelet activation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of proteolysis;regulation of Ras protein signal transduction;regulation of receptor catabolic process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of sterol transport;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of transport;regulation of tube size;regulation of wound healing;response to abiotic stimulus;response to axon injury;response to chemical stimulus;response to cholesterol;response to cytokine stimulus;response to dietary excess;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to hormone stimulus;response to inorganic substance;response to insulin stimulus;response to interleukin-1;response to light stimulus;response to lipid;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to radiation;response to reactive oxygen species;response to retinoic acid;response to stimulus;response to stress;response to vitamin;response to vitamin A;response to wounding;retinoid metabolic process;reverse cholesterol transport;second-messenger-mediated signaling;signal transduction;signaling;small molecule metabolic process;steroid catabolic process;steroid metabolic process;sterol catabolic process;sterol homeostasis;sterol metabolic process;sterol transport;synaptic transmission;synaptic transmission, cholinergic;system process;terpenoid metabolic process;transport;triglyceride metabolic process;triglyceride-rich lipoprotein particle clearance;triglyceride-rich lipoprotein particle remodeling;vascular process in circulatory system;vasodilation;very-low-density lipoprotein particle clearance;very-low-density lipoprotein particle remodeling;vesicle-mediated transport"

antioxidant activity;beta-amyloid binding;binding;carbohydrate binding;cation binding;cholesterol transporter activity;enzyme activator activity;enzyme regulator activity;glycosaminoglycan binding;heparin binding;hydroxyapatite binding;identical protein binding;ion binding;lipid binding;lipid transporter activity;lipoprotein particle binding;lipoprotein particle receptor binding;low-density lipoprotein particle receptor binding;metal chelating activity;metal ion binding;pattern binding;phosphatidylcholine-sterol O-acyltransferase activator activity;phospholipid binding;polysaccharide binding;protein binding;protein dimerization activity;protein homodimerization activity;protein-lipid complex binding;receptor binding;sterol transporter activity;substrate-specific transporter activity;transporter activity;very-low-density lipoprotein particle receptor binding cell body;cell part;cell projection;chylomicron;cytoplasmic part;dendrite;early endosome;endosome;extracellular region;extracellular region part;extrinsic to external side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus;high-density lipoprotein particle;intermediate-density lipoprotein particle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;late endosome;low-density lipoprotein particle;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuron projection;neuronal cell body;organelle;plasma lipoprotein particle;plasma membrane;plasma membrane part;protein-lipid complex;triglyceride-rich lipoprotein particle;very-low-density lipoprotein particle

Alzheimer's disease

O15143;C9J4Z7;C9JEY1;C9JQM8;C9JFG9;C9J6C8;C9JTT6;C9JBJ7;C9K057 Actin-related protein 2/3 complex subunit 1B ARPC1B >sp|O15143|ARC1B_HUMAN Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3;>tr|C9J4Z7|C9J4Z7_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=2 SV=1;>tr|C9JEY1|C9JEY1_HUMAN Actin-relate0.69 1.19 0.9 2.34 0.4 0.51 0.51 0.9 3.37E-13 5 17.2 biological regulation;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular process;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization structural constituent of cytoskeleton;structural molecule activity Arp2/3 protein complex;cell part;cytoplasm;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis P59998;F8WCF6;P59998-3;F8WDD7;H7C0A3;P59998-2;R4GN08;P59998-4;F8WE39 Actin-related protein 2/3 complex subunit 4 ARPC4;ARPC4-TTLL3 >sp|P59998|ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3;>tr|F8WCF6|F8WCF6_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=2 SV=1;>sp|P59998-3|ARPC4_HUMAN Isoform 3 of Actin-related 0.63 2.44 0.73 3.19 0.23 0.59 0.43 0.94 2.03E-24 5 28 actin cytoskeleton organization;actin filament organization;actin filament polymerization;actin filament-based process;actin nucleation;actin polymerization or depolymerization;Arp2/3 complex-mediated actin nucleation;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;protein complex assembly;protein complex subunit organization;protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stress Arp2/3 protein complex;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis Q12797;Q12797-10;E5RHJ2;Q12797-7;Q12797-6;Q12797-2;E5RG56;E5RHK2;G3XAN5;E5RG29;Q12797-4;Q12797-3;Q12797-9;Q12797-5;Q12797-8 Aspartyl/asparaginyl beta-hydroxylase ASPH >sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3;>sp|Q12797-10|ASPH_HUMAN Isoform 10 of Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH 1.17 0.96 1.55 0.52 1.34 0.81 1.16 1.36 1.53E-66 5 11.7 "activation of store-operated calcium channel activity;anatomical structure development;anatomical structure morphogenesis;appendage morphogenesis;biological regulation;calcium ion transmembrane transport;calcium ion transport;calcium-mediated signaling;cation transport;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;detection of calcium ion;detection of chemical stimulus;detection of stimulus;developmental process;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;face morphogenesis;intracellular signal transduction;ion transmembrane transport;ion transport;limb morphogenesis;macromolecule metabolic process;macromolecule modification;metabolic process;metal ion transport;multicellular organismal process;muscle contraction;muscle system process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;palate development;pattern specification process;peptidyl-amino acid modification;peptidyl-aspartic acid hydroxylation;peptidyl-aspartic acid modification;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of calcium ion transport;positive regulation of calcium ion transport into cytosol;positive regulation of calcium ion transport via store-operated calcium channel activity;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of homeostatic process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of ion transmembrane transporter activity;positive regulation of ion transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein metabolic process;positive regulation of protein transport;positive regulation of proteolysis;positive regulation of RNA metabolic process;positive regulation of ryanodine-sensitive calcium-release channel activity;positive regulation of transcription, DNA-dependent;positive regulation of transport;positive regulation of transporter activity;primary metabolic process;protein hydroxylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of calcium ion transport via store-operated calcium channel activity;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cell communication;regulation of cell communication by electrical coupling;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of establishment of protein localization;regulation of gene expression;regulation of heart contraction;regulation of homeostatic process;regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of proteolysis;regulation of receptor activity;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of response to stimulus;regulation of RNA metabolic process;regulation of ryanodine-sensitive calcium-release channel activity;regulation of signal transduction;regulation of signaling;regulation of striated muscle contraction;regulation of system process;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to ATP;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to stimulus;second-messenger-mediated signaling;signal transduction;system process;transmembrane transport;transport" "binding;calcium ion binding;catalytic activity;cation binding;dioxygenase activity;electron carrier activity;ion binding;ion channel binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptide-aspartate beta-dioxygenase activity;protein binding;structural constituent of muscle;structural molecule activity" calcium channel complex;cation channel complex;cell cortex part;cell part;cortical endoplasmic reticulum;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;ion channel complex;junctional sarcoplasmic reticulum membrane;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle membrane;organelle part;plasma membrane;protein complex;sarcoplasmic reticulum lumen;sarcoplasmic reticulum membrane

Q9HD20-2;Q9HD20;H7C3H2;Q9HD20-3 Probable cation-transporting ATPase 13A1 ATP13A1 >sp|Q9HD20-2|AT131_HUMAN Isoform B of Probable cation-transporting ATPase 13A1 OS=Homo sapiens GN=ATP13A1;>sp|Q9HD20|AT131_HUMAN Probable cation-transporting ATPase 13A1 OS=Homo sapiens GN=ATP13A1 PE=1 SV=2 NaN NaN 1.29 0.88 0.94 1.11 NaN NaN 2.09E-14 5 5.2 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;ion transmembrane transporter activity;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;integral to membrane;intrinsic to membrane;membrane part

P54709;C9JXZ1;C9JA36;B7Z1N7;H7C547;F8WBY4 Sodium/potassium-transporting ATPase subunit beta-3 ATP1B3 >sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1;>tr|C9JXZ1|C9JXZ1_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 (Fragment) OS=Homo sapiens GN=ATP1B3 PE=2 SV=1;>tr|C9JA36|C9JA36_HUMA 0.85 1.09 1.64 0.73 0.66 0.59 0.99 1.04 1.11E-35 5 21.5 biological regulation;blood coagulation;cation transport;cell migration;cell motility;cellular component movement;cellular process;coagulation;establishment of localization;hemostasis;immune system process;ion transport;leukocyte migration;locomotion;metal ion transport;monovalent inorganic cation transport;multicellular organismal process;potassium ion transport;regulation of biological quality;regulation of body fluid levels;sodium ion transport;transport "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;potassium ion transmembrane transporter activity;potassium-transporting ATPase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;pyrophosphatase activity;sodium ion transmembrane transporter activity;sodium:potassium-exchanging ATPase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" caveola;cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;melanosome;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;plasma membrane part;protein complex;sodium:potassium-exchanging ATPase complex;vesicle Aldosterone-regulated sodium reabsorption;Bile secretion;Carbohydrate digestion and absorption;Cardiac muscle contraction;Endocrine and other factor-regulated calcium reabsorption;Gastric acid secretion;Mineral absorption;Pancreatic secretion;Protein digestion and absorption;Proximal tubule bicarbonate reclamation;Salivary secretion

Q9BXK5;Q9BXK5-4;B7Z238;E9PDD6;Q9BXK5-2 Bcl-2-like protein 13 BCL2L13 >sp|Q9BXK5|B2L13_HUMAN Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=1 SV=1;>sp|Q9BXK5-4|B2L13_HUMAN Isoform 3 of Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13;>tr|B7Z238|B7Z238_HUMAN Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=2 SV=1 1.14 1.38 1.79 0.51 1.1 0.56 1.14 1.42 3.02E-15 5 19.4 biological regulation;induction of apoptosis;induction of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death apoptotic protease activator activity;caspase activator activity;caspase regulator activity;enzyme activator activity;enzyme regulator activity;peptidase activator activity;peptidase regulator activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle membrane;organelle part

P62158;H0Y7A7;E7ETZ0;E7EMB3;F8WBR5;M0QZ52;G3V479;G3V361;Q96HY3;G3V226 Calmodulin CALM1;CALM2;CALM3 >sp|P62158|CALM_HUMAN Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2;>tr|H0Y7A7|H0Y7A7_HUMAN Calmodulin (Fragment) OS=Homo sapiens GN=CALM2 PE=2 SV=1;>tr|E7ETZ0|E7ETZ0_HUMAN Calmodulin OS=Homo sapiens GN=CALM1 PE=2 SV=1;>tr|E7EMB3|E7EMB3_HUMAN Calmodulin OS 0.98 1.63 1.15 1.6 0.21 0.35 0.68 1.06 5.55E-108 5 34.2 activation of phospholipase C activity;alcohol metabolic process;biological regulation;calcium-mediated signaling;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell activation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization or biogenesis;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;defense response;detection of calcium ion;detection of chemical stimulus;detection of stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;fibroblast growth factor receptor signaling pathway;generation of precursor metabolites and energy;glucan catabolic process;glucan metabolic process;glucose metabolic process;glycogen catabolic process;glycogen metabolic process;G-protein coupled receptor protein signaling pathway;hexose metabolic process;immune response;immune system process;innate immune response;inositol phosphate metabolic process;intracellular signal transduction;macromolecule catabolic process;macromolecule metabolic process;membrane organization;metabolic process;monosaccharide metabolic process;multicellular organismal process;muscle contraction;muscle system process;negative regulation of biological process;negative regulation of ion transmembrane transporter activity;negative regulation of molecular function;negative regulation of ryanodine-sensitive calcium-release channel activity;negative regulation of transport;negative regulation of transporter activity;nerve growth factor receptor signaling pathway;nitric oxide metabolic process;nitrogen compound metabolic process;organophosphate metabolic process;oxidation-reduction process;platelet activation;platelet degranulation;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cyclic nucleotide metabolic process;positive regulation of cyclic-nucleotide phosphodiesterase activity;positive regulation of dephosphorylation;positive regulation of hydrolase activity;positive regulation of ion transmembrane transporter activity;positive regulation of lipase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleotide metabolic process;positive regulation of phosphatase activity;positive regulation of phosphate metabolic process;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphoprotein phosphatase activity;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of ryanodine-sensitive calcium-release channel activity;positive regulation of transport;positive regulation of transporter activity;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of catalytic activity;regulation of cell division;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclic nucleotide metabolic process;regulation of cyclic-nucleotide phosphodiesterase activity;regulation of cytokinesis;regulation of dephosphorylation;regulation of heart contraction;regulation of heart rate;regulation of homeostatic process;regulation of hydrolase activity;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of lipase activity;regulation of lipoprotein lipase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide metabolic process;regulation of oxidoreductase activity;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to stimulus;response to stress;second-messenger-mediated signaling;secretion;secretion by cell;signal transduction;signaling;small molecule metabolic process;synaptic transmission;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport "binding;calcium ion binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;ion binding;kinase activity;metal ion binding;phosphatase activator activity;phosphatase regulator activity;protein phosphatase activator activity;protein phosphatase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;centrosome;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;plasma membrane;protein complex;sarcomere;spindle microtubule;spindle pole Alzheimer's disease;Calcium signaling pathway;Gastric acid secretion;Glioma;GnRH signaling pathway;Insulin signaling pathway;ko05152;Long-term potentiation;Melanogenesis;Neurotrophin signaling pathway;Olfactory transduction;Oocyte meiosis;Phosphatidylinositol signaling system;Phototransduction;Phototransduction - fly;Plant-pathogen interaction;Salivary secretion;Vascular smooth muscle contraction

P52907 F-actin-capping protein subunit alpha-1 CAPZA1 >sp|P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 0.8 1.41 1.11 2.19 0.41 0.66 0.56 1.01 1.23E-91 5 25.9 actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;defense response;hemostasis;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;protein complex assembly;protein complex subunit organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to stimulus;response to stress actin binding;binding;cytoskeletal protein binding;protein binding cell part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region;F-actin capping protein complex;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex;WASH complex

B1AK87;P47756-2;B1AK88;P47756;F6Q0E3;F6USW4;B1AK85 F-actin-capping protein subunit beta CAPZB ">tr|B1AK87|B1AK87_HUMAN Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=2 SV=1;>sp|P47756-2|CAPZB_HUMAN Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB;>tr|B1AK88|B1AK88_HUMAN Cappi" 0.76 1.36 1 2 0.42 0.66 0.59 0.91 1.88E-33 5 18.1 actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;hemostasis;lamellipodium assembly;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell morphogenesis;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization actin binding;binding;cytoskeletal protein binding;protein binding cell cortex part;cell part;cell projection;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;F-actin capping protein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;protein complex;WASH complex

P20810-9;B7Z468;P20810-5;E7ESM9;P20810-7;P20810-6;H0Y7F0;H0Y9H6;P20810-3;E9PDE4;E7ES10;P20810-4;E9PCH5;P20810-8;E7EVY3;B7Z574;P20810-2;P20810;E7EQ12;E7EQA0;H0YD33;D6RC54;F8W7E0;D6RAA8;D6RGF7;D6RBR1;E7EN75;H0Y944;H0YA91;E9PSG1 Calpastatin CAST >sp|P20810-9|ICAL_HUMAN Isoform 9 of Calpastatin OS=Homo sapiens GN=CAST;>tr|B7Z468|B7Z468_HUMAN DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CAST PE=2 SV=1;>sp|P20810-5|ICAL_HUMAN Isoform 5 of Calpastatin OS=Homo sapiens GN=CAST;>tr|E7ES 1.43 0.5 NaN 0.27 0.83 1.44 2.67 1.89 5.80E-38 5 9.3 biological regulation;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;regulation of biological process;regulation of catalytic activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity cell part;membrane

P48643;E7ENZ3;B7ZAR1;E9PCA1;B4DYD8;D6RIZ7 T-complex protein 1 subunit epsilon CCT5 >sp|P48643|TCPE_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1;>tr|E7ENZ3|E7ENZ3_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1;>tr|B7ZAR1|B7ZAR1_HUMAN T-complex protein 1 subunit epsilon OS=Homo sa 1.43 NaN 0.74 NaN 1.67 NaN 1.57 NaN 8.14E-15 5 15.7 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;multi-organism process;primary metabolic process;protein folding;protein metabolic process;response to biotic stimulus;response to other organism;response to stimulus;response to virus adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;centrosome;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex

H0YD13;P16070-18;P16070-12;P16070-14;P16070-13;P16070-11;P16070-10;P16070-16;P16070-8;P16070-17;P16070-6;P16070-4;P16070-3;P16070-7;E7EPC6;P16070-5;P16070;H0Y2P0;H0YE40;H0YDW7;H0YCV9;P16070-15;H0Y5E4;P16070-9;E9PKC6;Q86UZ1;P16070-19;H0YDX6;H0YD17;J3KN83 CD44 antigen CD44 >tr|H0YD13|H0YD13_HUMAN CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1;>sp|P16070-18|CD44_HUMAN Isoform 18 of CD44 antigen OS=Homo sapiens GN=CD44;>sp|P16070-12|CD44_HUMAN Isoform 12 of CD44 antigen OS=Homo sapiens GN=CD44;>sp|P16070-14|CD44_HUM 0.95 1.21 1.38 0.71 0.77 0.45 0.89 1.24 7.57E-25 5 31.4 "amine metabolic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biological adhesion;biological regulation;branching involved in prostate gland morphogenesis;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;carbohydrate catabolic process;carbohydrate metabolic process;cartilage development;catabolic process;cell adhesion;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-matrix adhesion;cell-substrate adhesion;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;developmental process involved in reproduction;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;homotypic cell-cell adhesion;hyaluronan catabolic process;hyaluronan metabolic process;interferon-gamma-mediated signaling pathway;leukocyte aggregation;leukocyte cell-cell adhesion;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monocyte aggregation;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular process;negative regulation of DNA damage response, signal transduction by p53 class mediator;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nitrogen compound metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell-cell adhesion;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ERK1 and ERK2 cascade;positive regulation of gene expression;positive regulation of heterotypic cell-cell adhesion;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of peptidyl-serine phosphorylation;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;prostate gland epithelium morphogenesis;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell-cell adhesion;regulation of cell-cell adhesion involved in gastrulation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of DNA damage response, signal transduction by p53 class mediator;regulation of embryonic development;regulation of endopeptidase activity;regulation of ERK1 and ERK2 cascade;regulation of gastrulation;regulation of gene expression;regulation of heterotypic cell-cell adhesion;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of peptidase activity;regulation of peptidyl-serine phosphorylation;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to interferon-gamma;response to organic substance;response to stimulus;response to stress;response to wounding;signal transduction;small molecule metabolic process;tissue development;tissue morphogenesis;tube morphogenesis;Wnt receptor signaling pathway;wound healing;wound healing involved in inflammatory response" "binding;carbohydrate binding;catalytic activity;collagen binding;glycosaminoglycan binding;hexosaminidase activity;hyaluronic acid binding;hyalurononglucosaminidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;pattern binding;polysaccharide binding;protein binding" basolateral plasma membrane;cell part;cell surface;cytoplasmic part;external side of plasma membrane;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;organelle;plasma membrane;plasma membrane part ECM-receptor interaction;Hematopoietic cell lineage;Shigellosis

Q99459 Cell division cycle 5-like protein CDC5L >sp|Q99459|CDC5L_HUMAN Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2 1.27 0.96 1.12 1.82 0.76 0.51 0.79 0.81 8.02E-17 5 9.4 "biological regulation;biosynthetic process;cell cycle;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;chromatin binding;DNA binding;nucleic acid binding;protein binding;protein domain specific binding;RNA binding;WD40-repeat domain binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;protein complex;Prp19 complex;ribonucleoprotein complex;spliceosomal complex Spliceosome

F5GWX5;Q14839;Q14839-2;Q5TG85;K7EMY3;Q8TDI0;Q12873-2;Q12873;Q12873-3 Chromodomain-helicase-DNA-binding protein 4 CHD4 >tr|F5GWX5|F5GWX5_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=2 SV=1;>sp|Q14839|CHD4_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2;>sp|Q14839-2|CHD4_HUMAN Isoform 2 of Chromodomain-heli 1.18 1.14 1.22 2.47 0.45 0.41 0.63 0.5 2.54E-17 5 3 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;centrosome organization;chromatin modification;chromatin organization;chromosome organization;cytoskeleton organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;spindle organization;transcription, DNA-dependent""adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;cation binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transition metal ion binding;zinc ion binding" cell part;centrosome;chromatin remodeling complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;histone deacetylase complex;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;protein complex;transcriptional repressor complex

P02452;CON__Q862S4 Collagen alpha-1(I) chain COL1A1 >sp|P02452|CO1A1_HUMAN Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5 NaN NaN 1.49 NaN 3.65 NaN NaN NaN 7.85E-12 5 4.1 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;biomineral tissue development;biosynthetic process;blood vessel development;bone trabecula formation;cartilage development;cartilage development involved in endochondral bone morphogenesis;cell activation;cell communication;cell differentiation;cell migration;cell motility;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to abiotic stimulus;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to growth factor stimulus;cellular response to mechanical stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to organic nitrogen;cellular response to organic substance;cellular response to retinoic acid;cellular response to stimulus;cellular response to transforming growth factor beta stimulus;cellular response to vitamin;cellular response to vitamin A;collagen biosynthetic process;collagen catabolic process;collagen fibril organization;collagen metabolic process;developmental process;embryonic skeletal system development;endochondral ossification;epidermis morphogenesis;establishment of localization;establishment of protein localization;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;face morphogenesis;immune system process;intramembranous ossification;leukocyte migration;localization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular process;neurological system process;ossification;osteoblast differentiation;platelet activation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cell communication;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell morphogenesis involved in differentiation;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of epithelial to mesenchymal transition;positive regulation of gene expression;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription, DNA-dependent;positive regulation of Wnt receptor signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein localization;protein localization to nucleus;protein localization to organelle;protein oligomerization;protein transport;protein trimerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of cell adhesion;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell-substrate adhesion;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of epithelial to mesenchymal transition;regulation of gene expression;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;response to abiotic stimulus;response to acid;response to amine stimulus;response to amino acid stimulus;response to cAMP;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to mechanical stimulus;response to nutrient;response to nutrient levels;response to organic nitrogen;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to reactive oxygen species;response to retinoic acid;response to steroid hormone stimulus;response to stimulus;response to stress;response to transforming growth factor beta stimulus;response to vitamin;response to vitamin A;sensory perception;sensory perception of light stimulus;sensory perception of mechanical stimulus;sensory perception of sound;skeletal system development;skin morphogenesis;system development;system process;tissue development;tissue morphogenesis;tooth mineralization;trabecula formation;transport;visual perception"binding;cation binding;extracellular matrix structural constituent;growth factor binding;identical protein binding;ion binding;metal ion binding;platelet-derived growth factor binding;protein binding;structural molecule activity cell part;collagen;collagen type I;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;extracellular space;fibrillar collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Amoebiasis;ECM-receptor interaction;Focal adhesion;Protein digestion and absorption

P53618;E9PP73;E9PP63;E9PKQ1Coatomer subunit beta COPB1 >sp|P53618|COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3;>tr|E9PP73|E9PP73_HUMAN Coatomer subunit beta (Fragment) OS=Homo sapiens GN=COPB1 PE=2 SV=1 0.71 1.24 0.4 0.95 1.7 1.45 1.1 1.37 1.06E-09 5 7.8 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;multi-organism process;organelle organization;protein transport;reproductive process;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport;viral reproductive process;virus-host interaction" structural molecule activity cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;endoplasmic reticulum-Golgi intermediate compartment;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;vesicle coat

P13073;Q86WV2;H3BN72;H3BNV9;H3BNI5;H3BPG0 "Cytochrome c oxidase subunit 4 isoform 1, mitochondrial" COX4I1 ">sp|P13073|COX41_HUMAN Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1;>tr|Q86WV2|Q86WV2_HUMAN COX4I1 protein OS=Homo sapiens GN=COX4I1 PE=2 SV=1;>tr|H3BN72|H3BN72_HUMAN Cytochrome c oxidase subunit 4 isoform 1," 1.22 1.64 1.45 1.47 0.46 0.44 0.65 0.74 3.53E-13 5 31.4 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to stimulus;small molecule metabolic process "catalytic activity;cation transmembrane transporter activity;cytochrome-c oxidase activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P20674;H3BRM5;H3BV69;H3BNX8 "Cytochrome c oxidase subunit 5A, mitochondrial" COX5A ">sp|P20674|COX5A_HUMAN Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2;>tr|H3BRM5|H3BRM5_HUMAN Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=2 SV=1;>tr|H3BV69|H3BV69_HUMAN Cytochrome c oxidase" 1.3 1.68 1.44 1.6 0.46 0.56 0.59 0.91 2.22E-12 5 36.7 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process "binding;catalytic activity;cation binding;cation transmembrane transporter activity;cytochrome-c oxidase activity;electron carrier activity;heme-copper terminal oxidase activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on a heme group of donors, oxygen as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P51398-2;P51398-3;P51398 "28S ribosomal protein S29, mitochondrial" DAP3 ">sp|P51398-2|RT29_HUMAN Isoform 2 of 28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3;>sp|P51398-3|RT29_HUMAN Isoform 3 of 28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3;>sp|P51398|RT29_HUMAN 28S ribosomal protein S29, mit" NaN NaN 2.22 NaN 1.02 NaN NaN NaN 9.38E-21 5 21 apoptotic mitochondrial changes;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;mitochondrion organization;organelle organization cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial part;mitochondrial ribosome;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit

Q96GQ7 Probable ATP-dependent RNA helicase DDX27 DDX27 >sp|Q96GQ7|DDX27_HUMAN Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2 1.3 1.18 1.23 2.31 0.4 1.03 0.55 0.51 1.73E-15 5 6.9 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q14195;Q14195-2;H0YBT4;F5GWI3 Dihydropyrimidinase-related protein 3 DPYSL3 >sp|Q14195|DPYL3_HUMAN Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1;>sp|Q14195-2|DPYL3_HUMAN Isoform LCRMP-4 of Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3;>tr|H0YBT4|H0YBT4_HUMAN Dihydropyrimidinase-related NaN NaN NaN 2.85 NaN 0.6 NaN NaN 6.44E-13 5 11.8 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;anatomical structure development;axon guidance;biological regulation;catabolic process;cell development;cellular aromatic compound metabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;heterocycle catabolic process;heterocycle metabolic process;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell projection organization;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of locomotion;negative regulation of neuron projection development;neuron development;nitrogen compound metabolic process;nucleobase catabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;organelle organization;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of filopodium assembly;positive regulation of neuron projection development;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;pyrimidine base catabolic process;pyrimidine base metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of filopodium assembly;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;response to axon injury;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to organic substance;response to stimulus;response to stress;response to wounding;small molecule metabolic process;taxis "binding;carbohydrate binding;catalytic activity;chondroitin sulfate binding;glycosaminoglycan binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides;pattern binding;polysaccharide binding;protein binding;protein domain specific binding;SH3 domain binding" cell body;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region part;extracellular space;filamentous actin;growth cone;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;organelle part;protein complex;site of polarized growth

Q14126 Desmoglein-2 DSG2 >sp|Q14126|DSG2_HUMAN Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2 1.41 1.65 1.08 1.48 0.48 0.37 0.63 1.1 1.75E-12 5 5.2 biological adhesion;cell adhesion;cell-cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;desmosome;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Arrhythmogenic right ventricular cardiomyopathy (ARVC)

Q96C19;H0Y4Y4;C9JTV4;Q8WYH2;Q9BUP0-2;Q9BUP0 EF-hand domain-containing protein D2 EFHD2 >sp|Q96C19|EFHD2_HUMAN EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=11.11 1.05 2.42 2.48 0.58 0.34 0.62 1.03 1.72E-15 5 20 cell projection organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;neuron projection development binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

Q504U8;E9PFD7;P00533;P00533-2;P00533-4;P00533-3;C9JYS6;J3KTI5;H3BLT0;J3QLU9;Q15303-4;Q15303-3;Q15303-2;Q15303 Epidermal growth factor receptor EGFR >tr|Q504U8|Q504U8_HUMAN EGFR protein OS=Homo sapiens GN=EGFR PE=2 SV=1;>tr|E9PFD7|E9PFD7_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=2 SV=2;>sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 1.13 1.24 1 0.82 2.33 0.59 0.84 0.91 1.78E-19 5 6.3 "activation of phospholipase A2 activity;activation of phospholipase A2 activity by calcium-mediated signaling;activation of phospholipase C activity;ameboidal cell migration;anatomical structure development;anatomical structure morphogenesis;apoptosis;axon guidance;biological adhesion;biological regulation;biosynthetic process;body fluid secretion;calcium-mediated signaling;cardiac muscle tissue regeneration;cell adhesion;cell death;cell differentiation;cell fate commitment;cell migration;cell morphogenesis;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;central nervous system morphogenesis;cerebral cortex cell migration;chemotaxis;death;defense response;developmental growth;developmental process;digestive tract morphogenesis;embryonic organ development;embryonic pattern specification;embryonic placenta development;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epidermis development;epithelial cell differentiation;establishment of localization;fibroblast growth factor receptor signaling pathway;forebrain cell migration;gland morphogenesis;growth;hair cycle process;hair follicle development;heart development;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;intracellular signal transduction;lactation;localization;localization within membrane;locomotion;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;macromolecule modification;mammary gland alveolus development;mammary gland epithelial cell differentiation;metabolic process;molting cycle;molting cycle process;morphogenesis of an epithelial fold;morphogenesis of an epithelium;multicellular organismal process;multicellular organismal reproductive process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;neural crest cell migration;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;olfactory bulb interneuron differentiation;organ development;ossification;pattern specification process;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cardiac muscle cell proliferation;positive regulation of catalytic activity;positive regulation of catenin import into nucleus;positive regulation of cell communication;positive regulation of cell cycle;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cyclin-dependent protein kinase activity;positive regulation of cyclin-dependent protein kinase activity involved in G1/S;positive regulation of developmental process;positive regulation of DNA metabolic process;positive regulation of DNA repair;positive regulation of DNA replication;positive regulation of epithelial cell proliferation;positive regulation of ERK1 and ERK2 cascade;positive regulation of fibroblast proliferation;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JAK-STAT cascade;positive regulation of kinase activity;positive regulation of lipase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phospholipase A2 activity;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein import into nucleus;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of protein transport;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of STAT protein import into nucleus;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of tyrosine phosphorylation of STAT protein;positive regulation of tyrosine phosphorylation of Stat5 protein;primary metabolic process;programmed cell death;protein autophosphorylation;protein insertion into membrane;protein localization;protein metabolic process;protein modification process;protein phosphorylation;regeneration;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cardiac muscle cell proliferation;regulation of cardiac muscle tissue development;regulation of cardiac muscle tissue growth;regulation of catabolic process;regulation of catalytic activity;regulation of catenin import into nucleus;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cyclin-dependent protein kinase activity;regulation of cyclin-dependent protein kinase activity involved in G1/S;regulation of developmental growth;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA repair;regulation of DNA replication;regulation of epidermal growth factor receptor signaling pathway;regulation of epithelial cell proliferation;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of fibroblast proliferation;regulation of gene expression;regulation of growth;regulation of heart growth;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of lipase activity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organ growth;regulation of oxidoreductase activity;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phospholipase A2 activity;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of STAT protein import into nucleus;regulation of striated muscle tissue development;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmembrane transport;regulation of transport;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat5 protein;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to light stimulus;response to organic substance;response to radiation;response to stimulus;response to stress;response to UV;response to UV-A;RNA biosynthetic process;RNA metabolic process;salivary gland morphogenesis;second-messenger-mediated signaling;secretion;signal transduction;signal transduction via phosphorylation event;taxis;telencephalon cell migration;tissue development;tissue morphogenesis;tissue regeneration;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;transport" "actin binding;actin filament binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cytoskeletal protein binding;DNA binding;double-stranded DNA binding;epidermal growth factor-activated receptor activity;kinase activity;MAP kinase kinase kinase activity;molecular transducer activity;nucleic acid binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein dimerization activity;protein heterodimerization activity;protein kinase activity;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;receptor signaling protein tyrosine kinase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;signal transducer activity;signaling receptor activity;structure-specific DNA binding;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity" basolateral plasma membrane;cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endocytic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;endosomal part;endosome;endosome membrane;extracellular region;extracellular region part;extracellular space;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nuclear membrane;nuclear part;nucleoplasm;nucleus;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;Shc-EGFR complex;vesicle Adherens junction;Bladder cancer;Calcium signaling pathway;Cytokine-cytokine receptor interaction;Dorso-ventral axis formation;Endocytosis;Endometrial cancer;Epithelial cell signaling in Helicobacter pylori infection;ErbB signaling pathway;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;Hepatitis C;MAPK signaling pathway;MAPK signaling pathway - fly;Melanoma;Non-small cell lung cancer;Pancreatic cancer;Pathways in cancer;Prostate cancer;Regulation of actin cytoskeleton

P50402;Q5HY57 Emerin EMD >sp|P50402|EMD_HUMAN Emerin OS=Homo sapiens GN=EMD PE=1 SV=1;>tr|Q5HY57|Q5HY57_HUMAN Emerin OS=Homo sapiens GN=EMD PE=2 SV=1 1.2 NaN 1.7 0.97 0.83 0.86 0.93 NaN 6.15E-109 5 26 anaphase;anatomical structure development;biological regulation;cell cycle phase;cell cycle process;cell differentiation;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;developmental process;M phase;M phase of mitotic cell cycle;membrane disassembly;membrane organization;mitotic anaphase;mitotic nuclear envelope disassembly;mitotic nuclear envelope reassembly;mitotic prophase;multicellular organismal process;muscle cell differentiation;muscle contraction;muscle organ development;muscle structure development;muscle system process;negative regulation of biological process;negative regulation of catenin import into nucleus;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of fibroblast proliferation;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of nucleocytoplasmic transport;negative regulation of protein import into nucleus;negative regulation of protein transport;negative regulation of transmembrane transport;negative regulation of transport;nuclear envelope disassembly;nuclear envelope organization;nuclear envelope reassembly;organ development;positive regulation of biological process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein export from nucleus;positive regulation of protein transport;positive regulation of transport;prophase;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of catenin import into nucleus;regulation of cell proliferation;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of fibroblast proliferation;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of nucleocytoplasmic transport;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transmembrane transport;regulation of transport;regulation of Wnt receptor signaling pathway;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;skeletal muscle cell differentiation;striated muscle cell differentiation;system process	actin binding;beta-tubulin binding;binding;cytoskeletal protein binding;protein binding;tubulin binding	cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;nuclear inner membrane;nuclear membrane;nuclear outer membrane;nuclear part;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex	Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM)

H7BXI1;A0FGR8-6;A0FGR8-2;A0FGR8;F2Z3K9;A0FGR8-5;A0FGR8-4	Extended synaptotagmin-2	ESYT2	>tr|H7BXI1|H7BXI1_HUMAN Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=2 SV=1;>sp|A0FGR8-6|ESYT2_HUMAN Isoform 6 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2;>sp|A0FGR8-2|ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sa	0.83	0.99	1.6	0.68	1.55	1.31	0.86	0.9	2.80E-32	5	7.4		cell part;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane

B0V109;B4DVY7;O75955;B0S8A9;B0V111;A2AB09;B0S8B0;B0V108;A2ABJ5;B0V112;B0V110;A2AB12;A2AB10	Flotillin-1	FLOT1	>tr|B0V109|B0V109_HUMAN Flotillin-1 (Fragment) OS=Homo sapiens GN=FLOT1 PE=2 SV=1;>tr|B4DVY7|B4DVY7_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=2 SV=1;>sp|O75955|FLOT1_HUMAN Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3;>tr|B0S8A9|B0S8A9_HUMAN Flotillin	1.17	1.86	1.85	2.67	0.41	0.41	0.44	0.42	5.22E-29	5	14.8	anatomical structure morphogenesis;axonogenesis;biological regulation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;developmental process;localization;macromolecule localization;membrane organization;neuron projection morphogenesis;plasma membrane organization;protein localization;protein localization in membrane;protein localization in plasma membrane;regulation of biological process;regulation of cellular process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction		caveola;cell part;centriolar satellite;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;endosome;flotillin complex;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center part;organelle;organelle part;pigment granule;plasma membrane;plasma membrane part;protein complex;sarcolemma;vesicle	Insulin signaling pathway

Q14254;J3QLD9;E7EMK3;K7EKW9	Flotillin-2	FLOT2	>sp|Q14254|FLOT2_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2;>tr|J3QLD9|J3QLD9_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=4 SV=1;>tr|E7EMK3|E7EMK3_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=2 SV=1	NaN	NaN	1.74	1.67	0.67	1.11	NaN	NaN	7.56E-15	5	13.8	anatomical structure development;biological adhesion;cell adhesion;cellular process;developmental process;epidermis development;tissue development	acrosomal membrane;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endosome;flotillin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;secretory granule membrane;vesicle;vesicle membrane	Insulin signaling pathway

Q96AE4;Q96AE4-2;E9PEB5;B4DT31;C9JSZ1	Far upstream element-binding protein 1	FUBP1	>sp|Q96AE4|FUBP1_HUMAN Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3;>sp|Q96AE4-2|FUBP1_HUMAN Isoform 2 of Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1;>tr|E9PEB5|E9PEB5_HUMAN Far upstream element-binding prot	1.45	NaN	1.55	NaN	0.47	NaN	1.92	NaN	1.20E-08	5	9.9	"biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;primary metabolic process;regulation of biological process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent"	binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;RNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding	cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

O94925-3;O94925;O94925-2;B8ZZC5;H7BZD1;B8ZZA8	"Glutaminase kidney isoform, mitochondrial"	GLS	">sp|O94925-3|GLSK_HUMAN Isoform 3 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS;>sp|O94925|GLSK_HUMAN Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1;>sp|O94925-2|GLSK_HUMAN Isoform 2 of Glutaminase kidney i"	0.6	0.83	1.02	0.3	1.27	1.32	1.91	3.32	5.44E-23	5	12.9	amine biosynthetic process;amine catabolic process;amine metabolic process;behavior;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;glutamate biosynthetic process;glutamate metabolic process;glutamate secretion;glutamine catabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multicellular organismal process;neurological system process;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;regulation of biological process;regulation of biological quality;regulation of multicellular organismal process;regulation of neurotransmitter levels;regulation of respiratory gaseous exchange;regulation of respiratory gaseous exchange by neurological system process;regulation of respiratory system process;regulation of system process;response to stimulus;secretion;secretion by cell;signal release;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;system process;transport "catalytic activity;glutaminase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides" cell part;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;D-Glutamine and D-glutamate metabolism;Nitrogen metabolism;Proximal tubule bicarbonate reclamation" P08754;P11488;P19087;A8MTJ3;P09471-2;P09471;H3BTM2;P38405-3 Guanine nucleotide-binding protein G(k) subunit alpha GNAI3 >sp|P08754|GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 1.27 1.72 1.5 1.1 0.32 0.28 0.56 0.83 1.61E-16 5 17.8 "aging;anatomical structure development;behavior;biological regulation;calcium ion homeostasis;cAMP-mediated signaling;catabolic process;cation homeostasis;cell activation;cell communication;cell cycle;cell development;cell division;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to electrical stimulus;cellular response to stimulus;chemical homeostasis;cyclic-nucleotide-mediated signaling;cytosolic calcium ion homeostasis;detection of abiotic stimulus;detection of chemical stimulus;detection of chemical stimulus involved in sensory perception;detection of chemical stimulus involved in sensory perception of bitter taste;detection of chemical stimulus involved in sensory perception of taste;detection of external stimulus;detection of light stimulus;detection of light stimulus involved in sensory perception;detection of light stimulus involved in visual perception;detection of stimulus;detection of stimulus involved in sensory perception;detection of visible light;developmental process;divalent inorganic cation homeostasis;dopamine receptor signaling pathway;elevation of cytosolic calcium ion concentration;establishment of localization;eye photoreceptor cell development;forebrain development;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;ion homeostasis;locomotory behavior;membrane fusion;membrane organization;metabolic process;metal ion homeostasis;multicellular organismal process;muscle contraction;muscle system process;negative regulation of adenylate cyclase activity;negative regulation of biological process;negative regulation of calcium ion transport;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of cyclic-nucleotide phosphodiesterase activity;negative regulation of hydrolase activity;negative regulation of ion transport;negative regulation of lyase activity;negative regulation of molecular function;negative regulation of transport;neurological system process;neuron development;neuron projection development;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle fusion;organelle organization;photoreceptor cell development;phototransduction;phototransduction, visible light;platelet activation;positive regulation of catalytic activity;positive regulation of cyclic-nucleotide phosphodiesterase activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of adenylate cyclase activity;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcium ion transport;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of cyclic-nucleotide phosphodiesterase activity;regulation of GTP catabolic process;regulation of GTPase activity;regulation of heart contraction;regulation of hydrolase activity;regulation of ion transport;regulation of localization;regulation of lyase activity;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of system process;regulation of transport;response to abiotic stimulus;response to alkaloid;response to chemical stimulus;response to cytokine stimulus;response to drug;response to electrical stimulus;response to external stimulus;response to hydrogen peroxide;response to inorganic substance;response to isoquinoline alkaloid;response to light intensity;response to light stimulus;response to morphine;response to nicotine;response to organic cyclic compound;response to organic substance;response to oxidative stress;response to radiation;response to reactive oxygen species;response to stimulus;response to stress;retina development in camera-type eye;retinal cone cell development;rhodopsin mediated signaling pathway;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;second-messenger-mediated signaling;sensory perception;sensory perception of chemical stimulus;sensory perception of sweet taste;sensory perception of taste;sensory perception of umami taste;signal transduction;signaling;small molecule metabolic process;synaptic transmission;system process;transport;vesicle fusion;vesicle organization" "acyl binding;binding;catalytic activity;cation binding;enzyme binding;GDP binding;G-protein beta/gamma-subunit complex binding;G-protein coupled photoreceptor activity;G-protein coupled receptor activity;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;kinase binding;metabotropic serotonin receptor binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;photoreceptor activity;protein binding;protein complex binding;protein kinase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor activity;receptor binding;ribonucleotide binding;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity" apical plasma membrane;cell body;cell part;cell projection;cell projection part;centrosome;cilium;cilium part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus;heterotrimeric G-protein complex;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;midbody;neuron projection;neuronal cell body;non-membrane-bounded organelle;nonmotile primary cilium;organelle;organelle part;photoreceptor connecting cilium;photoreceptor inner segment;photoreceptor outer segment;photoreceptor outer segment membrane;plasma membrane part;primary cilium;protein complex;stored secretory granule;vesicle;zymogen granule Axon guidance;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Gap junction;Gastric acid secretion;Leukocyte transendothelial migration;Long-term depression;Melanogenesis;Phototransduction;Progesterone-mediated oocyte maturation;Tight junction;Toxoplasmosis

P62879;C9JZN1;C9JIS1;C9JXA5;Q9HAV0;C9JD14;B3KPU1 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2;Guanine nucleotide-binding protein subunit beta-4 GNB2;GNB4 >sp|P62879|GBB2_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3;>tr|C9JZN1|C9JZN1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (Fragment) OS=Homo sapiens GN=GNB2 PE=2 SV=1;> 0.93 1.8 1.11 1.28 0.45 0.53 0.61 0.89 1.38E-26 5 13.2 biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to glucagon stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;G-protein coupled receptor protein signaling pathway;metabolic process;oxidation-reduction process;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to glucagon stimulus;response to hormone stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;signaling;small molecule metabolic process;synaptic transmission "calcium channel regulator activity;catalytic activity;channel regulator activity;GTPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;molecular transducer activity;nucleoside-triphosphatase activity;pyrophosphatase activity;signal transducer activity" cell body;cell part;cytoplasmic part;intracellular part;macromolecular complex;membrane;perinuclear region of cytoplasm;plasma membrane;protein complex Chemokine signaling pathway

P07305;P07305-2 Histone H1.0 H1F0 >sp|P07305|H10_HUMAN Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3;>sp|P07305-2|H10_HUMAN Isoform 2 of Histone H1.0 OS=Homo sapiens GN=H1F0 1.24 1.35 0.32 1.75 1.37 1.3 0.64 0.57 5.57E-42 5 26.3 "catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization" binding;DNA binding;nucleic acid binding cell part;chromatin;chromosomal part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear part;nucleoplasm;nucleosome;organelle;organelle part;protein-DNA complex

P17096;P17096-3;H7BYM6;P17096-2;E5RIT9 High mobility group protein HMG-I/HMG-Y HMGA1 >sp|P17096|HMGA1_HUMAN High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3;>sp|P17096-3|HMGA1_HUMAN Isoform HMG-R of High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1;>tr|H7BYM6|H7BYM6_HUMAN High mobility group protein 1.2 1.25 0.94 2.52 0.64 0.29 0.35 0.38 1.29E-15 5 44.9 "aging;base-excision repair;biological regulation;biosynthetic process;cell aging;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;cellular senescence;chromatin assembly;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA repair;DNA unwinding involved in replication;heterochromatin formation;heterochromatin organization;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of chromatin silencing;negative regulation of gene expression;negative regulation of gene silencing;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;oncogene-induced senescence;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell aging;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular senescence;positive regulation of developmental process;positive regulation of gene expression;positive regulation of gene expression, epigenetic;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cell aging;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of cellular senescence;regulation of chromatin silencing;regulation of developmental process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of gene silencing;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to biotic stimulus;response to DNA damage stimulus;response to other organism;response to stimulus;response to stress;response to virus;RNA biosynthetic process;RNA metabolic process;senescence-associated heterochromatin focus formation;transcription, DNA-dependent" 5'-deoxyribose-5-phosphate lyase activity;AT DNA binding;binding;carbon-oxygen lyase activity;catalytic activity;DNA binding;DNA-(apurinic or apyrimidinic site) lyase activity;hormone receptor binding;ligand-dependent nuclear receptor transcription coactivator activity;lyase activity;nuclear hormone receptor binding;nucleic acid binding;nucleic acid binding transcription factor activity;peroxisome proliferator activated receptor binding;protein binding;protein binding transcription factor activity;receptor binding;retinoic acid receptor binding;retinoid X receptor binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity cell part;chromatin;chromosomal part;cytoplasmic part;cytosol;heterochromatin;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;senescence-associated heterochromatin focus;transcription factor complex

Q13151 Heterogeneous nuclear ribonucleoprotein A0 HNRNPA0 >sp|Q13151|ROA0_HUMAN Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 1.16 0.84 1.66 1.81 0.38 0.36 0.78 0.68 1.11E-38 5 25.9 "3'-UTR-mediated mRNA stabilization;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;inflammatory response;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;response to stress;response to wounding;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization" AU-rich element binding;binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex

D6RAF8;Q14103-3;Q14103;H0YA96;H0Y8G5;Q14103-4;B4DTC3;Q14103-2;D6RF44;D6RBQ9;F5H6R6;D6RD83 Heterogeneous nuclear ribonucleoprotein D0 HNRNPD >tr|D6RAF8|D6RAF8_HUMAN Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Homo sapiens GN=HNRNPD PE=2 SV=1;>sp|Q14103-3|HNRPD_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD;>sp|Q14103|HNRPD_HUMAN Heterogeneou 1.05 1.04 1.1 1.68 0.34 0.3 0.99 0.73 4.02E-48 5 27.6 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;sequence-specific DNA binding;telomeric DNA binding cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex

Q58FF6 Putative heat shock protein HSP 90-beta 4 HSP90AB4P >sp|Q58FF6|H90B4_HUMAN Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1 NaN NaN NaN 1.31 NaN 0.52 NaN NaN 1.08E-38 5 9.5 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;response to stimulus;response to stress adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;intracellular part

Q16666-3;Q16666-6;Q16666-2;E7EPR3;Q16666;Q16666-7;H3BM18;H3BVE6;H3BR88;Q6K0P9-6;Q6K0P9-5;Q6K0P9-4;Q6K0P9-3;Q6K0P9-2;Q6K0P9 Gamma-interferon-inducible protein 16 IFI16 >sp|Q16666-3|IF16_HUMAN Isoform 3 of Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16;>sp|Q16666-6|IF16_HUMAN Isoform 4 of

Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16;>sp|Q16666-2|IF16_HUMAN Isoform 2 of Gamma-interferon-in 1.55 0.78 1.26 0.9 0.8 0.26 1.32 0.76 4.12E-17 5 10.1 "activation of immune response;activation of innate immune response;autophagy;biological regulation;biosynthetic process;catabolic process;cell communication;cell cycle;cell differentiation;cell proliferation;cellular biosynthetic process;cellular catabolic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to ionizing radiation;cellular response to nutrient levels;cellular response to radiation;cellular response to starvation;cellular response to stimulus;cellular response to stress;defense response;defense response to virus;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;immune effector process;immune response;immune system process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;inflammatory response;innate immune response;intracellular signal transduction;leukocyte differentiation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monocyte differentiation;multi-organism process;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cysteine-type endopeptidase activity;negative regulation of defense response;negative regulation of DNA binding;negative regulation of endopeptidase activity;negative regulation of gene expression;negative regulation of hydrolase activity;negative regulation of immune response;negative regulation of immune system process;negative regulation of innate immune response;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of peptidase activity;negative regulation of reproductive process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of gene expression;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of interleukin-1 beta production;positive regulation of interleukin-1 production;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of type I interferon production;primary metabolic process;regulation of apoptosis;regulation of autophagy;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cytokine production;regulation of defense response;regulation of DNA binding;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interleukin-1 beta production;regulation of interleukin-1 production;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of type I interferon production;regulation of viral genome replication;regulation of viral reproduction;response to abiotic stimulus;response to biotic stimulus;response to DNA damage stimulus;response to external stimulus;response to extracellular stimulus;response to ionizing radiation;response to nutrient levels;response to other organism;response to radiation;response to starvation;response to stimulus;response to stress;response to virus;response to wounding;RNA biosynthetic process;RNA metabolic process;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;transcription, DNA-dependent" binding;DNA binding;double-stranded DNA binding;nucleic acid binding;protein binding;structure-specific DNA binding;transcription factor binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part

Q27J81-2;Q27J81;H7BXE4 Inverted formin-2 INF2 >sp|Q27J81-2|INF2_HUMAN Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2;>sp|Q27J81|INF2_HUMAN Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 1.16 0.81 1.52 NaN 2.7 NaN 0.92 0.62 1.25E-30 5 5.3 actin cytoskeleton organization;actin filament-based process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm

Q14571 "Inositol 1,4,5-trisphosphate receptor type 2" ITPR2 ">sp|Q14571|ITPR2_HUMAN Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2" 1.15 0.88 0.48 1.72 1.09 0.36 1.03 0.99 7.03E-08 5 1.7 activation of phospholipase C activity;biological regulation;cell activation;cell surface receptor linked signaling pathway;cellular metabolic process;cellular process;cellular response to cAMP;cellular response to chemical stimulus;cellular response to ethanol;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;defense response;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway;generation of precursor metabolites and energy;immune response;immune system process;innate immune response;metabolic process;nerve growth factor receptor signaling pathway;oxidation-reduction process;platelet activation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;regulation of biological process;regulation of catalytic activity;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of lipase activity;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phospholipase activity;regulation of secretion;regulation of signaling;regulation of transport;response to cAMP;response to chemical stimulus;response to endogenous stimulus;response to ethanol;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hypoxia;response to organic substance;response to oxygen levels;response to stimulus;response to stress;signal transduction;small molecule metabolic process;transmembrane receptor protein tyrosine kinase signaling pathway "binding;calcium channel activity;calcium-release channel activity;cation channel activity;cation transmembrane transporter activity;channel activity;gated channel activity;inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity;intracellular ligand-gated ion channel activity;ion channel activity;ion transmembrane transporter activity;ligand-gated channel activity;ligand-gated ion channel activity;lipid binding;molecular transducer activity;passive transmembrane transporter activity;phosphatidylinositol binding;phospholipid binding;receptor activity;signal transducer activity;signaling receptor activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell cortex;cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part;plasma membrane;platelet dense tubular network membrane;sarcoplasmic reticulum membrane Alzheimer's disease;Calcium signaling pathway;Gap junction;Gastric acid secretion;GnRH signaling pathway;Long-term depression;Long-term potentiation;Oocyte meiosis;Pancreatic secretion;Phosphatidylinositol signaling system;Salivary secretion;Vascular smooth muscle contraction

Q5T749 Keratinocyte proline-rich protein KPRP >sp|Q5T749|KPRP_HUMAN Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1 NaN 1.77 0.73 1.62 4.96 2.46 NaN 0.94 4.97E-15 5 8.6 cell part;cytoplasm;intracellular part

Q2M2I5;CON__Q2M2I5 "Keratin, type I cytoskeletal 24" KRT24 ">sp|Q2M2I5|K1C24_HUMAN Keratin, type I cytoskeletal 24 OS=Homo sapiens GN=KRT24 PE=1 SV=1;>Q2M2I5 SWISS-PROT:Q2M2I5 Tax_Id=9606 Gene_Symbol=KRT24 Keratin, type I cytoskeletal 24" NaN NaN NaN NaN NaN NaN NaN NaN 1.53E-34 5 9 structural molecule activity cell part;cytoplasm;cytoskeletal part;cytoskeleton;intermediate filament;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;protein complex

CON__Q8IUT8;CON__O76011;O76011;O76009;CON__Q6NTB9;CON__O76009 "Keratin, type I cuticular Ha4" KRT34 ">Q8IUT8 TREMBL:Q8IUT8 Type I hair keratin 4 - Homo sapiens (Human).;>O76011 SWISS-PROT:O76011 Keratin, type I cuticular HA4 (Hair keratin, type I HA4);>sp|O76011|KRT34_HUMAN Keratin, type I cuticular Ha4 OS=Homo sapiens GN=KRT34 PE=2 SV=2" 1.25 1.28 0.97 0.81 1.14 2.06 0.96 1.34 3.62E-25 5 13.1 anatomical structure development;developmental process;epidermis development;tissue development structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex

P11279;B4DWL3 Lysosome-associated membrane glycoprotein 1 LAMP1 >sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3;>tr|B4DWL3|B4DWL3_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=2 SV=1 0.62 0.84 0.63 0.35 2.4 0.77 1.82 1.33 1.47E-15 5 11.8 autophagic cell death;autophagy;catabolic process;cell death;cellular catabolic process;cellular metabolic process;cellular process;death;metabolic process;programmed cell death cell body;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;dendrite;endosomal part;endosome;endosome membrane;external side of plasma membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome;lysosomal membrane;lysosome;lytic vacuole;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;multivesicular body;neuron projection;neuronal cell body;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;plasma membrane part;sarcolemma;vacuolar membrane;vacuolar part;vacuole;vesicle ko05152;Lysosome;Phagosome

Q9Y4W2-4;Q9Y4W2-2;Q9Y4W2;Q9Y4W2-3 Ribosomal biogenesis protein LAS1L LAS1L >sp|Q9Y4W2-4|LAS1L_HUMAN Isoform 4 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L;>sp|Q9Y4W2-2|LAS1L_HUMAN Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L;>sp|Q9Y4W2|LAS1L_HUMAN Ribosomal biogenesis protein LAS1L OS 1.42 NaN 1.81 1.25 0.88 0.45 0.92 NaN 1.16E-14 5 24.4 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;cytoplasm;histone methyltransferase complex;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL1 complex;nuclear part;nucleoplasm part;organelle part;protein complex

P09382;F8WEI7 Galectin-1 LGALS1 >sp|P09382|LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 0.58 0.66 1.26 1.6 0.25 0.2 0.58 0.62 5.07E-19 5 37 apoptosis;B cell activation;B cell activation involved in immune response;B cell differentiation;biological regulation;carbohydrate homeostasis;cell activation;cell activation involved in immune response;cell death;cell differentiation;cellular chemical homeostasis;cellular developmental process;cellular glucose homeostasis;cellular homeostasis;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to monosaccharide stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;death;developmental process;glucose homeostasis;homeostatic process;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;leukocyte differentiation;lymphocyte activation;lymphocyte activation involved in immune response;lymphocyte costimulation;lymphocyte differentiation;mature B cell differentiation;mature B cell differentiation involved in immune response;multicellular organismal process;multicellular organismal response to stress;muscle cell differentiation;myoblast differentiation;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell projection organization;negative regulation of cell-substrate adhesion;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of neuron projection development;plasma cell differentiation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell-cell adhesion;positive regulation of cellular process;positive regulation of erythrocyte aggregation;positive regulation of homotypic cell-cell adhesion;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of T cell activation;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell activation;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell-cell adhesion;regulation of cell-substrate adhesion;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of erythrocyte aggregation;regulation of homotypic cell-cell adhesion;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell activation;response to axon injury;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to glucose stimulus;response to hexose stimulus;response to monosaccharide stimulus;response to organic cyclic compound;response to organic substance;response to stimulus;response to stress;response to wounding;T cell costimulation binding;carbohydrate binding;disaccharide binding;galactoside binding;lactose binding;molecular transducer activity;monosaccharide binding;signal transducer activity;sugar binding cell part;cell surface;cytoplasm;extracellular matrix;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;proteinaceous extracellular matrix

E9PMS6;Q8WWI1-3;E9PLH4;E9PMT2;Q8WWI1-4;F8WD26;Q8WWI1-2;J3KP06;Q8WWI1;E9PMP7;H0Y424;E9PLU6;E9PK58;E9PJ10 LIM domain only protein 7 LMO7 >tr|E9PMS6|E9PMS6_HUMAN LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=2 SV=1;>sp|Q8WWI1-3|LMO7_HUMAN Isoform 3 of LIM domain only protein 7 OS=Homo sapiens GN=LMO7;>tr|E9PLH4|E9PLH4_HUMAN LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=2 SV=1;> 1.25 1.09 1 0.1 6.14 0.32 0.97 0.8 2.94E-12 5 6 "acid-amino acid ligase activity;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;ubiquitin ligase complex Adherens junction

Q86V48-2;Q86V48-3;Q86V48;E5RFK8 Leucine zipper protein 1 LUZP1 >sp|Q86V48-2|LUZP1_HUMAN Isoform 2 of Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1;>sp|Q86V48-3|LUZP1_HUMAN Isoform 3 of Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1;>sp|Q86V48|LUZP1_HUMAN Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV 1.02 0.69 1.07 1.06 0.78 0.61 1.05 1.25 2.38E-11 5 5.6 anatomical structure development;anatomical structure morphogenesis;artery development;blood vessel development;cardiac septum development;developmental process;embryonic morphogenesis;morphogenesis of an epithelial fold;morphogenesis of an epithelium;neural fold bending;tissue morphogenesis;ventricular septum development cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

P21397-2;P21397;B7Z5H3;B7Z242;P27338 Amine oxidase [flavin-containing] A MAOA >sp|P21397-2|AOFA_HUMAN Isoform 2 of Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA;>sp|P21397|AOFA_HUMAN Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 NaN 1.39 1.22 0.74 0.95 1.15 NaN 1.5 8.93E-28 5 16 alcohol catabolic process;alcohol metabolic process;amine catabolic process;amine metabolic process;behavior;benzene-containing compound metabolic process;biological regulation;biosynthetic process;catabolic process;catecholamine catabolic process;catecholamine metabolic process;catechol-containing compound catabolic process;catechol-containing compound metabolic process;cellular amine metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;diol catabolic process;diol metabolic process;dopamine catabolic process;dopamine metabolic process;establishment of localization;establishment of localization in cell;metabolic process;negative regulation of amine transport;negative regulation of biological process;negative regulation of cellular process;negative regulation of secretion;negative regulation of serotonin secretion;negative regulation of transport;neurotransmitter biosynthetic process;neurotransmitter catabolic process;neurotransmitter metabolic process;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;phenol-containing compound metabolic process;positive regulation of biological process;positive regulation of catecholamine metabolic process;positive regulation of cellular amine metabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of dopamine metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;regulation of amine transport;regulation of biological process;regulation of biological quality;regulation of catecholamine metabolic process;regulation of cell communication;regulation of cellular amine metabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of dopamine metabolic process;regulation of localization;regulation of metabolic process;regulation of neurotransmitter levels;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of secretion;regulation of serotonin secretion;regulation of signaling;regulation of transport;response to aluminum ion;response to biotic stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to corticosterone stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to glucocorticoid stimulus;response to hormone stimulus;response to inorganic substance;response to lipopolysaccharide;response to metal ion;response to mineralocorticoid stimulus;response to molecule of bacterial origin;response to organic substance;response to selenium ion;response to steroid hormone stimulus;response to stimulus;response to toxin;secretion;secretion by cell;signal release;small molecule catabolic process;small molecule metabolic process;transport;xenobiotic metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;electron carrier activity;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH2 group of donors;oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor;primary amine oxidase activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane "Arginine and proline metabolism;Drug metabolism - cytochrome P450;Glycine, serine and threonine metabolism;Histidine metabolism;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Tryptophan metabolism;Tyrosine metabolism"

Q9Y6C9;E9PIE4;F5H3Y2 Mitochondrial carrier homolog 2 MTCH2 >sp|Q9Y6C9|MTCH2_HUMAN Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1;>tr|E9PIE4|E9PIE4_HUMAN Mitochondrial carrier homolog 2 (Fragment) OS=Homo sapiens GN=MTCH2 PE=2 SV=1 0.92 1.27 1.5 1.49 0.54 0.69 0.71 0.98 7.41E-20 5 17.8 establishment of localization;transport cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part

O95299;E7ESZ7;Q8WXC9;H7C2W5;H7C1Y7;H7C2X4;Q8N1B9;C9J6X0 "NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial" NDUFA10 ">sp|O95299|NDUAA_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1;>tr|E7ESZ7|E7ESZ7_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN" 0.96 1.59 1.23 2.04 0.32 0.34 0.56 0.79

1.67E-23 5 17.5 "cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;oxidation-reduction process;primary metabolic process;respiratory electron transport chain;response to chemical stimulus;response to drug;response to stimulus;small molecule metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle lumen;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

B4DFA2;I3L0N3;P46459;I3L2G1;K7EQD6 Vesicle-fusing ATPase NSF >tr|B4DFA2|B4DFA2_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1;>tr|I3L0N3|I3L0N3_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1;>sp|P46459|NSF_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3 0.48 2.37 0.45 1.4 1.29 2.15 0.58 1.41 1.34E-30 5 8.5 biological regulation;cation transport;cell communication;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular membrane fusion;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;ion transport;membrane fusion;membrane organization;metal ion transport;monovalent inorganic cation transport;plasma membrane fusion;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of receptor recycling;positive regulation of signaling;potassium ion transport;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of receptor recycling;regulation of signaling;secretion;secretion by cell;signaling;synaptic transmission;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Vasopressin-regulated water reabsorption

P57740;Q6PJE1;B4DZ67;G3V1T4;H0YG15 Nuclear pore complex protein Nup107 NUP107 >sp|P57740|NU107_HUMAN Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1;>tr|Q6PJE1|Q6PJE1_HUMAN NUP107 protein OS=Homo sapiens GN=NUP107 PE=2 SV=1;>tr|B4DZ67|B4DZ67_HUMAN Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 NaN NaN 1.3 NaN 1.35 NaN NaN NaN 2.56E-09 5 6.6 anaphase;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular transport;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear export;nuclear pore complex assembly;nuclear pore organization;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process channel activity;nucleocytoplasmic transporter activity;passive transmembrane transporter activity;porin activity;structural constituent of nuclear pore;structural molecule activity;transmembrane transporter activity;transporter activity;wide pore channel activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;Nup107-160 complex;organelle;organelle membrane;organelle part;pore complex;protein complexRNA transport

P07237;F5H8J2;H7BZ94;I3L398;H0Y3Z3;I3NI03;I3L312;I3L4M2;I3L3P5;I3L3U6 Protein disulfide-isomerase P4HB >sp|P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3;>tr|F5H8J2|F5H8J2_HUMAN Uncharacterized protein OS=Homo sapiens GN=P4HB PE=2 SV=1;>tr|H7BZ94|H7BZ94_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=2 SV=2;>tr 0.99 0.76 0.54 0.64 1.32 0.97 1.75 1.28 6.02E-23 5 15 4-hydroxyproline metabolic process;amine metabolic process;biological regulation;carboxylic acid metabolic process;cell redox homeostasis;cellular amine metabolic process;cellular amino acid metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;extracellular matrix organization;extracellular structure organization;glycerol ether metabolic process;heterocycle metabolic process;homeostatic process;lipid metabolic process;lipoprotein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid metabolic process;organic ether metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-proline hydroxylation;peptidyl-proline hydroxylation to 4-hydroxy-L-proline;peptidyl-proline modification;primary metabolic process;protein metabolic process;protein modification process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;peptidyl-proline 4-dioxygenase activity;peptidyl-proline dioxygenase activity;procollagen-proline 4-dioxygenase activity;procollagen-proline dioxygenase activity;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;plasma membrane;vesicle Protein processing in endoplasmic reticulum

Q86U42-2;Q86U42;B4DEH8;G3V4T2;Q92843-2;H0YJH9Polyadenylate-binding protein 2 PABPN1 >sp|Q86U42-2|PABP2_HUMAN Isoform 2 of Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1;>sp|Q86U42|PABP2_HUMAN Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1 PE=1 SV=3;>tr|B4DEH8|B4DEH8_HUMAN Polyadenylate-binding protein 2 OS=Homo sapie 1.45 1.24 1.65 1.8 0.34 0.25 0.66 0.63 1.29E-16 5 30.4 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;macromolecule metabolic process;metabolic process;modification by symbiont of host morphology or physiology;modification by virus of host mRNA processing;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by symbiont of host cellular process;modulation by virus of host cellular process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;multicellular organismal process;multi-organism process;muscle contraction;muscle system process;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;poly(A)+ mRNA export from nucleus;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;reproductive process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;system process;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport;viral infectious cycle;viral reproductive process;virus-host interaction" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex mRNA surveillance pathway

P09874 Poly [ADP-ribose] polymerase 1 PARP1 >sp|P09874|PARP1_HUMAN Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 NaN NaN 0.68 NaN 1.09 NaN NaN NaN 6.54E-17 5 7.3 "anatomical structure homeostasis;base-excision repair;biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chromosome organization;detection of stimulus;DNA damage response, detection of DNA damage;DNA metabolic process;DNA repair;double-strand break repair;enzyme linked receptor protein signaling pathway;homeostatic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;protein ADP-ribosylation;protein autoprocessing;protein maturation;protein metabolic process;protein modification process;protein poly-ADP-ribosylation;protein processing;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of growth rate;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;telomere maintenance;telomere organization;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway" "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;DNA binding;ion binding;metal ion binding;NAD binding;NAD+ ADP-ribosyltransferase activity;nucleic acid binding;nucleotide binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups;transition metal ion binding;zinc ion binding" cell part;envelope;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleolus;nucleoplasm part;organelle;organelle envelope;organelle part;protein complex;transcription factor complex Base excision repair

Q16822;H0YML5;B4DW73;Q16822-2;H0YM31;H0YMU6;H0YNG4;H0YMA5 "Phosphoenolpyruvate carboxykinase [GTP], mitochondrial" PCK2 ">sp|Q16822|PCKGM_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3;>tr|H0YML5|H0YML5_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=2 SV=1;>tr|B4DW73|B4DW73_HUMAN Phospho" NaN NaN 1.02 2.6 3.62 2.27 NaN NaN 5.46E-14 5 10.3 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;gluconeogenesis;glucose metabolic process;hexose biosynthetic process;hexose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process "binding;carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;cation binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ion binding;kinase activity;lyase activity;metal ion binding;nucleotide binding;phosphoenolpyruvate carboxykinase (GTP) activity;phosphoenolpyruvate carboxykinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Adipocytokine signaling pathway;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Insulin signaling pathway;PPAR signaling pathway;Proximal tubule bicarbonate reclamation;Pyruvate metabolism

Q9BY77-2;Q9BY77;Q6R954;B4DMM2;F8WEE2;F8WCX5 Polymerase delta-interacting protein 3 POLDIP3 >sp|Q9BY77-2|PDIP3_HUMAN Isoform 2 of Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3;>sp|Q9BY77|PDIP3_HUMAN Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2 0.67 2.5 1.61 2.25 0.61 1.88 0.6 1.29 3.10E-15 5 19.4 biological regulation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part

Q8WXF1-2;Q8WXF1 Paraspeckle component 1 PSPC1 >sp|Q8WXF1-2|PSPC1_HUMAN Isoform 2 of Paraspeckle component 1 OS=Homo sapiens GN=PSPC1;>sp|Q8WXF1|PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1 1.35 0.98 0.99 1.21 0.56 0.55 0.94 1.08 2.72E-12 5 14 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;paraspeckles

Q6WKZ4;E7EX40;Q6WKZ4-3;Q6WKZ4-2;Q6WKZ4-1;REV__Q8N9Q2;Q7L804;Q3I768 Rab11 family-interacting protein 1 RAB11FIP1 >sp|Q6WKZ4|RFIP1_HUMAN Rab11 family-interacting protein 1 OS=Homo sapiens GN=RAB11FIP1 PE=1 SV=3;>tr|E7EX40|E7EX40_HUMAN Rab11 family-interacting protein 1 OS=Homo sapiens GN=RAB11FIP1 PE=2 SV=1;>sp|Q6WKZ4-3|RFIP1_HUMAN Isoform 2 of Rab11 family-interactin 0.99 1.06 0.56 0.47 2.96 1.37 0.95 0.95 1.26E-10 5 4.5 cellular process;establishment of cell polarity;establishment of localization;establishment of protein localization;establishment or maintenance of cell polarity;fluid transport;protein transport;transmembrane transport;transport;water transport cell part;cytoplasm;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;recycling endosome;recycling endosome membrane;vesicle membrane Endocytosis

Q9NP72;Q9NP72-2;Q5W0J0;Q9NP72-3;H0Y6T8 Ras-related protein Rab-18 RAB18 >sp|Q9NP72|RAB18_HUMAN Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1;>sp|Q9NP72-2|RAB18_HUMAN Isoform 2 of Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18;>tr|Q5W0J0|Q5W0J0_HUMAN Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=2 1.23 1.54 1.71 0.58 0.97 0.86 0.97 0.9 7.20E-18 5 29.6 anatomical structure development;biological regulation;brain development;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;developmental process;endocytosis;establishment of localization;establishment of protein localization;eye development;intracellular signal transduction;membrane invagination;membrane organization;organ development;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;sensory organ development;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;intracellular;membrane;plasma membrane

P61019;P61019-2;E9PKL7;Q8WUD1;E9PE37;H7C125;H0YD31 Ras-related protein Rab-2A;Ras-related protein Rab-2B RAB2A;RAB2B >sp|P61019|RAB2A_HUMAN Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1;>sp|P61019-2|RAB2A_HUMAN Isoform 2 of Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A;>tr|E9PKL7|E9PKL7_HUMAN Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=2 0.94 1.62 1.05 0.8 1.01 1.1 0.95 0.96 1.45E-125 5 31.6 biological regulation;cell cycle phase;cell cycle process;cellular process;cellular response to stimulus;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular signal transduction;intracellular transport;M phase;M phase of mitotic cell cycle;mitotic prophase;positive regulation of biological process;positive regulation of cellular process;positive regulation of exocytosis;positive regulation of secretion;positive regulation of transport;prophase;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;vesicle

P51148;P51148-2;F8VVK3;K7ERI8;K7ERQ8;F8VWU4;F8VVZ0;F8VUA5;K7ENY4;K7EIP6;F8WCY6;F8WD79;F8VPW9;F8VSF8;F8VWZ7 Ras-related protein Rab-5C RAB5C >sp|P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2;>sp|P51148-2|RAB5C_HUMAN Isoform 2 of Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C;>tr|F8VVK3|F8VVK3_HUMAN Ras-related protein Rab-5C (Fragment) OS=Homo sapiens GN= 0.78 2.02 1.28 0.93 1.02 1.21 0.84 0.98 1.12E-52 5 30.1 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;endosome organization;establishment of localization;establishment of protein localization;histone acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of endocytosis;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport" "acetyltransferase activity;binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;histone acetyltransferase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lysine N-acetyltransferase activity;N-acetyltransferase activity;N-acyltransferase activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome membrane;endocytic vesicle;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;vesicle Amoebiasis;Endocytosis;ko05152;Phagosome;Vasopressin-regulated water reabsorption

P61006 Ras-related protein Rab-8A RAB8A >sp|P61006|RAB8A_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1 NaN 1.39 1.68 NaN 0.89 NaN NaN 0.84 5.43E-43 5 27.5 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;axonogenesis;biological regulation;cell cycle process;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane fusion;cellular membrane organization;cellular process;cellular response to stimulus;cilium assembly;developmental process;establishment of localization;establishment of protein localization;G2/M transition of mitotic cell cycle;Golgi vesicle fusion to target membrane;intracellular signal transduction;membrane docking;membrane fusion;membrane organization;neuron projection morphogenesis;organelle fusion;organelle organization;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular process;regulation of establishment of protein localization;regulation of localization;regulation of long-term neuronal synaptic plasticity;regulation of multicellular organismal process;regulation of neurological system process;regulation of neuronal synaptic plasticity;regulation of protein localization;regulation of protein transport;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle fusion;vesicle organization "binding;catalytic activity;enzyme binding;GDP binding;GTP binding;GTPase activity;GTPase binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;Rab GTPase binding;Ras GTPase binding;ribonucleotide binding;small GTPase binding" cell body;cell part;cell projection;cell projection part;cilium;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;endocytic vesicle;endocytic vesicle membrane;endosome;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule basal body;microtubule organizing center;neuronal cell body;nonmotile primary cilium;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;postsynaptic density;primary cilium;recycling endosome;synapse part;vesicle;vesicle membrane Pancreatic secretion

Q9P0K7-4;Q9P0K7-3;E7EMX7;Q9P0K7;Q9P0K7-2 Ankycorbin RAI14 >sp|Q9P0K7-4|RAI14_HUMAN Isoform 4 of Ankycorbin OS=Homo sapiens GN=RAI14;>sp|Q9P0K7-3|RAI14_HUMAN Isoform 3 of Ankycorbin OS=Homo sapiens GN=RAI14;>tr|E7EMX7|E7EMX7_HUMAN Ankycorbin OS=Homo sapiens GN=RAI14 PE=2 SV=1;>sp|Q9P0K7|RAI14_HUMAN Ankycorbin OS=H 0.88 NaN 0.56 1.38 1.16 0.77 0.95 NaN 7.78E-09 5 5.6 cell cortex;cell part;cytoplasmic part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nucleus;organelle

P62826;B5MDF5;J3KQE5;H0YFC6;F5H018;B4DV51 GTP-binding nuclear protein Ran RAN >sp|P62826|RAN_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3;>tr|B5MDF5|B5MDF5_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=2 SV=1;>tr|J3KQE5|J3KQE5_HUMAN GTP-binding nuclear protein Ran (Fragment) OS=Homo sapien 0.58 2.94 0.52 2.83 0.27 0.66 0.48 0.64 9.99E-14 5 23.6 "androgen receptor signaling pathway;biological regulation;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cytoskeleton organization;DNA metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;gene expression;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitosis;mitotic spindle organization;nitrogen compound metabolic process;nuclear division;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;organelle fission;organelle organization;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein binding;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein export from nucleus;protein targeting;protein transport;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein binding;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small GTPase mediated signal transduction;spindle organization;steroid hormone receptor signaling pathway;transport;viral infectious cycle;viral reproductive process" "androgen receptor binding;binding;catalytic activity;chromatin binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nuclear part;nuclear pore;nucleoplasm;organelle;organelle part;pigment granule;pore complex;protein complex;vesicle Ribosome biogenesis in eukaryotes;RNA transport

Q09028-3;Q09028;Q09028-4;Q09028-2;H0YF10;E9PC52;H0YEU5;B4DRT0;Q5JP02;H0YCT5;H0YDK2;E9PNS2;Q5JNZ6;C9JPP3;E9PIC4;E9PNS6 Histone-binding protein RBBP4 RBBP4;RBBP7 >sp|Q09028-3|RBBP4_HUMAN Isoform 3 of Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4;>sp|Q09028|RBBP4_HUMAN Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3;>sp|Q09028-4|RBBP4_HUMAN Isoform 4 of Histone-binding protein RBBP4 OS=Homo 1.01 1.39 1.23 2.38 0.43 0.38 0.55 0.78 1.41E-13 5 12.7 "ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cell cycle;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;DNA metabolic process;DNA replication;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;histone exchange;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitotic cell cycle;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;histone binding;protein binding CAF-1 complex;cell part;chromatin assembly complex;chromatin remodeling complex;chromosomal part;ESC/E(Z) complex;histone deacetylase complex;histone methyltransferase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ISWI complex;macromolecular complex;membrane-bounded organelle;methyltransferase complex;nuclear chromosome part;nuclear part;nucleoplasm part;nucleus;NuRD complex;NURF complex;organelle;organelle part;PcG protein complex;protein complex;Sin3 complex;Sin3-type complex;transcriptional repressor complex

Q9NW13;Q9NW13-2;C9JE21;C9JAA9;H7C5G8 RNA-binding protein 28 RBM28 >sp|Q9NW13|RBM28_HUMAN RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3;>sp|Q9NW13-2|RBM28_HUMAN Isoform 2 of RNA-binding protein 28 OS=Homo sapiens GN=RBM28 1.2 1.43 1.74 2.39 0.46 0.4 0.45 0.47 4.92E-17 5 7.5 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Ribosome biogenesis in eukaryotes

P62906 60S ribosomal protein L10a RPL10A >sp|P62906|RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 1.39 0.86 1.21 0.79 0.69 0.6 1.46 0.93 4.07E-13 5 19.4 "anatomical structure morphogenesis;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

P61313;E7EQV9;E7EX53;E7ENU7;P61313-2;E7ERA2 60S ribosomal protein L15;Ribosomal protein L15 RPL15 >sp|P61313|RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2;>tr|E7EQV9|E7EQV9_HUMAN Ribosomal protein L15 (Fragment) OS=Homo sapiens GN=RPL15 PE=2 SV=1;>tr|E7EX53|E7EX53_HUMAN Ribosomal protein L15 (Fragment) OS=Homo sapiens GN=RPL15 1.28 0.76 1.19 0.63 0.84 1.14 1.36 1.01 1.23E-18 5 22.5 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

J3QQT2;J3KRX5;P18621;P18621-3;P18621-2;J3QLC8;J3QS96;J3KRB3;J3KSJ0 60S ribosomal protein L17 RPL17 >tr|J3QQT2|J3QQT2_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1;>tr|J3KRX5|J3KRX5_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1;>sp|P18621|RL17_HUMAN 60S ribosomal protein L17 OS=Homo sapiens 1.38 0.71 0.39 0.75 1.07 1.02 1.25 0.94 1.50E-31 5 28.7 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

G3V203;Q07020;J3QQ67;F8VYV2;F8VWC5;H0YHA7;F8VUA6;F8VXR6 60S ribosomal protein L18 RPL18 >tr|G3V203|G3V203_HUMAN 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=2 SV=1;>sp|Q07020|RL18_HUMAN 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2;>tr|J3QQ67|J3QQ67_HUMAN 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE1.32 0.77 0.63 0.66 1.4 0.91 1.42 0.99 1.41E-164 5 32.9 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P62899;H7C2W9;C9JU56;B7Z4E3;P62899-3;P62899-2;B7Z4C8;B8ZZK4 60S ribosomal protein L31 RPL31 >sp|P62899|RL31_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1;>tr|H7C2W9|H7C2W9_HUMAN 60S ribosomal protein L31 (Fragment) OS=Homo sapiens GN=RPL31 PE=4 SV=1;>tr|C9JU56|C9JU56_HUMAN 60S ribosomal protein L31 (Fragment) OS=Homo sapiens 1.55 0.8 0.47 0.68 0.95 0.8 1.25 0.97 1.87E-79 5 34.4 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P62917;E9PP36;E9PKZ0;E9PKU4;G3V1A1 60S ribosomal protein L8 RPL8 >sp|P62917|RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2;>tr|E9PP36|E9PP36_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=2 SV=1;>tr|E9PKZ0|E9PKZ0_HUMAN 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=2 SV=1 1.4 0.72 0.6 0.62 1.45 0.91 1.49 1 2.36E-20 5 18.7 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P05387;H0YDD8;P05386-2 60S acidic ribosomal protein P2 RPLP2 >sp|P05387|RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1;>tr|H0YDD8|H0YDD8_HUMAN 60S acidic ribosomal protein P2 (Fragment) OS=Homo sapiens GN=RPLP2 PE=3 SV=1 1.61 0.58 1.44 0.45 1.02 0.68 1.91 1.07 1.23E-122 5 67.8 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

M0R210;P62249;M0R3H0;M0QX76;M0R1M5;Q6IPX4 40S ribosomal protein S16 RPS16 >tr|M0R210|M0R210_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=3 SV=1;>sp|P62249|RS16_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2;>tr|M0R3H0|M0R3H0_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=3 SV=1 1.67 0.9 1.36 0.63 1.03 0.79 1.01 0.73 5.13E-17 5 34.9 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal small subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

Q5JR95;P62241 40S ribosomal protein S8 RPS8 >tr|Q5JR95|Q5JR95_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=2 SV=1;>sp|P62241|RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 1.38 0.82 0.59 0.69 1.6 1.11 1.37 0.98 1.33E-265 5 29.3 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maturation of SSU-rRNA;maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

F5H456;Q5JTH9-2;Q5JTH9-3;Q5JTH9 RRP12-like protein RRP12 >tr|F5H456|F5H456_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=2 SV=1;>sp|Q5JTH9-2|RRP12_HUMAN Isoform 2 of RRP12-like protein OS=Homo sapiens GN=RRP12;>sp|Q5JTH9-3|RRP12_HUMAN Isoform 3 of RRP12-like protein OS=Homo sapiens GN=RRP12;>sp|Q5JTH9|RRP 1.05 NaN 1.27 NaN 1.1 NaN 0.68 NaN 3.72E-25 5 6.8 cell part;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;organelle;organelle membrane;organelle part

F8W914;Q9NQC3-2;Q9NQC3-5;Q9NQC3;Q9NQC3-4;F8WAM4;Q9NQC3-3;H7C106;Q9NQC3-6 Reticulon-4 RTN4 >tr|F8W914|F8W914_HUMAN Reticulon-4 OS=Homo sapiens GN=RTN4 PE=2 SV=1;>sp|Q9NQC3-2|RTN4_HUMAN Isoform 2 of Reticulon-4 OS=Homo sapiens GN=RTN4;>sp|Q9NQC3-5|RTN4_HUMAN Isoform 5 of Reticulon-4 OS=Homo sapiens GN=RTN4;>sp|Q9NQC3|RTN4_HUMAN Reticulon-4 OS=Hom 0.66 0.51 0.83 0.16 2.68 1.49 1.55 1.12 9.57E-18 5 22.9 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;apoptosis;axonal fasciculation;biological regulation;cardiac epithelial to mesenchymal transition;cell death;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell recognition;cell surface receptor linked signaling pathway;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;cerebral cortex cell migration;cerebral cortex radial glia guided migration;cerebral cortex radially oriented cell migration;death;developmental process;endoplasmic reticulum organization;endoplasmic reticulum tubular network organization;enzyme linked receptor protein signaling pathway;epithelial to mesenchymal transition;forebrain cell migration;locomotion;negative regulation of axon extension;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental growth;negative regulation of developmental process;negative regulation of growth;negative regulation of neurogenesis;nerve growth factor receptor signaling pathway;neuron recognition;organelle organization;programmed cell death;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of branching morphogenesis of a nerve;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of localization;regulation of locomotion;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;response to stimulus;signal transduction;telencephalon cell migration;transmembrane receptor protein tyrosine kinase signaling pathway cell body;cell part;cell projection;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum part;envelope;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;neuronal cell body;nuclear envelope;nuclear part;organelle;organelle envelope;organelle part;plasma membrane

P60903 Protein S100-A10 S100A10 >sp|P60903|S10AA_HUMAN Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2 0.87 0.79 0.61 0.11 2.71 2 1.33 0.52 2.20E-15 5 45.4 biological regulation;cellular process;cellular response to acid;cellular response to chemical stimulus;cellular response to stimulus;positive regulation of binding;positive regulation of molecular function;regulation of binding;regulation of biological process;regulation of cellular process;regulation of molecular function;response to acid;response to chemical stimulus;response to stimulus;signal transduction binding;calcium ion binding;cation binding;ion binding;metal ion binding;protein binding;receptor binding cell part;extrinsic to membrane;extrinsic to plasma membrane;membrane part;plasma membrane part

P31949 Protein S100-A11 S100A11 >sp|P31949|S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 0.97 1.04 0.63 0.11 2.55 2.53 1.31 0.52 6.24E-32 5 41.9 biological regulation;cellular process;cellular response to stimulus;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to stimulus;signal transduction binding;calcium ion binding;calcium-dependent protein binding;cation binding;identical protein binding;ion binding;metal ion binding;protein binding;protein dimerization activity;protein homodimerization activity cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;ruffle

P05109 "Protein S100-A8;Protein S100-A8, N-terminally processed" S100A8 >sp|P05109|S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 0.24 0.33 0.04 0.13 4.15 3.17 1.62 1.64 2.37E-13 5 48.4 "activation of caspase activity;acute inflammatory response;autophagy;biological adhesion;biological regulation;catabolic process;cell adhesion;cell chemotaxis;cell migration;cell motility;cell-cell adhesion;cellular catabolic process;cellular component movement;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemokine production;chemotaxis;chronic inflammatory response;cytokine production;defense response;defense response to bacterium;defense response to fungus;homotypic cell-cell adhesion;immune response;immune system process;induction of apoptosis;induction of programmed cell death;inflammatory response;innate immune response;leukocyte aggregation;leukocyte cell-cell adhesion;leukocyte chemotaxis;leukocyte migration;leukocyte migration involved in inflammatory response;locomotion;maintenance of location;metabolic process;multicellular organismal process;multi-organism process;neutrophil aggregation;neutrophil chemotaxis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular process;positive regulation of defense response;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of inflammatory response;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytoskeleton organization;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of inflammatory response;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to ethanol;response to external stimulus;response to fungus;response to inorganic substance;response to lipopolysaccharide;response to metal ion;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;response to wounding;response to zinc ion;sequestering of metal ion;sequestering of zinc ion;taxis;wound healing" arachidonic acid binding;binding;calcium ion binding;carboxylic acid binding;cation binding;cytoskeletal protein binding;fatty acid binding;icosanoid binding;icosatetraenoic acid binding;ion binding;lipid binding;metal ion binding;microtubule binding;monocarboxylic acid binding;protein binding;RAGE receptor binding;receptor binding;Toll-like receptor 4 binding;Toll-like receptor binding;transition metal ion binding;tubulin binding;zinc ion binding cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;extracellular region part;extracellular space;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;non-membrane-bounded organelle;organelle;plasma membrane

Q14151 Scaffold attachment factor B2 SAFB2 >sp|Q14151|SAFB2_HUMAN Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1 NaN 0.84 NaN NaN NaN NaN NaN 0.75 4.40E-41 5 6.5 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q15758;Q15758-3;Q15758-2;M0QXM4;M0R144;M0QX44 Neutral amino acid transporter B(0) SLC1A5 >sp|Q15758|AAAT_HUMAN Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2;>sp|Q15758-3|AAAT_HUMAN Isoform 3 of Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5;>sp|Q15758-2|AAAT_HUMAN Isoform 2 of Neutral amino acid transpo 0.89 1.5 1.46 1.3 0.53 0.21 0.51 0.78 2.46E-65 5 11.6 active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;anion transmembrane transporter activity;anion:cation symporter activity;carboxylic acid transmembrane transporter activity;cation transmembrane transporter activity;dicarboxylic acid transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;L-amino acid transmembrane transporter activity;L-glutamine transmembrane transporter activity;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;neutral amino acid transmembrane transporter activity;organic acid transmembrane transporter activity;organic acid:sodium symporter activity;receptor activity;secondary active transmembrane transporter activity;sodium ion transmembrane transporter activity;sodium:dicarboxylate symporter activity;solute:cation symporter activity;solute:sodium symporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;plasma membrane part;vesicle Protein digestion and absorption

P11166;C9JIM8 "Solute carrier family 2, facilitated glucose transporter member 1" SLC2A1 ">sp|P11166|GTR1_HUMAN Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2;>tr|C9JIM8|C9JIM8_HUMAN Solute carrier family 2, facilitated glucose transporter member 1 (Fragment) OS=Homo sapiens GN=SLC2A1 PE=2" 1.09 1.73 1.46 1.7 0.28 0.17 0.42 0.5 7.65E-61 5 10.2 biological regulation;carboxylic acid metabolic process;cell communication;cellular ketone metabolic process;cellular metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;L-ascorbic acid metabolic process;metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;response to abiotic stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient levels;response to osmotic stress;response to starvation;response to stimulus;response to stress;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process carbohydrate transmembrane transporter activity;dehydroascorbic acid transporter activity;D-glucose transmembrane transporter activity;glucose transmembrane transporter activity;hexose transmembrane transporter activity;monosaccharide transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;sugar transmembrane transporter activity;transmembrane transporter activity;transporter activity;vitamin transporter activity;xenobiotic transporter activity basolateral plasma membrane;caveola;cell junction;cell part;cell-cell junction;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;female pronucleus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;midbody;nucleus;organelle;pigment granule;plasma membrane;plasma membrane part;pronucleus;vesicle Adipocytokine signaling pathway;Bile secretion;Pathways in cancer;Renal cell carcinoma

Q15005;E9PI68;E9PL01;E9PRB9;H0YE04 Signal peptidase complex subunit 2 SPCS2 >sp|Q15005|SPCS2_HUMAN Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3;>tr|E9PI68|E9PI68_HUMAN Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=2 SV=1;>tr|E9PL01|E9PL01_HUMAN Signal peptidase complex subunit 2 OS=Homo sa 1.17 1.19 1.83 1.18 0.59 0.59 0.74 0.95 7.05E-10 5 19.5 biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;peptide metabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;proteolysis;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;signal peptide processing;SRP-dependent cotranslational protein targeting to membrane;translation;transport catalytic activity;hydrolase activity;peptidase activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;protein complex;signal peptidase complex Protein export

Q9Y5M8;H7C4H2;C9J5Z8 Signal recognition particle receptor subunit beta SRPRB >sp|Q9Y5M8|SRPRB_HUMAN Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3;>tr|H7C4H2|H7C4H2_HUMAN Signal recognition particle receptor subunit beta (Fragment) OS=Homo sapiens GN=SRPRB PE=4 SV=1 NaN 0.84 1.83 NaN 0.86 NaN NaN 1.05 5.02E-19 5 25.5 activation of signaling protein activity involved in unfolded protein response;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular signal transduction;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;signal transduction;small GTPase mediated signal transduction;SRP-dependent cotranslational protein targeting to membrane;translation;transport binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;microtubule;organelle membrane;organelle part;protein complex Protein export

Q16629-3;Q16629-2;Q16629-4;C9JAB2;Q16629;F8WEA1 Serine/arginine-rich splicing factor 7 SRSF7 >sp|Q16629-3|SRSF7_HUMAN Isoform 3 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7;>sp|Q16629-2|SRSF7_HUMAN Isoform 2 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7;>sp|Q16629-4|SRSF7_HUMAN Isoform 4 of Serine/arginin 1.27 1.08 1.33 1.66 0.59 0.49 0.91 0.76 4.78E-62 5 37.9 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part Spliceosome

O43815-2;O43815 Striatin STRN >sp|O43815-2|STRN_HUMAN Isoform 2 of Striatin OS=Homo sapiens GN=STRN;>sp|O43815|STRN_HUMAN Striatin OS=Homo sapiens GN=STRN PE=1 SV=4 NaN NaN 0.82 NaN 1.27 NaN NaN NaN 1.14E-11 5 11.2 anatomical structure development;behavior;biological regulation;cell junction assembly;cell junction organization;cell projection organization;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;dendrite development;developmental process;locomotory behavior;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;neuron projection development;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to stimulus;signal transduction;tight junction assembly;Wnt receptor signaling pathway binding;calmodulin binding;enzyme binding;phosphatase binding;protein binding;protein complex binding;protein phosphatase 2A binding;protein phosphatase binding cell body;cell junction;cell part;cell-cell junction;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;membrane;neuronal cell body;occluding junction;organelle part;postsynaptic density;postsynaptic membrane;synapse part;synaptic membrane;tight junction

P46977;E9PNQ1;E9PIJ8;E9PN73;E9PI32;H0YET6 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A STT3A >sp|P46977|STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2;>tr|E9PNQ1|E9PNQ1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=S 1.04 1.25 1.54 0.82 0.77 0.6 0.94 0.98 8.48E-17 5 7.1 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;co-translational protein modification;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;oligosaccharyltransferase complex;organelle part;protein complex N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis

O00204-2;O00204 Sulfotransferase family cytosolic 2B member 1 SULT2B1 >sp|O00204-2|ST2B1_HUMAN Isoform 2 of Sulfotransferase family cytosolic 2B member 1 OS=Homo sapiens GN=SULT2B1;>sp|O00204|ST2B1_HUMAN Sulfotransferase family cytosolic 2B member 1 OS=Homo sapiens GN=SULT2B1 PE=1 SV=2 NaN 0.57 0.69 0.17 2.64 3.5 NaN 1.16 3.47E-10 5 15.4 3'-phosphoadenosine 5'-phosphosulfate metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle metabolic process;lipid metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside bisphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside bisphosphate metabolic process;purine-containing compound metabolic process;ribonucleoside bisphosphate metabolic process;small molecule metabolic process;steroid metabolic process;sulfate assimilation;sulfur compound metabolic process;xenobiotic metabolic process "alcohol sulfotransferase activity;catalytic activity;steroid sulfotransferase activity;sulfotransferase activity;transferase activity;transferase activity, transferring sulfur-containing groups" cell part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Steroid hormone biosynthesis;Sulfur metabolism

P09758 Tumor-associated calcium signal transducer 2 TACSTD2 >sp|P09758|TACD2_HUMAN Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3 0.93 1.47 1.66 0.67 0.74 0.62 0.88 0.97 7.08E-51 5 16.4 anatomical structure morphogenesis;biological regulation;cell proliferation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;developmental process;epithelial tube morphogenesis;morphogenesis of an epithelium;multicellular organismal process;negative regulation of actin filament bundle assembly;negative regulation of biological process;negative regulation of branching involved in ureteric bud morphogenesis;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of developmental process;negative regulation of epithelial cell migration;negative regulation of locomotion;negative regulation of multicellular organismal process;negative regulation of organelle organization;negative regulation of stress fiber assembly;neurological system process;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of branching involved in ureteric bud morphogenesis;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of epithelial cell migration;regulation of epithelial cell proliferation;regulation of kidney development;regulation of localization;regulation of locomotion;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of organ morphogenesis;regulation of organelle organization;regulation of stress fiber assembly;response to stimulus;sensory perception;sensory perception of light stimulus;signal transduction;system process;tissue morphogenesis;tube morphogenesis;ureteric bud morphogenesis;visual perception receptor activity basal plasma membrane;cell part;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lateral plasma membrane;membrane part;plasma membrane part

Q9BTV4 Transmembrane protein 43 TMEM43 >sp|Q9BTV4|TMM43_HUMAN Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1 0.91 1.12 1.68 1.41 0.89 0.72 0.75 0.98 1.46E-11 5 17.8 cell part;cytoplasmic part;endoplasmic reticulum;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nuclear inner membrane;nuclear membrane;nuclear part;organelle;organelle inner membrane;organelle membrane;organelle part

Q9C0C2;Q9C0C2-2;E9PKK0 182 kDa tankyrase-1-binding protein TNKS1BP1 >sp|Q9C0C2|TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4 1.22 NaN 0.77 0.73 1.72 1.56 0.93 NaN 1.03E-10 5 5.2 anatomical structure homeostasis;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome organization;DNA metabolic process;DNA replication;homeostatic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological quality;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;RNA-dependent DNA replication;telomere maintenance;telomere maintenance via telomerase;telomere maintenance via telomere lengthening;telomere organization ankyrin binding;binding;cytoskeletal protein binding;enzyme binding;protein binding CCR4-NOT complex;cell part;chromatin;chromosomal part;cytoplasmic part;cytoskeleton;cytosol;heterochromatin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear heterochromatin;nuclear part;nuclear telomeric heterochromatin;nucleoplasm part;organelle;organelle part;protein complex;telomeric heterochromatin;transcription factor complex

O96008;O96008-2;K7EKG4;K7EJ57 Mitochondrial import receptor subunit TOM40 homolog TOMM40 >sp|O96008|TOM40_HUMAN Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1;>sp|O96008-2|TOM40_HUMAN Isoform 2 of Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40;>tr|K7EKG4|K7EKG4_HUMAN Mitoc 1.11 1.4 1.4 1.72 0.45 0.57 0.59 0.97 2.09E-34 5 14.4 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;ion transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transmembrane transport;transport channel activity;macromolecule transmembrane transporter activity;passive transmembrane transporter activity;porin activity;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;wide pore channel activity cell part;cytoplasmic part;integral to membrane;integral to mitochondrial membrane;integral to mitochondrial outer membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to mitochondrial outer membrane;intrinsic to organelle membrane;macromolecular complex;membrane;membrane part;mitochondrial membrane;mitochondrial membrane part;mitochondrial outer membrane;mitochondrial outer membrane translocase complex;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane;pore complex;protein complex	Amyotrophic lateral sclerosis (ALS)

P11387;E5RIC7;Q969P6-2;Q969P6	DNA topoisomerase 1	TOP1	>sp|P11387|TOP1_HUMAN DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2	1.21 1.36 0.87 1.72 1	0.56 0.86 0.71 2.33E-12 5	7.7	biosynthetic process;cell death;cell division;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;chromosome segregation;death;DNA conformation change;DNA metabolic process;DNA replication;DNA topological change;embryonic cleavage;interaction with host;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;programmed cell death;reproductive process;response to chemical stimulus;response to drug;response to stimulus;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;chromatin binding;DNA binding;DNA topoisomerase (ATP-hydrolyzing) activity;DNA topoisomerase activity;DNA topoisomerase type I activity;DNA-dependent ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;isomerase activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	cell part;chromosomal part;chromosome;cytoplasmic mRNA processing body;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoid;nucleolus;nucleoplasm;organelle;organelle part;perikaryon;protein complex;replication fork protection complex;ribonucleoprotein complex;RNA granule

P49411	"Elongation factor Tu, mitochondrial"	TUFM	">sp|P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2"	1.07 0.56 0.96 0.18 3.41 1.87 1.62 0.99 2.04E-16 5	16.2 catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process	"binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding"	cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle part	Plant-pathogen interaction

J3QS39;J3QTR3;F5H6Q2;P62987;F5GYU3;F5H2Z3;F5H265;F5H7Y5;B4DV12;F5H388;P62979;F5H747;F5GXK7;J3QKN0;P0CG47;Q96C32;F5H7K6;F5H041;P0CG48;M0R1V7;F5H4D8;M0R1M6;M0R2S1;J3QLP7;J3QRK5;J3QSA3;K7EMA8;F5GZ39;J3KSM4	Ubiquitin-60S ribosomal protein L40;Ubiquitin;60S ribosomal protein L40;Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Polyubiquitin-B;Ubiquitin;Polyubiquitin-C;Ubiquitin	UBB;RPS27A;UBC;UBA52;UBBP4	>tr|J3QS39|J3QS39_HUMAN Ubiquitin (Fragment) OS=Homo sapiens GN=UBB PE=4 SV=1;>tr|J3QTR3|J3QTR3_HUMAN Ubiquitin (Fragment) OS=Homo sapiens GN=RPS27A PE=1 SV=1;>tr|F5H6Q2|F5H6Q2_HUMAN Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=2 SV=1;>sp|P62987|RL	1.17 1.37 0.9	1.54 1.42 0.79 0.68 0.71 1.72E-215	5	50.5 "activation of immune response;activation of innate immune response;activation of MAPK activity;adipose tissue development;anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen receptor-mediated signaling pathway;biological regulation;biosynthetic process;catabolic process;cell cycle phase;cell cycle process;cell development;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;central nervous system neuron development;cotranslational protein targeting to membrane;cytokine-mediated signaling pathway;cytoplasmic pattern recognition receptor signaling pathway;defense response;developmental process;developmental process involved in reproduction;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA metabolic process;DNA repair;egress of virus within host cell;endosome transport;energy homeostasis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;fat pad development;female gonad development;female meiosis I;fibroblast growth factor receptor signaling pathway;forebrain neuron development;G1 phase;G1 phase of mitotic cell cycle;G1/S transition of mitotic cell cycle;gonad development;homeostatic process;hypothalamus gonadotrophin-releasing hormone neuron development;I-kappaB kinase/NF-kappaB cascade;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;intracellular protein kinase cascade;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;ion transmembrane transport;ion transport;JNK cascade;M phase;M phase of mitotic cell cycle;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;male meiosis I;MAPKKK cascade;meiosis I;membrane organization;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA catabolic process;mRNA metabolic process;multicellular organismal homeostasis;multicellular organismal process;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cytokine production;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of gene expression;negative regulation of ligase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of type I interferon production;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nerve growth factor receptor signaling pathway;neuron development;nitrogen compound metabolic process;Notch receptor processing;Notch signaling pathway;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;nucleotide-binding oligomerization domain containing signaling pathway;organ development;pattern recognition receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of gene expression;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of ligase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of NF-kappaB transcription factor activity;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein serine/threonine kinase activity;positive regulation of protein ubiquitination;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of type I interferon production;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex disassembly;protein complex subunit organization;protein maturation;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein phosphorylation;protein polyubiquitination;protein processing;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of defense response;regulation of epidermal growth factor receptor signaling pathway;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of ligase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein ubiquitination;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of type I interferon production;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;reproductive structure development;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;response to stress;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;S phase;S phase of mitotic cell cycle;seminiferous tubule development;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;SRP-dependent cotranslational protein targeting to membrane;stress-activated protein kinase signaling cascade;T cell receptor signaling pathway;tissue development;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transforming growth factor beta receptor signaling pathway;translation;translational elongation;translational initiation;translational termination;transmembrane receptor protein serine/threonine kinase signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport;TRIF-dependent toll-like receptor signaling pathway;ubiquitin homeostasis;ubiquitin-dependent protein catabolic process;vesicle-mediated transport;viral protein processing;viral reproductive process;viral transcription;virion assembly" binding;cation binding;ion binding;metal ion binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;cytosolic large ribosomal subunit;cytosolic small ribosomal subunit;endocytic vesicle membrane;endosomal part;endosome membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle membrane;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit;vesicle membrane Parkinson's disease;Ribosome

O94874-2;O94874;O94874-3 E3 UFM1-protein ligase 1 UFL1 >sp|O94874-2|UFL1_HUMAN Isoform 2 of E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1;>sp|O94874|UFL1_HUMAN E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2;>sp|O94874-3|UFL1_HUMAN Isoform 3 of E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 NaN NaN 1.26 NaN 1.52 NaN NaN NaN 6.35E-13 5 9.3 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of sequence-specific DNA binding transcription factor activity;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ufmylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent" "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;UFM1 conjugating enzyme activity" cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q92900-2;Q92900 Regulator of nonsense transcripts 1 UPF1 >sp|Q92900-2|RENT1_HUMAN Isoform 2 of Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1;>sp|Q92900|RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2 NaN NaN 0.63 NaN 8.18 NaN NaN NaN 3.37E-09 5 6.4 "biological regulation;biosynthetic process;catabolic process;cell cycle;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;DNA replication;dosage compensation;dosage compensation, by inactivation of X chromosome;establishment of localization;establishment of localization in cell;establishment of RNA localization;gene expression;histone mRNA catabolic process;histone mRNA metabolic process;intracellular transport;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein complex disassembly;regulation of protein metabolic process;regulation of translation;regulation of translational termination;response to DNA damage stimulus;response to stimulus;response to stress;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA transport;transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;cation binding;chromatin binding;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;transition metal ion binding;zinc ion binding" cell part;chromatin;chromosomal part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;exon-exon junction complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;organelle;organelle part;protein complex;ribonucleoprotein complex;RNA granule mRNA surveillance pathway;RNA transport

P31930 "Cytochrome b-c1 complex subunit 1, mitochondrial" UQCRC1">sp|P31930|QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3" 1.16 1.62 1.34 1.85 0.45 0.4 0.57 0.86 6.53E-17 5 8.5 "aerobic respiration;cellular metabolic process;cellular process;cellular respiration;electron transport chain;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, ubiquinol to cytochrome c;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;respiratory electron transport chain;response to activity;response to alkaloid;response to chemical stimulus;response to organic substance;response to stimulus;small molecule metabolic process" "binding;catalytic activity;cation binding;cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on diphenols and related substances as donors;oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;ubiquinol-cytochrome-c reductase activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain;mitochondrial respiratory chain complex III;organelle part;protein complex;respiratory chain;respiratory chain complex III Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P21399;Q9HBB2;Q5VZA6 Cytoplasmic aconitate hydratase ACO1;IRP1 >sp|P21399|ACOC_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3;>tr|Q9HBB2|Q9HBB2_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=IRP1 PE=2 SV=1;>tr|Q5VZA6|Q5VZA6_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO NaN NaN 0.11 NaN 0.06 NaN NaN NaN 5.03E-13 6 10.5 acetyl-CoA catabolic process;acetyl-CoA metabolic process;biological regulation;carboxylic acid metabolic process;catabolic process;cation homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;chemical homeostasis;citrate metabolic process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental process;digestive system process;homeostatic process;intestinal absorption;ion homeostasis;iron ion homeostasis;metabolic process;metal ion homeostasis;multicellular organismal process;organic acid metabolic process;oxoacid metabolic process;post-embryonic development;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;response to chemical stimulus;response to inorganic substance;response to iron ion;response to iron(II) ion;response to metal ion;response to stimulus;small molecule metabolic process;system process;tricarboxylic acid cycle;tricarboxylic acid metabolic process "4 iron, 4 sulfur cluster binding;aconitate hydratase activity;binding;carbon-oxygen lyase activity;catalytic activity;cation binding;citrate hydro-lyase (cis-aconitate-forming) activity;hydro-lyase activity;ion binding;iron-responsive element binding;iron-sulfur cluster binding;isocitrate hydro-lyase (cis-aconitate-forming) activity;lyase activity;metal cluster binding;metal ion binding;mRNA binding;nucleic acid binding;RNA binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism

P61160;P61160-2;F5H6T1 Actin-related protein 2 ACTR2 >sp|P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1;>sp|P61160-2|ARP2_HUMAN Isoform 2 of Actin-related protein 2 OS=Homo sapiens GN=ACTR2;>tr|F5H6T1|F5H6T1_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=2 SV=1 0.62 2.01 0.68 3.15 0.3 0.64 0.45 0.94 8.61E-36 6 16 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin nucleation;Arp2/3 complex-mediated actin nucleation;biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stress adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding Arp2/3 protein complex;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex

P23526-2;P23526 Adenosylhomocysteinase AHCY >sp|P23526-2|SAHH_HUMAN Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHCY;>sp|P23526|SAHH_HUMAN Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4 0.08 30.35 0.07 18.62 0.07 0.98 0.12 1.07 2.32E-26 6 17.1 amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;methylation;nitrogen compound metabolic process;one-carbon metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound metabolic process;xenobiotic metabolic process "adenosylhomocysteinase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ether bonds;trialkylsulfonium hydrolase activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;vesicle Cysteine and methionine metabolism

Q5QNZ2;P24539 "ATP synthase subunit b, mitochondrial" ATP5F1 ">tr|Q5QNZ2|Q5QNZ2_HUMAN ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=2 SV=1;>sp|P24539|AT5F1_HUMAN ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2" 0.99 1.45 1.46 1.34 0.61 0.44 0.77 0.76 1.34E-18 6 31.8 "ATP biosynthetic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;cation transport;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle lumen;organelle part;protein complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex, proton-transporting domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P48047;H7C068;H7C0C1;H7C086 "ATP synthase subunit O, mitochondrial" ATP5O ">sp|P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1" 1.14 1.37 1.94 1.33 0.64 0.53 0.69 0.86 1.09E-69 6 40.4 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "binding;cation transmembrane transporter activity;drug binding;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;lipid binding;monovalent inorganic cation transmembrane transporter activity;steroid binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle part;plasma membrane;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P51572;P51572-2;C9JMD7;C9JSP1;C9JQ75;C9J0M4;C9JM14 B-cell receptor-associated protein 31 BCAP31 >sp|P51572|BAP31_HUMAN B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3;>sp|P51572-2|BAP31_HUMAN Isoform 2 of B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31;>tr|C9JMD7|C9JMD7_HUMAN B-cell receptor-associated protei 0.89 0.51 1.02 0.31 2.05 1.28 1.42 1.24 9.31E-17 6 21.5 antigen processing and presentation;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;calcium ion homeostasis;calcium-mediated signaling;calcium-mediated signaling using intracellular calcium source;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;cytosolic calcium ion homeostasis;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion concentration;elevation of mitochondrial calcium ion concentration;endoplasmic reticulum calcium ion homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;gamete generation;homeostatic process;immune response;immune system process;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;male gamete generation;metal ion homeostasis;mitochondrial calcium ion homeostasis;multicellular organismal process;multicellular organismal reproductive process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;protein transport;reduction of endoplasmic reticulum calcium ion concentration;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;reproductive process;response to stimulus;second-messenger-mediated signaling;signal transduction;spermatogenesis;transport;vesicle-mediated transport binding;protein binding;receptor binding cell part;cytoplasmic part;cytosol;endoplasmic reticulum;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;intrinsic to plasma membrane;lipid particle;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part Protein processing in endoplasmic reticulum

Q14692 Ribosome biogenesis protein BMS1 homolog BMS1 >sp|Q14692|BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1 1.11 0.99 1.17 2.47 0.57 0.38 0.59 0.53 2.30E-28 6 6.8 catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle assembly;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;ribosome assembly;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes

P35613-3;P35613-4;P35613-2;P35613;R4GMX5;I3L192;R4GN83 Basigin BSG>sp|P35613-3|BASI_HUMAN Isoform 3 of Basigin OS=Homo sapiens GN=BSG;>sp|P35613-4|BASI_HUMAN Isoform 4 of Basigin OS=Homo sapiens GN=BSG;>sp|P35613-2|BASI_HUMAN Isoform 2 of Basigin OS=Homo sapiens GN=BSG;>sp|P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG 0.71 1.5 1.23 1.24 0.31 0.39 0.65 1.12 3.99E-18 6 34.1 anatomical structure development;anatomical structure morphogenesis;biological regulation;blood coagulation;carboxylic acid metabolic process;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component movement;cellular ketone metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;coagulation;decidualization;developmental process;developmental process involved in reproduction;embryo implantation;hemostasis;immune system process;leukocyte migration;locomotion;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;organic acid metabolic process;oxoacid metabolic process;pyruvate metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;reproductive process;response to cAMP;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to inorganic substance;response to mercury ion;response to metal ion;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;small molecule metabolic process;tissue development binding;carbohydrate binding;mannose binding;monosaccharide binding;sugar binding acrosomal membrane;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;sarcolemma;secretory granule membrane;vesicle;vesicle membrane

F8VPD4;P27708;H7BZB3 CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyltransferase;Dihydroorotase CAD >tr|F8VPD4|F8VPD4_HUMAN DNA fragmentation factor subunit beta OS=Homo sapiens GN=CAD PE=2 SV=1;>sp|P27708|PYR1_HUMAN CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 NaN 0.47 0.94 NaN 1.72 NaN NaN 1.13 3.02E-24 6 4.3 amine catabolic process;amine metabolic process;anatomical structure morphogenesis;biological regulation;biosynthetic process;body fluid secretion;carbamoyl phosphate biosynthetic process;carbamoyl phosphate metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to drug;cellular response to endogenous stimulus;cellular response to epidermal growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;'de novo' pyrimidine base biosynthetic process;'de novo' UMP biosynthetic process;developmental process;drug metabolic process;embryo development;establishment of localization;female pregnancy;glutamine catabolic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;lactation;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organ morphogenesis;organ regeneration;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-threonine modification;peptidyl-threonine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;pyrimidine base biosynthetic process;pyrimidine base metabolic process;pyrimidine nucleoside biosynthetic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside monophosphate biosynthetic process;pyrimidine nucleoside monophosphate metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside monophosphate biosynthetic process;pyrimidine ribonucleoside monophosphate metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;regeneration;regulation of biological quality;regulation of body fluid levels;reproductive process;response to alkaloid;response to amine stimulus;response to caffeine;response to chemical stimulus;response to corticosteroid stimulus;response to cortisol stimulus;response to drug;response to endogenous stimulus;response to epidermal growth factor stimulus;response to glucocorticoid stimulus;response to growth factor stimulus;response to hormone stimulus;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to purine-containing compound;response to steroid hormone stimulus;response to stimulus;response to testosterone stimulus;ribonucleoside metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;small molecule catabolic process;small molecule metabolic process;transport;UMP biosynthetic process;UMP metabolic process;UTP biosynthetic process;UTP metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;aspartate binding;aspartate carbamoyltransferase activity;ATP binding;binding;carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;carbon-nitrogen ligase activity, with glutamine as amido-N-donor;carboxyl- or carbamoyltransferase activity;carboxylic acid binding;catalytic activity;cation binding;dihydroorotase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides;identical protein binding;ion binding;kinase activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring one-carbon groups;transferase activity, transferring phosphorus-containing groups" axon part;cell body;cell part;cell projection part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;neuronal cell body;nuclear matrix;nuclear part;organelle part;protein complex;synapse part;terminal button "Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism"

P07384;E9PLX0;E9PJJ3;E9PLC9;E9PMC6;E9PJA6;E9PSA6;E9PLQ6;E9PL37;E9PQB3;E9PRM1 Calpain-1 catalytic subunit CAPN1 >sp|P07384|CAN1_HUMAN Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 NaN NaN 0.4 0.82 3.29 1.93 NaN NaN 5.46E-12 6 9.1 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein metabolic process;proteolysis;receptor catabolic process;receptor metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process "binding;calcium ion binding;calcium-dependent cysteine-type endopeptidase activity;catalytic activity;cation binding;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasm;intracellular;intracellular part;membrane;plasma membrane Alzheimer's disease;Apoptosis;Protein processing in endoplasmic reticulum

Q03135;E9PCT5;C9JKI3;Q03135-2;P56539 Caveolin-1;Caveolin CAV1 >sp|Q03135|CAV1_HUMAN Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4;>tr|E9PCT5|E9PCT5_HUMAN Caveolin OS=Homo sapiens GN=CAV1 PE=2 SV=1;>tr|C9JKI3|C9JKI3_HUMAN Caveolin (Fragment) OS=Homo sapiens GN=CAV1 PE=2 SV=1;>sp|Q03135-2|CAV1_HUMAN Isoform Beta of Cave 1.14 1.16 0.72 1.2 0.79 0.71 0.83 1.26 1.12E-61 6 34.8 "actin cytoskeleton organization;actin filament organization;actin filament-based process;acylglycerol metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;angiogenesis;biological regulation;blood coagulation;body fluid secretion;calcium ion homeostasis;calcium ion transport;carbohydrate homeostasis;cardiac cell development;cardiac muscle cell development;cation homeostasis;cation transport;caveola assembly;caveolin-mediated endocytosis;cell communication;cell development;cell differentiation;cell growth;cell migration;cell motility;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein localization;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to hyperoxia;cellular response to nutrient levels;cellular response to oxygen levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;chemical homeostasis;cholesterol homeostasis;cholesterol transport;circulatory system process;coagulation;cytoplasmic microtubule organization;cytoskeleton organization;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of cytosolic calcium ion concentration;endocytosis;establishment of localization;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;gas homeostasis;glucose homeostasis;glycerol ether metabolic process;glycerolipid metabolic process;growth;heart trabecula formation;hemostasis;homeostatic process;immune system process;inactivation of MAPK activity;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;ion homeostasis;ion transport;lactation;leukocyte migration;lipid homeostasis;lipid localization;lipid metabolic process;lipid storage;lipid transport;localization;locomotion;lymphocyte costimulation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;mammary gland involution;MAPKKK cascade;membrane depolarization;membrane invagination;membrane organization;membrane raft assembly;membrane raft organization;metabolic process;metal ion homeostasis;metal ion transport;microtubule cytoskeleton organization;microtubule-based process;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell development;muscle cell homeostasis;muscle organ development;muscle structure development;muscle tissue development;myoblast fusion;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of BMP signaling pathway;negative regulation of calcium ion transport;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cardiac muscle hypertrophy;negative regulation of cardiac muscle tissue growth;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell growth involved in cardiac muscle cell development;negative regulation of cell proliferation;negative regulation of cell size;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cytokine-mediated signaling pathway;negative regulation of cytoskeleton organization;negative regulation of developmental growth;negative regulation of developmental process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell differentiation;negative regulation of epithelial cell proliferation;negative regulation of gene expression;negative regulation of growth;negative regulation of heart growth;negative regulation of intracellular protein kinase cascade;negative regulation of ion transport;negative regulation of JAK-STAT cascade;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of monooxygenase activity;negative regulation of multicellular organismal process;negative regulation of muscle cell differentiation;negative regulation of muscle hypertrophy;negative regulation of nitric oxide biosynthetic process;negative regulation of nitric-oxide synthase activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organ growth;negative regulation of organelle organization;negative regulation of oxidoreductase activity;negative regulation of peptidyl-serine phosphorylation;negative regulation of peptidyl-tyrosine phosphorylation;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of programmed cell death;negative regulation of protein binding;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of protein serine/threonine kinase activity;negative regulation of protein ubiquitination;negative regulation of response to cytokine stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sarcomere organization;negative regulation of signal transduction;negative regulation of signaling;negative regulation of striated muscle cell differentiation;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of transport;negative regulation of tyrosine phosphorylation of STAT protein;negative regulation of tyrosine phosphorylation of Stat5 protein;negative regulation of Wnt receptor signaling pathway;neutral lipid metabolic process;nitric oxide homeostasis;nitric oxide metabolic process;nitrogen compound metabolic process;nucleus localization;organ development;organelle localization;organelle organization;organic ether metabolic process;organic substance transport;plasma membrane organization;plasma membrane repair;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of calcium ion transport into cytosol;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of homeostatic process;positive regulation of immune system process;positive regulation of ion transport;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of metalloenzyme activity;positive regulation of microtubule polymerization;positive regulation of microtubule polymerization or depolymerization;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle cell differentiation;positive regulation of myotube differentiation;positive regulation of organelle organization;positive regulation of peptidyl-serine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein complex assembly;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein polymerization;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of skeletal muscle cell differentiation;positive regulation of striated muscle cell differentiation;positive regulation of T cell activation;positive regulation of transport;positive regulation of vasoconstriction;positive regulation of Wnt receptor signaling pathway;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein localization;protein localization in membrane;protein localization in plasma membrane;protein oligomerization;receptor internalization;receptor internalization involved in canonical Wnt receptor signaling pathway;receptor metabolic process;receptor-mediated endocytosis;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of anoikis;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood coagulation;regulation of blood vessel size;regulation of BMP signaling pathway;regulation of body fluid levels;regulation of branching involved in mammary gland duct morphogenesis;regulation of calcium ion import;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac muscle cell differentiation;regulation of cardiac muscle contraction;regulation of cardiac muscle hypertrophy;regulation of cardiac muscle tissue development;regulation of cardiac muscle tissue growth;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell growth involved in cardiac muscle cell development;regulation of cell proliferation;regulation of cell size;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular ketone metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of coagulation;regulation of cytokine-mediated signaling pathway;regulation of cytoskeleton organization;regulation of developmental growth;regulation of developmental process;regulation of endothelial cell proliferation;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of fatty acid metabolic process;regulation of gene expression;regulation of growth;regulation of heart contraction;regulation of heart growth;regulation of heart rate;regulation of homeostatic process;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of lipid metabolic process;regulation of localization;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of membrane depolarization;regulation of membrane potential;regulation of membrane repolarization;regulation of metabolic process;regulation of metal ion transport;regulation of metalloenzyme activity;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of molecular function;regulation of monooxygenase activity;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle adaptation;regulation of muscle cell differentiation;regulation of muscle contraction;regulation of muscle hypertrophy;regulation of muscle organ development;regulation of muscle system process;regulation of myotube differentiation;regulation of nerve growth factor receptor activity;regulation of nerve growth factor receptor signaling pathway;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ growth;regulation of organ morphogenesis;regulation of organelle organization;regulation of oxidoreductase activity;regulation of peptidyl-serine phosphorylation;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein binding;regulation of protein complex assembly;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of protein serine/threonine kinase activity;regulation of protein ubiquitination;regulation of receptor activity;regulation of response to cytokine stimulus;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sarcomere organization;regulation of signal transduction;regulation of signal transduction by receptor internalization;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of skeletal muscle contraction;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of smooth muscle contraction;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of striated muscle cell differentiation;regulation of striated muscle contraction;regulation of striated muscle tissue development;regulation of system process;regulation of T cell activation;regulation of the force of heart contraction;regulation of the force of heart contraction by chemical signal;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;regulation of tube size;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat5 protein;regulation of vasoconstriction;regulation of ventricular cardiomyocyte membrane depolarization;regulation of ventricular cardiomyocyte membrane repolarization;regulation of Wnt receptor signaling pathway;regulation of wound healing;reproductive process;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to hyperoxia;response to hypoxia;response to inorganic substance;response to metal ion;response to nutrient levels;response to organic substance;response to oxygen levels;response to progesterone stimulus;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;secretion;signal transduction;skeletal muscle tissue development;small molecule metabolic process;sterol homeostasis;sterol transport;striated muscle tissue development;syncytium formation;syncytium formation by plasma membrane fusion;system process;T cell costimulation;tissue development;tissue remodeling;trabecula formation;transport;triglyceride metabolic process;T-tubule organization;vascular process in circulatory system;vasculogenesis;vasoconstriction;vesicle organization;vesicle-mediated transport;viral reproductive process;virus-host interaction" binding;calcium channel regulator activity;channel regulator activity;cholesterol binding;connexin binding;enzyme activator activity;enzyme regulator activity;lipid binding;peptidase activator activity;peptidase regulator activity;protein binding;protein complex binding;protein complex scaffold;protein C-terminus binding;sodium channel regulator activity;steroid binding;sterol binding;structural molecule activity acrosomal membrane;apical plasma membrane;basolateral plasma membrane;caveola;cell cortex;cell part;cell surface;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;dystrophin-associated glycoprotein complex;endocytic vesicle membrane;endoplasmic reticulum;endoplasmic reticulum part;endosome;Golgi apparatus part;Golgi membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lipid particle;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;neuromuscular junction;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex;secretory granule membrane;synapse;T-tubule;vesicle;vesicle membrane Bacterial invasion of epithelial cells;Endocytosis;Focal adhesion;Viral myocarditis

B7Z9L0;P50991;B7Z2F4;P50991-2 T-complex protein 1 subunit delta CCT4 >tr|B7Z9L0|B7Z9L0_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1;>sp|P50991|TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4;>tr|B7Z2F4|B7Z2F4_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens 0.74 1.6 0.46 1.27 0.39 0.94 0.89 1 1.84E-28 6 13.9 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein bindingcell part;centrosome;chaperonin-containing T-complex;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;cytosolic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane-bounded organelle;membrane-bounded vesicle;microtubule;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;pigment granule;protein complex;vesicle

B4DZI8;P35606;D6RBZ7;D6RCL6;D6RBG7;D6RBT6;H0YAC7;D6R997;H0Y938 Coatomer subunit beta COPB2 ">tr|B4DZI8|B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1;>sp|P35606|COPB2_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB2 PE=1 SV=2" NaN NaN 0.45 NaN 1.8 NaN NaN NaN 6.10E-19 6 9.6 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;organelle organization;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport"structural molecule activity actin cytoskeleton;cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytoskeleton;cytosol;Golgi apparatus;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle coat

Q9Y678;H0Y8X7 Coatomer subunit gamma-1 COPG1 >sp|Q9Y678|COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 NaN NaN 0.37 NaN 2.08 NaN NaN NaN 1.02E-17 6 8.1 "cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;cytoskeleton-dependent intracellular transport;establishment of Golgi localization;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;microtubule-based movement;microtubule-based process;microtubule-based transport;organelle organization;organelle transport along microtubule;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" structural molecule activity cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;vesicle coat

O75131;E5RHZ0;E5RG68;E5RJ85;H0YB26;E5RG97;Q86VY2;Q7Z6C8;Q719H8;Q96FN4;E7ENV7;Q8IYJ1;Q96A23;O95741;Q9UBL6-2;Q86YQ8;Q96A23-2;Q9HCH3;F5GXN1;Q9UBL6 Copine-3 CPNE3 >sp|O75131|CPNE3_HUMAN Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1;>tr|E5RHZ0|E5RHZ0_HUMAN Copine-3 (Fragment) OS=Homo sapiens GN=CPNE3 PE=2 SV=1;>tr|E5RG68|E5RG68_HUMAN Copine-3 (Fragment) OS=Homo sapiens GN=CPNE3 PE=2 SV=1 0.85 0.72 0.92 0.17 2.5 2.63

1.38 0.44 7.69E-13 6 11.7 anatomical structure development;cell communication;cell-cell signaling;cellular process;developmental process;establishment of localization;lipid metabolic process;metabolic process;nervous system development;primary metabolic process;signaling;synaptic transmission;system development;transport;vesicle-mediated transport "binding;calcium ion binding;calcium-dependent phospholipid binding;catalytic activity;cation binding;ion binding;kinase activity;lipid binding;metal ion binding;phosphatidylserine binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transporter activity" axon;cell body;cell part;cell projection;cytoplasmic part;cytosol;dendrite;intracellular part;membrane;neuron projection;neuronal cell body

E9PR44;P02511;E9PNH7;E9PJL7;E9PRA8;H0YCW8;E9PRS4;E9PS12 Alpha-crystallin B chain CRYAB >tr|E9PR44|E9PR44_HUMAN Alpha-crystallin B chain (Fragment) OS=Homo sapiens GN=CRYAB PE=2 SV=1;>sp|P02511|CRYAB_HUMAN Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2;>tr|E9PNH7|E9PNH7_HUMAN Alpha-crystallin B chain (Fragment) OS=Homo sapiens GN 0.3 0.54 0.06 0.2 3.13 2.94 1.04 1.24 2.17E-42 6 42.5 aging;alcohol metabolic process;anatomical structure development;apoptosis;apoptosis involved in morphogenesis;biological regulation;carbohydrate metabolic process;cell death;cellular carbohydrate metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cytoskeleton organization;death;developmental process;developmental programmed cell death;glucose metabolic process;hexose metabolic process;intracellular protein kinase cascade;intracellular signal transduction;lens development in camera-type eye;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;MAPKKK cascade;metabolic process;microtubule cytoskeleton organization;microtubule polymerization or depolymerization;microtubule-based process;monosaccharide metabolic process;multicellular organismal process;muscle contraction;muscle organ development;muscle structure development;muscle system process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cell growth;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of growth;negative regulation of hydrolase activity;negative regulation of intracellular transport;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of reactive oxygen species metabolic process;negative regulation of transport;organ development;organelle organization;primary metabolic process;programmed cell death;protein complex assembly;protein complex subunit organization;protein folding;protein homooligomerization;protein metabolic process;protein oligomerization;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of intracellular transport;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of programmed cell death;regulation of reactive oxygen species metabolic process;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to hormone stimulus;response to hydrogen peroxide;response to hypoxia;response to inorganic substance;response to organic substance;response to oxidative stress;response to oxygen levels;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;signal transduction;small molecule metabolic process;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;system process;tubulin complex assembly binding;cation binding;ion binding;metal ion binding;structural constituent of eye lens;structural molecule activity actin filament bundle;cell part;cell surface;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microtubule cytoskeleton;mitochondrion;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;Z disc Protein processing in endoplasmic reticulum

Q9NVP1;H7C452 ATP-dependent RNA helicase DDX18 DDX18 >sp|Q9NVP1|DDX18_HUMAN ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 0.82 1.35 1.16 2.16 0.37 0.3 0.5 0.47 2.78E-14 6 9.6 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

Q68CR9;P14868;C9J7S3;C9JLC1;C9JQM9;H7BZ35;H7C278 "Aspartate--tRNA ligase, cytoplasmic" DKFZp781B11202;DARS ">tr|Q68CR9|Q68CR9_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DKFZp781B11202 PE=2 SV=1;>sp|P14868|SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2;>tr|C9J7S3|C9J7S3_HUMAN Aspartate--tRNA ligase, cytoplasmic" 1.18 0.92 0.48 0.56 0.93 1.08 1.42 1.09 7.53E-15 6 17 amine metabolic process;amino acid activation;aspartyl-tRNA aminoacylation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacylase activity;aminoacyl-tRNA ligase activity;aspartate-tRNA ligase activity;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Aminoacyl-tRNA biosynthesis

P36957;B7Z5W8;Q86SW4;H0YJF9;G3V5M3;G3V3F0 "Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial" DLST ">sp|P36957|ODO2_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4;>tr|B7Z5W8|B7Z5W8_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-" 0.89 1.34 1.72 0.9 0.86 1.01 0.92 1.31 3.64E-88 6 19.6 acetyl-CoA catabolic process;acetyl-CoA metabolic process;amine catabolic process;amine metabolic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;L-lysine catabolic process;L-lysine catabolic process to acetyl-CoA;L-lysine catabolic process to acetyl-CoA via saccharopine;L-lysine metabolic process;lysine catabolic process;lysine metabolic process;metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;dihydrolipoyllysine-residue succinyltransferase activity;S-acyltransferase activity;S-succinyltransferase activity;succinyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part;oxoglutarate dehydrogenase complex;protein complex Citrate cycle (TCA cycle);Lysine degradation

Q9NVH1-3;Q9NVH1-2;F5H1N1;Q9NVH1;B4DGD5;B1AK20;Q9UMU8;Q5TH61 DnaJ homolog subfamily C member 11 DNAJC11 >sp|Q9NVH1-3|DJC11_HUMAN Isoform 3 of DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11;>sp|Q9NVH1-2|DJC11_HUMAN Isoform 2 of DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11;>tr|F5H1N1|F5H1N1_HUMAN DnaJ homolog subfamily C member 1.88 0.64 1.15 1.35 0.77 0.72 1.24 0.8 1.12E-21 6 13 cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

Q5QJE6;J3KP30;E9PRB3 Deoxynucleotidyltransferase terminal-interacting protein 2 DNTTIP2 >sp|Q5QJE6|TDIF2_HUMAN Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens GN=DNTTIP2 PE=1 SV=2;>tr|J3KP30|J3KP30_HUMAN Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens GN=DNTTIP2 PE=4 SV=1 1.13 1.42 1.12 2.24 0.49 0.28 0.41 0.49 2.99E-25 6 10.8 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

P26641;B4DTG2 Elongation factor 1-gamma EEF1G >sp|P26641|EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3;>tr|B4DTG2|B4DTG2_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=2 SV=1 0.68 1.87 0.31 1.17 0.48 1.04 1.12 1.2 2.99E-37 6 13 multi-organism process;response to biotic stimulus;response to other organism;response to stimulus;response to virus "binding;nucleic acid binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular part;macromolecular complex;protein complex

F5H335;Q14152 Eukaryotic translation initiation factor 3 subunit A EIF3A >tr|F5H335|F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1;>sp|Q14152|EIF3A_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1 NaN NaN 0.35 NaN 6.19 NaN NaN NaN 1.44E-15 6 6.1 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;formation of translation initiation complex;macromolecular complex assembly;macromolecular complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization "binding;nucleic acid binding;RNA binding;structural molecule activity;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex RNA transport

E7ER77;Q7Z2K6;B3KSB1;Q6ZMD3 Endoplasmic reticulum metallopeptidase 1 ERMP1 >tr|E7ER77|E7ER77_HUMAN Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=2 SV=1;>sp|Q7Z2K6|ERMP1_HUMAN Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=1 SV=2;>tr|B3KSB1|B3KSB1_HUMAN Endoplasmic reticulum metallopept 0.94 1.06 1.39 0.94 1.05 0.71 1.01 0.77 3.86E-14 6 7.6 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "binding;catalytic activity;cation binding;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part

P04899;P04899-4;F5GZL8;B4E2X5;P04899-3;P04899-2;B3KTZ0 Guanine nucleotide-binding protein G(i) subunit alpha-2 GNAI2 >sp|P04899|GNAI2_HUMAN Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3;>sp|P04899-4|GNAI2_HUMAN Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2;>tr|F5GZL8|F5GZL8_HU 0.93 1.88 1.2 1.21 0.46 0.44 0.54 1.01 3.00E-60 6 20.8 "activation of MAPKK activity;activation of protein kinase activity;adenosine receptor signaling pathway;biological regulation;cAMP-mediated signaling;catabolic process;cell activation;cell communication;cell cycle;cell division;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cyclic-nucleotide-mediated signaling;gamma-aminobutyric acid signaling pathway;G-protein coupled purinergic receptor signaling pathway;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;metabolic process;muscarinic acetylcholine receptor signaling pathway;negative regulation of adenylate cyclase activity;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cellular process;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of neurological system process;negative regulation of signaling;negative regulation of synaptic transmission;negative regulation of transmission of nerve impulse;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;purinergic receptor signaling pathway;regulation of adenylate cyclase activity;regulation of biological process;regulation of biosynthetic process;regulation of calcium ion transport;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of ion transport;regulation of kinase activity;regulation of localization;regulation of lyase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of signaling;regulation of synaptic transmission;regulation of system process;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of transport;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;second-messenger-mediated signaling;signal transduction;signaling;small molecule metabolic process;synaptic transmission" "binding;catalytic activity;cation binding;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity" cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;microtubule organizing center;midbody;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex Axon guidance;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Gap junction;Gastric acid secretion;Leukocyte transendothelial migration;Long-term depression;Melanogenesis;Progesterone-mediated oocyte maturation;Tight junction;Toxoplasmosis

P63092-3;P63092-2;P63092;P63092-4;Q5JWF2-2;Q5JWF2;Q5JWE9;H0Y7F4;A2A2R6;Q5JWD1;H0Y7E8;Q14344;Q03113;P38405;P38405-2 Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas GNAS >sp|P63092-3|GNAS2_HUMAN Isoform 3 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS;>sp|P63092-2|GNAS2_HUMAN Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapie 0.71 1.47 0.86 1.05 0.79 1 0.73 0.9 8.36E-16 6 17.9 "activation of adenylate cyclase activity;activation of adenylate cyclase activity by dopamine receptor signaling pathway;activation of adenylate cyclase activity by G-protein signaling pathway;activation of phospholipase D activity;anatomical structure development;anatomical structure homeostasis;anatomical structure morphogenesis;appendage morphogenesis;behavior;biological regulation;blood coagulation;body morphogenesis;branching morphogenesis of a tube;cAMP-mediated signaling;cartilage development;catabolic process;cell activation;cell communication;cell differentiation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular catabolic process;cellular component movement;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to amine stimulus;cellular response to catecholamine stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to glucagon stimulus;cellular response to hormone stimulus;cellular response to lipid;cellular response to monoamine stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to prostaglandin E stimulus;cellular response to prostaglandin stimulus;cellular response to stimulus;chordate embryonic development;coagulation;cyclic-nucleotide-mediated signaling;developmental process;DNA alkylation;DNA metabolic process;DNA methylation;DNA modification;dopamine receptor signaling pathway;embryo development;embryo development ending in birth or egg hatching;embryonic appendage morphogenesis;embryonic cranial skeleton morphogenesis;embryonic digit morphogenesis;embryonic hindlimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;embryonic skeletal system morphogenesis;endochondral ossification;energy derivation by oxidation of organic compounds;energy reserve metabolic process;epidermis development;establishment of localization;establishment of localization in cell;fluid transport;generation of precursor metabolites and energy;genetic imprinting;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;growth;GTP catabolic process;GTP metabolic process;hemostasis;heterocycle catabolic process;heterocycle metabolic process;hindlimb morphogenesis;homeostatic process;in utero embryonic development;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;intracellular transport;limb morphogenesis;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organism growth;multicellular organismal process;negative regulation of adenylate cyclase activity;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of molecular function;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;one-carbon metabolic process;organ morphogenesis;ossification;oxidation-reduction process;pattern specification process;patterning of blood vessels;platelet activation;positive regulation of adenylate cyclase activity;positive regulation of adenylate cyclase activity by G-protein signaling pathway;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of cyclase activity;positive regulation of developmental process;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of lyase activity;positive regulation of molecular function;positive regulation of myeloid cell differentiation;positive regulation of myeloid leukocyte differentiation;positive regulation of osteoblast differentiation;positive regulation of osteoclast differentiation;positive regulation of phospholipase activity;post-embryonic body morphogenesis;post-embryonic morphogenesis;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;Ras protein signal transduction;regulation of adenylate cyclase activity;regulation of adenylate cyclase activity involved in G-protein signaling pathway;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell motility;regulation of cell shape;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of developmental process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of hormone secretion;regulation of hydrolase activity;regulation of immune system process;regulation of insulin secretion;regulation of lipase activity;regulation of localization;regulation of locomotion;regulation of lyase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoclast differentiation;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phospholipase activity;regulation of primary metabolic process;regulation of secretion;regulation of signaling;regulation of transport;response to alkaloid;response to amine stimulus;response to amphetamine;response to caffeine;response to catecholamine stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to glucagon stimulus;response to hormone stimulus;response to lipid;response to monoamine stimulus;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to peptide hormone stimulus;response to prostaglandin E stimulus;response to prostaglandin stimulus;response to purine-containing compound;response to stimulus;Rho protein signal transduction;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;second-messenger-mediated signaling;sensory perception;sensory perception of chemical stimulus;sensory perception of smell;signal transduction;signaling;skeletal system morphogenesis;skin development;small GTPase mediated signal transduction;small molecule metabolic process;synaptic transmission;system process;tissue development;tissue homeostasis;tissue morphogenesis;transmembrane transport;transport;tube morphogenesis;water transport" "adenylate cyclase activity;angiotensin receptor binding;binding;catalytic activity;cation binding;cyclase activity;D5 dopamine receptor binding;dopamine receptor binding;glutamate receptor binding;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;ionotropic glutamate receptor binding;lyase activity;metal ion binding;molecular transducer activity;mu-type opioid receptor binding;nucleoside-triphosphatase activity;nucleotide binding;opioid receptor binding;phosphorus-oxygen lyase activity;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity;type 1 angiotensin receptor binding" brush border membrane;cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;dendrite;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus part;Golgi membrane;heterotrimeric G-protein complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuron projection;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;protein complex;trans-Golgi network membrane;vesicle Amoebiasis;Bile secretion;Calcium signaling pathway;Chagas disease (American trypanosomiasis);Dilated cardiomyopathy;Endocrine and other factor-regulated calcium reabsorption;Gap junction;Gastric acid secretion;GnRH signaling pathway;Long-term depression;MAPK signaling pathway;Melanogenesis;Olfactory transduction;Pancreatic secretion;Regulation of actin cytoskeleton;Salivary secretion;Taste transduction;Vascular smooth muscle contraction;Vasopressin-regulated water reabsorption;Vibrio cholerae infection Q99878;Q96KK5;Q93077;Q7L7L0;P20671;P0C0S8;P04908;Q9BTM1;Q6FI13;H0YFX9;Q16777;Q9BTM1-2;Q96QV6;Q71UI9-5;REV__H0Y672 Histone H2A type 1-J;Histone H2A type 1-H;Histone H2A type 1-C;Histone H2A type 3;Histone H2A type 1-D;Histone H2A type 1;Histone H2A type 1-B/E;Histone H2A.J;Histone H2A type 2-A;Histone H2A;Histone H2A type 2-C;Histone H2A type 1-A HIST1H2AJ;HIST1H2AH;HIST1H2AC;HIST3H2A;HIST1H2AD;HIST1H2AG;HIST1H2AB;H2AFJ;HIST2H2AA3;HIST2H2AC;HIST1H2AA >sp|Q99878|H2A1J_HUMAN Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3;>sp|Q96KK5|H2A1H_HUMAN Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3;>sp|Q93077|H2A1C_HUMAN Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3;>sp|Q7L 1.08 1.7 1.19 2.96 0.42 0.44 0.33 0.32 6.90E-107 6 60.9 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus B0S7Z4;P30508;B0S7Z5;B0S7Z6;Q5SRN7;P30455;P30443;P16188;P13746;P04439;Q29963;Q07000;P30505;P30501;B0UY12;Q5SRN5;P13746-2;B0UY14;B0UY15;B0UXQ1;A2BDY9;A2ARK8;Q29960-2;Q04826;P30480;P30479;P30460;P01889;P01893;Q31612;P30447;P05534;P30512;P30459;P30457;P30456;P30453;P30450;P18462;P16190;P16189;P10314;B0UXQ0;P30510;P30504;P10321;Q9TNN7;Q29960;A2BF24;Q5SPM3;A2AEA2;A2BF25;A2BF26;F5GXA6;A9R9N8;B0V0C2;Q29940;P30685;P30498;P30495;P30493;P30492;P30491;P30490;P30484;P30464;P18465;P18464;P10319;Q09160;P10316;P01892;P01891;Q29865;P04222;B0V0B9;A9R9N7;B0V0C1;F6U0H7;P17693;Q5RJ85;Q95365;Q29836;Q29718;P30488;P30487;P30485;P30483;P30481;P30475;P30466;P30462;P30461;P18463;P03989;P30499;Q31611;Q5SPT7;B1AZU4 "HLA class I histocompatibility antigen, Cw-12 alpha chain;HLA class I histocompatibility antigen, A-36 alpha chain;HLA class I histocompatibility antigen, A-1 alpha chain;HLA class I histocompatibility antigen, A-30 alpha chain;HLA class I histocompatibility antigen, A-11 alpha chain;HLA class I histocompatibility antigen, A-3 alpha chain;HLA class I histocompatibility antigen, Cw-6 alpha chain;HLA class I histocompatibility antigen, Cw-15 alpha chain;HLA class I histocompatibility antigen, Cw-8 alpha chain;HLA class I histocompatibility antigen, Cw-2 alpha chain;HLA class I histocompatibility antigen, B-40 alpha chain;HLA class I histocompatibility antigen, B-42 alpha chain;HLA class I histocompatibility antigen, B-41 alpha chain;HLA class I histocompatibility antigen, B-8 alpha chain;HLA class I histocompatibility antigen, B-7 alpha chain;Putative HLA class I histocompatibility antigen, alpha chain H;HLA class I histocompatibility antigen, B-73 alpha chain;HLA class I histocompatibility antigen, A-23 alpha chain;HLA class I histocompatibility antigen, A-24 alpha chain;HLA class I histocompatibility antigen, A-29 alpha chain;HLA class I histocompatibility antigen, A-74 alpha chain;HLA class I histocompatibility antigen, A-66 alpha chain;HLA class I histocompatibility antigen, A-43 alpha chain;HLA class I histocompatibility antigen, A-34 alpha chain;HLA class I histocompatibility antigen, A-26 alpha chain;HLA class I histocompatibility antigen, A-25 alpha chain;HLA class I histocompatibility antigen, A-33 alpha chain;HLA class I histocompatibility antigen, A-31 alpha chain;HLA class I histocompatibility antigen, A-32 alpha chain;HLA class I histocompatibility antigen, Cw-14 alpha chain;HLA class I histocompatibility antigen, Cw-4 alpha chain;HLA class I histocompatibility antigen, Cw-7 alpha chain;HLA class I histocompatibility antigen, Cw-5 alpha chain;HLA class I histocompatibility antigen, Cw-16 alpha chain;HLA class I histocompatibility antigen, B-59 alpha chain;HLA class I histocompatibility antigen, B-35 alpha chain;HLA class I histocompatibility antigen, B-78 alpha chain;HLA class I histocompatibility antigen, B-56 alpha chain;HLA class I histocompatibility antigen, B-55 alpha chain;HLA class I histocompatibility antigen, B-54 alpha chain;HLA class I histocompatibility antigen, B-53 alpha chain;HLA class I histocompatibility antigen, B-52 alpha chain;HLA class I histocompatibility antigen, B-46 alpha chain;HLA class I histocompatibility antigen, B-15 alpha chain;HLA class I histocompatibility antigen, B-57 alpha chain;HLA class I histocompatibility antigen, B-51 alpha chain;HLA class I histocompatibility antigen, B-58 alpha chain;HLA class I histocompatibility antigen, A-80 alpha chain;HLA class I histocompatibility antigen, A-69 alpha chain;HLA class I histocompatibility antigen, A-2 alpha chain;HLA class I histocompatibility antigen, A-68 alpha chain;HLA class I histocompatibility antigen, Cw-18 alpha chain;HLA class I histocompatibility antigen, Cw-3 alpha chain" HLA-C;HLA-A;HLA-B;HLA-H ">tr|B0S7Z4|B0S7Z4_HUMAN HLA class I histocompatibility antigen, Cw-14 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=1;>sp|P30508|1C12_HUMAN HLA class I histocompatibility antigen, Cw-12 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=2;>tr|B0S7Z5|B0S7Z5_HUMAN" 0.82 1.23 1.46 0.86 0.35 0.41 0.68 0.92 4.43E-85 6 22.1 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;cell surface receptor linked signaling pathway;cellular defense response;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;detection of bacterium;detection of biotic stimulus;detection of external stimulus;detection of stimulus;immune response;immune response-inhibiting cell surface receptor signaling pathway;immune response-inhibiting signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cell activation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of mononuclear cell proliferation;negative regulation of T cell activation;negative regulation of T cell proliferation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of developmental process;positive regulation of immune system process;positive regulation of interleukin-12 production;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of multicellular organismal process;positive regulation of regulatory T cell differentiation;positive regulation of T cell activation;positive regulation of T cell differentiation;positive regulation of T cell tolerance induction;positive regulation of tolerance induction;regulation of biological process;regulation of cell activation;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular process;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of developmental process;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of interleukin-12 production;regulation of interleukin-6 production;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte anergy;regulation of lymphocyte differentiation;regulation of lymphocyte proliferation;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of regulatory T cell differentiation;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of T cell activation;regulation of T cell anergy;regulation of T cell differentiation;regulation of T cell proliferation;regulation of T cell tolerance induction;regulation of tolerance induction;reproductive process;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;signal transduction;type I interferon-mediated signaling pathway;viral reproduction;viral reproductive process;virus-host interaction" binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity cell part;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome membrane;endocytic vesicle membrane;endoplasmic reticulum part;endosomal part;endosome membrane;ER to Golgi transport vesicle membrane;extracellular region;Golgi apparatus part;Golgi membrane;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;MHC class I protein complex;MHC protein complex;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;plasma membrane part;protein complex;transport vesicle membrane;vesicle membrane Allograft rejection;Antigen processing and presentation;Autoimmune thyroid disease;Cell adhesion molecules (CAMs);Endocytosis;Graft-versus-host disease;Natural killer cell mediated cytotoxicity;Phagosome;Type I diabetes mellitus;Viral myocarditis

Q8TCT9-5;Q8TCT9;Q8TCT9-2;Q8TCT9-4 Minor histocompatibility antigen H13 HM13 >sp|Q8TCT9-5|HM13_HUMAN Isoform 5 of Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13;>sp|Q8TCT9|HM13_HUMAN Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1;>sp|Q8TCT9-2|HM13_HUMAN Isoform 2 of Minor histocompatibility ant 0.93 1.12 1.5 0.81 0.76 0.89 0.95 1.18 3.56E-56 6 21.2 macromolecule metabolic process;membrane protein proteolysis;metabolic process;primary metabolic process;protein metabolic process;proteolysis "aspartic endopeptidase activity, intramembrane cleaving;aspartic-type endopeptidase activity;aspartic-type peptidase activity;binding;catalytic activity;endopeptidase activity;hydrolase activity;identical protein binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;protein dimerization activity;protein homodimerization activity" cell part;cell surface;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum part;integral to cytosolic side of endoplasmic reticulum membrane;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle part;plasma membrane;rough endoplasmic reticulum

P51991-2;P51991;H7C1J8 Heterogeneous nuclear ribonucleoprotein A3 HNRNPA3 >sp|P51991-2|ROA3_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3;>sp|P51991|ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 1.28 1.09 1.27 1.62 0.44 0.47 0.8 0.67 4.96E-81 6 22.5 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

E9PCY7;P31943;G8JLB6;D6RIU0;D6RBM0;E5RGH4;E7EQJ0;D6RAM1;E5RGV0;D6R9T0;D6RFM3;D6RIT2;D6RDU3;D6RJ04;D6RIH9;H0YB39;P55795;H0YAQ2;F5GZT4;E7EN40;H0YBG7;H0YBD7;D6RDL0 "Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed;Heterogeneous nuclear ribonucleoprotein H2" HNRNPH1;HNRNPH2 >tr|E9PCY7|E9PCY7_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1;>sp|P31943|HNRH1_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4;>tr|G8JLB6|G8JLB6_HUMAN Heterogeneous nuclear ribon 1.2 0.97 0.88 1.43 0.89 0.73 1.05 0.85 5.55E-228 6 20.3 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;poly(U) RNA binding;poly-pyrimidine tract binding;RNA binding;single-stranded RNA binding actin cytoskeleton;catalytic step 2 spliceosome;cell part;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex

Q9Y6M1-1;Q9Y6M1;F8W930;Q9Y6M1-5;Q9Y6M1-6;Q9Y6M1-3;Q9Y6M1-4;Q9NZI8-2;Q9NZI8 Insulin-like growth factor 2 mRNA-binding protein 2 IGF2BP2 >sp|Q9Y6M1-1|IF2B2_HUMAN Isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2;>sp|Q9Y6M1|IF2B2_HUMAN Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2;>tr|F8W930|F8W930_HUMAN Ins 1.93 0.6 1.11 0.67 1.39 0.78 1.74 1.05 3.24E-20 6 15.3 anatomical structure morphogenesis;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;CRD-mediated mRNA stabilization;developmental process;gene expression;localization;macromolecule localization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA stabilization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of mRNA stability involved in response to stress;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of translation;RNA localization;RNA metabolic process;RNA stabilization binding;mRNA 3'-UTR binding;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;translation regulator activity cell part;cell projection;cell projection part;CRD-mediated mRNA stability complex;cytoplasmic part;cytoskeleton;cytosol;dendritic spine;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;macromolecular complex;membrane;membrane-bounded organelle;neuron projection;neuron spine;non-membrane-bounded organelle;nucleus;organelle;plasma membrane;protein complex;ribonucleoprotein complex;RNA granule;stress granule

Q92945;M0R0I5;M0QXW7;M0QYH3;M0QYG1;M0R0C6 Far upstream element-binding protein 2 KHSRP >sp|Q92945|FUBP2_HUMAN Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4;>tr|M0R0I5|M0R0I5_HUMAN Far upstream element-binding protein 2 (Fragment) OS=Homo sapiens GN=KHSRP PE=4 SV=1 1.34 NaN 1.45 0.96 1.14 0.39 1.67 NaN 2.04E-24 6 15 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of RNA localization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA transport;transcription, DNA-dependent;transport" binding;DNA binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;RNA granule;stress granule

Q08380;K7EKQ5;K7EP36;K7EQT9;K7ES75;K7EN99;K7ERZ6;K7EJY8;K7EJD3 Galectin-3-binding protein LGALS3BP >sp|Q08380|LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 2.07 1.33 1.27 0.77 0.52 0.39 0.77 0.71 2.88E-21 6 13.3 biological adhesion;biological regulation;cell adhesion;cellular defense response;cellular process;cellular response to stimulus;defense response;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;signal transduction cargo receptor activity;receptor activity;scavenger receptor activity cell part;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;proteinaceous extracellular matrix;vesicle

Q96AG4;I3L223 Leucine-rich repeat-containing protein 59 LRRC59 >sp|Q96AG4|LRC59_HUMAN Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 1.17 0.73 1.17 0.42 1.15 0.97 1.37 1.47 9.27E-45 6 23.5 cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleoid;organelle;organelle envelope;organelle membrane;organelle part

Q9NX58;D6RDJ1 Cell growth-regulating nucleolar protein LYAR >sp|Q9NX58|LYAR_HUMAN Cell growth-regulating nucleolar protein OS=Homo sapiens GN=LYAR PE=1 SV=2 1.17 1.07 1.38 1.81 0.5 0.6 0.62 0.62 4.91E-37 6 21.4 binding;cation binding;ion binding;metal ion binding cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

Q9BYG3;C9J6C5;H7BZL0;C9J808 MKI67 FHA domain-interacting nucleolar phosphoprotein MKI67IP >sp|Q9BYG3|MK67I_HUMAN MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens GN=MKI67IP PE=1 SV=1;>tr|C9J6C5|C9J6C5_HUMAN MKI67 FHA domain-interacting nucleolar phosphoprotein (Fragment) OS=Homo sapiens GN=MKI67IP PE=2 SV=1 1.1 1.53 0.94 2.08 0.69 0.29 0.67 0.45 4.82E-29 6 29.7 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;RNA biosynthetic process;RNA metabolic process;rRNA metabolic process;rRNA transcription;transcription, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;chromosome;condensed chromosome;condensed nuclear chromosome;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleolus;nucleoplasm;organelle;organelle part

Q14165;F5H1S8;H0YG07;F5GX14 Malectin MLEC >sp|Q14165|MLEC_HUMAN Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1;>tr|F5H1S8|F5H1S8_HUMAN Malectin (Fragment) OS=Homo sapiens GN=MLEC PE=2 SV=1;>tr|H0YG07|H0YG07_HUMAN Malectin (Fragment) OS=Homo sapiens GN=MLEC PE=4 SV=1;>tr|F5GX14|F5GX14_HUMAN Malectin OS 1.02 1.24 1.48 1.07 0.75 0.76 0.89 1.01 1.54E-76 6 25.7 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine binding;carbohydrate binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part

O94776;Q68DB1 Metastasis-associated protein MTA2 MTA2;DKFZp686F2281 >sp|O94776|MTA2_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1;>tr|Q68DB1|Q68DB1_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=DKFZp686F2281 PE=2 SV=1 1.54 NaN 1.24 0.92 0.58 0.84 1.13 NaN 1.69E-11 6 10.6 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin assembly or disassembly;chromatin organization;chromosome organization;DNA alkylation;DNA metabolic process;DNA methylation;DNA modification;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;small molecule metabolic process" "binding;catalytic activity;cation binding;chromatin binding;deacetylase activity;DNA binding;histone deacetylase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding transcription factor activity;protein deacetylase activity;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transition metal ion binding;zinc ion binding" cell part;chromatin remodeling complex;histone deacetylase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;protein complex;transcription factor complex;transcriptional repressor complex

P11586;G3V2B8;F5H2F4;G3V3L6 "C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase;Methenyltetrahydrofolate cyclohydrolase;Formyltetrahydrofolate synthetase" MTHFD1 ">sp|P11586|C1TC_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3;>tr|G3V2B8|G3V2B8_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1;>tr|F5H2F4|F5H2F4_HUMAN C-1-tetrahydrofolate synthas" 0.67 1 0.72 0.74 2.7 1.76 1.12 0.96 5.21E-12 6 8.7 amine biosynthetic process;amine metabolic process;aromatic compound biosynthetic process;aspartate family amino acid biosynthetic process;aspartate family amino acid metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;folic acid metabolic process;folic acid-containing compound biosynthetic process;folic acid-containing compound metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;histidine biosynthetic process;histidine family amino acid biosynthetic process;histidine family amino acid metabolic process;histidine metabolic process;metabolic process;methionine biosynthetic process;methionine metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;one-carbon metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pteridine-containing compound biosynthetic process;pteridine-containing compound metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid biosynthetic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;tetrahydrofolate interconversion;tetrahydrofolate metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cyclohydrolase activity;formate-tetrahydrofolate ligase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;ligase activity;ligase activity, forming carbon-nitrogen bonds;methenyltetrahydrofolate cyclohydrolase activity;methylenetetrahydrofolate dehydrogenase (NADP+) activity;methylenetetrahydrofolate dehydrogenase [NAD(P)+] activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH group of donors;oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle One carbon pool by folate

P19105;O14950;J3QRS3;P24844;J3KTJ1;P24844-2 Myosin regulatory light chain 12A;Myosin regulatory light chain 12B;Myosin regulatory light polypeptide 9 MYL12A;MYL12B;MYL9 >sp|P19105|ML12A_HUMAN Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2;>sp|O14950|ML12B_HUMAN Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2;>tr|J3QRS3|J3QRS3_HUMAN Myosin regulatory light chain 12A OS=Homo sapi 1.06 0.92 1.31 0.72 2.26 0.92 1.2 1.67 2.80E-161 6 40.4 axon guidance;biological regulation;chemotaxis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;intracellular protein transport;intracellular transport;locomotion;multicellular organismal process;muscle contraction;muscle system process;protein targeting;protein targeting to plasma membrane;protein transport;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of system process;response to chemical stimulus;response to external stimulus;response to stimulus;system process;taxis;transport binding;calcium ion binding;cation binding;ion binding;metal ion binding;structural constituent of muscle;structural molecule activity actin filament bundle;actomyosin;apical part of cell;cell part;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;muscle myosin complex;myosin complex;myosin II complex;organelle part;protein complex;stress fiber;Z disc Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Tight junction;Vascular smooth muscle contraction

F8W1R7;P60660-2;P60660;G3V1V0;G3V1Y7;J3KND3;G8JLA2;B7Z6Z4;F8VPF3;F8VZU9;F8W180;H0YI43;F8VXL3;F8W1I5;P14649 Myosin light polypeptide 6 MYL6 >tr|F8W1R7|F8W1R7_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1;>sp|P60660-2|MYL6_HUMAN Isoform Smooth muscle of Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6;>sp|P60660|MYL6_HUMAN Myosin light polypeptide 6 OS=Homo sapiens GN=MYL 0.97 0.82 1.37 0.64 1.09 1.16 1.21 1.68 4.25E-153 6 49 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;anatomical structure development;axon guidance;cellular component movement;cellular process;chemotaxis;developmental process;locomotion;muscle filament sliding;muscle tissue development;response to chemical stimulus;response to external stimulus;response to stimulus;skeletal muscle tissue development;striated muscle tissue development;taxis;tissue development "actin-dependent ATPase activity;ATPase activity;ATPase activity, coupled;binding;calcium ion binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;motor activity;nucleoside-triphosphatase activity;pyrophosphatase activity;structural constituent of muscle;structural molecule activity" cell part;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;muscle myosin complex;myosin complex;myosin II complex;organelle part;protein complex;unconventional myosin complex Vascular smooth muscle contraction

O75306-2;O75306;B7Z9L2 "NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial" NDUFS2 ">sp|O75306-2|NDUS2_HUMAN Isoform 2 of NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2;>sp|O75306|NDUS2_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1" 1.13 1.3 1.72 1.73 0.85 0.48 0.61 0.86 5.46E-85 6 18.8 "cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;oxidation-reduction process;respiratory electron transport chain;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;small molecule metabolic process" "4 iron, 4 sulfur cluster binding;binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;electron carrier activity;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;NAD binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;quinone binding" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q9Y3T9 Nucleolar complex protein 2 homolog NOC2L >sp|Q9Y3T9|NOC2L_HUMAN Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 NaN NaN 2.12 NaN 0.72 NaN NaN NaN 1.62E-11 6 6.9 "apoptosis;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to light stimulus;cellular response to radiation;cellular response to stimulus;cellular response to UV;death;establishment of localization;establishment of localization in cell;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of B cell apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of histone acetylation;negative regulation of histone modification;negative regulation of leukocyte apoptosis;negative regulation of lymphocyte apoptosis;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of peptidyl-lysine acetylation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleolus to nucleoplasm transport;primary metabolic process;programmed cell death;regulation of apoptosis;regulation of B cell apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of gene expression;regulation of histone acetylation;regulation of histone modification;regulation of leukocyte apoptosis;regulation of lymphocyte apoptosis;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-lysine acetylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to light stimulus;response to radiation;response to stimulus;response to UV;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;transport" binding;chromatin binding;histone binding;nucleosome binding;protein binding;protein binding transcription factor activity;repressing transcription factor binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding;transcription factor binding transcription factor activitycell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part

E9PLK3;P55786;B7Z463;E9PP11;F5GZY4;E5RJ24;E7EWZ2;A6NEC2;H0YCQ5 Puromycin-sensitive aminopeptidase NPEPPS >tr|E9PLK3|E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1;>sp|P55786|PSA_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2;>tr|B7Z463|B7Z463_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sa NaN NaN 0.36 NaN 0.18 NaN NaN NaN 9.75E-12 6 7.3 antigen processing and presentation;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hypoxia;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;immune system process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q9UQ80;F8VR77;H0YIN7;F8W0A3 Proliferation-associated protein 2G4 PA2G4 >sp|Q9UQ80|PA2G4_HUMAN Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3;>tr|F8VR77|F8VR77_HUMAN Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=2 SV=1 1.46 1.12 0.9 0.88 0.82 0.67 1.3 0.84 2.84E-21 6 18.8 "biological regulation;biosynthetic process;cell cycle arrest;cell cycle process;cell proliferation;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;RNA biosynthetic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;transcription, DNA-dependent" binding;catalytic activity;DNA binding;hydrolase activity;nucleic acid binding;nucleic acid binding transcription factor activity;RNA binding;sequence-specific DNA binding transcription factor activity cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex

F8WDZ1;Q8IZL8;C9JFV4;Q8IZL8-2;I3L3A8;I3L4M7;E7EV54;I3L1P4;I3L445 "Proline-, glutamic acid- and leucine-rich protein 1" PELP1 ">tr|F8WDZ1|F8WDZ1_HUMAN Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens GN=PELP1 PE=2 SV=1;>sp|Q8IZL8|PELP1_HUMAN Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens GN=PELP1 PE=1 SV=2;>tr|C9JFV4|C9JFV4_HUMAN Proline-, g" 1.22 NaN 1.24 1.36 3.67 0.43 0.73 NaN 4.92E-22 6 11.3 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" cell part;cytoplasm;histone methyltransferase complex;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL1 complex;nuclear part;nucleoplasm part;organelle part;protein complex

Q99959-2;Q99959 Plakophilin-2 PKP2 >sp|Q99959-2|PKP2_HUMAN Isoform 1 of Plakophilin-2 OS=Homo sapiens GN=PKP2;>sp|Q99959|PKP2_HUMAN Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2 1.67 1.93 1.32 1.45 0.29 0.28 0.39 0.69 2.94E-18 6 8.4 adherens junction maintenance;adherens junction organization;anatomical structure morphogenesis;biological adhesion;biological regulation;cardiac muscle tissue morphogenesis;cell adhesion;cell junction assembly;cell junction maintenance;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component maintenance;cellular component maintenance at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemical homeostasis;cytoskeleton organization;desmosome assembly;developmental process;gap junction assembly;homeostatic process;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;lipid homeostasis;maintenance of organ identity;muscle tissue morphogenesis;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of developmental process;negative regulation of locomotion;organelle organization;positive regulation of biological process;positive regulation of ion transport;positive regulation of sodium ion transport;positive regulation of transport;regulation of biological process;regulation of biological quality;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of ion transport;regulation of localization;regulation of locomotion;regulation of metal ion transport;regulation of sodium ion transport;regulation of tight junction assembly;regulation of transport;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis binding;channel regulator activity;intermediate filament binding;ion channel binding;protein binding;protein complex binding;protein complex scaffold;sodium channel regulator activity;structural molecule activity adherens junction;anchoring junction;cell junction;cell part;cell-cell contact zone;cell-cell junction;cytoskeletal part;desmosome;integral to membrane;intercalated disc;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC)

Q15269;C9J544;H7C455 Periodic tryptophan protein 2 homolog PWP2 >sp|Q15269|PWP2_HUMAN Periodic tryptophan protein 2 homolog OS=Homo sapiens GN=PWP2 PE=1 SV=2 NaN NaN 1.35 2.21 0.67 0.34 NaN NaN 2.42E-19 6 9.4 molecular transducer activity;signal transducer activitycell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes

P61106 Ras-related protein Rab-14 RAB14 >sp|P61106|RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 0.59 2.48 0.68 1.39 0.69 1.21 0.67 1.13 8.08E-54 6 39.5 biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;developmental process;embryo development;endocytic recycling;endosome transport;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;fibroblast growth factor receptor signaling pathway;Golgi to endosome transport;Golgi vesicle transport;intracellular signal transduction;intracellular transport;membrane organization;neurotransmitter secretion;neurotransmitter transport;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of localization;regulation of neurotransmitter levels;regulation of protein localization;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;secretion;secretion by cell;signal release;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;early endosome;early endosome membrane;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum;endosomal part;endosome;endosome membrane;Golgi apparatus part;Golgi membrane;Golgi stack;Golgi-associated vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nuclear outer membrane-endoplasmic reticulum membrane network;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;recycling endosome;rough endoplasmic reticulum;trans-Golgi network transport vesicle;transport vesicle;vacuole;vesicle;vesicle membrane

P11233;H7C3P7;F8WEQ6;C9JPE8;C9JYR1;C9JQB3 Ras-related protein Ral-A RALA >sp|P11233|RALA_HUMAN Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1;>tr|H7C3P7|H7C3P7_HUMAN Ras-related protein Ral-A (Fragment) OS=Homo sapiens GN=RALA PE=4 SV=1 0.79 1.32 0.93 0.88 1.12 1.05 0.69 1.2 1.24E-18 6 29.1 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;biological regulation;cell cycle;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;cytokinesis;cytoskeleton organization;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;interaction with host;interspecies interaction between organisms;intracellular signal transduction;localization;localization within membrane;locomotion;membrane organization;membrane raft localization;multi-organism process;nerve growth factor receptor signaling pathway;organelle organization;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of filopodium assembly;Ras protein signal transduction;regulation of biological process;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of filopodium assembly;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;secretion;secretion by cell;signal transduction;small GTPase mediated signal transduction;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction "binding;catalytic activity;Edg-2 lysophosphatidic acid receptor binding;endothelial differentiation G-protein coupled receptor binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding" cell division site part;cell part;cell surface;cleavage furrow;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;intracellular organelle part;intracellular part;membrane;midbody;organelle membrane;organelle part;plasma membrane;vesicle membrane Pancreatic cancer;Pathways in cancer

Q8IXI1;H3BST5;I3L2C6;H3BUX4;Q8IXI1-2;H3BMP9;H3BVI5;J3KSX7 Mitochondrial Rho GTPase 2 RHOT2 >sp|Q8IXI1|MIRO2_HUMAN Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2;>tr|H3BST5|H3BST5_HUMAN Mitochondrial Rho GTPase 2 (Fragment) OS=Homo sapiens GN=RHOT2 PE=2 SV=2;>tr|I3L2C6|I3L2C6_HUMAN Mitochondrial Rho GTPase 2 (Fragment) OS=Homo sapi0.77 1.47 1.61 1.35 0.6 0.41 0.86 0.96 8.91E-17 6 11.3 "apoptosis;biological regulation;catabolic process;cell death;cellular catabolic process;cellular component movement;cellular homeostasis;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cytoskeleton-dependent intracellular transport;death;establishment of localization;establishment of localization in cell;establishment of mitochondrion localization;establishment of mitochondrion localization, microtubule-mediated;establishment of organelle localization;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;intracellular signal transduction;intracellular transport;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrion transport along microtubule;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle transport along microtubule;primary metabolic process;programmed cell death;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process;transport" "binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;integral to membrane;integral to mitochondrial membrane;integral to mitochondrial outer membrane;integral to organelle membrane;intracellular;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to mitochondrial outer membrane;intrinsic to organelle membrane;membrane;membrane part;mitochondrial membrane;mitochondrial membrane part;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane;plasma membrane

P62424;Q5T8U3;Q5T8U2 60S ribosomal protein L7a RPL7A >sp|P62424|RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1

SV=2;>tr|Q5T8U3|Q5T8U3_HUMAN 60S ribosomal protein L7a (Fragment) OS=Homo sapiens GN=RPL7A PE=2 SV=1 1.27 0.78 0.61 0.63 0.99 0.88 1.45 1 1.01E-113 6 24.1 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;polysomal ribosome;ribonucleoprotein complex;ribosome Ribosome

H0YEN5;E9PQD7;P15880;E9PMM9;H3BNG3;H0YE27;I3L404;E9PPT0;E9PM36 40S ribosomal protein S2 RPS2 >tr|H0YEN5|H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=2 SV=1;>tr|E9PQD7|E9PQD7_HUMAN 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=2 SV=1;>sp|P15880|RS2_HUMAN 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 1.21 0.81 0.51 0.63 1.11 0.98 1.34 0.95 3.45E-28 6 32.8 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

P62081;B5MCP9 40S ribosomal protein S7 RPS7 >sp|P62081|RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1;>tr|B5MCP9|B5MCP9_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=2 SV=1 1.48 0.78 0.93 0.53 1.24 0.67 1.35 0.83 6.55E-17 6 34.5 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal small subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity 90S preribosome;cell part;cytoplasmic part;cytoskeletal part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;ribonucleoprotein complex;ribosome;small ribosomal subunit;small-subunit processome Ribosome

C9J9K3;P08865;A6NE09;C9JQR9 40S ribosomal protein SA RPSA;RPSAP58 >tr|C9J9K3|C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1;>sp|P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4;>tr|A6NE09|A6NE09_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSAP58 PE=2 0.49 2.54 0.15 1.31 0.5 1.46 0.85 1.02 4.82E-62 6 24.6 "biological adhesion;biosynthetic process;catabolic process;cell adhesion;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cleavage involved in rRNA processing;cotranslational protein targeting to membrane;endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage involved in rRNA processing;endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA);establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;establishment of RNA localization;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA 3'-end processing;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;rRNA 3'-end processing;rRNA export from nucleus;rRNA metabolic process;rRNA processing;rRNA transport;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;laminin receptor activity;receptor activity;ribonucleoprotein binding;ribosome binding;structural constituent of ribosome;structural molecule activity 90S preribosome;cell part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;preribosome;ribonucleoprotein complex;small ribosomal subunit Ribosome

Q9HCY8 Protein S100-A14 S100A14 >sp|Q9HCY8|S10AE_HUMAN Protein S100-A14 OS=Homo sapiens GN=S100A14 PE=1 SV=1 1.13 1.82 1.53 0.86 0.94 0.65 0.73 0.88 0 6 61.5 activation of immune response;activation of innate immune response;apoptosis;biological regulation;calcium ion homeostasis;cation homeostasis;cell death;cellular process;cellular response to stimulus;chemical homeostasis;death;defense response;defense response to bacterium;divalent inorganic cation homeostasis;homeostatic process;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response-activating signal transduction;ion homeostasis;metal ion homeostasis;multi-organism process;pattern recognition receptor signaling pathway;positive regulation of behavior;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of defense response;positive regulation of granulocyte chemotaxis;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of monocyte chemotaxis;positive regulation of response to external stimulus;positive regulation of response to stimulus;programmed cell death;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of chemotaxis;regulation of defense response;regulation of granulocyte chemotaxis;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of monocyte chemotaxis;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;signal transduction;toll-like receptor 4 signaling pathway;toll-like receptor signaling pathway binding;calcium ion binding;cation binding;chemokine receptor binding;cytokine receptor binding;G-protein-coupled receptor binding;ion binding;metal ion binding;protein binding;receptor binding cell junction;cell part;cytoplasmic part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;plasma membrane

P82979;Q567R9;F8VZQ9;H0YHG0;F8VS12 SAP domain-containing ribonucleoprotein SARNP;CIP29 >sp|P82979|SARNP_HUMAN SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3;>tr|Q567R9|Q567R9_HUMAN CIP29 protein OS=Homo sapiens GN=CIP29 PE=2 SV=1;>tr|F8VZQ9|F8VZQ9_HUMAN SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SA 1.38 1.31 2 1.79 0.71 0.33 0.58 0.51 3.17E-67 6 31.9 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part

Q8NC51-4;Q8NC51-3;Q8NC51-2;Q8NC51 Plasminogen activator inhibitor 1 RNA-binding protein SERBP1 >sp|Q8NC51-4|PAIRB_HUMAN Isoform 4 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1;>sp|Q8NC51-3|PAIRB_HUMAN Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1;>sp|Q8NC51-2|PAIRB_H 1.6 0.69 1.68 0.72 0.77 0.51 1.65 0.91 7.41E-169 6 21.7 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;RNA metabolic process binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;RNA binding cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane

Q9H9B4;D6RDG7;D6RFI0;D6RAE9 Sideroflexin-1 SFXN1 >sp|Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4;>tr|D6RDG7|D6RDG7_HUMAN Sideroflexin-1 (Fragment) OS=Homo sapiens GN=SFXN1 PE=2 SV=1;>tr|D6RFI0|D6RFI0_HUMAN Sideroflexin-1 (Fragment) OS=Homo sapiens GN=SFXN1 PE=2 SV=1 1.27 1.61 1.75 2.23 0.5 0.28 0.54 0.78 4.02E-190 6 21.7 biological regulation;cation homeostasis;cation transport;cell differentiation;cellular developmental process;cellular process;chemical homeostasis;developmental process;erythrocyte differentiation;establishment of localization;homeostatic process;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;metal ion transport;myeloid cell differentiation;regulation of biological quality;transition metal ion transport;transport cation transmembrane transporter activity;ion transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part

I3L1P8;Q02978;Q02978-2 Mitochondrial 2-oxoglutarate/malate carrier protein SLC25A11 >tr|I3L1P8|I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=2 SV=1;>sp|Q02978|M2OM_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3;>sp|Q02978-2|M2OM_H 0.98 1.4 1.37 2.14 0.58 0.58 0.54 0.64 2.12E-24 6 19.6 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;establishment of localization;gluconeogenesis;glucose metabolic process;hexose biosynthetic process;hexose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;transport active transmembrane transporter activity;anion transmembrane transporter activity;anion:anion antiporter activity;antiporter activity;C4-dicarboxylate transmembrane transporter activity;carboxylic acid transmembrane transporter activity;dicarboxylic acid transmembrane transporter activity;ion transmembrane transporter activity;malate transmembrane transporter activity;organic acid transmembrane transporter activity;oxoglutarate:malate antiporter activity;secondary active transmembrane transporter activity;solute:solute antiporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;plasma membrane part

F6TQG2;P28370-2;P28370 Probable global transcription activator SNF2L1 SMARCA1 >tr|F6TQG2|F6TQG2_HUMAN Probable global transcription activator SNF2L1 (Fragment) OS=Homo sapiens GN=SMARCA1 PE=2 SV=1;>sp|P28370-2|SMCA1_HUMAN Isoform 2 of Probable global transcription activator SNF2L1 OS=Homo sapiens GN=SMARCA1;>sp|P28370|SMCA1_HUMAN Pr NaN NaN 1.68 NaN 0.62 NaN NaN NaN 1.63E-14 6 6.1 "anatomical structure development;ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;brain development;cell differentiation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;neuron differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;chromatin binding;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleosome binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromatin remodeling complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ISWI complex;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;NURF complex;organelle;organelle part;protein complex

Q9UQE7 Structural maintenance of chromosomes protein 3SMC3 >sp|Q9UQE7|SMC3_HUMAN Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 NaN NaN 1.69 NaN 0.78 NaN NaN NaN 9.95E-16 6 7.6 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;cytokinesis;cytoskeleton organization;developmental process;DNA metabolic process;DNA repair;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;meiosis;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;mitotic spindle organization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA endoreduplication;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA endoreduplication;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to DNA damage stimulus;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle;signal transduction;sister chromatid cohesion;spindle organization;stem cell maintenance "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;chromatin binding;dynein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" "basement membrane;cell part;chromatin;chromosomal part;chromosome, centromeric region;cohesin complex;cytoplasmic part;cytoskeletal part;cytosol;extracellular matrix part;extracellular region part;intracellular organelle part;intracellular part;lateral element;macromolecular complex;meiotic cohesin complex;nuclear chromosome part;nuclear cohesin complex;nuclear matrix;nuclear meiotic cohesin complex;nuclear part;nucleoplasm;organelle part;protein complex;spindle pole" Cell cycle;Cell cycle - yeast;Meiosis - yeast;Oocyte meiosis

O15020-2;O15020 "Spectrin beta chain, non-erythrocytic 2" SPTBN2 ">sp|O15020-2|SPTN2_HUMAN Isoform 2 of Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2;>sp|O15020|SPTN2_HUMAN Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3" 1.39 1.09 1.13 0.62 1.4 1.24 1 0.79 5.48E-12 6 3.8 actin filament capping;adult behavior;anatomical structure morphogenesis;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;behavior;biological regulation;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cerebellar Purkinje cell layer morphogenesis;chemotaxis;death;developmental process;establishment of localization;growth;immune system process;locomotion;multicellular organism growth;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;synapse assembly;synapse organization;taxis;transport;vesicle-mediated transport actin binding;binding;cytoskeletal protein binding;lipid binding;phospholipid binding;protein binding;structural constituent of cytoskeleton;structural molecule activitycell body;cell cortex part;cell part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;neuronal cell body;organelle part;spectrin

Q07955-3;Q07955;J3KTL2;Q07955-2;J3QQV5;J3KSW7;J3KSR8 Serine/arginine-rich splicing factor 1 SRSF1 >sp|Q07955-3|SRSF1_HUMAN Isoform ASF-3 of Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1;>sp|Q07955|SRSF1_HUMAN Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2;>tr|J3KTL2|J3KTL2_HUMAN Serine/arginine-rich-splicing 1.27 0.84 1.14 1.68 3.52 0.98 1.03 0.96 1.40E-14 6 31.8 "biosynthetic process;cardiac muscle contraction;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;establishment of localization;establishment of localization in cell;establishment of RNA localization;in utero embryonic development;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA splice site selection;mRNA transport;multicellular organismal process;muscle contraction;muscle system process;nitrogen compound metabolic process;nuclear export;nuclear mRNA 5'-splice site recognition;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA transport;striated muscle contraction;system process;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

Q13428-2;Q13428-8;J3KQ96;Q13428-6;Q13428-7;Q13428;E7ETY2;Q13428-3;Q13428-4;E9PHK9;Q13428-5;H0YA99 Treacle protein TCOF1 >sp|Q13428-2|TCOF_HUMAN Isoform 2 of Treacle protein OS=Homo sapiens GN=TCOF1;>sp|Q13428-8|TCOF_HUMAN Isoform 8 of Treacle protein OS=Homo sapiens GN=TCOF1;>tr|J3KQ96|J3KQ96_HUMAN Treacle protein (Fragment) OS=Homo sapiens GN=TCOF1 PE=4 SV=1;>sp|Q13428-6|T 1.88 0.9 1.37 1.16 0.34 0.29 0.73 0.71 1.54E-19 6 5.2 "anatomical structure development;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;rRNA transcription;skeletal system development;system development;transcription from RNA polymerase I promoter;transcription of nuclear large rRNA transcript from RNA polymerase I promoter;transcription, DNA-dependent" transporter activity cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes

Q9NXF1-2;Q9NXF1;B7Z9D5 Testis-expressed sequence 10 protein TEX10 >sp|Q9NXF1-2|TEX10_HUMAN Isoform 2 of Testis-expressed sequence 10 protein OS=Homo sapiens GN=TEX10;>sp|Q9NXF1|TEX10_HUMAN Testis-expressed sequence 10 protein OS=Homo sapiens GN=TEX10 PE=1 SV=2;>tr|B7Z9D5|B7Z9D5_HUMAN Testis-expressed sequence 10 protein NaN NaN 1.83 NaN 0.93 NaN NaN NaN 1.58E-20 6 10.1 cell part;cytoplasm;histone methyltransferase complex;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;methyltransferase complex;MLL1 complex;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;nucleoplasm part;organelle;organelle membrane;organelle part;protein complex

P49755;G3V2K7 Transmembrane emp24 domain-containing protein 10 TMED10 >sp|P49755|TMEDA_HUMAN Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2;>tr|G3V2K7|G3V2K7_HUMAN Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=2 SV=1 0.97 0.99 1.78 0.8 0.84 0.81 1.07 1.1 5.87E-65 6 34.7 "amyloid precursor protein catabolic process;amyloid precursor protein metabolic process;anatomical structure development;beta-amyloid formation;beta-amyloid metabolic process;cargo loading into vesicle;catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;COPI coating of Golgi vesicle;COPII vesicle coating;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;glycoprotein catabolic process;glycoprotein metabolic process;Golgi organization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;kidney development;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;organ development;organelle organization;protein complex assembly;protein complex subunit organization;protein oligomerization;protein transport;regulated secretory pathway;response to acid;response to alkaloid;response to chemical stimulus;response to organic substance;response to stimulus;retrograde vesicle-mediated transport, Golgi to ER;secretion;secretion by cell;transport;vesicle coating;vesicle organization;vesicle-mediated transport" cell part;cis-Golgi network;clathrin-coated vesicle;coated vesicle;COPI-coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;gamma-secretase complex;Golgi apparatus part;Golgi-associated vesicle;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;protein complex;secretory granule membrane;trans-Golgi network transport vesicle;transport vesicle;transport vesicle membrane;vesicle;vesicle membrane;zymogen granule membrane

Q6ZXV5-2;Q6ZXV5;F6V107;H7C3Z6;F8VRY4;Q9NRD5;E7EX83;C9J840;H7C0P6;E7ENQ1;O95819-4;G3XAA2;H7C360;O95819-2;O95819;O95819-5;E7EN19;E7ESS2;O95819-3;G5E948 Transmembrane and TPR repeat-containing protein 3 TMTC3 >sp|Q6ZXV5-2|TMTC3_HUMAN Isoform 2 of Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3;>sp|Q6ZXV5|TMTC3_HUMAN Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2 0.99 1 1.32 0.81 0.76 1.33 1.07 1.27 1.19E-16 6 8.4 "activation of protein kinase activity;activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway;amine transport;anatomical structure development;axis elongation;biological regulation;branch elongation of an epithelium;bud outgrowth involved in lung branching;cell communication;cell development;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein localization;cellular protein metabolic process;cellular response to stimulus;developmental growth;developmental growth involved in morphogenesis;developmental process;DNA alkylation;DNA metabolic process;DNA methylation;DNA methylation involved in embryo development;DNA methylation involved in gamete generation;DNA modification;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;G-protein coupled receptor protein signaling pathway;growth;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;localization;lung alveolus development;macromolecule localization;macromolecule metabolic process;macromolecule methylation;macromolecule modification;membrane organization;metabolic process;methylation;monoamine transport;muscle cell development;muscle fiber development;neuronal ion channel clustering;nitrogen compound metabolic process;nitrogen compound transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organic substance transport;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;post-embryonic development;primary metabolic process;protein localization;protein localization in membrane;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein transport;receptor clustering;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of gene expression;regulation of gene expression, epigenetic;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;reproductive process;response to stimulus;response to stress;retrograde vesicle-mediated transport, Golgi to ER;signal transduction;signaling;small molecule metabolic process;striated muscle cell development;synaptic transmission;transport;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cation binding;enzyme binding;enzyme regulator activity;GTPase regulator activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;kinase activity;kinase binding;metal ion binding;nucleoside-triphosphatase activity;nucleoside-triphosphatase regulator activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein kinase binding;protein kinase C binding;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;small GTPase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell junction;cell part;cytoplasm;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;presynaptic membrane;synapse part;synaptic membrane;vesicle membrane MAPK signaling pathway

P11388;P11388-2;P11388-3;P11388-4;J3KTB7 DNA topoisomerase 2-alpha TOP2A >sp|P11388|TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3;>sp|P11388-2|TOP2A_HUMAN Isoform 2 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A;>sp|P11388-3|TOP2A_HUMAN Isoform 3 of DNA topoisomerase 2-alpha OS=Homo sapiens GN= NaN NaN NaN NaN NaN NaN NaN NaN 1.22E-22 6 4.8 "apoptotic chromosome condensation;biological regulation;biosynthetic process;cell cycle;cell cycle process;cell division;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome condensation;chromosome organization;chromosome segregation;chromosome separation;DNA conformation change;DNA ligation;DNA metabolic process;DNA packaging;DNA recombination;DNA repair;DNA replication;DNA topological change;DNA-dependent DNA replication;embryonic cleavage;inositol lipid-mediated signaling;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;meiotic chromosome separation;metabolic process;mitotic cell cycle;mitotic recombination;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;phosphatidylinositol-mediated signaling;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of reproductive process;positive regulation of retroviral genome replication;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of retroviral genome replication;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral genome replication;regulation of viral reproduction;resolution of meiotic recombination intermediates;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;sister chromatid segregation" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cation binding;chromatin binding;DNA bending activity;DNA binding;DNA topoisomerase (ATP-hydrolyzing) activity;DNA topoisomerase activity;DNA-dependent ATPase activity;drug binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;isomerase activity;magnesium ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;small conjugating protein binding;ubiquitin binding" cell part;chromosomal part;chromosome;condensed chromosome;cytoplasm;DNA topoisomerase complex (ATP-hydrolyzing);intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;protein complex;synaptonemal complex

A6NNK5;Q12888;F8VY86;Q12888-2;C9JXV0;H7C3N7;M0R142;H7BZY0 Tumor suppressor p53-binding protein 1 TP53BP1 >tr|A6NNK5|A6NNK5_HUMAN Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=2 SV=2;>sp|Q12888|TP53B_HUMAN Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2;>tr|F8VY86|F8VY86_HUMAN Tumor suppressor p53-binding prot1.14 1.62 1.38 NaN 0.6 NaN 0.55 0.85 9.66E-22 6 5.8 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via homologous recombination;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;recombinational repair;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress" binding;damaged DNA binding;DNA binding;histone binding;methylated histone residue binding;nucleic acid binding;protein binding;protein binding transcription factor activity;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;sequence-specific DNA binding;telomeric DNA binding;transcription cofactor activity;transcription factor binding transcription factor activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;replication fork

Q96QK1;I3L4S0;I3L4P4 Vacuolar protein sorting-associated protein 35 VPS35 >sp|Q96QK1|VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 NaN 1.59 0.27 NaN 0.83 NaN NaN 1.06 9.53E-12 6 9.3 "cell death;cellular process;death;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;protein transport;retrograde transport, endosome to Golgi;transport;vesicle-mediated transport" cell part;cytoplasmic part;cytosol;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle

Q8NI36;D6R922 WD repeat-containing protein 36 WDR36 >sp|Q8NI36|WDR36_HUMAN WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1 NaN NaN 0.95 NaN 0.73 NaN NaN NaN 1.11E-13 6 7.6 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;multicellular organismal process;ncRNA metabolic process;ncRNA processing;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;response to stimulus;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;sensory perception;sensory perception of light stimulus;system process;visual perception cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;ribonucleoprotein complex;small-subunit processome Ribosome biogenesis in eukaryotes

P16989-2;P16989;P16989-3 Y-box-binding protein 3 YBX3 >sp|P16989-2|YBOX3_HUMAN Isoform 2 of Y-box-binding protein 3 OS=Homo sapiens GN=YBX3;>sp|P16989|YBOX3_HUMAN Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4;>sp|P16989-3|YBOX3_HUMAN Isoform 3 of Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 1.95 0.7 0.93 0.57 0.75 0.38 1.78 1.08 3.30E-32 6 28.1 "3'-UTR-mediated mRNA stabilization;anatomical structure development;biological regulation;biosynthetic process;cellular biosynthetic process;cellular hyperosmotic response;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to osmotic stress;cellular response to stimulus;cellular response to stress;cellular response to tumor necrosis factor;chordate embryonic development;developmental process;developmental process involved in reproduction;embryo development;embryo development ending in birth or egg hatching;fertilization;gonad development;hyperosmotic response;in utero embryonic development;macromolecule biosynthetic process;macromolecule metabolic process;male gonad development;metabolic process;mRNA metabolic process;mRNA stabilization;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of muscle organ development;negative regulation of necrotic cell death;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of skeletal muscle tissue development;negative regulation of striated muscle tissue development;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytoplasmic translation;positive regulation of growth;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of organ growth;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoplasmic translation;regulation of developmental process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of necrotic cell death;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ growth;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of skeletal muscle tissue development;regulation of striated muscle tissue development;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;reproductive structure development;response to abiotic stimulus;response to chemical stimulus;response to cold;response to cytokine stimulus;response to organic substance;response to osmotic stress;response to stimulus;response to stress;response to temperature stimulus;response to tumor necrosis factor;RNA biosynthetic process;RNA metabolic process;RNA stabilization;transcription, DNA-dependent" binding;DNA binding;double-stranded DNA binding;enzyme binding;GTPase binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein binding transcription factor activity;Ras GTPase binding;Rho GTPase binding;RNA binding;sequence-specific DNA binding transcription factor activity;small GTPase binding;structure-specific DNA binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell junction;cell part;cell-cell junction;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;occluding junction;organelle;perinuclear region of cytoplasm;polysome;ribonucleoprotein complex;tight junction Tight junction

Q96TA2-3;Q96TA2-2;Q96TA2;R4GNA5;Q5T8D2;Q5T8D1 ATP-dependent zinc metalloprotease YME1L1 YME1L1 >sp|Q96TA2-3|YMEL1_HUMAN Isoform 3 of ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1;>sp|Q96TA2-2|YMEL1_HUMAN Isoform 2 of ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1;>sp|Q96TA2|YMEL1_HUMAN ATP-dependent zinc me 0.77 1.52 1.57 1.77 0.51 0.33 0.45 0.5 6.16E-17 6 11.6 cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;macromolecule metabolic process;metabolic process;misfolded or incompletely synthesized protein catabolic process;mitochondrion organization;organelle organization;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

Q04917 14-3-3 protein eta YWHAH >sp|Q04917|1433F_HUMAN 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 0.71 2.99 NaN 2.38 NaN 0.48 0.82 1.42 7.16E-211 6 26.8 "biological regulation;C21-steroid hormone catabolic process;C21-steroid hormone metabolic process;catabolic process;cellular component organization;cellular component organization or biogenesis;cellular hormone metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular response to stimulus;corticosteroid receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;glucocorticoid catabolic process;glucocorticoid metabolic process;glucocorticoid receptor signaling pathway;hormone catabolic process;hormone metabolic process;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular transport;lipid catabolic process;lipid metabolic process;membrane organization;metabolic process;negative regulation of biological process;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of dendrite morphogenesis;negative regulation of developmental process;negative regulation of neurogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein transport;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of gene expression;regulation of hormone levels;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of signaling;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transmission of nerve impulse;regulation of transport;regulation of transporter activity;response to stimulus;signal transduction;steroid catabolic process;steroid hormone receptor signaling pathway;steroid metabolic process;transport" binding;channel regulator activity;insulin-like growth factor receptor binding;ion channel binding;protein binding;protein domain specific binding;receptor binding;sodium channel regulator activity cell junction;cell part;cell-cell contact zone;cell-cell junction;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intercalated disc;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis

Q70UQ0-4 >sp|Q70UQ0-4|IKIP_HUMAN Isoform 4 of Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP 0.89 0.98 1.26 0.85 0.93 0.62 1.1 1.26 4.95E-55 6 17

P28288-2;P28288;E7EUE1;F5GYC1;P28288-3 ATP-binding cassette sub-family D member 3 ABCD3 >sp|P28288-2|ABCD3_HUMAN Isoform 2 of ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3;>sp|P28288|ABCD3_HUMAN ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1;>tr|E7EUE1|E7EUE1_HUMAN ATP-binding cassette sub- NaN 0.93 1.04 1 0.57 0.92 NaN 0.96 2.58E-20 7 16.4 ATP catabolic process;ATP metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;heterocycle catabolic process;heterocycle metabolic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;peroxisome organization;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule catabolic process;small molecule metabolic process;transmembrane transport;transport;very long-chain fatty acid catabolic process;very long-chain fatty acid metabolic process "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;cytosol;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody

lumen;microbody membrane;microbody part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part ABC transporters;Peroxisome
P61158;B4DXW1;F5H3P5;Q9P1U1-2;Q9P1U1 Actin-related protein 3 ACTR3 >sp|P61158|ARP3_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3;>tr|B4DXW1|B4DXW1_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=2 SV=1;>tr|F5H3P5|F5H3P5_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=2 SV=1 0.74 2.03 0.77 3.02 0.31 0.61 0.48 1.14 4.57E-82 7 19.9 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin nucleation;anatomical structure morphogenesis;Arp2/3 complex-mediated actin nucleation;asymmetric cell division;biological regulation;cell cycle;cell cycle cytokinesis;cell cycle process;cell division;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular process;cilium morphogenesis;cytokinesis;cytokinesis after meiosis;cytoskeleton organization;defense response;developmental process;establishment or maintenance of cell polarity;immune response;immune system process;innate immune response;localization;meiotic cell cycle;organelle localization;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of dendrite morphogenesis;positive regulation of developmental process;positive regulation of filopodium assembly;positive regulation of lamellipodium assembly;positive regulation of neurogenesis;positive regulation of neuron differentiation;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of filopodium assembly;regulation of lamellipodium assembly;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myosin II filament organization;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to antibiotic;response to carbohydrate stimulus;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;spindle localizationadenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding Arp2/3 protein complex;cell junction;cell part;cell projection;cell-substrate junction;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;excitatory synapse;Golgi apparatus part;Golgi membrane;hemidesmosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;podosome;protein complex;synapse
O95831-3;O95831;O95831-6;O95831-4;O95831-2;E9PMA0;O95831-5 "Apoptosis-inducing factor 1, mitochondrial" AIFM1 ">sp|O95831-3|AIFM1_HUMAN Isoform 3 of Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1;>sp|O95831|AIFM1_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1;>sp|O95831-6|AIFM1_HUMAN Isoform 6 of Apoptosis-i" 0.76 1.15 1.54 0.86 0.59 0.66 1.01 1.39 6.47E-21 7 14.6 "activation of caspase activity;apoptosis;apoptosis in response to endoplasmic reticulum stress;biological regulation;catabolic process;cell death;cell differentiation;cell redox homeostasis;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;death;developmental process;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mitochondrial respiratory chain complex assembly;mitochondrial respiratory chain complex I assembly;mitochondrial respiratory chain complex I biogenesis;NADH dehydrogenase complex assembly;neuron apoptosis;neuron death;neuron differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;primary metabolic process;programmed cell death;protein complex assembly;protein complex biogenesis;protein complex subunit organization;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity" binding;catalytic activity;coenzyme binding;cofactor binding;DNA binding;electron carrier activity;flavin adenine dinucleotide binding;nucleic acid binding;oxidoreductase activity cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part;perinuclear region of cytoplasm Apoptosis
P00352;Q5SYQ7;Q5SYQ9;Q5SYQ8 Retinal dehydrogenase 1 ALDH1A1 >sp|P00352|AL1A1_HUMAN Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=20.15 12.84 0.22 5.95 0.03 0.5 0.36 0.43 6.74E-23 7 12 alcohol metabolic process;biological regulation;cellular aldehyde metabolic process;cellular hormone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;diterpenoid metabolic process;ethanol metabolic process;ethanol oxidation;fat-soluble vitamin metabolic process;hormone metabolic process;isoprenoid metabolic process;lipid metabolic process;metabolic process;oxidation-reduction process;primary alcohol metabolic process;primary metabolic process;regulation of biological quality;regulation of hormone levels;retinoid metabolic process;retinol metabolic process;small molecule metabolic process;terpenoid metabolic process;vitamin A metabolic process;vitamin metabolic process;xenobiotic metabolic process "aldehyde dehydrogenase (NAD) activity;androgen binding;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;hormone binding;lipid binding;nucleoside-triphosphatase regulator activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;Ras

GTPase activator activity;retinal dehydrogenase activity;small GTPase regulator activity;steroid binding" cell part;cytoplasmic part;cytosol;intracellular part Retinol metabolism

P05091;F8W0A9;P05091-2;F8VP50 "Aldehyde dehydrogenase, mitochondrial" ALDH2 ">sp|P05091|ALDH2_HUMAN Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2;>tr|F8W0A9|F8W0A9_HUMAN Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=2 SV=1;>sp|P05091-2|ALDH2_HUMAN Isoform 2 of Aldehyde dehydrogenase, m" 0.08 12.41 0.13 7.06 0.17 1.99 0.23 1.39 3.89E-56 7 19.9 alcohol catabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular metabolic process;cellular process;ethanol catabolic process;ethanol metabolic process;ethanol oxidation;metabolic process;neurotransmitter biosynthetic process;neurotransmitter metabolic process;oxidation-reduction process;primary alcohol catabolic process;primary alcohol metabolic process;primary metabolic process;regulation of biological quality;regulation of neurotransmitter levels;small molecule catabolic process;small molecule metabolic process;xenobiotic metabolic process "aldehyde dehydrogenase (NAD) activity;aldehyde dehydrogenase [NAD(P)+] activity;catalytic activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Chloroalkane and chloroalkene degradation;Fatty acid metabolism;Glycerolipid metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Limonene and pinene degradation;Lysine degradation;Pentose and glucuronate interconversions;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation"

P36542;B4DL14;P36542-2 "ATP synthase subunit gamma, mitochondrial;ATP synthase subunit gamma" ATP5C1 ">sp|P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1;>tr|B4DL14|B4DL14_HUMAN ATP synthase subunit gamma OS=Homo sapiens GN=ATP5C1 PE=2 SV=1;>sp|P36542-2|ATPG_HUMAN Isoform Heart of ATP synthase subunit gamma," 1.2 1.45 1.73 1.2 0.62 0.55 0.74 0.8 2.92E-34 7 24.8 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex, catalytic core F(1);organelle inner membrane;organelle lumen;organelle membrane;organelle part;protein complex;proton-transporting ATP synthase complex, catalytic core F(1);proton-transporting two-sector ATPase complex, catalytic domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

O75947;O75947-2;F5H608 "ATP synthase subunit d, mitochondrial" ATP5H ">sp|O75947|ATP5H_HUMAN ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3;>sp|O75947-2|ATP5H_HUMAN Isoform 2 of ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H;>tr|F5H608|F5H608_HUMAN ATP synthase subunit d, mitochondri" 0.97 1.47 1.88 1.27 0.56 0.48 0.71 0.81 8.17E-57 7 49.7 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity "cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle part;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P21281;H0YC04;C9JL73;P15313;C9J5E3;C9JNS9 "V-type proton ATPase subunit B, brain isoform" ATP6V1B2 ">sp|P21281|VATB2_HUMAN V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3;>tr|H0YC04|H0YC04_HUMAN V-type proton ATPase subunit B, brain isoform (Fragment) OS=Homo sapiens GN=ATP6V1B2 PE=4 SV=1" 0.55 2.14 0.52 1.66 0.71 1.38 0.64 0.88 1.02E-78 7 17 "anatomical structure morphogenesis;ATP hydrolysis coupled proton transport;ATP metabolic process;biological regulation;calcium ion homeostasis;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;developmental process;divalent inorganic cation homeostasis;embryonic morphogenesis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;excretion;ferric iron transport;heterocycle metabolic process;homeostatic process;hydrogen transport;inner ear morphogenesis;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;multicellular organismal process;multi-organism process;neurological system process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;organelle organization;ossification;pH reduction;phagosome maturation;primary metabolic process;protein transport;proton transport;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of pH;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;secretion;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal transduction;small molecule metabolic process;system process;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "apical plasma membrane;basolateral plasma membrane;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endomembrane system;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lateral plasma membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microvillus;organelle;organelle part;pigment granule;plasma membrane;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain;proton-transporting V-type ATPase complex;proton-transporting V-type ATPase, V1 domain;vacuolar part;vacuolar proton-transporting V-type ATPase complex;vesicle" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

P27797;K7EM77;K7EJB9 Calreticulin CALR >sp|P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 0.72 0.29 0.52 0.21 1.87 1.23 2.13 1.22 3.61E-21 7 15.6 "actin cytoskeleton organization;actin filament-based process;activation of signaling protein activity involved in unfolded protein response;aging;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;carbohydrate metabolic process;cardiac cell differentiation;cardiac muscle cell differentiation;cell aging;cell cycle arrest;cell cycle process;cell differentiation;cellular carbohydrate metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to lithium ion;cellular response to metal ion;cellular response to stimulus;cellular response to stress;cellular senescence;cortical actin cytoskeleton organization;cortical cytoskeleton organization;corticosteroid receptor signaling pathway;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;gamete generation;glucocorticoid receptor signaling pathway;glycosylation;immune system process;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule glycosylation;macromolecule localization;macromolecule metabolic process;macromolecule modification;maintenance of location;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;muscle cell differentiation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of retinoic acid receptor signaling pathway;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;nuclear export;nuclear transport;nucleocytoplasmic transport;organelle organization;peptide antigen assembly with MHC class I protein complex;peptide antigen assembly with MHC protein complex;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell cycle;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of dendritic cell chemotaxis;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of endocytosis;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nuclease activity;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phagocytosis;positive regulation of protein kinase activity;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of transferase activity;positive regulation of transport;posttranscriptional regulation of gene expression;post-translational protein modification;primary metabolic process;protein complex assembly;protein complex subunit organization;protein export from nucleus;protein folding;protein glycosylation;protein localization;protein localization to nucleus;protein localization to organelle;protein maturation;protein maturation by protein folding;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein stabilization;protein targeting;protein transport;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of dendritic cell chemotaxis;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of endocytosis;regulation of gene expression;regulation of hydrolase activity;regulation of immune system process;regulation of kinase activity;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of meiosis;regulation of meiotic cell cycle;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of response to external stimulus;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to hormone stimulus;response to inorganic substance;response to lithium ion;response to metal ion;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;sequestering of calcium ion;sequestering of metal ion;signal transduction;spermatogenesis;steroid hormone receptor signaling pathway;striated muscle cell differentiation;transport" androgen receptor binding;binding;calcium ion binding;carbohydrate binding;cation binding;chaperone binding;complement binding;complement component C1q binding;DNA binding;hormone binding;hormone receptor binding;ion binding;iron ion binding;metal ion binding;mRNA binding;nuclear hormone receptor binding;nucleic acid binding;opsonin binding;peptide binding;protein binding;protein binding involved in protein folding;receptor binding;RNA binding;steroid hormone receptor binding;transition metal ion binding;unfolded protein binding;zinc ion binding acrosomal vesicle;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;external side of plasma membrane;extracellular matrix;extracellular region part;extracellular space;Golgi apparatus;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;MHC class I peptide loading complex;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane part;polysome;protein complex;proteinaceous extracellular matrix;ribonucleoprotein complex;sarcoplasmic reticulum lumen;stored secretory granule;vesicle Antigen processing and presentation;Chagas disease (American trypanosomiasis);Phagosome;Protein processing in endoplasmic reticulum

Q86VP6;Q86VP6-2 Cullin-associated NEDD8-dissociated protein 1 CAND1 >sp|Q86VP6|CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens

GN=CAND1 PE=1 SV=2;>sp|Q86VP6-2|CAND1_HUMAN Isoform 2 of Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 0.19 8.36 0.15 5.69 0.79 0.76 0.31 0.98 7.69E-21 7 7.8 "biological regulation;cell differentiation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;developmental process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of catalytic activity;negative regulation of molecular function;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA polymerase II transcriptional preinitiation complex assembly;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein complex assembly;regulation of RNA metabolic process;regulation of RNA polymerase II transcriptional preinitiation complex assembly;regulation of transcription from RNA polymerase II promoter;regulation of transcription initiation from RNA polymerase II promoter;regulation of transcription initiation, DNA-dependent;regulation of transcription, DNA-dependent;SCF complex assembly" cell part;cullin-RING ubiquitin ligase complex;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;ubiquitin ligase complex

Q76M96;Q76M96-2;H7C5K4 Coiled-coil domain-containing protein 80 CCDC80 >sp|Q76M96|CCD80_HUMAN Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 PE=1 SV=1;>sp|Q76M96-2|CCD80_HUMAN Isoform 2 of Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 NaN NaN 0.76 NaN 16.02 NaN NaN NaN 5.59E-19 7 9.3 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular structure organization;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;regulation of biological process;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular process binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding basement membrane;extracellular matrix;extracellular matrix part;extracellular region part;interstitial matrix;proteinaceous extracellular matrix

P40227;B4DPJ8;P40227-2;Q92526-3;Q92526;Q92526-2 T-complex protein 1 subunit zeta CCT6A >sp|P40227|TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3;>tr|B4DPJ8|B4DPJ8_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=2 SV=1;>sp|P40227-2|TCPZ_HUMAN Isoform 2 of T-complex protein 1 subunit zeta OS=H 1.1 1.08 0.9 0.9 1.4 1 1.18 1.15 2.81E-36 7 17.7 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chaperone-mediated protein complex assembly;'de novo' posttranslational protein folding;'de novo' protein folding;gamete generation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;reproductive process;spermatogenesis adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;protein transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;substrate-specific transporter activity;transporter activity;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular organelle part;intracellular part;macromolecular complex;microtubule;organelle part;protein complex

B4DEM7;P50990;B4DQH4;H7C4C8;H7C2U0 T-complex protein 1 subunit theta CCT8 >tr|B4DEM7|B4DEM7_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1;>sp|P50990|TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4;>tr|B4DQH4|B4DQH4_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens 0.97 0.97 0.5 0.93 1.07 0.8 1.23 1.03 1.38E-25 7 15.3 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" aggresome;cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;inclusion body;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex

Q6YHK3-4;Q6YHK3;Q6YHK3-3;Q6YHK3-2;C9JZB3;Q16821CD109 antigen CD109 >sp|Q6YHK3-4|CD109_HUMAN Isoform 4 of CD109 antigen OS=Homo sapiens GN=CD109;>sp|Q6YHK3|CD109_HUMAN CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2;>sp|Q6YHK3-3|CD109_HUMAN Isoform 3 of CD109 antigen OS=Homo sapiens GN=CD109;>sp|Q6YHK3-2|CD109_HUMAN Isofo 0.95 1.33 1.11 1.11 0.63 0.55 0.7 0.82 4.15E-53 7 6.2 biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan metabolic process;glycogen metabolic process;macromolecule metabolic process;metabolic process;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;oxidation-reduction process;polysaccharide metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity anchored to membrane;cell part;extracellular region part;extracellular space;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Insulin signaling pathway

P00387-2;P00387;P00387-3;B1AHF3 NADH-cytochrome b5 reductase 3;NADH-cytochrome b5 reductase 3 membrane-bound form;NADH-cytochrome b5 reductase 3 soluble form CYB5R3 >sp|P00387-2|NB5R3_HUMAN Isoform 2 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3;>sp|P00387|NB5R3_HUMAN NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3;>sp|P00387-3|NB5R3_HUMAN Isoform 3 of NADH-cytochrome b5 reductase 3 OS 0.87 1 1.64 0.53 1.5 1.1 1.05 1.18 5.30E-31 7 22.7 alcohol metabolic process;biosynthetic process;blood circulation;carboxylic acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;circulatory system process;L-ascorbic acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;multicellular organismal process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;system process;vitamin metabolic process;water-soluble vitamin metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;AMP binding;binding;catalytic activity;coenzyme binding;cofactor binding;cytochrome-b5 reductase activity;FAD binding;flavin adenine dinucleotide binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosolic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;hemoglobin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex Amino sugar and nucleotide sugar metabolism

Q14203-5;Q14203-2;Q14203-3;Q14203-4;E7EX90;Q14203-6;Q14203;Q6AWB1;E7EWF7 Dynactin subunit 1 DCTN1 >sp|Q14203-5|DCTN1_HUMAN Isoform 5 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1;>sp|Q14203-2|DCTN1_HUMAN Isoform p135 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1;>sp|Q14203-3|DCTN1_HUMAN Isoform 3 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1;>sp|Q14 NaN NaN 0.77 NaN 15.65 NaN NaN NaN 4.07E-16 7 7.7 activation of signaling protein activity involved in unfolded protein response;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;cell cycle phase;cell cycle process;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;developmental process;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;macromolecule metabolic process;metabolic process;mitosis;nervous system development;nuclear division;organelle fission;organelle organization;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;system development;transport "catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;pyrophosphatase activity" cell leading edge;cell part;centrosome;chromosomal part;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;spindle pole Huntington's disease;Vasopressin-regulated water reabsorption

Q08554-2;Q08554 Desmocollin-1DSC1 >sp|Q08554-2|DSC1_HUMAN Isoform 1B of Desmocollin-1 OS=Homo sapiens GN=DSC1;>sp|Q08554|DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2 0.86 1.47 1.98 1.51 2.1 2.87 1.2 1.13 6.90E-21 7 11.4 biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;desmosome;gap junction;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane

Q14574-2;Q14574;J3QRL9 Desmocollin-3DSC3 >sp|Q14574-2|DSC3_HUMAN Isoform 3B of Desmocollin-3 OS=Homo sapiens GN=DSC3;>sp|Q14574|DSC3_HUMAN Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3 1.04 1.49 1.09 1.22 0.64 0.36 0.5 0.64 1.90E-16 7 8 biological adhesion;biological regulation;cell adhesion;cell-cell adhesion;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;homophilic cell adhesion;in utero embryonic development;posttranscriptional regulation of gene expression;protein stabilization;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;cytoplasm;desmosome;extracellular region;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;plasma membrane

Q99848;H7C2Q8 Probable rRNA-processing protein EBP2 EBNA1BP2 ">sp|Q99848|EBP2_HUMAN Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2;>tr|H7C2Q8|H7C2Q8_HUMAN EBNA1 binding protein 2, isoform CRA_d OS=Homo sapiens GN=EBNA1BP2 PE=2 SV=1" 1.17 1.6 1.02 2.9 0.52 0.35 0.4 0.45 1.08E-29 7 25.5 cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

H3BRV0;Q99613;B5ME19;H3BPE3;H3BPE4 Eukaryotic translation initiation factor 3 subunit C EIF3C;EIF3CL >tr|H3BRV0|H3BRV0_HUMAN Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=2 SV=1;>sp|Q99613|EIF3C_HUMAN Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1;>sp|B5ME19|EIFCL_HUMAN Eukaryotic NaN NaN 0.5 NaN 1.94 NaN NaN NaN 1.11E-16 7 9 cellular process;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport

P29317;Q9UF33-2;J3KR66;D6RAL5;Q5JY90;B3KTB2;Q06187;F8W9W0;C9JXA2;Q96L35;B1AKC9;P54756-3;P29320;P54762;P29323-2;P54760;P29323-3;Q15375-2;Q15375-4;Q15375;P54753;F8VP57;P29322;P54756-2;Q9UF33;P54756;P29323 Ephrin type-A receptor 2 EPHA2 >sp|P29317|EPHA2_HUMAN Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2 1.09 1.48 0.88 0.98 0.76 0.57 0.59 0.71 3.53E-39 7 9.6 "activation of immune response;activation of innate immune response;activation of Rac GTPase activity;activation of Ras GTPase activity;activation of Rho GTPase activity;adaptive immune response;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;antigen receptor-mediated signaling pathway;apoptosis;axial mesoderm formation;axon guidance;axonal fasciculation;axonogenesis;B cell activation;B cell receptor signaling pathway;behavior;biological adhesion;biological regulation;biosynthetic process;blood vessel endothelial cell migration;bone remodeling;brain development;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a nerve;branching morphogenesis of a tube;calcium-mediated signaling;camera-type eye morphogenesis;cAMP-mediated signaling;cell activation;cell adhesion;cell chemotaxis;cell communication;cell death;cell development;cell differentiation;cell maturation;cell migration;cell migration involved in sprouting angiogenesis;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell recognition;cell surface receptor linked signaling pathway;cell-substrate adhesion;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;central nervous system neuron axonogenesis;central nervous system projection neuron axonogenesis;chemotaxis;cognition;commissural neuron axon guidance;corpus callosum development;cranial nerve morphogenesis;cyclic-nucleotide-mediated signaling;death;defense response;dendritic spine morphogenesis;dendritic spine organization;detection of abiotic stimulus;detection of external stimulus;detection of stimulus;detection of stimulus involved in sensory perception;detection of temperature stimulus;detection of temperature stimulus involved in sensory perception;detection of temperature stimulus involved in sensory perception of pain;developmental maturation;developmental process;digestive tract morphogenesis;embryonic morphogenesis;endothelial cell migration;enzyme linked receptor protein signaling pathway;ephrin receptor signaling pathway;epidermal cell differentiation;epithelial cell differentiation;epithelial cell proliferation;establishment of cell polarity;establishment or maintenance of cell polarity;eye morphogenesis;fasciculation of motor neuron axon;fasciculation of sensory neuron axon;formation of primary germ layer;heart morphogenesis;hemopoietic or lymphoid organ development;hippocampus development;I-kappaB kinase/NF-kappaB cascade;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;inner ear morphogenesis;intracellular protein kinase cascade;intracellular signal transduction;keratinocyte differentiation;learning;learning or memory;lens fiber cell morphogenesis;leukocyte activation;leukocyte differentiation;locomotion;lymphocyte activation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;mammary gland epithelial cell proliferation;mesoderm development;mesoderm formation;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;MyD88-dependent toll-like receptor signaling pathway;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of intracellular protein kinase cascade;negative regulation of nervous system development;negative regulation of neurogenesis;negative regulation of protein kinase B signaling cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of synapse assembly;neural precursor cell proliferation;neural tube development;neurological system process;neuron differentiation;neuron maturation;neuron projection morphogenesis;neuron recognition;neuron remodeling;nitrogen compound metabolic process;notochord cell development;notochord formation;nucleic acid metabolic process;nucleobase-containing compound metabolic process;optic nerve morphogenesis;organ development;organ morphogenesis;osteoblast differentiation;osteoclast differentiation;palate development;pattern recognition receptor signaling pathway;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of B cell activation;positive regulation of B cell differentiation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component biogenesis;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of CREB transcription factor activity;positive regulation of defense response;positive regulation of developmental process;positive regulation of establishment of protein localization in plasma membrane;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of long-term neuronal synaptic plasticity;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nervous system development;positive regulation of neurogenesis;positive regulation of neuron apoptosis;positive regulation of neuron projection development;positive regulation of NF-kappaB transcription factor activity;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of programmed cell death;positive regulation of Rac GTPase activity;positive regulation of Ras GTPase activity;positive regulation of response to stimulus;positive regulation of Rho GTPase activity;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of synapse assembly;positive regulation of transferase activity;primary metabolic process;programmed cell death;protein autophosphorylation;protein kinase B signaling cascade;protein metabolic process;protein modification process;protein phosphorylation;regulation of actin cytoskeleton

organization;regulation of actin filament-based process;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of axonogenesis;regulation of B cell activation;regulation of B cell apoptosis;regulation of B cell cytokine production;regulation of B cell differentiation;regulation of B cell mediated immunity;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood vessel endothelial cell migration;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of Cdc42 GTPase activity;regulation of cell activation;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell-cell adhesion;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of cytokine production involved in immune response;regulation of cytoskeleton organization;regulation of defense response;regulation of developmental process;regulation of endopeptidase activity;regulation of endothelial cell migration;regulation of epithelial to mesenchymal transition;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of focal adhesion assembly;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of homeostatic process;regulation of hormone secretion;regulation of hydrolase activity;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of insulin secretion;regulation of insulin secretion involved in cellular response to glucose stimulus;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of lamellipodium assembly;regulation of leukocyte activation;regulation of leukocyte apoptosis;regulation of leukocyte mediated immunity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of long-term neuronal synaptic plasticity;regulation of lymphocyte activation;regulation of lymphocyte apoptosis;regulation of lymphocyte differentiation;regulation of lymphocyte mediated immunity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron apoptosis;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of production of molecular mediator of immune response;regulation of programmed cell death;regulation of protein autophosphorylation;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Rac GTPase activity;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of secretion;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of synapse assembly;regulation of synapse organization;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of transport;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to retinoic acid;response to stimulus;response to stress;response to temperature stimulus;response to vitamin;response to vitamin A;retinal ganglion cell axon guidance;RNA biosynthetic process;RNA metabolic process;second-messenger-mediated signaling;signal transduction;skeletal system development;substrate adhesion-dependent cell spreading;substrate-dependent cell migration;system development;system process;taxis;thymus development;tissue development;tissue morphogenesis;tissue remodeling;toll-like receptor 2 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor signaling pathway;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;tube morphogenesis;urogenital system development;vasculogenesis" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;axon guidance receptor activity;binding;catalytic activity;cation binding;chemorepellent activity;ephrin receptor activity;GPI-linked ephrin receptor activity;ion binding;kinase activity;lipid binding;metal ion binding;molecular transducer activity;non-membrane spanning protein tyrosine kinase activity;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-3,4,5-trisphosphate binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;ribonucleotide binding;signal transducer activity;signaling receptor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity;transmembrane-ephrin receptor activity" adherens junction;anchoring junction;axon;cell body;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell surface;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic part;cytoplasmic vesicle;cytosol;dendrite;early endosome;early endosome membrane;endoplasmic reticulum;endosomal part;endosome;endosome membrane;external side of plasma membrane;extracellular region;focal adhesion;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium membrane;leading edge membrane;membrane;membrane part;membrane raft;membrane-bounded organelle;neuromuscular junction;neuron projection;neuronal cell body;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;postsynaptic membrane;rough endoplasmic reticulum;ruffle membrane;synapse;synapse part;synaptic membrane;vesicle Axon guidance;B cell receptor signaling pathway;Fc epsilon RI signaling pathway;Osteoclast differentiation;Primary immunodeficiency
P22087;M0R299;M0QXL5;M0R0P1;M0R2Q4;M0R2U2;M0R1H0;M0R2B0;A6NHQ2;R4GMW7 rRNA 2-O-methyltransferase fibrillarin FBL >sp|P22087|FBRL_HUMAN rRNA 2-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2;>tr|M0R299|M0R299_HUMAN rRNA 2-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=3 SV=1;>tr|M0QXL5|M0QXL5_HUMAN rRNA 2-O-methyltransferase f 1.07 1.14 1.22 2.1 0.58 0.5 0.71 0.62 9.39E-41 7 24.9 cellular macromolecule metabolic

process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;methylation;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;small molecule metabolic process;snoRNA metabolic process;tRNA metabolic process;tRNA processing "binding;catalytic activity;methyltransferase activity;nucleic acid binding;RNA binding;transferase activity;transferase activity, transferring one-carbon groups" box C/D snoRNP complex;Cajal body;cell part;granular component;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleolar part;nucleolus;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes

P04406;P04406-2;E7EUT5 Glyceraldehyde-3-phosphate dehydrogenase GAPDH >sp|P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3;>sp|P04406-2|G3P_HUMAN Isoform 2 of Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH;>tr|E7EUT5|E7EUT5_HUMAN Glyceraldehyde-3-phosphate dehydr 0.83 0.68 0.45 0.48 1 1.3 1.5 0.93 2.01E-71 7 30.7 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;apoptosis;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell death;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;death;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;microtubule cytoskeleton organization;microtubule-based process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;neuron apoptosis;neuron death;organelle organization;peptidyl-amino acid modification;peptidyl-cysteine modification;peptidyl-cysteine S-nitrosylation;peptidyl-cysteine S-trans-nitrosylation;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein metabolic process;protein modification process;protein nitrosylation;protein stabilization;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein stability;regulation of translation;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;cytoskeletal protein binding;glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity;microtubule binding;NAD binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;peptidyl-cysteine S-nitrosylase activity;protein binding;transferase activity;transferase activity, transferring nitrogenous groups;tubulin binding" cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lipid particle;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule cytoskeleton;non-membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane;ribonucleoprotein complex;vesicle Alzheimer's disease;Glycolysis / Gluconeogenesis

Q9BZE4;B7Z7A3;B4DY13;Q5T3R7 Nucleolar GTP-binding protein 1 GTPBP4 >sp|Q9BZE4|NOG1_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3;>tr|B7Z7A3|B7Z7A3_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=2 SV=1;>tr|B4DY13|B4DY13_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens GN 1.08 1.37 0.93 2.23 0.41 0.38 0.55 0.54 6.87E-34 7 14.2 biological regulation;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell adhesion;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cell-cell adhesion;negative regulation of cellular biosynthetic process;negative regulation of cellular component movement;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of collagen binding;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of locomotion;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein binding;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;posttranscriptional regulation of gene expression;protein stabilization;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell cycle;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cell-cell adhesion;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of collagen binding;regulation of cyclin-dependent protein kinase activity;regulation of DNA metabolic process;regulation of DNA replication;regulation of gene expression;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein binding;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein stability;regulation of protein ubiquitination;regulation of transferase activity;ribonucleoprotein complex biogenesis;ribosome biogenesis "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm Ribosome biogenesis in eukaryotes

P16403 Histone H1.2 HIST1H1C >sp|P16403|H12_HUMAN Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 1.11 1.36 0.28 4.3 0.22 0.29 0.35 0.28 8.77E-36 7 34.3 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex

P34932 Heat shock 70 kDa protein 4 HSPA4 >sp|P34932|HSP74_HUMAN Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 0.73 2.34 0.35 1.99 0.82 0.63 0.78 1.23 3.13E-22 7 11.8 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;cellular protein complex assembly;chaperone-mediated protein complex assembly;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;membrane organization;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;organelle organization;outer mitochondrial membrane organization;protein complex assembly;protein complex subunit organization;protein import;protein import into mitochondrial outer membrane;protein targeting;protein targeting to membrane;protein targeting to mitochondrion;protein transport;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;transport adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Antigen processing and presentation

F6SBX2;Q9NSE4 "Isoleucine--tRNA ligase, mitochondrial" IARS2 ">tr|F6SBX2|F6SBX2_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=2 SV=1;>sp|Q9NSE4|SYIM_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2" NaN NaN 0.95 NaN 4.05 NaN NaN NaN 9.01E-17 7 8.4 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;isoleucyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;isoleucine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis"

Q70UQ0;Q70UQ0-2 Inhibitor of nuclear factor kappa-B kinase-interacting protein IKBIP >sp|Q70UQ0|IKIP_HUMAN Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP PE=1 SV=1;>sp|Q70UQ0-2|IKIP_HUMAN Isoform 2 of Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP 1.03 1.09 1.35 0.94 0.79 0.61 0.94 1.27 3.70E-31 7 23.1 biological regulation;induction of apoptosis;induction of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to abiotic stimulus;response to ionizing radiation;response to radiation;response to stimulus;response to X-ray cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part

Q15046;Q15046-2;H3BRC9;H3BVA8 Lysine--tRNA ligase KARS >sp|Q15046|SYK_HUMAN Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3;>sp|Q15046-2|SYK_HUMAN Isoform Mitochondrial of Lysine--tRNA ligase OS=Homo sapiens GN=KARS 1.63 NaN 0.83 NaN 1.06 NaN 2.09 NaN 1.09E-14 7 13.4 amine metabolic process;amino acid activation;biosynthetic process;bis(5'-nucleosidyl) oligophosphate biosynthetic process;bis(5'-nucleosidyl) oligophosphate metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;diadenosine polyphosphate biosynthetic process;diadenosine polyphosphate metabolic process;diadenosine tetraphosphate biosynthetic process;diadenosine tetraphosphate metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;interaction with host;interspecies interaction between organisms;lysyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;multi-organism process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;reproductive process;ribonucleoside biosynthetic process;ribonucleoside metabolic process;RNA metabolic process;RNA processing;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tRNA processing;viral reproductive process;virus-host interaction"adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic acid binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;lysine-tRNA ligase activity;metal ion binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-enclosed lumen;microtubule cytoskeleton;mitochondrial matrix;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle lumen;organelle part;plasma membrane;protein complex Aminoacyl-tRNA biosynthesis

Q07666-2;Q07666;Q07666-3;Q5VWX1 "KH domain-containing, RNA-binding, signal transduction-associated protein 1" KHDRBS1 ">sp|Q07666-2|KHDR1_HUMAN Isoform 2 of KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1;>sp|Q07666|KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens" 0.99 1.05 0.88 1.73 0.74 0.41 0.73 0.9 4.70E-21 7 17.9 "biological regulation;biosynthetic process;cell cycle arrest;cell cycle process;cell proliferation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;G2/M transition of mitotic cell cycle;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nucleobase-containing compound transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein metabolic process;positive regulation of RNA export from nucleus;positive regulation of translation;positive regulation of translational initiation;positive regulation of transport;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleobase-containing compound transport;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA export from nucleus;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;regulation of transport;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;signal transduction;transcription, DNA-dependent" binding;DNA binding;mRNA binding;nucleic acid binding;poly(A) RNA binding;poly(U) RNA binding;poly-purine tract binding;poly-pyrimidine tract binding;RNA binding;single-stranded RNA binding cell part;cytoplasm;Grb2-Sos complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane part;protein complex

P48449-3;P48449;P48449-2;C9J315 Lanosterol synthaseLSS >sp|P48449-3|ERG7_HUMAN Isoform 3 of Lanosterol synthase OS=Homo sapiens GN=LSS;>sp|P48449|ERG7_HUMAN Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1;>sp|P48449-2|ERG7_HUMAN Isoform 2 of Lanosterol synthase OS=Homo sapiens GN=LSS;>tr|C9J315|C9J315_HUM 0.66 0.52 0.57 0.23 3.1 2.17 1.38 1.09 3.58E-18 7 14 alcohol metabolic process;biosynthetic process;cholesterol biosynthetic process;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process catalytic activity;intramolecular transferase activity;isomerase activity;lanosterol synthase activity;oxidosqualene cyclase activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;lipid particle;membrane;membrane part;organelle membrane;organelle part Steroid biosynthesis

P29966 Myristoylated alanine-rich C-kinase substrate MARCKS >sp|P29966|MARCS_HUMAN Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4 0.9 1.27 2.01 0.55 0.6 0.53 0.91 1.05 2.92E-66 7 35.8 biological regulation;cellular metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;small molecule metabolic process actin binding;actin filament binding;binding;calmodulin binding;cytoskeletal protein binding;protein binding actin cytoskeleton;cell cortex;cell part;centrosome;cytoplasmic part;cytoskeletal part;cytoskeleton;female germ cell nucleus;germ cell nucleus;germinal vesicle;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane Fc gamma R-mediated phagocytosis

P56192;A6NC17;H0YIP0;H0YI94;H0YHV5;B3KVK7;H0YIC2;H0YHL6;H0YI27 "Methionine--tRNA ligase, cytoplasmic" MARS ">sp|P56192|SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2;>tr|A6NC17|A6NC17_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=2 SV=3" 1.52 0.55 0.99 0.42 1.96 1 1.7 1.1 2.88E-21 7 9.9 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;methionyl-tRNA aminoacylation;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;methionine-tRNA ligase activity;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Aminoacyl-tRNA biosynthesis;Selenocompound metabolism

J3KSW8;Q6WCQ1-3;Q6WCQ1;Q6WCQ1-2 Myosin phosphatase Rho-interacting protein MPRIP >tr|J3KSW8|J3KSW8_HUMAN Myosin phosphatase Rho-interacting protein (Fragment) OS=Homo sapiens GN=MPRIP PE=4 SV=1;>sp|Q6WCQ1-3|MPRIP_HUMAN Isoform 3 of Myosin phosphatase Rho-interacting protein OS=Homo sapiens GN=MPRIP;>sp|Q6WCQ1|MPRIP_HUMAN Myosin phospha 1.19 1.49 0.9 1.48 3.29 1.01 0.59 0.95 4.10E-28 7 10.7 binding;lipid binding;phospholipid binding cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

Q86UE4;E5RJU9;H0YB56;H0YBJ8 Protein LYRIC MTDH >sp|Q86UE4|LYRIC_HUMAN Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2;>tr|E5RJU9|E5RJU9_HUMAN Protein LYRIC OS=Homo sapiens GN=MTDH PE=2 SV=1 1.26 0.74 1.01 0.47 1.19 0.73 1.49 1.21 1.79E-35 7 16 "biological regulation;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to biotic stimulus;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to stimulus;lipopolysaccharide-mediated signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;positive regulation of angiogenesis;positive regulation of autophagy;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of protein kinase B signaling cascade;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of autophagy;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cell communication;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;signal transduction;tight junction assembly" protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity apical plasma membrane;cell junction;cell part;cell-cell junction;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intercellular canaliculus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear membrane;nuclear part;nucleolus;nucleoplasm part;occluding junction;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;tight junction

O75489;B4DFM8;E9PS48;E9PKL8;G3V194 "NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial" NDUFS3 ">sp|O75489|NDUS3_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1 SV=1" 1.15 1.5 1.62 1.79 0.54 0.55 0.69 0.87 9.75E-145 7 36.4 "biological regulation;cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;induction of apoptosis;induction of programmed cell death;metabolic process;mitochondrial electron transport, NADH to ubiquinone;negative regulation of biological process;negative regulation of cell growth;negative regulation of cellular process;negative regulation of growth;oxidation-reduction process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;regulation of programmed cell death;respiratory electron transport chain;small molecule metabolic process" "catalytic activity;electron carrier activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

G5EA52;P30101 Protein disulfide-isomerase A3 PDIA3 ">tr|G5EA52|G5EA52_HUMAN Protein disulfide isomerase family A, member 3, isoform CRA_b OS=Homo sapiens GN=PDIA3 PE=2 SV=1;>sp|P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4" 0.86 1.03 0.51 0.89 0.88 0.81 1.18 1.05 5.01E-46 7 17.3 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;carbohydrate metabolic process;cell redox homeostasis;cellular carbohydrate metabolic process;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;glycerol ether metabolic process;glycosylation;homeostatic process;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;maintenance of location;maintenance of location in cell;maintenance of protein localization in endoplasmic reticulum;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;metabolic process;nuclear import;nuclear transport;nucleocytoplasmic transport;organic ether metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;post-translational protein modification;primary metabolic process;protein glycosylation;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein retention in ER lumen;protein targeting;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to stimulus;signal transduction;small molecule metabolic process;transport" "catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;disulfide oxidoreductase activity;electron carrier activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;lipase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;peptidase activity;peptidase activity, acting on L-amino acid peptides;phospholipase activity;phospholipase C activity;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;vesicle Antigen processing and presentation;Protein processing in endoplasmic reticulum

P36871;P36871-2;P36871-3 Phosphoglucomutase-1 PGM1 >sp|P36871|PGM1_HUMAN Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3;>sp|P36871-2|PGM1_HUMAN Isoform 2 of Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1;>sp|P36871-3|PGM1_HUMAN Isoform 3 of Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 0.18 17.38 0.09 7.47 0.05 1.45 0.16 0.94 2.61E-40 7 16.9 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;galactose catabolic process;galactose metabolic process;generation of precursor metabolites and energy;glucan biosynthetic process;glucan catabolic process;glucan metabolic process;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycogen biosynthetic process;glycogen catabolic process;glycogen metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;oxidation-reduction process;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;intramolecular transferase activity;intramolecular transferase activity, phosphotransferases;ion binding;isomerase activity;magnesium ion binding;metal ion binding;phosphoglucomutase activity" actin cytoskeleton;cell part;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle Amino sugar and nucleotide sugar metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway;Purine metabolism;Starch and sucrose metabolism;Streptomycin biosynthesis

Q06830;H7C3T4;Q13162 Peroxiredoxin-1 PRDX1 >sp|Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 0.7 0.95 0.97 0.5 1.2 1.79 1.3 0.92 8.83E-18 7 33.7 anatomical structure development;biological regulation;catabolic process;cell killing;cell proliferation;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to oxygen radical;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cellular response to superoxide;defense response;developmental process;erythrocyte homeostasis;homeostasis of number of cells;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;I-kappaB phosphorylation;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;leukocyte mediated cytotoxicity;leukocyte mediated immunity;lymphocyte mediated immunity;macromolecule metabolic process;macromolecule modification;metabolic process;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular localization;regulation of cellular process;regulation of cellular response to stress;regulation of establishment of protein localization;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of MAPKKK cascade;regulation of NF-kappaB import into nucleus;regulation of nucleocytoplasmic transport;regulation of programmed cell death;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of transcription factor import into nucleus;regulation of transmembrane transport;regulation of transport;removal of superoxide radicals;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to oxygen radical;response to reactive oxygen species;response to stimulus;response to stress;response to superoxide;skeletal system development;superoxide metabolic process;system development "antioxidant activity;binding;catalytic activity;cation binding;heme binding;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;peroxiredoxin activity;tetrapyrrole binding;thioredoxin peroxidase activity;transition metal ion binding" cell part;chromatin;chromosomal part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;euchromatin;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microbody lumen;microbody part;mitochondrial matrix;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleolus;nucleus;organelle;organelle lumen;organelle part;peroxisomal matrix;peroxisomal part;pigment granule;vesicle Peroxisome

Q96EY7;B8ZZQ4;B4DF73;Q96EY7-2;F8WE76 "Pentatricopeptide repeat domain-containing protein 3, mitochondrial" PTCD3 ">sp|Q96EY7|PTCD3_HUMAN Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3" NaN NaN 1.63 NaN 0.72 NaN NaN NaN 1.84E-17 7 12.2 biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrial translation;mitochondrion organization;organelle organization;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;translation binding;nucleic acid binding;ribonucleoprotein binding;ribosomal small subunit binding;RNA binding;rRNA binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle

P61026;Q15286-2;P59190-2;P59190;H0YLJ8;H0YL94;C9JB90;E9PI18;C9JFM7;E9PJQ5;Q6MZX6;E9PRF7;E9PNB9;E9PS06;J3QSF4;G3V562;E9PBQ0;Q6MZH2;G3V196;H0YDK7;E9PMJ1;M0R1E0;A6NDJ8;A8MSP2;Q96AX2-4;A8MTC6;A8MZI4;M0R0X1;B7Z3L0;P51153;Q15771;Q86YS6;Q96DA2;P61018;Q96AX2-2;Q14964;P20338;Q96AX2;Q96AX2-3;Q9H082;P61018-2 Ras-related protein Rab-10 RAB10 >sp|P61026|RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 0.79 1.06 0.76 0.33 1.87 1.83 1.16 0.89 5.59E-102 7 39 "anatomical structure morphogenesis;autophagy;axonogenesis;biological adhesion;biological regulation;catabolic process;cation homeostasis;cell adhesion;cell differentiation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular metabolic process;cellular monovalent inorganic cation homeostasis;cellular process;cellular protein localization;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;developmental process;endoplasmic reticulum organization;endoplasmic reticulum tubular network organization;endosome transport;epithelial cell differentiation;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of neuroblast polarity;establishment of protein localization;establishment of protein localization in endoplasmic reticulum membrane;establishment of protein localization in membrane;establishment or maintenance of cell polarity;establishment or maintenance of neuroblast polarity;Golgi organization;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;homeostatic process;intracellular pH reduction;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;localization;macromolecule localization;membrane organization;metabolic process;monovalent inorganic cation homeostasis;neuron projection morphogenesis;organelle fusion;organelle organization;pH reduction;phagosome acidification;phagosome maturation;phagosome-lysosome fusion;plasma membrane organization;polarized epithelial cell differentiation;post-Golgi vesicle-mediated transport;protein localization;protein localization in membrane;protein localization in plasma membrane;protein transport;regulation of autophagic vacuole assembly;regulation of autophagy;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular pH;regulation of cellular process;regulation of cellular response to stress;regulation of endocytosis;regulation of intracellular pH;regulation of intracellular transport;regulation of localization;regulation of macroautophagy;regulation of metabolic process;regulation of organelle organization;regulation of pH;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress;regulation of retrograde vesicle-mediated transport, Golgi to ER;regulation of transport;regulation of vacuole organization;regulation of vesicle-mediated transport;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;retrograde transport, plasma membrane to Golgi;signal transduction;small GTPase mediated signal transduction;synapse organization;transport;vesicle-mediated transport" "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transporter activity;transporter activity" cell junction;cell part;cell projection;cell-cell junction;cilium;cis-Golgi network;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum tubular network;endoplasmic reticulum-Golgi intermediate compartment;endosomal part;endosome;endosome membrane;Golgi apparatus;Golgi apparatus part;Golgi cisterna;Golgi lumen;Golgi membrane;insulin-responsive compartment;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;occluding junction;organelle;organelle lumen;organelle membrane;organelle part;organelle subcompartment;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;primary cilium;recycling endosome;recycling endosome membrane;stored secretory granule;tight junction;trans-Golgi network;vesicle;vesicle membrane Endocytosis;Tight junction

P20340-2;P20340;H7BYW1;P20340-4;H0YGL6;F5H3K7;F5GX61;P20340-3;C9JU14;J3KR73;B7Z337 Ras-related protein Rab-6A RAB6A >sp|P20340-2|RAB6A_HUMAN Isoform 2 of Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A;>sp|P20340|RAB6A_HUMAN Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3;>tr|H7BYW1|H7BYW1_HUMAN Ras-related protein Rab-6A (Fragment) OS=Homo sapiens GN= 0.67 2.29 1.17 1.05 1.02 1.64 0.71 1.06 5.83E-42 7 32.2 "biological regulation;cellular component movement;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cytoskeleton-dependent intracellular transport;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;Golgi vesicle transport;intracellular protein transport;intracellular signal transduction;intracellular transport;intra-Golgi vesicle-mediated transport;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;microtubule-based movement;microtubule-based process;microtubule-based transport;minus-end-directed organelle transport along microtubule;one-carbon metabolic process;organelle transport along microtubule;peptidyl-amino acid modification;peptidyl-cysteine methylation;peptidyl-cysteine modification;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;protein targeting;protein targeting to Golgi;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;retrograde transport, vesicle recycling within Golgi;retrograde vesicle-mediated transport, Golgi to ER;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process;transport;vesicle-mediated transport" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;trans-Golgi network;vesicle

F8W181;Q02878;F8VR69;F8VZ45 60S ribosomal protein L6 RPL6 >tr|F8W181|F8W181_HUMAN 60S ribosomal protein L6 (Fragment) OS=Homo sapiens GN=RPL6 PE=2 SV=1;>sp|Q02878|RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3 1.32 0.73 0.88 0.7 0.85 0.75 1.52 1 7.57E-60 7 29.6 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;DNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P62277;J3KMX5;E9PS50 40S ribosomal protein S13 RPS13 >sp|P62277|RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2;>tr|J3KMX5|J3KMX5_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=4 SV=1 2.11 1.09 1.54 0.6 0.81 0.57 0.91 0.63 7.87E-51 7 43 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of

cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit
Ribosome

P62753;A2A3R5;A2A3R7 40S ribosomal protein S6 RPS6 >sp|P62753|RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1;>tr|A2A3R5|A2A3R5_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=2 SV=1 1.3 0.78 0.44 0.66 1.3 1.08 1.31 0.89 1.95E-36 7 22.9 "biological regulation;biosynthetic process;carbohydrate homeostasis;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;cotranslational protein targeting to membrane;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glucose homeostasis;homeostatic process;insulin receptor signaling pathway;intracellular protein transport;intracellular signal transduction;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;regulation of programmed cell death;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex biogenesis;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;ribosomal small subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;signal transduction;SRP-dependent cotranslational protein targeting to membrane;TOR signaling cascade;translation;translational elongation;translational initiation;translational termination;transmembrane receptor protein tyrosine kinase signaling pathway;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Insulin signaling pathway;mTOR signaling pathway;Ribosome

Q9Y230;B3KQ59;M0R0Y3;M0R0Z0;M0QXI6 RuvB-like 2 RUVBL2 >sp|Q9Y230|RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3;>tr|B3KQ59|B3KQ59_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=2 SV=1 1.14 0.97 0.85 0.94 1.03 1.08 1.06 0.95 1.84E-23 7 17.3 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to light stimulus;cellular response to radiation;cellular response to stimulus;cellular response to stress;cellular response to UV;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA recombination;DNA repair;histone acetylation;histone H2A acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein folding;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "5'-3' DNA helicase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent 5'-3' DNA helicase activity;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;damaged DNA binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;unfolded protein binding" cell part;chromatin remodeling complex;chromosomal part;cytoplasm;DNA helicase complex;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;histone methyltransferase complex;Ino80 complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;methyltransferase complex;MLL1 complex;NuA4 histone acetyltransferase complex;nuclear chromosome part;nuclear matrix;nuclear part;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex

Q96FQ6 Protein S100-A16 S100A16 >sp|Q96FQ6|S10AG_HUMAN Protein S100-A16 OS=Homo sapiens GN=S100A16 PE=1 SV=1 1.2 1.59 1.27 0.76 1.36 0.97 0.74 0.67 1.13E-41 7 58.3 response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulusbinding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane

Q15393;Q15393-2;Q15393-3;J3QRB2;J3QL37;I3L4G7 Splicing factor 3B subunit 3 SF3B3 >sp|Q15393|SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 1.38 0.83 1.41 1.35 2.24 0.45 1.1 0.64 1.74E-28 7 8.1 "cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome

Q6P1M0;Q96G53;B7Z662;Q6PCB7 Long-chain fatty acid transport protein 4 SLC27A4 >sp|Q6P1M0|S27A4_HUMAN Long-chain fatty acid transport protein 4 OS=Homo sapiens GN=SLC27A4 PE=1 SV=1 0.95 0.78 1.18 0.34 2.7 1.45 1.31 1.01 1.26E-27 7 15.1 adiponectin-mediated signaling pathway;alcohol metabolic process;amine biosynthetic process;amine metabolic process;anatomical structure development;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;carboxylic acid transport;cardiolipin biosynthetic process;cardiolipin metabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular amine metabolic process;cellular biogenic amine biosynthetic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;epidermis development;establishment of localization;ethanolamine biosynthetic process;ethanolamine metabolic process;ethanolamine-containing compound metabolic process;fatty acid catabolic process;fatty acid metabolic process;fatty acid transport;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid transport;long-chain fatty acid transport;medium-chain fatty acid transport;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of metabolic process;negative regulation of phospholipid biosynthetic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;organic acid transport;organic substance transport;organophosphate metabolic process;oxoacid metabolic process;phosphatidic acid biosynthetic process;phosphatidic acid metabolic process;phosphatidylcholine biosynthetic process;phosphatidylcholine metabolic process;phosphatidylethanolamine biosynthetic process;phosphatidylethanolamine metabolic process;phosphatidylglycerol biosynthetic process;phosphatidylglycerol metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phosphatidylserine biosynthetic process;phosphatidylserine metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of heat generation;positive regulation of homeostatic process;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of heat generation;regulation of homeostatic process;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of phosphate metabolic process;regulation of phospholipid biosynthetic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of transferase activity;response to abiotic stimulus;response to chemical stimulus;response to cold;response to cytokine stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;signal transduction;skin development;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;tissue development;transmembrane transport;transport;very long-chain fatty acid catabolic process;very long-chain fatty acid metabolic process "binding;catalytic activity;fatty acid ligase activity;fatty acid transporter activity;ligase activity;ligase activity, forming carbon-sulfur bonds;lipid transporter activity;long-chain fatty acid-CoA ligase activity;nucleotide binding;substrate-specific transporter activity;transporter activity;very long-chain fatty acid-CoA ligase activity" brush border membrane;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic part;endomembrane system;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microvillus;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part PPAR signaling pathway

B4E2V5;P27105;P27105-2 Erythrocyte band 7 integral membrane protein STOM >tr|B4E2V5|B4E2V5_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=2 SV=1;>sp|P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3 0.77 0.94 1.22 1.24 0.51 0.45 1.07 1.01 1.21E-42 7 35.4 cellular component assembly;cellular component organization;cellular component organization or biogenesis;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;pigment granule;plasma membrane part;vesicle

O95425-2;O95425;F5H2Q5 Supervillin SVIL >sp|O95425-2|SVIL_HUMAN Isoform 2 of Supervillin OS=Homo sapiens GN=SVIL;>sp|O95425|SVIL_HUMAN Supervillin OS=Homo sapiens GN=SVIL PE=1 SV=2 0.85 1.57 1.05 1.57 0.73 0.86 0.71 1.67 1.65E-21 7 5.5 anatomical structure development;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;muscle tissue development;organelle organization;skeletal muscle tissue development;striated muscle tissue development;tissue development actin binding;actin filament binding;binding;cytoskeletal protein binding;protein binding actin cytoskeleton;cell junction;cell part;cell projection;contractile fiber part;costamere;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;invadopodium;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;podosome;protein complex

Q12788;J3KNP2 Transducin beta-like protein 3 TBL3 >sp|Q12788|TBL3_HUMAN Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2;>tr|J3KNP2|J3KNP2_HUMAN Transducin beta-like protein 3 (Fragment) OS=Homo sapiens GN=TBL3 PE=4 SV=1 1.32 NaN 1.38 NaN 0.44 NaN 0.61 NaN 2.51E-38 7 11.6 "biological regulation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cGMP-mediated signaling;cyclic-nucleotide-mediated signaling;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cGMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;intracellular signal transduction;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;second-messenger-mediated signaling;signal transduction" molecular transducer activity;receptor signaling protein activity;signal transducer activity cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;ribonucleoprotein complex;small-subunit processome Ribosome biogenesis in eukaryotes

O94826 Mitochondrial import receptor subunit TOM70 TOMM70A >sp|O94826|TOM70_HUMAN Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1 0.98 1.46 1.54 1.25 0.69 0.65 0.77 0.86 1.91E-25 7 11.7 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transport macromolecule transmembrane transporter activity;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial outer membrane translocase complex;mitochondrial part;organelle part;protein complex

Q5JTV8;H0YD16;H0Y4R4;Q5JTV8-2;H0YDU3 Torsin-1A-interacting protein 1 TOR1AIP1 >sp|Q5JTV8|TOIP1_HUMAN Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2 1.17 1.98 1.84 1.25 0.68 0.75 0.68 0.87 2.82E-43 7 18 cellular component organization;cellular component organization or biogenesis;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;localization;macromolecule localization;membrane organization;nuclear membrane organization;protein localization;protein localization to nucleus;protein localization to organelle cell part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;nuclear inner membrane;nuclear membrane;nuclear part;organelle inner membrane;organelle membrane;organelle part

Q9P0L0;Q9P0L0-2;J3QKM9 Vesicle-associated membrane protein-associated protein A VAPA >sp|Q9P0L0|VAPA_HUMAN Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3;>sp|Q9P0L0-2|VAPA_HUMAN Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA 1.06 1.21 1.98 1 0.96 0.66 0.79 0.91 4.91E-28 7 26.9 biological regulation;biosynthetic process;cell death;cell projection organization;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;death;lipid biosynthetic process;lipid metabolic process;localization;macromolecule localization;membrane fusion;membrane lipid biosynthetic process;membrane lipid metabolic process;membrane organization;metabolic process;neuron projection development;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein localization;protein localization in endoplasmic reticulum;protein localization to organelle;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;small molecule metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process molecular transducer activity;signal transducer activity;structural molecule activity cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;microtubule;organelle;organelle membrane;organelle part;plasma membrane;protein complex;vesicle Tight junction

Q9Y277;Q9Y277-2;F5H740;E5RK27;E5RFP6;E5RJN6;E5RHZ6;E5RHE1 Voltage-dependent anion-selective channel protein 3 VDAC3 >sp|Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1;>sp|Q9Y277-2|VDAC3_HUMAN Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3;>tr|F5H740|F5H740_HUMAN Voltage 1.03 1.43 1.63 1.8 0.5 0.62 0.61 0.93 1.35E-45 7 29 adenine transport;cellular process;establishment of localization;nitrogen compound transport;nucleobase transport;nucleobase-containing compound transport;purine base transport;purine-containing compound transmembrane transport;transmembrane transport;transport anion channel activity;anion transmembrane transporter activity;binding;channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;nucleotide binding;passive transmembrane transporter activity;porin activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated ion channel activity;wide pore channel activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;pore complex;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease

P62258;P62258-2;B4DJF2;I3L3T1;K7EM20;I3L0W5;K7EIT4 14-3-3 protein epsilon YWHAE >sp|P62258|1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1;>sp|P62258-2|1433E_HUMAN Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE 1.09 1.4 0.63 1.43 0.26 0.53 1.39 1.32 1.01E-208 7 29 anatomical structure development;biological regulation;cell cycle process;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;cerebral cortex development;developmental process;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;G2/M transition of mitotic cell cycle;hippo signaling cascade;hippocampus development;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotion;membrane organization;multi-organism process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of dephosphorylation;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of protein dephosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;nerve growth factor receptor signaling pathway;neuron migration;protein targeting;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;reproductive process;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;viral reproductive process;virus-host interaction axon part;cell part;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinesin complex;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule associated complex;mitochondrion;organelle;organelle membrane;organelle part;pigment granule;protein complex;vesicle;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis

P27348;E9PG15 14-3-3 protein theta YWHAQ >sp|P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1;>tr|E9PG15|E9PG15_HUMAN 14-3-3 protein theta (Fragment) OS=Homo sapiens GN=YWHAQ PE=2 SV=1 0.65 2.86 0.21 2.02 0.26 0.89 0.84 1.3 9.73E-254 7 34.3 "biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular signal transduction;intracellular transport;membrane organization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;protein targeting;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport" cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis

O15144;C9JTV5;G5E9J0;H7C3F9;G5E9S7 Actin-related protein 2/3 complex subunit 2 ARPC2 >sp|O15144|ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 0.59 1.91 0.81 2.54 0.3 0.54 0.42 0.93 1.57E-102 8 26.3 biological regulation;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular process;defense response;immune response;immune system process;innate immune response;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stressstructural constituent of cytoskeleton;structural molecule activity adherens junction;anchoring junction;Arp2/3 protein complex;cell junction;cell leading edge;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;endosome;focal adhesion;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis

Q93050-1;Q93050;F5H569;Q93050-3;B7Z641;B7Z2A9;K7EM24;K7EN36;K7EPG4;K7ELZ6;K7EQW2 V-type proton ATPase 116 kDa subunit a isoform 1 ATP6V0A1 >sp|Q93050-1|VPP1_HUMAN Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1;>sp|Q93050|VPP1_HUMAN V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3;>tr|F5H569|F5H569_HUMAN V-type pr 0.86 1.06 0.56 0.81 1.97 1.63 1.06 1.12 1.77E-28 8 11.2 "ATP hydrolysis coupled proton transport;biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organelle organization;phagosome maturation;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity "cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosomal part;endosome membrane;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle membrane;organelle part;phagocytic vesicle membrane;pigment granule;plasma membrane;protein complex;proton-transporting two-sector ATPase complex, proton-transporting domain;proton-transporting V-type ATPase, V0 domain;vacuolar part;vacuolar proton-transporting V-type ATPase, V0 domain;vesicle;vesicle membrane" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

Q99832-3;Q99832;F5GZK5;Q99832-4;B7Z1C9;Q99832-2;F8WAM2 T-complex protein 1 subunit eta CCT7 >sp|Q99832-3|TCPH_HUMAN Isoform 3 of T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7;>sp|Q99832|TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2;>tr|F5GZK5|F5GZK5_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=0.78 1.6 0.35 1.21 0.76 0.87 0.91 0.97 8.16E-23 8 21.8 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic processadenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;mitochondrion;organelle;organelle part;protein complex

P12830;Q9UII8;H3BNC6;H3BVI7;J3QKP1 Cadherin-1;E-Cad/CTF1;E-Cad/CTF2;E-Cad/CTF3 CDH1 ">sp|P12830|CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3;>tr|Q9UII8|Q9UII8_HUMAN Cadherin 1, type 1, E-cadherin (Epithelial), isoform CRA_c OS=Homo sapiens GN=CDH1 PE=2 SV=1;>tr|H3BNC6|H3BNC6_HUMAN Fizzy-related protein homolog OS=Homo sapiens G" 1.13 1.15 1.17 0.77 0.6 0.59 1.01 1.03 1.59E-73 8 12 "adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to indole-3-methanol;cellular response to inorganic substance;cellular response to lithium ion;cellular response to metal ion;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cochlea development;developmental process;gland development;homeostatic process;homophilic cell adhesion;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;multicellular organismal process;multicellular organismal water homeostasis;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell-cell adhesion;negative regulation of cellular process;neurological system process;neuron projection development;organ development;pituitary gland development;plasma membrane organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of RNA metabolic process;positive regulation of transcription factor import into nucleus;positive regulation of transcription, DNA-dependent;positive regulation of transmembrane transport;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein localization;protein localization in membrane;protein localization in plasma membrane;protein metabolic process;protein oligomerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of branching involved in salivary gland morphogenesis;regulation of catalytic activity;regulation of cell adhesion;regulation of cell-cell adhesion;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of gene expression;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organ morphogenesis;regulation of peptidase activity;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein localization at cell surface;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of

transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of water loss via skin;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to indole-3-methanol;response to inorganic substance;response to lithium ion;response to metal ion;response to organic nitrogen;response to organic substance;response to stimulus;response to toxin;salivary gland cavitation;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;synapse assembly;synapse organization;system process;tight junction assembly;trophectodermal cell differentiation;tube formation;tube lumen cavitation;water homeostasis" beta-catenin binding;binding;calcium ion binding;cation binding;cell adhesion molecule binding;ion binding;metal ion binding;protein binding actin cytoskeleton;adherens junction;aggresome;anchoring junction;apical junction complex;apical part of cell;axon part;axon terminus;basolateral plasma membrane;catenin complex;cell junction;cell part;cell projection part;cell surface;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic part;cytoskeleton;endosome;extrinsic to membrane;extrinsic to plasma membrane;focal adhesion;Golgi apparatus;Golgi apparatus part;inclusion body;integral to membrane;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lateral loop;lateral plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuron projection terminus;node of Ranvier;non-membrane-bounded organelle;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;Schmidt-Lanterman incisure;trans-Golgi network Adherens junction;Bacterial invasion of epithelial cells;Bladder cancer;Cell adhesion molecules (CAMs);Endometrial cancer;Melanoma;Pathogenic Escherichia coli infection;Pathways in cancer;Thyroid cancer
B4DGU4;P35222;P35222-2 Catenin beta-1 CTNNB1 >tr|B4DGU4|B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1;>sp|P35222|CTNB1_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 0.86 1.4 0.77 0.82 0.72 0.67 0.83 0.88 6.21E-18 8 12.7 "adherens junction assembly;adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;anatomical structure morphogenesis;androgen receptor signaling pathway;anterior/posterior axis specification;apoptosis;appendage morphogenesis;axis specification;biological adhesion;biological regulation;biosynthetic process;bone resorption;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling pathway involved in heart development;canonical Wnt receptor signaling pathway involved in negative regulation of apoptosis;canonical Wnt receptor signaling pathway involved in positive regulation of cardiac outflow tract cell proliferation;canonical Wnt receptor signaling pathway involved in positive regulation of epithelial to mesenchymal transition;canonical Wnt receptor signaling pathway involved in regulation of cell proliferation;cell activation;cell adhesion;cell communication;cell death;cell development;cell differentiation;cell fate commitment;cell fate commitment involved in formation of primary germ layers;cell fate determination;cell fate specification;cell junction assembly;cell junction organization;cell maturation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cell surface receptor linked signaling pathway involved in heart development;cell-cell adhesion;cell-cell junction organization;cell-cell signaling;cell-cell signaling involved in cell fate commitment;cell-matrix adhesion;cell-substrate adhesion;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein localization;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to indole-3-methanol;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;central nervous system vasculogenesis;chordate embryonic development;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;death;determination of bilateral symmetry;determination of dorsal/ventral asymmetry;developmental induction;developmental maturation;developmental process;developmental process involved in reproduction;digestive tract development;dorsal/ventral axis specification;ectoderm development;ectodermal placode formation;embryo development;embryo development ending in birth or egg hatching;embryonic appendage morphogenesis;embryonic axis specification;embryonic digit morphogenesis;embryonic epithelial tube formation;embryonic foregut morphogenesis;embryonic forelimb morphogenesis;embryonic heart tube development;embryonic hindlimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic pattern specification;endodermal cell fate commitment;endothelial tube morphogenesis;epidermal cell differentiation;epidermis development;epithelial cell differentiation;epithelial cell differentiation involved in prostate gland development;epithelial cell morphogenesis;epithelial to mesenchymal transition;epithelial tube branching involved in lung morphogenesis;epithelial tube formation;epithelial tube morphogenesis;epithelium development;establishment of localization;forebrain development;forelimb morphogenesis;fungiform papilla formation;gastrulation;gastrulation with mouth forming second;genitalia development;genitalia morphogenesis;germ cell development;glial cell fate determination;glial cell proliferation;hair cell differentiation;hair cycle process;hair follicle morphogenesis;hair follicle placode formation;hemopoietic or lymphoid organ development;hindbrain development;hindlimb morphogenesis;homeostatic process;immune system process;in utero embryonic development;intracellular receptor mediated signaling pathway;lens morphogenesis in camera-type eye;leukocyte activation;leukocyte differentiation;limb morphogenesis;liver development;localization;locomotion;lung cell differentiation;lung induction;lung-associated mesenchyme development;lymphocyte activation;lymphocyte differentiation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;male genitalia development;mesenchymal cell proliferation;mesenchymal cell proliferation involved in lung development;mesenchymal to epithelial transition;mesenchymal to epithelial transition involved in metanephros morphogenesis;mesenchyme development;metabolic process;midgut development;molting cycle;molting cycle process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an endothelium;morphogenesis of an epithelium;multicellular organismal process;muscle cell differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;myoblast differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cardiac cell fate specification;negative regulation of cardioblast cell fate specification;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell fate commitment;negative regulation of cell fate specification;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of chondrocyte differentiation;negative regulation of developmental process;negative regulation of gene expression;negative regulation of glial cell differentiation;negative regulation of gliogenesis;negative regulation of heart induction by canonical Wnt receptor signaling pathway;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte

differentiation;negative regulation of neurogenesis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of oligodendrocyte differentiation;negative regulation of osteoclast differentiation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein sumoylation;negative regulation of RNA metabolic process;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nephron tubule formation;neural plate development;neuron migration;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;odontogenesis;odontogenesis of dentine-containing tooth;oocyte development;organ development;organ formation;organ induction;organ morphogenesis;organelle organization;osteoclast differentiation;oviduct development;pancreas development;pattern specification process;patterning of blood vessels;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of branching involved in lung morphogenesis;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of determination of dorsal identity;positive regulation of developmental process;positive regulation of endothelial cell differentiation;positive regulation of epithelial cell differentiation;positive regulation of epithelial cell proliferation;positive regulation of epithelial cell proliferation involved in prostate gland development;positive regulation of fibroblast growth factor receptor signaling pathway;positive regulation of gene expression;positive regulation of glycoprotein biosynthetic process;positive regulation of heparan sulfate proteoglycan biosynthetic process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of muscle cell differentiation;positive regulation of neural precursor cell proliferation;positive regulation of neuroblast proliferation;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of osteoblast differentiation;positive regulation of programmed cell death;positive regulation of reproductive process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of sulfur metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;programmed cell death;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein localization;protein localization at cell surface;protein oligomerization;proximal/distal pattern formation;regionalization;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of branching involved in lung morphogenesis;regulation of calcium ion import;regulation of calcium ion transport;regulation of cardiac cell fate specification;regulation of cardioblast cell fate specification;regulation of cardioblast differentiation;regulation of cardioblast proliferation;regulation of cartilage development;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell fate commitment;regulation of cell fate specification;regulation of cell proliferation;regulation of cell proliferation involved in heart morphogenesis;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of centriole-centriole cohesion;regulation of centromeric sister chromatid cohesion;regulation of chondrocyte differentiation;regulation of chromosome organization;regulation of chromosome segregation;regulation of cytoskeleton organization;regulation of determination of dorsal identity;regulation of developmental process;regulation of embryonic development;regulation of endothelial cell differentiation;regulation of epithelial cell differentiation;regulation of epithelial cell differentiation involved in kidney development;regulation of epithelial cell proliferation;regulation of epithelial cell proliferation involved in prostate gland development;regulation of fibroblast growth factor receptor signaling pathway;regulation of fibroblast proliferation;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of glycoprotein biosynthetic process;regulation of heart induction;regulation of heart morphogenesis;regulation of heparan sulfate proteoglycan biosynthetic process;regulation of homeostatic process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transport;regulation of kidney development;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of localization;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of mesenchymal cell proliferation;regulation of metabolic process;regulation of metal ion transport;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of mononuclear cell proliferation;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of myelination;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nephron tubule epithelial cell differentiation;regulation of nervous system development;regulation of neural precursor cell proliferation;regulation of neurogenesis;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oligodendrocyte differentiation;regulation of organ formation;regulation of organ morphogenesis;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoclast differentiation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein localization;regulation of protein localization at cell surface;regulation of protein metabolic process;regulation of protein modification process;regulation of protein sumoylation;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of secondary heart field cardioblast proliferation;regulation of signal transduction;regulation of signaling;regulation of sister chromatid cohesion;regulation of smooth muscle cell proliferation;regulation of sulfur metabolic process;regulation of system process;regulation of T cell activation;regulation of T cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmission of nerve impulse;regulation of transport;renal inner medulla development;renal outer medulla development;renal vesicle formation;reproductive process;reproductive structure development;response to cadmium ion;response to chemical stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to growth factor stimulus;response to hormone stimulus;response to indole-3-methanol;response to inorganic substance;response to metal ion;response to organic cyclic compound;response to organic substance;response to steroid hormone stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;Schwann cell proliferation;signal transduction;signaling;skin development;smooth muscle cell differentiation;specification of symmetry;steroid hormone receptor signaling pathway;synapse organization;synaptic vesicle transport;T cell activation;T cell differentiation;T cell differentiation in thymus;thymus development;tissue development;tissue homeostasis;tissue morphogenesis;tongue morphogenesis;trachea formation;transcription, DNA-dependent;transport;tube development;tube formation;tube morphogenesis;vasculogenesis;vesicle-mediated transport;Wnt receptor signaling pathway;Wnt receptor signaling pathway involved in heart development"   androgen receptor binding;binding;chromatin binding;DNA binding;double-stranded DNA binding;enzyme binding;hormone receptor binding;kinase binding;molecular transducer activity;nuclear hormone receptor binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein binding transcription factor activity;protein kinase binding;receptor binding;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding transcription factor activity;signal transducer activity;steroid hormone receptor binding;structural molecule activity;structure-specific DNA binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;transcription regulatory region DNA binding adherens junction;anchoring junction;apical junction complex;apical part of cell;basolateral plasma membrane;beta-catenin destruction complex;beta-catenin-TCF7L2 complex;catenin complex;catenin-TCF7L2 complex;cell cortex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;dendritic shaft;desmosome;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;internal side of plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;lateral plasma membrane;macromolecular complex;membrane;membrane part;microtubule organizing center;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleoplasm part;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;protein-DNA complex;Scrib-APC-beta-catenin complex;spindle pole;synapse;transcription factor complex;Z disc;zonula adherens Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Basal cell carcinoma;Colorectal cancer;Endometrial cancer;Focal adhesion;Leukocyte transendothelial migration;Melanogenesis;Pathogenic Escherichia coli infection;Pathways in cancer;Prostate cancer;Thyroid cancer;Tight junction;Wnt signaling pathway

P39656;E7EWT1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit DDOST >sp|P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4;>tr|E7EWT1|E7EWT1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN 1.14 1.18 1.67 0.9 0.83 0.66 0.92 0.98 4.66E-58 8 18.2 biosynthetic process;carbohydrate metabolic process;cell activation;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glycosylation;immune response;immune system process;innate immune response;intracellular protein transport;intracellular transport;leukocyte activation;lymphocyte activation;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;response to stress;SRP-dependent cotranslational protein targeting to membrane;T cell activation;translation;transport "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;oligosaccharyltransferase complex;organelle membrane;organelle part;protein complex N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis

O00148;Q13838;Q13838-2;F8VQ10;B4DP52;Q5STU3;F6WLT2;O00148-2;H0Y400;F6S4E6;F6UN21;F6TRA5;K7EQN7;B1Q2N1;B4DIJ6;F6UJC5;K7EN69;F6QYI9;K7EPJ3;F6R6M7;K7ENP6;F6QWI5;K7EL56;K7EIL8;F6U6E2;F6S2B7;F6SXL5;E7EMX2;H0YCC6;K7EN25 ATP-dependent RNA helicase DDX39A;Spliceosome RNA helicase DDX39B DDX39A;DDX39B;DDX39 >sp|O00148|DX39A_HUMAN ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2;>sp|Q13838|DX39B_HUMAN Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1;>sp|Q13838-2|DX39B_HUMAN Isoform 2 of Spliceosome RNA helicase DDX39B OS1.27 1.64 1.64 1.99 0.3 0.3 0.51 0.5 1.20E-50 8 16.4 "cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;intronless viral mRNA export from host nucleus;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA export from nucleus;RNA metabolic process;RNA processing;RNA secondary structure unwinding;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;spliceosome assembly;transport;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent protein binding;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;snRNA binding;U4 snRNA binding;U6 snRNA binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex;transcription export complex mRNA surveillance pathway;RNA transport;Spliceosome

P10515;H0YDD4;E9PEJ4;F5H7M3 "Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial" DLAT ">sp|P10515|ODP2_HUMAN Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=1 SV=3;>tr|H0YDD4|H0YDD4_HUMAN Dihydrolipoyllysine-residue acetyltransferase component of pyruvate deh" 0.91 1.62 1.47 1.41 0.77 0.65 0.64 0.98 4.29E-82 8 13.6 acetyl-CoA biosynthetic process;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor catabolic process;cofactor metabolic process;glucose metabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of metabolic process;small molecule metabolic process;tricarboxylic acid cycle "acetyltransferase activity;catalytic activity;dihydrolipoamide S-acyltransferase activity;dihydrolipoyllysine-residue acetyltransferase activity;S-acetyltransferase activity;S-acyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial pyruvate dehydrogenase complex;organelle part;protein complex;pyruvate dehydrogenase complex Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Pyruvate metabolism

Q02487-2;Q02487 Desmocollin-2DSC2 >sp|Q02487-2|DSC2_HUMAN Isoform 2B of Desmocollin-2 OS=Homo sapiens GN=DSC2;>sp|Q02487|DSC2_HUMAN Desmocollin-2 OS=Homo sapiens GN=DSC2 PE=1 SV=1 0.94 1.11 0.7 0.49 1.7 1.38 1.08 1.1 5.27E-44 8 12 biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;desmosome;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Arrhythmogenic right ventricular cardiomyopathy (ARVC)

P29692;P29692-3;P29692-2;E9PRY8;E9PK01;E9PI39;E9PQZ1;P29692-4;E9PMW7;H0YE72;E9PPR1;E9PL12;E9PL71;E9PQ49;E9PN91;H0YE58;E9PIZ1;H0YCK7;E9PNW6;E9PQC9;E9PKK3;E9PK72;E9PJD0;E9PK06 Elongation factor 1-deltaEEF1D >sp|P29692|EF1D_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5;>sp|P29692-3|EF1D_HUMAN Isoform 3 of Elongation factor 1-delta OS=Homo sapiens GN=EEF1D;>sp|P29692-2|EF1D_HUMAN Isoform 2 of Elongation factor 1-delta OS=Homo sapiens GN=EEF 1.52 0.63 1.8 0.41 0.98 0.68 2.04 1.33 8.77E-90 8 37.4 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;translational elongation" "binding;DNA binding;molecular transducer activity;nucleic acid binding;RNA binding;signal transducer activity;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex

P55884;P55884-2;C9JZG1 Eukaryotic translation initiation factor 3 subunit B EIF3B >sp|P55884|EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3;>sp|P55884-2|EIF3B_HUMAN Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B NaN 0.83 0.58 0.68 1.7 0.91 NaN 1.25 4.01E-16 8 13.1 biological regulation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation "binding;nucleic acid binding;nucleotide binding;protein binding;protein complex scaffold;RNA binding;structural molecule activity;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport

Q5T0W9 Protein FAM83B FAM83B >sp|Q5T0W9|FA83B_HUMAN Protein FAM83B OS=Homo sapiens GN=FAM83B PE=1 SV=1 0.95 1.38 0.89 1.92 1.42 0.66 0.74 0.55 2.39E-23 8 9.3

Q13283;F5H4D6;E5RIZ6;E5RH00;D6R9X5;D6R9A4;D6RBM9;D6REX8;D6RBR0;E5RI46;E5RIF8;D6RE13;D6RBW8;E5RH42;Q5HYE9;D6RGJ4;D6RAC7;E5RJU8;D6RB17 Ras GTPase-activating protein-binding protein 1 G3BP1 >sp|Q13283|G3BP1_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1;>tr|F5H4D6|F5H4D6_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=2 SV=1 2.16 0.67 1.09 0.62 1.03 0.65 1.96 1.3 3.93E-86 8 21.9 biological regulation;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;establishment of localization;intracellular signal transduction;metabolic process;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;Ras protein signal transduction;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of Wnt receptor signaling pathway;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;endonuclease activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;hydrolase activity, acting on ester bonds;mRNA binding;nuclease activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;plasma membrane;ribonucleoprotein complex;RNA granule;stress granule

Q92616 Translational activator GCN1 GCN1L1 >sp|Q92616|GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 0.98 NaN 0.78 NaN 1.68 NaN 0.9 NaN 2.16E-19 8 4 biological regulation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome

P00367;B4DGN5;B3KV55;P49448 "Glutamate dehydrogenase 1, mitochondrial;Glutamate dehydrogenase;Glutamate dehydrogenase 2, mitochondrial" GLUD1;GLUD2 ">sp|P00367|DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2;>tr|B4DGN5|B4DGN5_HUMAN Glutamate dehydrogenase OS=Homo sapiens GN=GLUD1 PE=2 SV=1;>tr|B3KV55|B3KV55_HUMAN Glutamate dehydrogenase OS=Homo sapiens GN=GLUD1 PE" 0.65 0.91 1.32 0.35 1.15 0.79 1.6 1.72 2.40E-38 8 15.2 amine biosynthetic process;amine catabolic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutamate biosynthetic process;glutamate catabolic process;glutamate metabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular process;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of secretion;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;amine binding;amino acid binding;ATP binding;binding;carboxylic acid binding;catalytic activity;coenzyme binding;cofactor binding;glutamate dehydrogenase (NAD+) activity;glutamate dehydrogenase [NAD(P)+] activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;identical protein binding;leucine binding;NAD binding;NAD+ binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH2 group of donors;oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;D-Glutamine and D-glutamate metabolism;Nitrogen metabolism;Proximal tubule bicarbonate reclamation"

P16401 Histone H1.5 HIST1H1B >sp|P16401|H15_HUMAN Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 1.12 1.34 0.65 2.88 0.71 0.26 0.42 0.31 5.28E-124 8 35.4 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromatin;chromosomal part;intracellular organelle part;intracellular part;macromolecular complex;nuclear chromatin;nuclear chromosome part;nuclear part;nucleosome;organelle part;protein-DNA complex

P16402;P22492 Histone H1.3 HIST1H1D >sp|P16402|H13_HUMAN Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2 1.13 1.5 0.74 3.05 0.43 0.19 0.39 0.3 8.16E-41 8 36.7 binding of sperm to zona pellucida;cell differentiation;cell motility;cell recognition;cell-cell recognition;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular process involved in reproduction;chromatin organization;chromosome organization;developmental process;gamete generation;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;male gamete generation;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization;reproductive process;sperm motility;spermatogenesis;sperm-egg recognition binding;DNA binding;nucleic acid binding cell part;chromatin;chromosomal part;chromosome;condensed chromosome;condensed nuclear chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome;nuclear chromosome part;nuclear part;nucleosome;organelle;organelle part;protein-DNA complex

P10412 Histone H1.4 HIST1H1E >sp|P10412|H14_HUMAN Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2 0.96 1.19 0.27 3.42 0.37 0.36 0.45 0.29 6.72E-33 8 37 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin assembly;chromatin assembly or disassembly;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;nucleosome positioning;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex

Q99879;Q99877;Q93079;Q5QNW6;P62807;P58876;P57053;O60814;Q5QNW6-2;B4DR52;Q99880 Histone H2B type 1-M;Histone H2B type 1-N;Histone H2B type 1-H;Histone H2B type 2-F;Histone H2B type 1-C/E/F/G/I;Histone H2B type 1-D;Histone H2B type F-S;Histone H2B type 1-K;Histone H2B;Histone H2B type 1-L HIST1H2BM;HIST1H2BN;HIST1H2BH;HIST2H2BF;HIST1H2BC;HIST1H2BD;H2BFS;HIST1H2BK;HIST1H2BL >sp|Q99879|H2B1M_HUMAN Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3;>sp|Q99877|H2B1N_HUMAN Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3;>sp|Q93079|H2B1H_HUMAN Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3;>sp|Q5Q1.01 1.61 0.72 2.74 0.44 0.39 0.35 0.32 1.65E-21 8 46.8 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;defense response;defense response to bacterium;macromolecular complex assembly;macromolecular complex subunit organization;multi-organism process;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization;response to bacterium;response to biotic stimulus;response to other organism;response to stimulus;response to stress binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus

P62805 Histone H4 HIST1H4A >sp|P62805|H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 1.09 1.62 0.9 3 0.38 0.41 0.34 0.33 4.09E-167 8 58.3 anatomical structure homeostasis;ATP-dependent chromatin remodeling;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;DNA metabolic process;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;histone exchange;homeostatic process;inositol lipid-mediated signaling;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of megakaryocyte differentiation;negative regulation of myeloid cell differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;phosphatidylinositol-mediated signaling;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biological quality;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of megakaryocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;response to stimulus;signal transduction;telomere maintenance;telomere organization binding;DNA binding;nucleic acid binding actin cytoskeleton;cell part;chromosomal part;cytoskeleton;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleosome;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus

G3V5V7 HNRNPC >tr|G3V5V7|G3V5V7_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=2 SV=1 1.11 1.29 1.92 2.18 0.56 0.53 0.5 0.48 2.18E-154 8 41.1

O60812 Heterogeneous nuclear ribonucleoprotein C-like 1 HNRNPCL1 >sp|O60812|HNRCL_HUMAN Heterogeneous nuclear ribonucleoprotein C-like 1 OS=Homo sapiens GN=HNRNPCL1 PE=1 SV=1 1.02 1.38 1.87 2.56 0.41 0.4 0.42 0.49 4.54E-144 8 24.6 binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex

Q9NSB2;CON__Q9NSB2;CON__Q6ISB0 "Keratin, type II cuticular Hb4" KRT84 ">sp|Q9NSB2|KRT84_HUMAN Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=2 SV=2;>Q9NSB2 SWISS-PROT:Q9NSB2 Keratin, type II cuticular Hb4 (Hair keratin, type II Hb4) - Homo sapiens (Human).;>Q6ISB0 TREMBL:Q6ISB0 Keratin, hair, basic, 4 - Homo sapie" 1.16 1.1 1.47 NaN 0.62 NaN 0.82 0.98 6.86E-33 8 8 anatomical structure development;biological regulation;developmental process;epidermis development;hair cycle process;hair follicle development;molting cycle;molting cycle process;multicellular organismal process;nail development;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of keratinocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;tissue development structural constituent of cytoskeleton;structural constituent of epidermis;structural molecule activitycell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P07942;G3XAI2;E7EPA6 Laminin subunit beta-1 LAMB1 >sp|P07942|LAMB1_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2;>tr|G3XAI2|G3XAI2_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1 1.44 1.4 1.18 0.79 0.44 0.36 0.76 1.09 1.25E-61 8 6.7 anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;cell adhesion;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-substrate adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;chemotaxis;developmental process;embryo implantation;locomotion;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;odontogenesis;organ morphogenesis;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of epithelial cell proliferation;positive regulation of locomotion;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of epithelial cell proliferation;regulation of localization;regulation of locomotion;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;substrate adhesion-dependent cell spreading;taxis binding;extracellular matrix structural constituent;glycolipid binding;glycosphingolipid binding;lipid binding;sphingolipid binding;structural molecule activity cell part;cytoplasmic part;extracellular matrix

part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular part;laminin complex;laminin-1 complex;laminin-10 complex;laminin-2 complex;laminin-8 complex;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;perinuclear region of cytoplasm;plasma membrane part;protein complex;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis
P47929 Galectin-7 LGALS7 >sp|P47929|LEG7_HUMAN Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2 0.89 1.58 1.42 1.41 0.75 0.74 0.92 1.17 1.26E-268 8 61.8 apoptosis;biological adhesion;cell adhesion;cell death;cell-cell adhesion;cellular process;death;heterophilic cell-cell adhesion;programmed cell death binding;carbohydrate binding cell part;cytoplasm;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle
Q16706 Alpha-mannosidase 2 MAN2A1 >sp|Q16706|MA2A1_HUMAN Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2 1.48 1.26 1.16 1.08 2.77 0.6 1 1.01 1.15E-25 8 8.9 alcohol metabolic process;anatomical structure development;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;glycosylation;hexose metabolic process;in utero embryonic development;liver development;lung alveolus development;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;mannose metabolic process;metabolic process;mitochondrion organization;monosaccharide metabolic process;multicellular organismal process;N-glycan processing;oligosaccharide metabolic process;organ development;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;respiratory gaseous exchange;small molecule metabolic process;vacuole organization "binding;carbohydrate binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing N-glycosyl compounds;hydrolase activity, hydrolyzing O-glycosyl compounds;ion binding;mannosidase activity;mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity;mannosyl-oligosaccharide mannosidase activity;metal ion binding;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part N-Glycan biosynthesis;Various types of N-glycan biosynthesis
Q3KQU3-4;Q3KQU3;Q3KQU3-2;Q3KQU3-3;C9JIR3;E9PLH3;H0YF21 MAP7 domain-containing protein 1 MAP7D1 >sp|Q3KQU3-4|MA7D1_HUMAN Isoform 4 of MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1;>sp|Q3KQU3|MA7D1_HUMAN MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1;>sp|Q3KQU3-2|MA7D1_HUMAN Isoform 2 of MAP7 domain-containing protei 1 0.72 0.79 0.59 2.67 1.39 1.06 1.32 1.73E-19 8 15.2 cell part;cytoplasm;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;spindle
P46013-2;P46013 Antigen KI-67 MKI67 >sp|P46013-2|KI67_HUMAN Isoform Short of Antigen KI-67 OS=Homo sapiens GN=MKI67;>sp|P46013|KI67_HUMAN Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 1.35 2.19 0.96 3.24 0.32 0.29 0.46 0.18 8.02E-18 8 5.8 anatomical structure morphogenesis;cell cycle phase;cell cycle process;cell proliferation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;macromolecule metabolic process;meiosis;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ morphogenesis;organ regeneration;primary metabolic process;regeneration;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding "cell part;chromosomal part;chromosome;chromosome, centromeric region;condensed chromosome;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part"
Q15233-2;Q15233;H7C367;C9JYS8;C9IZL7 Non-POU domain-containing octamer-binding protein NONO >sp|Q15233-2|NONO_HUMAN Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO;>sp|Q15233|NONO_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4;>tr|H7C367|H7C367_HUMAN Non-POU domain- 1.19 1.04 1.19 1.73 0.63 0.52 0.83 0.88 2.85E-45 8 22.5 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA recombination;DNA repair;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;paraspeckles
Q9Y2X3;H7BZ72;F8WED0;REV__Q9Y2X3 Nucleolar protein 58 NOP58 >sp|Q9Y2X3|NOP58_HUMAN Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 0.97 1.15 1.32 2.18 0.52 0.57 0.63 0.65 2.25E-61 8 18.5 cell growth;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;growth;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;snRNP protein import into nucleus;transport binding;nucleic acid

binding;RNA binding;snoRNA binding box C/D snoRNP complex;Cajal body;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nucleolar part;nucleoplasm part;organelle part;pre-snoRNP complex;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes

P06748-2;P06748;P06748-3;E5RGW4;Q9C0A0-2;F5H107;Q9C0A0;E9PDN6 Nucleophosmin NPM1 >sp|P06748-2|NPM_HUMAN Isoform 2 of Nucleophosmin OS=Homo sapiens GN=NPM1;>sp|P06748|NPM_HUMAN Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2;>sp|P06748-3|NPM_HUMAN Isoform 3 of Nucleophosmin OS=Homo sapiens GN=NPM1 1.24 1.12 1.78 1.43 1.06 0.3 0.81 0.66 3.72E-83 8 38.5 "aging;ATP-dependent chromatin remodeling;biological adhesion;biological regulation;cell adhesion;cell aging;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;centrosome cycle;centrosome organization;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;developmental process;DNA metabolic process;DNA repair;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;establishment of localization;establishment of localization in cell;establishment of protein localization;histone exchange;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule organizing center organization;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of centrosome duplication;negative regulation of organelle organization;negative regulation of programmed cell death;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;nucleosome assembly;nucleosome organization;organelle assembly;organelle organization;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein transport;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of centriole replication;regulation of centrosome cycle;regulation of centrosome duplication;regulation of cytoskeleton organization;regulation of deoxyribonuclease activity;regulation of endodeoxyribonuclease activity;regulation of endoribonuclease activity;regulation of gene expression;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of ribonuclease activity;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;signal transduction;transport;viral reproduction;viral reproductive process;virus-host interaction" binding;histone binding;identical protein binding;NF-kappaB binding;nucleic acid binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein heterodimerization activity;protein homodimerization activity;ribonucleoprotein binding;ribosomal large subunit binding;ribosomal small subunit binding;RNA binding;Tat protein binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;unfolded protein binding cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spindle pole centrosome

P00558;B7Z7A9;E7ERH5;P07205 Phosphoglycerate kinase 1;Phosphoglycerate kinase PGK1 >sp|P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3;>tr|B7Z7A9|B7Z7A9_HUMAN Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1;>tr|E7ERH5|E7ERH5_HUMAN Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1 0.14 11.21 0.12 8.06 0.12 1.75 0.22 0.86 8.23E-27 8 20.9 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphoglycerate kinase activity;phosphotransferase activity, carboxyl group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis

Q3MJ16-2;C9JK77;Q3MJ16;B7WPN2 Cytosolic phospholipase A2 epsilon PLA2G4E >sp|Q3MJ16-2|PA24E_HUMAN Isoform 2 of Cytosolic phospholipase A2 epsilon OS=Homo sapiens GN=PLA2G4E;>tr|C9JK77|C9JK77_HUMAN Cytosolic phospholipase A2 epsilon OS=Homo sapiens GN=PLA2G4E PE=2 SV=1;>sp|Q3MJ16|PA24E_HUMAN Cytosolic phospholipase A2 epsilon OS 0.62 0.9 0.87 0.33 2.76 3.05 1.18 0.5 3.07E-49 8 17.7 biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;metabolic process;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid catabolic process;phospholipid metabolic process;primary metabolic process "binding;carboxylic ester hydrolase activity;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lipase activity;metal ion binding;phospholipase A2 activity;phospholipase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;lysosomal membrane;membrane;organelle membrane;organelle part;vacuolar membrane;vacuolar part alpha-Linolenic acid metabolism;Arachidonic acid metabolism;Ether lipid metabolism;Fat digestion and absorption;Fc epsilon RI signaling pathway;Glycerophospholipid metabolism;GnRH signaling pathway;Linoleic acid metabolism;Long-term depression;MAPK signaling pathway;Pancreatic secretion;Toxoplasmosis;Vascular smooth muscle contraction;VEGF signaling pathway

Q9H0U4;E9PLD0;P62820;B7Z8M7;Q92928;P62820-2;E7END7;H0YMN7;P62820-3;E7ETK2;H0YNE9;F5GY21;Q92930;B4DEK7 Ras-related protein Rab-1B;Ras-related protein Rab-1A;Putative Ras-related protein Rab-1CRAB1B;RAB1A;RAB1C >sp|Q9H0U4|RAB1B_HUMAN Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1;>tr|E9PLD0|E9PLD0_HUMAN Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=2 SV=1;>sp|P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3; 0.84 1.63 0.71 0.83 1.01 1.38 0.85 0.94 1.80E-133 8 43.8 adherens junction organization;biological regulation;cell cycle phase;cell cycle process;cell junction organization;cell-cell junction organization;cellular component organization;cellular component organization or biogenesis;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to peroxisome;intracellular protein transport;intracellular signal transduction;intracellular transport;M phase;M phase of mitotic cell cycle;mitotic prophase;peroxisomal transport;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of corticotropin secretion;positive regulation of hormone secretion;positive regulation of secretion;positive regulation of transport;prophase;protein import;protein import into peroxisome membrane;protein targeting;protein targeting to membrane;protein targeting to peroxisome;protein transport;regulation of biological process;regulation of cell communication;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of corticotropin secretion;regulation of endocrine process;regulation of hormone secretion;regulation of localization;regulation of multicellular organismal process;regulation of secretion;regulation of signaling;regulation of system process;regulation of transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cell pole;cell tip;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;microbody;microbody membrane;microbody part;mitochondrion;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;peroxisomal membrane;peroxisomal part;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;vesicle;vesicle membrane

P54136;P54136-2;E5RJM9;E5RH09;F5H3T8 "Arginine--tRNA ligase, cytoplasmic" RARS ">sp|P54136|SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2;>sp|P54136-2|SYRC_HUMAN Isoform Monomeric of Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS;>tr|E5RJM9|E5RJM9_HUMAN Arginine--tRNA ligase, cytoplasmic OS" 1.28 1.04 0.69 0.77 2.05 1.03 1.34 1.12 9.03E-26 8 14.4 amine metabolic process;amino acid activation;arginyl-tRNA aminoacylation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;aminoacyl-tRNA ligase activity;arginine binding;arginine-tRNA ligase activity;ATP binding;binding;carboxylic acid binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nucleus;organelle;protein complex Aminoacyl-tRNA biosynthesis

P39023;G5E9G0;B5MCW2;H7C3M2;H7C422;F8WCR1;Q92901 60S ribosomal protein L3 RPL3 >sp|P39023|RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2;>tr|G5E9G0|G5E9G0_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=2 SV=1;>tr|B5MCW2|B5MCW2_HUMAN 60S ribosomal protein L3 (Fragment) OS=Homo sapiens GN=RPL3 PE=2 SV=11.35 0.72 0.5 0.63 1.22 1.01 1.43 1.01 1.75E-34 8 19.1 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

P18124;A8MUD9;C9JZ88;C9JIJ5 60S ribosomal protein L7 RPL7 >sp|P18124|RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1;>tr|A8MUD9|A8MUD9_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=2 SV=1 1.39 0.66 1.32 0.52 2.41 0.91 1.47 0.93 3.56E-102 8 31.9

"biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;DNA binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome

M0QZC5;P62280;M0R1H6;M0R1H5 40S ribosomal protein S11 RPS11 >tr|M0QZC5|M0QZC5_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=4 SV=1;>sp|P62280|RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3;>tr|M0R1H6|M0R1H6_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=4 SV=1 1.67 0.98 0.86 0.57 0.96 0.59 0.96 0.63 8.01E-16 8 47.5 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

Q15424;Q15424-4;Q15424-3;Q15424-2;F5GZU3;B7Z2F6;K7ES42 Scaffold attachment factor B1 SAFB >sp|Q15424|SAFB1_HUMAN Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4;>sp|Q15424-4|SAFB1_HUMAN Isoform 4 of Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB;>sp|Q15424-3|SAFB1_HUMAN Isoform 3 of Scaffold attachment factor B1 OS=Homo s 1.15 1.28 1.19 2.32 1.48 0.4 0.54 0.59 6.15E-74 8 10.2 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chromatin organization;chromosome organization;estrogen receptor signaling pathway;growth;hormone metabolic process;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of hormone levels;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;steroid hormone receptor signaling pathway;transcription, DNA-dependent" binding;chromatin binding;core promoter binding;DNA binding;double-stranded DNA binding;nucleic acid binding;nucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;structure-specific DNA binding;transcription regulatory region DNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

P05120;H7C004;H7BYS2;E7ERB5;E7EPJ9;E9PDK7 Plasminogen activator inhibitor 2 SERPINB2;SERPINB10 >sp|P05120|PAI2_HUMAN Plasminogen activator inhibitor 2 OS=Homo sapiens GN=SERPINB2 PE=1 SV=2;>tr|H7C004|H7C004_HUMAN Serpin B10 (Fragment) OS=Homo sapiens GN=SERPINB10 PE=3 SV=1;>tr|H7BYS2|H7BYS2_HUMAN Serpin B10 (Fragment) OS=Homo sapiens GN=SERPINB10 PE 0.89 0.75 0.46 0.1 2.58 2.46 1.18 0.47 2.05E-43 8 21.4 biological regulation;blood coagulation;coagulation;fibrinolysis;hemostasis;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood coagulation;negative regulation of cell death;negative regulation of cellular process;negative regulation of coagulation;negative regulation of multicellular organismal process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of blood coagulation;regulation of body fluid levels;regulation of cell death;regulation of cellular process;regulation of coagulation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of proteolysis;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of wound healing;response to stimulus;response to stress;response to wounding;wound healing endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasm;extracellular region;extracellular region part;extracellular space;intracellular part;membrane;plasma membrane Amoebiasis

Q13435;E9PPJ0;E9PJ04;H0YCG1;E9PJT3;E9PIL8;H0YEX5 Splicing factor 3B subunit 2 SF3B2 >sp|Q13435|SF3B2_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2;>tr|E9PPJ0|E9PPJ0_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=2 SV=1;>tr|E9PJ04|E9PJ04_HUMAN Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens G 1.38 0.8 1.13 1.45 2.52 0.44 0.92 0.76 2.44E-20 8 11.3 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;reproductive process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;viral reproductive process;virus-host interaction" binding;nucleic acid binding catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome

Q9Y6N5;H3BNX3;H3BNP9;H3BMS6;H3BV36 "Sulfide:quinone oxidoreductase, mitochondrial" SQRDL ">sp|Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1;>tr|H3BNX3|H3BNX3_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1" 0.84 1.26 1.79 0.49 0.72 0.68 1.06 1.51 9.30E-173 8 23.3 "amine catabolic process;amine metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;sulfide oxidation;sulfide oxidation, using sulfide:quinone oxidoreductase;sulfur amino acid catabolic process;sulfur amino acid metabolic process;sulfur compound catabolic process;sulfur compound metabolic process" "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, quinone or similar compound as acceptor;sulfide:quinone oxidoreductase activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

B4E1K7;Q9UJZ1;F2Z2I8 "Stomatin-like protein 2, mitochondrial" STOML2 ">tr|B4E1K7|B4E1K7_HUMAN Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=2 SV=1;>sp|Q9UJZ1|STML2_HUMAN Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1" 1.12 1.6 1.31 1.69 0.6 0.59 0.61 0.83 1.12E-87 8 39.2 "activation of immune response;alpha-beta T cell activation;antigen receptor-mediated signaling pathway;ATP biosynthetic process;ATP metabolic process;ATP synthesis coupled proton transport;biological regulation;biosynthetic process;calcium ion homeostasis;calcium ion transport;cation homeostasis;cation transport;CD4-positive, alpha-beta T cell activation;cell activation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chemical homeostasis;cytokine production;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;heterocycle biosynthetic process;heterocycle metabolic process;homeostatic process;hydrogen transport;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;interleukin-2 production;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;leukocyte activation;lipid localization;localization;lymphocyte activation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;mitochondrial ATP synthesis coupled proton transport;mitochondrial calcium ion transport;mitochondrial protein processing;mitochondrial transport;monovalent inorganic cation transport;multicellular organismal process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of DNA-dependent DNA replication;positive regulation of immune response;positive regulation of immune system process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of membrane potential;positive regulation of metabolic process;positive regulation of mitochondrial DNA replication;positive regulation of mitochondrial membrane potential;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;primary metabolic process;protein complex assembly;protein complex subunit organization;protein maturation;protein metabolic process;protein oligomerization;protein processing;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of immune response;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of mitochondrial DNA replication;regulation of mitochondrial membrane potential;regulation of mitochondrion organization;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of response to stimulus;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;T cell activation;T cell receptor signaling pathway;transmembrane transport;transport" binding;protein binding;receptor binding cell part;cytoplasmic part;cytoskeleton;extrinsic to membrane;extrinsic to plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;organelle;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part;plasma membrane part

P22695;H3BRG4;H3BSJ9;H3BP04;H3BUE4;H3BUI9 "Cytochrome b-c1 complex subunit 2, mitochondrial" UQCRC2">sp|P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3;>tr|H3BRG4|H3BRG4_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=2 SV=1;>tr|H3BSJ9|H3BSJ9_HUMAN Cytochrome b-c1" 1.15 1.55 1.51 1.85 0.43 0.4 0.58 0.94 6.03E-243 8 24.7 aerobic respiration;cellular metabolic process;cellular process;cellular respiration;electron transport chain;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;macromolecule metabolic process;metabolic process;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein metabolic process;proteolysis;respiratory electron transport chain;small molecule metabolic process"binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex III;organelle inner membrane;organelle membrane;organelle part;protein complex;respiratory chain complex III Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q9BVJ6-3;Q9BVJ6;F8WD00;Q9BVJ6-2;Q5TAP6 U3 small nucleolar RNA-associated protein 14 homolog A UTP14A >sp|Q9BVJ6-3|UT14A_HUMAN Isoform 3 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A;>sp|Q9BVJ6|UT14A_HUMAN U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1;>tr|F8WD00|F8WD00_HUMAN 0.94 0.87 1.69 2 0.56 0.27 0.46 0.8 2.01E-25 8 14.9 cell cycle phase;cell cycle process;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;gamete generation;macromolecule metabolic process;male gamete generation;meiosis;metabolic process;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;reproductive process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;spermatogenesis cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;ribonucleoprotein complex;small-subunit processomeRibosome biogenesis in eukaryotes

P13010 X-ray repair cross-complementing protein 5 XRCC5 >sp|P13010|XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 1.41 0.42 0.85 0.54 1.38 0.41 2.09 1.02 4.94E-18 8 13.3 "anatomical structure homeostasis;biological regulation;biosynthetic process;cell differentiation;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;developmental process;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via nonhomologous end joining;hemopoietic stem cell differentiation;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of neurogenesis;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;stem cell differentiation;telomere maintenance;telomere organization;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;damaged DNA binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;double-stranded DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;sequence-specific DNA binding;structure-specific DNA binding;telomeric DNA binding;transcription regulatory region DNA binding" cell part;chromosomal part;cytoplasm;intracellular organelle part;intracellular part;Ku70:Ku80 complex;macromolecular complex;nonhomologous end joining complex;nuclear chromosome part;nuclear part;nuclear telomere cap complex;nucleoplasm;organelle part;protein complex;protein-DNA complex;telomere cap complex Non-homologous end-joining

P63104;E7EX29;E5RIR4;E9PD24;E7EVZ2;B7Z2E6;H0YB80;E7ESK7;B0AZS6;P63104-2;E7EX24;E5RGE1 14-3-3 protein zeta/delta YWHAZ >sp|P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1;>tr|E7EX29|E7EX29_HUMAN 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1;>tr|E5RIR4|E5RIR4_HUMAN 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens 1.33 0.85 0.81 0.76 0.56 0.52 1.94 1.25 0 8 38.8 amine transport;biological regulation;cell activation;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;gene expression;histamine secretion;histamine secretion by mast cell;histamine secretion involved in inflammatory response;histamine transport;hormone secretion;hormone transport;intracellular protein transport;intracellular transport;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial transport;mRNA metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nitrogen compound transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic substance transport;platelet activation;primary metabolic process;protein import;protein targeting;protein targeting to mitochondrion;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;regulation of hormone levels;regulation of programmed cell death;RNA metabolic process;secretion;secretion by cell;signal release;transport "catalytic activity;kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell leading edge;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;nuclear part;nucleoplasm;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;pigment granule;postsynaptic density;protein complex;synapse part;vesicle;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis

Q9UHD8-3;Q9UHD8-7;Q9UHD8-2;Q9UHD8-5;Q9UHD8;K7EL40;Q9UHD8-4;Q9UHD8-9;Q9UHD8-8;K7EK18;K7EJ51;K7ER52;K7EIE4;K7ER14;K7EQD7;K7ELJ9;K7EJL9;K7ERG1;K7EIR4;K7EKN4;K7EN52;K7ENQ5;K7EJZ2;B7Z686;B1AHR1;Q9UH03-2;Q9UH03 Septin-9 41891 >sp|Q9UHD8-3|SEPT9_HUMAN Isoform 3 of Septin-9 OS=Homo sapiens GN=SEPT9;>sp|Q9UHD8-7|SEPT9_HUMAN Isoform 7 of Septin-9 OS=Homo sapiens GN=SEPT9;>sp|Q9UHD8-2|SEPT9_HUMAN Isoform 2 of Septin-9 OS=Homo sapiens GN=SEPT9;>sp|Q9UHD8-5|SEPT9_HUMAN Isoform 5 of Se 1.62 1.02 0.76 0.82 0.88 0.86 1.67 1.14 1.27E-24 9 26.5 cell cycle;cell division;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular process;cytokinesis;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin filament bundle;actomyosin;cell cortex part;cell junction;cell part;cytoplasmic part;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;microtubule;organelle part;perinuclear region of cytoplasm;protein complex;septin complex;stress fiber;synapse

E7EQT4;Q9UKV3;Q9UKV3-5;G3V3B0;Q9UKV3-3;Q9UKV3-2;REV__H0Y7L4;REV__B1AK53-2;REV__G3V3B0;REV__Q9UKV3-3;REV__Q9UKV3-2;REV__B1AK53 Apoptotic chromatin condensation inducer in the nucleus ACIN1 >tr|E7EQT4|E7EQT4_HUMAN Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=2 SV=2;>sp|Q9UKV3|ACINU_HUMAN Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2;>sp|Q9UKV3-5|ACINU_HUMAN Is 1.26 1.34 1.73 2.24 0.51 0.52 0.64 0.65 6.03E-44 9 9.5 apoptotic chromosome condensation;biological regulation;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome condensation;chromosome organization;developmental process;DNA conformation change;DNA metabolic process;DNA packaging;erythrocyte differentiation;macromolecule metabolic process;metabolic process;myeloid cell differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of monocyte differentiation;positive regulation of myeloid cell differentiation;positive regulation of myeloid leukocyte differentiation;primary metabolic process;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of monocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation "ATPase activity;binding;catalytic activity;enzyme binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;pyrophosphatase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part mRNA surveillance pathway;RNA transport;Spliceosome

Q9Y4W6;K7EP56;B7Z651;E9PHW9;Q01484-5;Q01484-2;I6L894;Q01484 AFG3-like protein 2 AFG3L2 >sp|Q9Y4W6|AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 0.8 1.49 1.41 1.57 0.54 0.52 0.79 1.03 2.52E-44 9 11.4 anatomical structure development;anatomical structure morphogenesis;atrial septum development;axon ensheathment;axon guidance;axonogenesis;biological regulation;calcium ion homeostasis;calcium ion transport;calcium-mediated signaling;cardiac muscle contraction;cardiac septum development;catabolic process;cation homeostasis;cation transport;cell death;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to stimulus;chemical homeostasis;chemotaxis;cristae formation;death;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;ensheathment of neurons;establishment of localization;establishment of localization in cell;establishment of protein

localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;homeostatic process;inner mitochondrial membrane organization;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;ion transport;localization;locomotion;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;membrane fusion;membrane organization;metabolic process;metal ion homeostasis;metal ion transport;mitochondrial fusion;mitochondrial membrane organization;mitochondrial protein processing;mitochondrion organization;multicellular organismal process;muscle contraction;muscle system process;myelination;nerve development;neuromuscular junction development;neuron projection morphogenesis;organelle fusion;organelle organization;plasma membrane organization;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of gene expression;positive regulation of ion transport;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of potassium ion transport;positive regulation of transport;posttranscriptional regulation of gene expression;primary metabolic process;protein catabolic process;protein localization;protein localization at cell surface;protein localization in endoplasmic reticulum;protein localization in membrane;protein localization in plasma membrane;protein localization to organelle;protein maturation;protein metabolic process;protein processing;protein stabilization;protein targeting;protein targeting to plasma membrane;protein transport;proteolysis;reflex;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cellular localization;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of heart contraction;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transport;regulation of localization;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of membrane repolarization;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of potassium ion transport;regulation of protein stability;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of striated muscle contraction;regulation of system process;regulation of transport;regulation of ventricular cardiomyocyte membrane repolarization;response to chemical stimulus;response to external stimulus;response to stimulus;righting reflex;sarcoplasmic reticulum calcium ion transport;second-messenger-mediated signaling;signal transduction;striated muscle contraction;synapse organization;system process;taxis;transport;T-tubule organization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase binding;binding;binding, bridging;catalytic activity;cation binding;channel regulator activity;endopeptidase activity;enzyme binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;ion channel binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;potassium channel regulator activity;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transition metal ion binding;unfolded protein binding;zinc ion binding" apical plasma membrane;basolateral plasma membrane;cell junction;cell part;cell-cell contact zone;cell-cell junction;contractile fiber part;costamere;cytoplasmic part;cytoskeleton;cytosol;integral to membrane;integral to plasma membrane;intercalated disc;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;M band;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;non-membrane-bounded organelle;organelle;organelle inner membrane;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;postsynaptic membrane;synapse part;synaptic membrane;T-tubule;Z disc
K7EJT8;P63010;P63010-2;Q7Z451;Q10567-4;Q10567-3;Q10567-2;Q10567;C9J1E7;K7ERE4;K7EKZ5;K7EJX1;K7EN71;K7ERB2;K7EJ01;H7C034 AP-2 complex subunit beta;AP-1 complex subunit beta-1 AP2B1;AP1B1 >tr|K7EJT8|K7EJT8_HUMAN AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=4 SV=1;>sp|P63010|AP2B1_HUMAN AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1;>sp|P63010-2|AP2B1_HUMAN Isoform 2 of AP-2 complex subunit beta OS=Homo sapiens GN=AP2B 0.6 1.18 0.43 1.04 1.16 0.74 1.21 1.07 2.54E-20 9 11.9 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;cellular protein complex assembly;cellular response to stimulus;chemotaxis;clathrin coat assembly;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;organelle organization;post-Golgi vesicle-mediated transport;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of epidermal growth factor receptor signaling pathway;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;synaptic transmission;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle coating;vesicle organization;vesicle-mediated transport;viral reproduction protein transporter activity;substrate-specific transporter activity;transporter activity AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;clathrin coated vesicle membrane;clathrin-coated endocytic vesicle membrane;coated pit;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endocytic vesicle membrane;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;lysosomal membrane;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;plasma membrane;protein complex;trans-Golgi network;trans-Golgi network membrane;vacuolar membrane;vacuolar part;vesicle membrane Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease;Lysosome
P23634-7;P23634-6;P23634-8;P23634;P23634-5;P23634-4;P23634-3;P23634-2;P20020-5;P20020-2;P20020-6;P20020-3;P20020-4;P20020;E7ERY9;Q16720-8;Q16720-7;Q16720-6;Q16720-3;Q16720-5;Q16720-2;Q16720-4;Q16720;H0Y7S3;Q01814-4;Q01814-7;Q01814-3;Q01814-6;Q01814-2;Q01814-8;Q01814-5;Q01814 Plasma membrane calcium-

transporting ATPase 4 ATP2B4 >sp|P23634-7|AT2B4_HUMAN Isoform ZB of Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4;>sp|P23634-6|AT2B4_HUMAN Isoform XB of Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4;>sp|P23634-8|AT2B4_HUMAN Isoform Z 0.93 1.04 0.77 0.33 2.27 1.86 1.14 0.7 6.40E-126 9 12.4 amine metabolic process;anatomical structure development;auditory receptor cell stereocilium organization;behavior;biological regulation;biomineral tissue development;blood coagulation;body fluid secretion;calcium ion homeostasis;cation homeostasis;cell differentiation;cell differentiation in hindbrain;cell projection organization;cellular amine metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine metabolic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;central nervous system neuron differentiation;cerebellar granule cell differentiation;cerebellar Purkinje cell differentiation;cGMP metabolic process;chemical homeostasis;coagulation;cochlea development;cyclic nucleotide metabolic process;cytosolic calcium ion homeostasis;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection of mechanical stimulus involved in sensory perception;detection of mechanical stimulus involved in sensory perception of sound;detection of stimulus;detection of stimulus involved in sensory perception;developmental process;divalent inorganic cation homeostasis;establishment of localization;hemostasis;heterocycle metabolic process;homeostatic process;indolalkylamine metabolic process;indole-containing compound metabolic process;inner ear receptor stereocilium organization;ion homeostasis;lactation;locomotion;locomotory behavior;metabolic process;metal ion homeostasis;multicellular organismal process;multicellular organismal reproductive process;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organelle organization;otolith mineralization;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of ion transport;positive regulation of transport;primary metabolic process;purine nucleotide metabolic process;purine-containing compound metabolic process;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of calcium ion transport;regulation of cell communication;regulation of cell size;regulation of cellular component size;regulation of cellular process;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of multicellular organismal process;regulation of neurological system process;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;reproductive process;response to abiotic stimulus;response to external stimulus;response to mechanical stimulus;response to stimulus;secretion;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;serotonin metabolic process;small molecule metabolic process;synapse organization;system process;tissue development;transport "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;calcium ion binding;calcium ion transmembrane transporter activity;calcium-dependent ATPase activity;calcium-transporting ATPase activity;calmodulin binding;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;divalent inorganic cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;metal ion transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;PDZ domain binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;protein domain specific binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" apical plasma membrane;cell body;cell part;cell projection;cilium;cytoplasm;cytoplasmic part;endoplasmic reticulum;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;neuronal cell body;organelle;plasma membrane;plasma membrane partCalcium signaling pathway;Pancreatic secretion;Salivary secretion

Q9UQB8-3;Q9UQB8-5;Q9UQB8-4;Q9UQB8-6;Q9UQB8-2;Q9UQB8;I3L4C2;F8W878;I3L327;I3L2M4;I3L125;I3L1C8;B4DWA1;I3L4A3;I3L526;I3L3C5;I3L0Y9;I3L0M4;I3L3J7;I3L3C6;I3L2J6;I3L113 Brain-specific angiogenesis inhibitor 1-associated protein 2BAIAP2 >sp|Q9UQB8-3|BAIP2_HUMAN Isoform 3 of Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2;>sp|Q9UQB8-5|BAIP2_HUMAN Isoform 5 of Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2;>sp|Q9 1.27 0.91 1.19 0.43 2.24 2.21 1.17 0.66 1.05E-24 9 21.9 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;anatomical structure development;anatomical structure morphogenesis;axonogenesis;biological regulation;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytoskeleton organization;defense response;dendrite development;developmental process;enzyme linked receptor protein signaling pathway;filopodium assembly;immune response;immune system process;innate immune response;insulin receptor signaling pathway;microspike assembly;multi-organism process;neuron projection development;neuron projection morphogenesis;organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of multicellular organismal process;regulation of neurological system process;regulation of organelle organization;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to other organism;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway "binding;binding, bridging;cytoskeletal adaptor activity;cytoskeletal protein binding;proline-rich region binding;protein binding;protein binding, bridging;protein C-terminus binding" cell junction;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;filopodium;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nucleus;organelle;plasma membrane;ruffle Adherens junction;Regulation of actin cytoskeleton

F8VQ14;F5GWF6;P78371;P78371-2 T-complex protein 1 subunit beta CCT2 >tr|F8VQ14|F8VQ14_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=1;>tr|F5GWF6|F5GWF6_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=2 SV=2;>sp|P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN= 0.73 1.83 0.55 1.41 0.52 0.88 0.88 1.03 9.25E-61 9 31.2 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chaperone-mediated protein complex assembly;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;nucleus;organelle;organelle part;protein complex

P49368;B4DUR8;P49368-2;Q5SZX9;E9PRC8;Q5SZX6;E9PM09 T-complex protein 1 subunit gamma CCT3 >sp|P49368|TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4;>tr|B4DUR8|B4DUR8_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=2 SV=1;>sp|P49368-2|TCPG_HUMAN Isoform 2 of T-complex protein 1 subunit gamma OS= 0.86 1.25 0.4 1.03 0.85 1 0.99 0.98 6.12E-60 9 20.4 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;organelle part;plasma membrane;protein complex

O60716-24;O60716-23;O60716-21;O60716-19;O60716-22;O60716-20;O60716-16;O60716-18;O60716-15;O60716-17;O60716-13;O60716-11;O60716-14;O60716-12;O60716-10;O60716-8;O60716-9;O60716-7;O60716-5;C9JZR2;O60716-3;O60716-6;O60716-4;O60716-2;O60716;O60716-32;O60716-31;O60716-29;O60716-27;O60716-30;O60716-28;O60716-26;O60716-25;E9PRE2;H0YC95 Catenin delta-1 CTNND1>sp|O60716-24|CTND1_HUMAN Isoform 3 of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716-23|CTND1_HUMAN Isoform 3C of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716-21|CTND1_HUMAN Isoform 3A of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716- 1.01 1.17 1.15 0.88 1.01 0.86 0.93 0.77 6.92E-25 9 15.5 "adherens junction organization;anatomical structure morphogenesis;biological adhesion;biological regulation;biosynthetic process;cell adhesion;cell differentiation;cell differentiation involved in salivary gland development;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell junction organization;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;developmental process;epidermal cell differentiation;epithelial cell differentiation;epithelial cell differentiation involved in salivary gland development;gland morphogenesis;keratinocyte differentiation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;morphogenesis of a polarized epithelium;morphogenesis of an epithelium;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;response to stimulus;RNA biosynthetic process;RNA metabolic process;salivary gland morphogenesis;signal transduction;tissue morphogenesis;transcription, DNA-dependent;Wnt receptor signaling pathway" adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane;membrane-bounded organelle;midbody;nucleus;organelle;plasma membrane Adherens junction;Leukocyte transendothelial migration

Q92499 ATP-dependent RNA helicase DDX1 DDX1 >sp|Q92499|DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 0.94 1.3 0.64 1.01 1.24 1.04 1.04 1.02 4.48E-19 9 15 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;developmental process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA repair;double-strand break repair;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;response to biotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA biosynthetic process;RNA metabolic process;spliceosome assembly;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;chromatin binding;DNA binding;DNA/RNA helicase activity;double-stranded RNA binding;exonuclease activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;hydrolase activity, acting on ester bonds;mRNA binding;nuclease activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;single-stranded RNA binding;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cleavage body;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm part;organelle;organelle part;protein complex;ribonucleoprotein complex;RNA granule;stress granule;tRNA-splicing ligase complex

O43143 Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15DHX15 >sp|O43143|DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 1.18 0.96 1.02 1.82 0.75 0.47 0.81 0.65 2.82E-37 9 12.6 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA helicase activity" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome

E9PEX6;P09622;B4DHG0;B4DT69;F8WDM5;F2Z2E3 "Dihydrolipoyl dehydrogenase, mitochondrial;Dihydrolipoyl dehydrogenase" DLD ">tr|E9PEX6|E9PEX6_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=2 SV=1;>sp|P09622|DLDH_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2;>tr|B4DHG0|B4DHG0_HUMAN Dihydrolipoyl dehydrogenase, mitoc" 0.85 1.3 1.3 1.07 0.72 0.7 0.96 1.26 1.19E-36 9 19.8 "acetyl-CoA catabolic process;acetyl-CoA metabolic process;amine catabolic process;amine metabolic process;anatomical structure morphogenesis;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;biological regulation;branched chain family amino acid catabolic process;branched chain family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell maturation;cell redox homeostasis;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular chemical homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;chemical homeostasis;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental maturation;developmental process;developmental process involved in reproduction;electron transport chain;embryonic morphogenesis;gastrulation;generation of precursor metabolites and energy;homeostatic process;ion homeostasis;lysine catabolic process;lysine metabolic process;macromolecule metabolic process;metabolic process;mitochondrial electron transport, NADH to ubiquinone;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;protein metabolic process;proteolysis;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of membrane potential;regulation of metabolic process;reproductive process;respiratory electron transport chain;small molecule catabolic process;small molecule metabolic process;sperm capacitation;tricarboxylic acid cycle" "binding;catalytic activity;coenzyme binding;cofactor binding;dihydrolipoyl dehydrogenase activity;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on NADH or NADPH" acrosomal matrix;cell part;cytoplasmic part;cytoplasmic vesicle part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part;vacuolar part "Citrate cycle (TCA cycle);Glycine, serine and threonine metabolism;Glycolysis / Gluconeogenesis;Pyruvate metabolism;Valine, leucine and isoleucine degradation"

Q16555-2;Q16555;E5RFU4 Dihydropyrimidinase-related protein 2 DPYSL2 >sp|Q16555-2|DPYL2_HUMAN Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2;>sp|Q16555|DPYL2_HUMAN Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 0.19 19.93 0.23 7.26 0.13 0.39 0.26 0.73 6.15E-29 9 25.4 anatomical structure development;axon guidance;biological regulation;catabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;establishment of localization;heterocycle catabolic process;heterocycle metabolic process;locomotion;metabolic process;nitrogen compound metabolic process;nucleobase catabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;olfactory bulb development;organelle organization;positive regulation of biological process;positive regulation of cellular process;positive regulation of glutamate secretion;positive regulation of secretion;positive regulation of transport;primary metabolic process;pyrimidine base catabolic process;pyrimidine base metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cellular localization;regulation of cellular process;regulation of developmental process;regulation of glutamate secretion;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of secretion;regulation of signaling;regulation of transport;response to alkaloid;response to amine stimulus;response to amphetamine;response to chemical stimulus;response to cocaine;response to drug;response to endogenous stimulus;response to external stimulus;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to stimulus;response to tropane;signal transduction;small molecule metabolic process;spinal cord development;synaptic vesicle transport;taxis;transport;vesicle-mediated transport "catalytic activity;dihydropyrimidinase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides" axon;cell body;cell part;cell projection;cell projection part;cytoplasmic part;cytosol;dendrite;growth cone;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;neuron projection;neuronal cell body;organelle;protein complex;site of polarized growth Axon guidance

Q05639 Elongation factor 1-alpha 2 EEF1A2 >sp|Q05639|EF1A2_HUMAN Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 0.07 NaN 0.07 11.98 0.04 2.46 0.06 NaN 3.63E-40 9 27.2 biological regulation;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to chemical stimulus;response to inorganic substance;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell body;cell part;cytoplasmic part;eukaryotic translation elongation factor 1 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;neuronal cell body;nucleus;organelle;protein complex RNA transport

P60842;J3QL43;J3KT12;P60842-2;J3QR64;J3KTB5;J3QS69;J3QKZ9;J3QLN6;J3KS25;J3KSZ0;J3KTN0 Eukaryotic initiation factor 4A-I EIF4A1 >sp|P60842|IF4A1_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1;>tr|J3QL43|J3QL43_HUMAN Eukaryotic initiation factor 4A-I (Fragment) OS=Homo sapiens GN=EIF4A1 PE=3 SV=1;>tr|J3KT12|J3KT12_HUMAN Eukaryotic initiation factor 4A-I 0.82 0.64 0.42 0.49 1.73 1.72 1.76 0.92 2.34E-47 9 19.5 biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;signal transduction;translational initiation;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mRNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA cap binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex RNA transport

Q8IY81 pre-rRNA processing protein FTSJ3 FTSJ3 >sp|Q8IY81|SPB1_HUMAN pre-rRNA processing protein FTSJ3 OS=Homo sapiens GN=FTSJ3 PE=1 SV=2 0.99 1.3 0.64 2.52 0.3 0.37 0.5 0.49 3.09E-36 9 16.4 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;primary metabolic process;RNA metabolic process;RNA methylation;RNA modification;RNA processing;rRNA metabolic process;rRNA processing;small molecule metabolic process "catalytic activity;methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

F5H6X6;Q14697;Q14697-2;E9PKU7;E9PNH1;H0YFL4 Neutral alpha-glucosidase AB GANAB >tr|F5H6X6|F5H6X6_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=2 SV=1;>sp|Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3;>sp|Q14697-2|GANAB_HUMAN Isoform 2 of Neutral alpha-glucosidase AB OS=Homo sapien NaN 1.77 0.47 NaN 2.99 NaN NaN 1.1 2.00E-22 9 14.4 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine "alpha-glucosidase activity;binding;carbohydrate binding;catalytic activity;glucan 1,3-alpha-glucosidase activity;glucosidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum lumen;endoplasmic reticulum part;glucosidase II complex;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;protein complex;vesicle N-Glycan biosynthesis;Protein processing in endoplasmic reticulum

O75367-3;O75367;O75367-2;B4DJC3;D6RCF2 Core histone macro-H2A.1 H2AFY >sp|O75367-3|H2AY_HUMAN Isoform 3 of Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY;>sp|O75367|H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4;>sp|O75367-2|H2AY_HUMAN Isoform 1 of Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY 0.95 1.37 1.01 2.49 0.56 0.69 0.5 0.58 9.14E-102 9 31.8 "biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin modification;chromatin organization;chromosome organization;dosage compensation;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule metabolic process;regulation of metabolic process" binding;chromatin binding;DNA binding;nucleic acid binding Barr body;cell part;chromosomal part;chromosome;condensed chromosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleosome;nucleus;organelle;organelle part;protein-DNA complex;sex chromosome;X chromosome Systemic lupus erythematosus

O00425;O00425-2;F8WD15 Insulin-like growth factor 2 mRNA-binding protein 3 IGF2BP3 >sp|O00425|IF2B3_HUMAN Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2;>sp|O00425-2|IF2B3_HUMAN Isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 NaN 0.7 1.06 0.42 1.6 1.07 NaN 1.31 4.64E-24 9 19.2 anatomical structure morphogenesis;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;translation binding;mRNA 3'-UTR binding;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;translation regulator activity cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q12905 Interleukin enhancer-binding factor 2 ILF2 >sp|Q12905|ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 1.18 0.95 1.4 1.8 0.48 0.39 0.97 0.87 1.19E-62 9 24.1 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;immune response;immune system process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;double-stranded RNA binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;transferase activity cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex

P05556;P05556-2;P05556-5;P05556-4;P05556-3;C9JPK5;H7C4N8;E7ERX5;Q5T3E6;E9PLR6;E7EUI6;E7EQW5 Integrin beta-1 ITGB1 >sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2;>sp|P05556-2|ITB1_HUMAN Isoform Beta-1B of Integrin beta-1 OS=Homo sapiens GN=ITGB1;>sp|P05556-5|ITB1_HUMAN Isoform Beta-1D of Integrin beta-1 OS=Homo sapiens GN=ITGB1;>sp|P05556-4|IT 0.95 1.06 1.12 0.7 0.85 0.29 0.94 1.15 1.19E-28 9 13.3 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;anatomical structure homeostasis;axon guidance;B cell activation;B cell differentiation;biological adhesion;biological regulation;blood coagulation;blood vessel endothelial cell migration;calcium ion homeostasis;calcium-independent cell-matrix adhesion;cardiac cell differentiation;cardiac muscle cell differentiation;cation homeostasis;cell activation;cell adhesion;cell adhesion mediated by integrin;cell communication;cell cycle process;cell differentiation;cell fate specification;cell junction assembly;cell junction organization;cell migration;cell migration involved in sprouting angiogenesis;cell motility;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell adhesion mediated by integrin;cell-cell junction assembly;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular defense response;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular membrane organization;cellular metal ion homeostasis;cellular process;cellular process involved in reproduction;cellular response to abiotic stimulus;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to ionizing radiation;cellular response to mechanical stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to radiation;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin D;chemical homeostasis;chemotaxis;chordate embryonic development;coagulation;cytoskeleton organization;defense response;developmental process;divalent inorganic cation homeostasis;embryo development;embryo development ending in birth or egg hatching;endothelial cell migration;establishment of localization;establishment of localization in cell;establishment of protein localization;extracellular matrix organization;extracellular structure organization;G1/S transition of mitotic cell cycle;germ cell migration;hemostasis;homeostatic process;homophilic cell adhesion;immune system process;in utero embryonic development;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;ion homeostasis;leukocyte activation;leukocyte cell-cell adhesion;leukocyte differentiation;leukocyte migration;locomotion;lymphocyte activation;lymphocyte differentiation;maternal process involved in female pregnancy;membrane organization;metal ion homeostasis;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell differentiation;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neuron differentiation;negative regulation of programmed cell death;neuron projection development;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cell-substrate adhesion;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of endocytosis;positive regulation of intracellular protein kinase cascade;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of neuron differentiation;positive regulation of neuron projection development;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transport;protein transport;protein transport within lipid bilayer;regulation of anoikis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cell-substrate adhesion;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of endocytosis;regulation of G-protein coupled receptor protein signaling pathway;regulation of immune response;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to abiotic stimulus;response to activity;response to chemical stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to gonadotropin stimulus;response to growth factor stimulus;response to hormone stimulus;response to ionizing radiation;response to mechanical stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to radiation;response to stimulus;response to stress;response to transforming growth factor beta stimulus;response to vitamin;response to vitamin D;sarcomere organization;signal transduction;striated muscle cell differentiation;taxis;tight junction assembly;tissue homeostasis;transport;viral reproductive process;virus-host interaction	actin binding;binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;peptide binding;protein binding;protein dimerization activity;protein heterodimerization activity;receptor activity	acrosomal vesicle;adherens junction;alpha3-beta1 integrin complex;alpha8-beta1 integrin complex;alpha9-beta1 integrin complex;anchoring junction;basement membrane;cell division site part;cell junction;cell part;cell projection;cell surface;cell-cell contact zone;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cleavage furrow;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;external side of plasma membrane;extracellular matrix part;extracellular region part;filopodium;focal adhesion;hemidesmosome;integrin complex;intercalated disc;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;myelin sheath abaxonal region;neuromuscular junction;organelle;pigment granule;plasma membrane;plasma membrane part;protein complex;receptor complex;ruffle;sarcolemma;stored secretory granule;synapse;vesicle	Arrhythmogenic right ventricular cardiomyopathy (ARVC);Axon guidance;Bacterial invasion of epithelial cells;Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leishmaniasis;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Shigellosis;Small cell lung cancer;Toxoplasmosis

Q14573;Q14643-4;Q14643-3;G5E9P1;Q14643-8;Q14643-7;Q14643-5;Q14643-6;Q14643-2;E7EVP7;Q14643;REV__B4E0P7;REV__Q4G0S7;B7ZMI3	"Inositol 1,4,5-trisphosphate receptor type 3"	ITPR3	">sp|Q14573|ITPR3_HUMAN Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2"	0.94 1.12 1	1.33 0.67 0.95 0.77 1.17 1.20E-24 9	3.5	activation of phospholipase C activity;apoptosis;apoptosis in response to endoplasmic reticulum stress;biological regulation;calcium ion homeostasis;calcium ion transport;calcium ion transport into cytosol;cation homeostasis;cation transport;cell activation;cell death;cell surface receptor linked signaling pathway;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cytosolic calcium ion homeostasis;cytosolic calcium ion transport;death;defense response;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of cytosolic calcium ion concentration;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;fibroblast growth factor receptor signaling pathway;generation of precursor metabolites and energy;G-protein coupled receptor protein signaling pathway;homeostatic process;immune response;immune system process;innate immune response;inositol phosphate-mediated signaling;intracellular signal transduction;ion homeostasis;ion transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;metal ion homeostasis;metal ion transport;multicellular organismal process;negative regulation of biological process;negative regulation of sequestering of calcium ion;nerve growth factor receptor signaling pathway;neurological system process;oxidation-reduction process;platelet activation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;programmed cell death;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein homooligomerization;protein oligomerization;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of homeostatic process;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of ion homeostasis;regulation of lipase activity;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phospholipase activity;regulation of secretion;regulation of sequestering of calcium ion;regulation of signaling;regulation of transport;release of sequestered calcium ion into cytosol;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hypoxia;response to inorganic substance;response to metal ion;response to organic substance;response to oxygen levels;response to stimulus;response to stress;second-messenger-mediated signaling;sensory perception;sensory perception of bitter taste;sensory perception of chemical stimulus;sensory perception of sweet taste;sensory perception of taste;sensory perception of umami taste;signal transduction;small molecule metabolic process;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transport "alcohol binding;binding;calcium channel activity;calcium-release channel activity;cation channel activity;cation transmembrane transporter activity;channel activity;gated channel activity;inositol 1,3,4,5 tetrakisphosphate binding;inositol 1,4,5 trisphosphate binding;inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity;inositol hexakisphosphate binding;intracellular ligand-gated calcium channel activity;intracellular ligand-gated ion channel activity;ion channel activity;ion transmembrane transporter activity;ligand-gated channel activity;ligand-gated ion channel activity;lipid binding;molecular transducer activity;passive transmembrane transporter activity;phosphatidylinositol binding;phospholipid binding;receptor activity;signal transducer activity;signaling receptor activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" apical part of cell;brush border;cell body;cell part;cell projection;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;myelin sheath;neuronal cell body;non-membrane-bounded organelle;nuclear membrane;nuclear outer membrane;nuclear part;nucleolus;nucleoplasm;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;plasma membrane part;platelet dense granule membrane;platelet dense tubular network membrane;secretory granule membrane;vesicle membrane Alzheimer's disease;Calcium signaling pathway;Gap junction;Gastric acid secretion;GnRH signaling pathway;Huntington's disease;Long-term depression;Long-term potentiation;Oocyte meiosis;Pancreatic secretion;Phosphatidylinositol signaling system;Salivary secretion;Taste transduction;Vascular smooth muscle contraction

Q14974;J3QR48;B7ZAV6;F5H4R7;J3KTM9;J3QKQ5 Importin subunit beta-1 KPNB1 >sp|Q14974|IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2;>tr|J3QR48|J3QR48_HUMAN Importin subunit beta-1 (Fragment) OS=Homo sapiens GN=KPNB1 PE=4 SV=1 0.72 1.98 0.58 NaN 0.78 NaN 0.92 1.26 4.63E-63 9 12 "biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;protein import;protein import into nucleus;protein import into nucleus, translocation;protein targeting;protein transport;regulation of biological process;regulation of cellular process;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;ribosomal protein import into nucleus;signal transduction;small molecule metabolic process;transport;viral infectious cycle;viral reproductive process" binding;cation binding;ion binding;metal ion binding;nuclear localization sequence binding;peptide binding;protein transporter activity;signal sequence binding;substrate-specific transporter activity;transition metal ion binding;transporter activity;zinc ion binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear pore;nucleoplasm;organelle membrane;organelle part;pore complex;protein complex RNA transport

Q9BQG0;Q9BQG0-2;I3L1L3;I3L2H8 Myb-binding protein 1A MYBBP1A >sp|Q9BQG0|MBB1A_HUMAN Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2;>sp|Q9BQG0-2|MBB1A_HUMAN Isoform 2 of Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A;>tr|I3L1L3|I3L1L3_HUMAN Myb-binding protein 1A (Fragment) OS=Homo sapiens GN=MYBBP1A 1.16 0.93 1.26 1.79 1.48 0.4 0.76 0.77 2.54E-37 9 7 "biological regulation;biosynthetic process;cell communication;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;electron transport chain;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic

process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;oxidation-reduction process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;respiratory electron transport chain;response to external stimulus;response to extracellular stimulus;response to nutrient levels;response to starvation;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;transcription, DNA-dependent;transport"
"binding;catalytic activity;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;nucleic acid binding;nucleotidyltransferase activity;protein binding;sequence-specific DNA binding;transcription factor binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;NLS-dependent protein nuclear import complex;non-membrane-bounded organelle;nuclear part;nucleocytoplasmic shuttling complex;nucleolus;organelle;organelle part;protein complex

Q9H0A0;E7ESU4;E9PJN6;E9PMU0 N-acetyltransferase 10 NAT10 >sp|Q9H0A0|NAT10_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2;>tr|E7ESU4|E7ESU4_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=2 SV=1 1.16 0.92 1.55 NaN 0.77 NaN 0.7 0.58 3.42E-20 9 10.7 "acetyltransferase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;N-acetyltransferase activity;N-acyltransferase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part Ribosome biogenesis in eukaryotes

Q14978;Q14978-3;Q14978-2 Nucleolar and coiled-body phosphoprotein 1 NOLC1 >sp|Q14978|NOLC1_HUMAN Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2;>sp|Q14978-3|NOLC1_HUMAN Isoform 3 of Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1;>sp|Q14978-2|NOLC1_HUMAN Isoform Beta of Nucleola 1.29 1.12 1.28 1.33 0.28 0.33 0.54 0.48 6.60E-26 9 12.7 cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mitosis;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleolus organization;nucleus organization;organelle fission;organelle organization;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding Cajal body;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear part;nucleolus;nucleoplasm part;organelle;organelle part

P11498;E9PRE7;B4DN00;E9PS68 "Pyruvate carboxylase, mitochondrial" PC ">sp|P11498|PYC_HUMAN Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2" 0.78 0.86 1.26 0.42 6.34 1.03 1.6 1.9 1.29E-28 9 10.9 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;dicarboxylic acid metabolic process;gluconeogenesis;glucose metabolic process;hexose biosynthetic process;hexose metabolic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;organic acid metabolic process;oxaloacetate metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;small molecule biosynthetic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;biotin binding;biotin carboxylase activity;carboxylic acid binding;catalytic activity;cation binding;DNA binding;ion binding;ligase activity;ligase activity, forming carbon-carbon bonds;ligase activity, forming carbon-nitrogen bonds;metal ion binding;monocarboxylic acid binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyruvate carboxylase activity;ribonucleotide binding;vitamin binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part Citrate cycle (TCA cycle);Pyruvate metabolism

Q99460;Q99460-2;H7C378;H7BZR6;C9J9M4 26S proteasome non-ATPase regulatory subunit 1 PSMD1 >sp|Q99460|PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2;>sp|Q99460-2|PSMD1_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 1.03 0.99 0.51 0.81 1.64 1.21 1.65 1.41 1.43E-17 9 13.5 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular

function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" enzyme regulator activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome regulatory particle;protein complex Proteasome
P26599;P26599-2;P26599-3;A6NLN1;K7ES59;K7ELW5;K7EKJ7;K7EK45;O95758-1;O95758-6;O95758-2;O95758;O95758-5;O95758-4;B4DI28;Q9UKA9-5;Q9UKA9-6;O95758-7;Q9UKA9;Q9UKA9-2;Q9UKA9-4;Q9UKA9-3;B4DSS8 Polypyrimidine tract-binding protein 1 PTBP1 >sp|P26599|PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1;>sp|P26599-2|PTBP1_HUMAN Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1;>sp|P26599-3|PTBP1_HUMAN Isoform 3 of Polypyrimidine trac 1.29 0.85 1.77 1.79 0.6 0.27 0.95 0.83 1.19E-32 9 21.1 "anatomical structure morphogenesis;biological regulation;cell maturation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental maturation;developmental process;erythrocyte maturation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA splice site selection;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of muscle cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of muscle cell differentiation;regulation of neural precursor cell proliferation;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;mRNA binding;nucleic acid binding;nucleotide binding;poly-pyrimidine tract binding;pre-mRNA binding;RNA binding;single-stranded RNA binding cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex

B4DWJ2;P47897;C9JSG9;H7C0R3;C9J165;F2Z2V6;B7Z840 Glutamine--tRNA ligase QARS >tr|B4DWJ2|B4DWJ2_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=QARS PE=2 SV=1;>sp|P47897|SYQ_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1 NaN NaN 0.5 NaN 2.5 NaN NaN NaN 3.07E-25 9 14.7 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;glutaminyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;glutamine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part
Aminoacyl-tRNA biosynthesis

Q15907;P62491-2;J3KQP6;H3BMH2;B4DMK0;H3BSC1;P62491;B4DQU5 Ras-related protein Rab-11B;Ras-related protein Rab-11A RAB11B;RAB11A

>sp|Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4;>sp|P62491-2|RB11A_HUMAN Isoform 2 of Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A;>tr|J3KQP6|J3KQP6_HUMAN Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A 0.76 1.31 0.94 0.55 1.27 1.39 1.02 1.04 7.50E-59 9 37.6 biological regulation;cell cycle;cell projection organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cellular response to stimulus;cytokinesis;establishment of localization;establishment of localization in cell;establishment of melanosome localization;establishment of organelle localization;establishment of pigment granule localization;establishment of protein localization;establishment of vesicle localization;fluid transport;intracellular protein transport;intracellular signal transduction;intracellular transport;localization;macromolecule localization;melanosome transport;membrane organization;neuron projection development;pigment granule transport;plasma membrane organization;plasma membrane to endosome transport;protein localization;protein localization in membrane;protein localization in plasma membrane;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular process;regulation of establishment of protein localization;regulation of localization;regulation of long-term neuronal synaptic plasticity;regulation of multicellular organismal process;regulation of neurological system process;regulation of neuronal synaptic plasticity;regulation of protein localization;regulation of protein transport;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transmembrane transport;transport;water transport"binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;SNARE binding;syntaxin binding" cell division site part;cell part;cleavage furrow;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;organelle membrane;organelle part;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;protein complex;recycling endosome;recycling endosome membrane;trans-Golgi network;transport vesicle;vesicle;vesicle membrane Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Pancreatic secretion;Vasopressin-regulated water reabsorption

Q96PK6 RNA-binding protein 14 RBM14 >sp|Q96PK6|RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 1.38 1.18 0.98 1.15 0.66 0.54 0.99 0.64 7.99E-26 9 15.4 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromosome organization;corticosteroid receptor signaling pathway;covalent chromatin modification;DNA metabolic process;DNA recombination;DNA repair;DNA replication;estrogen receptor signaling pathway;glucocorticoid receptor signaling pathway;histone deacetylation;histone modification;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein deacetylation;protein deacylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;response to stress;signal transduction;steroid hormone receptor signaling pathway" "binding;binding, bridging;ligand-dependent nuclear receptor transcription coactivator activity;nucleic acid binding;nucleotide binding;protein binding;protein binding transcription factor activity;protein binding, bridging;RNA binding;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;intracellular organelle part;intracellular part;macromolecular complex;mediator complex;nuclear part;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex;transcription factor complex

P26373;P26373-2;J3QSB4;J3KS98;H3BUK8;H3BTH3 60S ribosomal protein L13 RPL13 >sp|P26373|RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4;>sp|P26373-2|RL13_HUMAN Isoform 2 of 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13;>tr|J3QSB4|J3QSB4_HUMAN 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 1.42 0.77 0.85 0.64 1.3 0.87 1.42 0.9 1.42E-51 9 41.7 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome

D6RAT0;P61247;D6RG13;D6RAS7;D6R9B6;F5H4F9;H0Y8L7;D6RB09;E9PFI5;H0Y9Y4;D6RED7;D6RGE0;D6RI02 40S ribosomal protein S3a RPS3A >tr|D6RAT0|D6RAT0_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=2 SV=1;>sp|P61247|RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2;>tr|D6RG13|D6RG13_HUMAN 40S ribosomal protein S3a (Fragment) OS=Homo sapiens GN=RPS3A PE 1.58 0.88 1.11 0.59 1.4 0.83 1.26 0.82 2.50E-184 9 37.4 "biological regulation;biosynthetic process;catabolic process;cell differentiation;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;induction of apoptosis;induction of programmed cell death;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

Q15050 Ribosome biogenesis regulatory protein homolog RRS1 >sp|Q15050|RRS1_HUMAN Ribosome biogenesis regulatory protein homolog OS=Homo sapiens GN=RRS1 PE=1 SV=2 1.04 1.3 0.65 3 0.28 0.39 0.47 0.6 3.28E-35 9 27.7 cell cycle process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;establishment of chromosome localization;establishment of localization;establishment of localization in cell;establishment of organelle localization;metaphase plate congression;mitotic metaphase plate congression;ribonucleoprotein complex biogenesis;ribosome biogenesis cell part;chromosome;condensed chromosome;condensed nuclear chromosome;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleolus;organelle;organelle part

J3QSV6;O76021;B4DJ58;I3L3U9;I3L3C4;I3L234 Ribosomal L1 domain-containing protein 1 RSL1D1 >tr|J3QSV6|J3QSV6_HUMAN Ribosomal L1 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=RSL1D1 PE=4 SV=1;>sp|O76021|RL1D1_HUMAN Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3;>tr|B4DJ58|B4DJ58_HUMAN Ribosomal L1 domain- 1.03 1.53 0.93 2.61 0.27 0.3 0.46 0.47 1.24E-80 9 22.3 biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;regulation of biological process;regulation of localization;regulation of protein localization;translation binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex

Q15459;E9PAW1;F8WB66;H7C1L2;F8WC79 Splicing factor 3A subunit 1 SF3A1 >sp|Q15459|SF3A1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1;>tr|E9PAW1|E9PAW1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=2 SV=1 1.06 0.98 1.32 1.67 0.92 0.49 0.83 0.85 2.43E-37 9 17.2 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA splice site selection;nitrogen compound metabolic process;nuclear mRNA 3'-splice site recognition;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA processing binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex;U2-type spliceosomal complex Spliceosome

P31947;P31947-2;A2IDB2;F8WEB6;A2IDB1 14-3-3 protein sigma SFN >sp|P31947|1433S_HUMAN 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1;>sp|P31947-2|1433S_HUMAN Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN 1.24 0.37 1.05 0.45 1.37 0.75 2.94 1.2 1.65E-31 9 38.7 "anatomical structure development;apoptotic mitochondrial changes;biological regulation;cell differentiation;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to stimulus;cellular response to stress;developmental process;DNA damage response, signal transduction resulting in induction of apoptosis;epidermal cell differentiation;epidermis development;epithelial cell differentiation;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;keratinocyte differentiation;keratinocyte proliferation;membrane organization;mitochondrion organization;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of programmed cell death;positive regulation of protein export from nucleus;positive regulation of protein transport;positive regulation of transport;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of growth;regulation of hydrolase activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nucleocytoplasmic transport;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein export from nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of transferase activity;regulation of transport;release of cytochrome c from mitochondria;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction in response to DNA damage;skin development;tissue development" enzyme inhibitor activity;enzyme regulator activity;kinase inhibitor activity;kinase regulator activity;protein kinase C inhibitor activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;vesicle membrane Aldosterone-regulated sodium reabsorption;Cell cycle;p53 signaling pathway

P17987;E7ERF2;F5H136;F5H726;F5GZI8;F5H676;F5H282;E7EQR6;F5GYL4;F5H7Y1;F5GZ03 T-complex protein 1 subunit alpha TCP1 >sp|P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1;>tr|E7ERF2|E7ERF2_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=2 SV=1;>tr|F5H136|F5H136_HUMAN T-complex protein 1 subunit alpha (Fragment) OS=Ho 0.94 0.98 0.76 1.09 1.11 0.99 1.14 0.98 2.34E-58 9 21.8 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;tubulin complex assembly adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell junction;cell part;centrosome;chaperonin-containing T-complex;chromatin;chromosomal part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;Golgi apparatus;heterochromatin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule;microtubule organizing center;microtubule organizing center part;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear heterochromatin;nuclear part;nucleus;organelle;organelle part;pericentriolar material;plasma membrane;protein complex

Q9Y2W1;B0AZU3;H0YF14 Thyroid hormone receptor-associated protein 3 THRAP3 >sp|Q9Y2W1|TR150_HUMAN Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 1.17 0.71 0.87 1.22 3.63 0.65 1.07 0.96 1.33E-28 9 10.3 "androgen receptor signaling pathway;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;induction of apoptosis;induction of programmed cell death;intracellular receptor mediated signaling pathway;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of RNA splicing;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA splicing;regulation of RNA stability;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA stabilization;signal transduction;steroid hormone receptor signaling pathway;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;hormone receptor binding;ligand-dependent nuclear receptor transcription coactivator activity;nuclear hormone receptor binding;nucleotide binding;phosphoprotein binding;protein binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;receptor binding;ribonucleotide binding;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;thyroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;vitamin D receptor binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mediator complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex

Q5TCU6;Q9Y490 Talin-1 TLN1 >tr|Q5TCU6|Q5TCU6_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1;>sp|Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 NaN NaN 0.32 NaN 0.53 NaN NaN NaN 3.85E-19 9 6.2 actin cytoskeleton organization;actin filament-based process;activation of signaling protein activity involved in unfolded protein response;axon guidance;biological adhesion;biological regulation;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell-cell junction assembly;cell-cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;locomotion;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;metabolic process;multicellular organismal process;muscle contraction;muscle system process;organelle organization;platelet activation;platelet degranulation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to chemical stimulus;response to external stimulus;response to stimulus;secretion;secretion by cell;system process;taxis;transport;vesicle-mediated transport structural constituent of cytoskeleton;structural molecule activity actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;plasma membrane part;ruffle;ruffle membrane;vesicle Focal adhesion

P31946-2;P31946;Q4VY20;Q4VY19 "14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed" YWHAB >sp|P31946-2|1433B_HUMAN Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB;>sp|P31946|1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 1.31 1.38 0.59 1.27 0.32 0.49 1.39 1.11 2.91E-49 9 44.3 "activation of MAPKK activity;activation of protein kinase activity;axon guidance;biological regulation;cell surface receptor linked signaling pathway;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemotaxis;cytoplasmic sequestering of protein;defense response;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;fibroblast growth factor receptor signaling pathway;gene expression;hippo signaling cascade;immune response;immune system process;innate immune response;insulin receptor signaling pathway;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;MAPKKK cascade;membrane organization;metabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of dephosphorylation;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of protein dephosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein transport;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;negative regulation of transport;nerve growth factor receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein metabolic process;protein modification process;protein oligomerization;protein phosphorylation;protein targeting;protein transport;Ras protein signal transduction;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of establishment of protein localization;regulation of gene expression;regulation of kinase activity;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein transport;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;RNA metabolic process;signal transduction;small GTPase mediated signal transduction;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport" protein binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;nuclear part;nucleoplasm part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;pigment granule;protein complex;transcriptional repressor complex;vesicle;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis

P61981 "14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed" YWHAG >sp|P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 0.88 1.44 0.59 1.11 0.43 0.63 1.43 1.29 5.89E-165 9 34.8 biological regulation;cell cycle process;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;G2/M transition of mitotic cell cycle;intracellular protein transport;intracellular transport;membrane organization;protein targeting;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;transport enzyme inhibitor activity;enzyme regulator activity;kinase inhibitor activity;kinase regulator activity;protein kinase C inhibitor activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis

P18583-6 >sp|P18583-6|SON_HUMAN Isoform E of Protein SON OS=Homo sapiens GN=SON 1.3 1.05 1 1.63 0.47 0.44 0.8 0.78 1.09E-36 9 5.4

Q86UK0-2;Q86UK0 ATP-binding cassette sub-family A member 12 ABCA12 >sp|Q86UK0-2|ABCAC_HUMAN Isoform 2 of ATP-binding cassette sub-family A member 12 OS=Homo sapiens GN=ABCA12;>sp|Q86UK0|ABCAC_HUMAN ATP-binding cassette sub-family A member 12 OS=Homo sapiens GN=ABCA12 PE=1 SV=3 1.12 0.6 0.4 0.21 2.19 2.56 1.4 0.74 1.21E-20 10 4.6 anatomical structure development;anatomical structure homeostasis;ATP catabolic process;ATP metabolic process;biological regulation;catabolic process;cellular catabolic process;cellular homeostasis;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;ceramide transport;chemical homeostasis;chemical homeostasis within a tissue;developmental process;establishment of localization;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;keratinization;lipid homeostasis;lipid transport;lung alveolus development;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organic substance transport;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological quality;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;surfactant homeostasis;tissue homeostasis;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part ABC transporters

Q562R1 Beta-actin-like protein 2 ACTBL2 >sp|Q562R1|ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 0.85 1.15 0.62 1.21 0.73 0.76 0.7 1.3 7.51E-255 10 20.2 adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

Q8N766-4;Q8N766-3;Q8N766-2;Q8N766;Q5TG59;H7C4E3 ER membrane protein complex subunit 1 EMC1 >sp|Q8N766-4|EMC1_HUMAN Isoform 4 of ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1;>sp|Q8N766-3|EMC1_HUMAN Isoform 3 of ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1;>sp|Q8N766-2|EMC1_HUMAN Isoform 2 of ER membrane protein c 1.37 1.45 1.21 1.1 0.95 0.56 0.99 0.85 2.73E-24 10 12.7 ER membrane protein complex;macromolecular complex;protein complex

P06733;K7EM90;P06733-2;F5H1C3;F5H5U1;F5GWQ3;E5RI09;E5RG95;K7EPM1;K7EKN2;E5RGZ4;F5H0C8;P13929-3;B7Z2X9;P13929-2;P13929;P09104 Alpha-enolase;Enolase ENO1 >sp|P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2;>tr|K7EM90|K7EM90_HUMAN Enolase (Fragment) OS=Homo sapiens GN=ENO1 PE=3 SV=1;>sp|P06733-2|ENOA_HUMAN Isoform MBP-1 of Alpha-enolase OS=Homo sapiens GN=ENO1 0.27 6.06 0.21 3.62 0.43 0.85 0.48 0.87 4.19E-67 10 25.6 "aging;alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental growth;developmental process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;growth;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regeneration;regulation of biological process;regulation of biosynthetic process;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to biotic stimulus;response to chemical stimulus;response to drug;response to other organism;response to stimulus;response to virus;RNA biosynthetic process;RNA metabolic process;skeletal muscle tissue regeneration;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;tissue development;tissue regeneration;transcription, DNA-dependent" binding;carbon-oxygen lyase activity;catalytic activity;cation binding;DNA binding;hydro-lyase activity;ion binding;lyase activity;magnesium ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;phosphopyruvate hydratase activity;protein binding transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;contractile fiber part;cytoplasmic part;cytosol;cytosolic part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;M band;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle part;perikaryon;phosphopyruvate hydratase complex;photoreceptor inner segment;plasma membrane;protein complex;vesicle Glycolysis / Gluconeogenesis;Methane metabolism;RNA degradation

E7EQR4;P15311 Ezrin EZR >tr|E7EQR4|E7EQR4_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=2 SV=2;>sp|P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 NaN NaN 0.56 NaN 1.05 NaN NaN NaN 4.18E-26 10 17.5 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;axon guidance;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;chemotaxis;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;developmental process;epithelial cell differentiation;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;leukocyte cell-cell adhesion;locomotion;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane docking;membrane to membrane docking;organelle organization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to chemical stimulus;response to external stimulus;response to stimulus;taxis actin binding;actin filament binding;binding;cytoskeletal protein binding;protein binding actin filament;apical part of cell;apical plasma membrane;basolateral plasma membrane;cell cortex part;cell part;cell projection;cell projection membrane;cell projection part;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extrinsic to membrane;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane;membrane part;microtubule basal body;microtubule organizing center;microvillus;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ruffle;ruffle membrane;uropod Gastric acid secretion;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton

Q9NYQ8 Protocadherin Fat 2 FAT2 >sp|Q9NYQ8|FAT2_HUMAN Protocadherin Fat 2 OS=Homo sapiens GN=FAT2 PE=1 SV=2 NaN NaN 1.98 NaN 0.76 NaN NaN NaN 5.33E-22 10 2.7 ameboidal cell migration;biological adhesion;cell adhesion;cell migration;cell motility;cell-cell adhesion;cellular component movement;cellular process;epithelial cell migration;homophilic cell adhesion;locomotion binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane

B4E2W0;P55084;F5GZQ3;B5MD38;C9JEY0;C9JE81;C9K0M0 "Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase" HADHB ">tr|B4E2W0|B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1;>sp|P55084|ECHB_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3;>tr|F5GZQ3|F5GZQ3_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=" 0.67 0.94 1.36 0.46 1.07 1.06 1.3 1.38 1.25E-49 10 22.8 biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;cardiolipin acyl-chain remodeling;cardiolipin metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;organophosphate metabolic process;oxidation-reduction process;oxoacid metabolic process;phosphatidylglycerol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "3-hydroxyacyl-CoA dehydrogenase activity;acetyl-CoA C-acyltransferase activity;binding;C-acyltransferase activity;carbon-oxygen lyase activity;carboxylic acid binding;catalytic activity;coenzyme binding;cofactor binding;enoyl-CoA hydratase activity;fatty acid binding;fatty-acyl-CoA binding;hydro-lyase activity;lipid binding;long-chain-3-hydroxyacyl-CoA dehydrogenase activity;long-chain-enoyl-CoA hydratase activity;lyase activity;monocarboxylic acid binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;endoplasmic reticulum;fatty acid beta-oxidation multienzyme complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial outer membrane;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex "Benzoate degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Valine, leucine and isoleucine degradation"

P09651-2;F8W6I7;P09651;P09651-3;Q32P51;F8VZ49;F8VTQ5;F8VYN5;H0YH80;F8W646 Heterogeneous nuclear ribonucleoprotein A1;Heterogeneous nuclear ribonucleoprotein A1-like 2 HNRNPA1;HNRNPA1L2 >sp|P09651-2|ROA1_HUMAN Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1;>tr|F8W6I7|F8W6I7_HUMAN Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=2 SV=1;>sp|P09651|ROA1_HUMAN Heterogeneous nuclea 1.24 1.27 1.72 2.03 0.55 0.29 0.61 0.61 5.81E-226 10 35.9 "alternative nuclear mRNA splicing, via spliceosome;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear export;nuclear import;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;reproductive process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;transport;viral reproductive process;virus-host interaction" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;single-stranded DNA binding;single-stranded RNA binding;structure-specific DNA binding catalytic step 2 spliceosome;cell part;cytoplasm;cytoskeleton;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

M0QXS5;P14866;P14866-2;M0QYT0;M0R076;M0QYL7;M0R1W6;B4DVF8 Heterogeneous nuclear ribonucleoprotein L HNRNPL >tr|M0QXS5|M0QXS5_HUMAN Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=4 SV=1;>sp|P14866|HNRPL_HUMAN Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2;>sp|P14866-2|HNRPL_HUMAN Isoform 2 of Hete 1.09 0.77 0.97 2.08 0.75 0.53 0.88 0.89 5.17E-52 10 28.7 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;catalytic activity;DNA binding;nucleic acid binding;nucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;transcription regulatory region DNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex

F5H698;B4DER1;Q9P2J5;B4DJ10 "Leucine--tRNA ligase, cytoplasmic" LARS ">tr|F5H698|F5H698_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1;>tr|B4DER1|B4DER1_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1;>sp|Q9P2J5|SYLC_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens" 1.1 NaN 0.67 0.34 5.56 0.94 2.19 NaN 3.09E-71 10 12.8 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;leucyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;leucine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis"

K7EIG7;J3QRN6;O94832;J3KRL0;J3QRR2 Unconventional myosin-Id MYO1D >tr|K7EIG7|K7EIG7_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=4 SV=1;>tr|J3QRN6|J3QRN6_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=4 SV=1;>sp|O94832|MYO1D_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2 0.91 1.5 1.1 1.55 0.68 0.96 0.48 0.99 8.77E-18 10 11.4 biological regulation;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process "actin-dependent ATPase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" axolemma;axon part;cell part;cell projection membrane;cell projection part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;myosin complex;neuron projection membrane;organelle;organelle part;plasma membrane part;protein complex;smooth endoplasmic reticulum

O00567;H0YDU4;H0Y653;Q5JXT2 Nucleolar protein 56 NOP56 >sp|O00567|NOP56_HUMAN Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4;>tr|H0YDU4|H0YDU4_HUMAN Nucleolar protein 56 (Fragment) OS=Homo sapiens GN=NOP56 PE=4 SV=1;>tr|H0Y653|H0Y653_HUMAN Nucleolar protein 56 (Fragment) OS=Homo sapiens GN=NOP56 PE=4 0.99 1.07 1.16 1.92 0.53 0.49 0.68 0.61 8.06E-49 10 19.9 cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing binding;nucleic acid binding;RNA binding;snoRNA binding box C/D snoRNP complex;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleolar part;organelle part;pre-snoRNP complex;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes

Q01813;Q01813-2;B1APP6;H0Y757;H0Y3Y3;B1APP8;Q5VSR6;Q5VSR5 6-phosphofructokinase type C PFKP >sp|Q01813|K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2;>sp|Q01813-2|K6PP_HUMAN Isoform 2 of 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP 0.51 0.76 0.23 0.62 1.89 2.43 1.17 0.99 1.59E-50 10 16.8 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;fructose 6-phosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "6-phosphofructokinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate kinase activity;catalytic activity;cation binding;ion binding;kinase activity;metal ion binding;nucleotide binding;phosphofructokinase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" 6-phosphofructokinase complex;cell part;cytoplasmic part;cytosolic part;intracellular part;macromolecular complex;protein complex Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Methane metabolism;Pentose phosphate pathway

Q6NZI2;Q6NZI2-2;Q6NZI2-3 Polymerase I and transcript release factor PTRF >sp|Q6NZI2|PTRF_HUMAN Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1;>sp|Q6NZI2-2|PTRF_HUMAN Isoform 2 of Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF 1.15 0.95 0.78 1.08 0.97 0.81 0.87 1.29 1.54E-233 10 34.4 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;termination of RNA polymerase I transcription;transcription initiation from RNA polymerase I promoter;transcription initiation, DNA-dependent;transcription termination, DNA-dependent" binding;nucleic acid binding;RNA binding;rRNA binding;rRNA primary transcript binding caveola;cell part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane part;membrane raft;membrane-bounded organelle;mitochondrion;nuclear part;nucleoplasm;organelle;organelle part;plasma membrane part

Q5QPL9;Q9UKM9-2;Q9UKM9;Q5QPM1;Q5QPM0;Q5QPM2;E5RIX9;E5RG71;B3KT61;Q86SE5;G3V129 RNA-binding protein Raly RALY >tr|Q5QPL9|Q5QPL9_HUMAN RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1;>sp|Q9UKM9-2|RALY_HUMAN Isoform 1 of RNA-binding protein Raly OS=Homo sapiens GN=RALY;>sp|Q9UKM9|RALY_HUMAN RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 1.09 1.17 1.65 2.15 0.57 0.49 0.54 0.66 9.87E-30 10 38.8 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;ribonucleoprotein complex;spliceosomal complex

Q9UGP8;A6PVC9 Translocation protein SEC63 homolog SEC63 >sp|Q9UGP8|SEC63_HUMAN Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2 1.61 1.25 1.81 0.79 0.96 0.79 1.21 0.98 3.98E-46 10 15.7 "cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transmembrane transport;intracellular protein transport;intracellular transport;posttranslational protein targeting to membrane, translocation;protein targeting;protein targeting to membrane;protein transmembrane transport;protein transport;transmembrane transport;transport" protein transporter activity;receptor activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Protein export;Protein processing in endoplasmic reticulum

P36952;P36952-2;C9JLM5 Serpin B5 SERPINB5 >sp|P36952|SPB5_HUMAN Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2;>sp|P36952-2|SPB5_HUMAN Isoform 2 of Serpin B5 OS=Homo sapiens GN=SERPINB5 0.63 0.42 0.9 0.27 5.16 2.64 1.55 0.98 4.75E-42 10 34.1 anatomical structure morphogenesis;biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;developmental process involved in reproduction;extracellular matrix organization;extracellular structure organization;gland morphogenesis;morphogenesis of an epithelium;organ morphogenesis;prostate gland morphogenesis;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of epithelial cell proliferation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;reproductive process;tissue morphogenesis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasm;extracellular region part;extracellular space;intracellular part p53 signaling pathway

Q6NUK1;Q6NUK1-2;J3KN42;H3BMI3 Calcium-binding mitochondrial carrier protein SCaMC-1 SLC25A24 >sp|Q6NUK1|SCMC1_HUMAN Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2;>sp|Q6NUK1-2|SCMC1_HUMAN Isoform 2 of Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24;>tr|J3KN42|J3KN42_HUM 1.04 1.29 1.21 1.41 0.57 0.5 0.8 1.29 7.82E-40 10 21.6 cellular process;establishment of localization;transmembrane transport;transport binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

P05141;Q9H0C2 ADP/ATP translocase 2 SLC25A5 >sp|P05141|ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 1.19 1.48 1.34 1.75 1.38 0.46 0.61 0.88 2.07E-59 10 32.6 biological regulation;cellular metabolic process;cellular process;chromosome segregation;energy derivation by oxidation of organic compounds;energy reserve metabolic process;establishment of localization;generation of precursor metabolites and energy;interaction with host;interspecies interaction between organisms;metabolic process;multi-organism process;oxidation-reduction process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;regulation of biological process;regulation of cell communication;regulation of cell proliferation;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;reproductive process;small molecule metabolic process;transmembrane transport;transport;viral reproduction;viral reproductive process;virus-host interaction adenine transmembrane transporter activity;nucleobase transmembrane transporter activity;nucleobase-containing compound transmembrane transporter activity;purine base transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cell projection;cilium;cytoplasmic part;cytoskeletal part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;mitochondrion;MMXD complex;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane part;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease

P12236;I7HJJ0 ADP/ATP translocase 3 SLC25A6 >sp|P12236|ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4;>tr|I7HJJ0|I7HJJ0_HUMAN ADP/ATP translocase 3 (Fragment) OS=Homo sapiens GN=SLC25A6 PE=4 SV=10.98 1.19 1.33 1.64 1.02 0.53 0.69 0.97 5.02E-40 10 32.6 active induction of host immune response by virus;apoptosis;biological regulation;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;energy derivation by oxidation of organic compounds;energy reserve metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;generation of precursor metabolites and energy;induction by organism of defense response of other organism involved in symbiotic interaction;induction by symbiont of host defense response;induction of host immune response by virus;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;modification by symbiont of host morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by organism of defense response of other organism involved in symbiotic interaction;modulation by symbiont of host defense response;multi-organism process;oxidation-reduction process;positive regulation by organism of defense response of other organism involved in symbiotic interaction;positive regulation by symbiont of host defense response;positive regulation of biological process;positive regulation of defense response;positive regulation of response to stimulus;primary metabolic process;programmed cell death;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of defense response;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of signaling;regulation of transport;reproductive process;response to biotic stimulus;response to defenses of other organism involved in symbiotic interaction;response to host;response to host defenses;response to other organism;response to stimulus;small molecule metabolic process;transmembrane transport;transport;viral infectious cycle;viral reproductive process;virus-host interaction active transmembrane transporter activity;antiporter activity;ATP:ADP antiporter activity;secondary active transmembrane transporter activity;solute:solute antiporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial inner membrane presequence translocase complex;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease

O60264;REV__J3KRF5;REV__K7EJJ5;REV__J3KS13;REV__Q00610-2;REV__Q00610 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 SMARCA5 >sp|O60264|SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 1.07 1.78 0.93 2.49 2.06 0.3 0.41 0.56 2.84E-110 10 10.7 "ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;chromatin assembly;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromatin silencing;chromatin silencing at rDNA;chromosome organization;developmental process;DNA metabolic process;DNA repair;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;double-strand break repair;embryo development;gene silencing;histone exchange;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of gene expression, epigenetic;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;nucleosome positioning;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription initiation, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;chromatin binding;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleosome binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromatin remodeling complex;chromatin silencing complex;chromosome;condensed chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ISWI complex;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;NURF complex;organelle;organelle part;protein complex;RSF complex

B4E022;P29401;P29401-2;E9PFF2;F8W888 Transketolase TKT>tr|B4E022|B4E022_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=2 SV=1;>sp|P29401|TKT_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3;>sp|P29401-2|TKT_HUMAN Isoform 2 of Transketolase OS=Homo sapiens GN=TKT 1.18 0.43 0.84 0.22 1.22 0.39 2.94 1.19 4.30E-65 10 24.1 "alcohol biosynthetic process;alcohol metabolic process;aldehyde biosynthetic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular aldehyde metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glyceraldehyde-3-phosphate biosynthetic process;glyceraldehyde-3-phosphate metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;organophosphate metabolic process;oxidation-reduction process;pentose biosynthetic process;pentose metabolic process;pentose-phosphate shunt, non-oxidative branch;primary metabolic process;regulation of biological process;regulation of growth;small molecule biosynthetic process;small molecule metabolic process;xylulose biosynthetic process;xylulose metabolic process" "binding;catalytic activity;cation binding;cofactor binding;identical protein binding;ion binding;metal ion binding;protein binding;protein dimerization activity;protein homodimerization activity;transferase activity;transferase activity, transferring aldehyde or ketonic groups;transketolase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microbody;nucleus;organelle;peroxisome Biosynthesis of ansamycins;Carbon fixation in photosynthetic organisms;Pentose phosphate pathway

P42167;G5E972;P42167-2;A2T926;P42166;H0YJH7 "Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopentin;Lamina-associated polypeptide 2, isoform alpha;Thymopoietin;Thymopentin" TMPO ">sp|P42167|LAP2B_HUMAN Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2;>tr|G5E972|G5E972_HUMAN Thymopentin OS=Homo sapiens GN=TMPO PE=2 SV=1;>sp|P42167-2|LAP2B_HUMAN Isoform Gamma of Lamina-associated polypeptide 2, i" 1.24 1.74 2.18 1.74 0.45 0.28 0.47 0.35 0 10 32.4 "biological regulation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent" binding;DNA binding;lamin binding;nucleic acid binding;protein binding cell part;chromatin;chromosomal part;envelope;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;nuclear envelope;nuclear inner membrane;nuclear membrane;nuclear part;organelle envelope;organelle inner membrane;organelle membrane;organelle part

Q5TCU3;P07951-2;P07951;CON__Q3SX28;Q5TCU8;P07951-3;H0YLS7 Tropomyosin beta chain TPM2 >tr|Q5TCU3|Q5TCU3_HUMAN Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=2 SV=1;>sp|P07951-2|TPM2_HUMAN Isoform 2 of Tropomyosin beta chain OS=Homo sapiens GN=TPM2;>sp|P07951|TPM2_HUMAN Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1;>Q3SX28 TREM NaN 0.68 NaN 0.74 NaN 0.62 NaN 1.64 8.45E-45 10 31 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;biological regulation;cellular component movement;cellular process;muscle filament sliding;regulation of ATPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process actin binding;binding;cytoskeletal protein binding;protein binding;structural constituent of muscle;structural molecule activity cell part;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;muscle thin filament tropomyosin;organelle part Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM)

P67936;K7EPV9;K7EMU5;K7EPB9 Tropomyosin alpha-4 chain TPM4 >sp|P67936|TPM4_HUMAN Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 1.11 0.36 0.42 0.41 1.29 0.87 2.4 1.35 4.44E-170 10 33.1 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;cellular component movement;cellular process;muscle filament sliding;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress binding;calcium ion binding;cation binding;ion binding;metal ion binding;structural constituent of muscle;structural molecule activity actin filament bundle;actomyosin;cell cortex part;cell part;contractile fiber part;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;muscle thin filament tropomyosin;non-membrane-bounded organelle;organelle;organelle part;podosome;protein complex;stress fiber Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM)

F5H897;Q12931;I3L0K7;I3L239;I3L253 "Heat shock protein 75 kDa, mitochondrial" TRAP1 ">tr|F5H897|F5H897_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=2 SV=1;>sp|Q12931|TRAP1_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3;>tr|I3L0K7|I3L0K7_HUMAN Heat shock protein 75 kDa, mitoch" NaN NaN 1.52 0.59 1.83 0.91 NaN NaN 6.27E-83 10 19.5 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cytokine receptor binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;tumor necrosis factor receptor binding;tumor necrosis factor receptor superfamily binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle

P45880-2;P45880;P45880-1;B4DKM5;Q5JSD2;Q5JSD1;A2A3S1 Voltage-dependent anion-selective channel protein 2 VDAC2 >sp|P45880-2|VDAC2_HUMAN Isoform 2 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2;>sp|P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2;>sp|P45880-1|VDAC2_HUMAN Isofor 1.05 1.31 0.94 1.35 2.46 0.8 0.79 1.11 4.59E-75 10 37.5 biological regulation;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of protein complex assembly;negative regulation of protein polymerization;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of protein complex assembly;regulation of protein polymerization anion channel activity;anion transmembrane transporter activity;binding;channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;nucleotide binding;passive transmembrane transporter activity;porin activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated ion channel activity;wide pore channel activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial outer membrane;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;pore complex;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease

P67809;H0Y449;C9J5V9;Q9Y2T7 Nuclease-sensitive element-binding protein 1 YBX1 >sp|P67809|YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3;>tr|H0Y449|H0Y449_HUMAN Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens GN=YBX1 PE=4 SV=1;>tr|C9J5V9|C9J5V9_HUMAN Nuclease-sensiti 2 0.75 1.18 0.67 0.43 0.33 1.66 1.13 2.50E-179 10 52.5 "anatomical structure development;biological regulation;biosynthetic process;cell development;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;chordate embryonic development;CRD-mediated mRNA stabilization;developmental process;developmental process involved in reproduction;embryo development;embryo development ending in birth or egg hatching;gamete generation;germ cell development;in utero embryonic development;macromolecule biosynthetic process;macromolecule metabolic process;male gamete generation;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;multicellular organismal process;multicellular organismal reproductive process;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of muscle cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of RNA metabolic process;negative regulation of striated muscle cell differentiation;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oocyte development;positive regulation of biological process;positive regulation of cell division;positive regulation of cellular process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cell division;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mRNA stability;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of striated muscle cell differentiation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization;spermatid development;spermatogenesis;transcription from RNA polymerase II promoter;transcription, DNA-dependent;translational attenuation" binding;chromatin binding;DNA binding;double-stranded DNA binding;lipid binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;ribonucleoprotein binding;RNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;translation regulator activity cell part;CRD-mediated mRNA stability complex;cytoplasm;cytoplasmic part;extracellular region;histone pre-mRNA 3'end processing complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;polysome;protein complex;ribonucleoprotein complex;RNA granule;spliceosomal complex;stress granule;U12-type spliceosomal complex

O95573;F5GWH2;H7BYZ7;H7C260;O60488-2;O60488 Long-chain-fatty-acid--CoA ligase 3 ACSL3 >sp|O95573|ACSL3_HUMAN Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 0.77 0.59 1.52 0.32 1.37 1.47 1.08 1.06 2.56E-40 11 16.7 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;anatomical structure development;biological regulation;biosynthetic process;brain development;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;dendritic spine development;developmental process;embryonic process involved in female pregnancy;establishment of localization;fatty acid biosynthetic process;fatty acid metabolic process;fatty acid transport;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;lipid transport;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of fatty acid transport;negative regulation of icosanoid secretion;negative regulation of lipid transport;negative regulation of organic acid transport;negative regulation of prostaglandin secretion;negative regulation of secretion;negative regulation of transport;neutral lipid biosynthetic process;neutral lipid metabolic process;organ development;organic acid biosynthetic process;organic acid metabolic process;organic acid transport;organic ether metabolic process;organic substance transport;oxoacid metabolic process;plasma lipoprotein particle assembly;plasma lipoprotein particle organization;positive regulation of biological process;positive regulation of cell growth;positive regulation of cellular process;positive regulation of Golgi to plasma membrane protein transport;positive regulation of growth;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of protein transport;positive regulation of secretion;positive regulation of transport;primary metabolic process;protein-lipid complex assembly;protein-lipid complex subunit organization;regulation of biological process;regulation of cell growth;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of fatty acid transport;regulation of Golgi to plasma membrane protein transport;regulation of growth;regulation of icosanoid secretion;regulation of intracellular protein transport;regulation of intracellular transport;regulation of lipid transport;regulation of localization;regulation of organic acid transport;regulation of prostaglandin secretion;regulation of protein localization;regulation of protein transport;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to extracellular stimulus;response to interleukin-15;response to nutrient;response to nutrient levels;response to organic cyclic compound;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;transport;triglyceride biosynthetic process;triglyceride metabolic process;very-low-density lipoprotein particle assembly"acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;arachidonate-CoA ligase activity;ATP binding;binding;catalytic activity;fatty acid ligase activity;ligase activity;ligase activity, forming carbon-sulfur bonds;long-chain fatty acid-CoA ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;very long-chain fatty acid-CoA ligase activity" cell body;cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lipid particle;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;neuronal cell body;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;perinuclear region of cytoplasm;peroxisomal membrane;peroxisomal part Adipocytokine signaling pathway;Fatty acid metabolism;Peroxisome;PPAR signaling pathway

P54886-2;P54886 Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate reductase ALDH18A1 >sp|P54886-2|P5CS_HUMAN Isoform Short of Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1;>sp|P54886|P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 0.84 0.94 1.16 0.64 0.99 1.01 1.23 1.37 1.09E-23 11 16.3 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;citrulline biosynthetic process;citrulline metabolic process;glutamate metabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;L-proline biosynthetic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;ornithine biosynthetic process;ornithine metabolic process;oxoacid metabolic process;primary metabolic process;proline biosynthetic process;proline metabolic process;small molecule biosynthetic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;amino acid kinase activity;ATP binding;binding;catalytic activity;glutamate 5-kinase activity;glutamate-5-semialdehyde dehydrogenase activity;kinase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;phosphotransferase activity, carboxyl group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Arginine and proline metabolism

P12109 Collagen alpha-1(VI) chain COL6A1 >sp|P12109|CO6A1_HUMAN Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3 NaN NaN 0.39 0.54 34.54 1.98 NaN NaN 5.57E-34 11 13.4 axon guidance;biological adhesion;cell adhesion;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;chemotaxis;collagen catabolic process;collagen metabolic process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein oligomerization;protein trimerization;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to organic nitrogen;response to organic substance;response to stimulus;taxis binding;growth factor binding;platelet-derived growth factor binding;protein binding anchoring collagen;cell part;collagen;collagen type VI;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;protein complex;sarcolemma ECM-receptor interaction;Focal adhesion;Protein digestion and absorption

P12110;P12110-3;P12110-2;C9JH44;H7C0M5 Collagen alpha-2(VI) chain COL6A2 >sp|P12110|CO6A2_HUMAN Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4;>sp|P12110-3|CO6A2_HUMAN Isoform 2C2A of Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2;>sp|P12110-2|CO6A2_HUMAN Isoform 2C2A of Collagen alpha-2(VI) chain OS=Homo NaN NaN 0.86 NaN 31.96 NaN NaN NaN 7.86E-39 11 13.3 axon guidance;biological adhesion;cell adhesion;cell-cell adhesion;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;collagen catabolic process;collagen metabolic process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein oligomerization;protein trimerization;response to chemical stimulus;response to external stimulus;response to stimulus;taxis "binding;binding, bridging;extracellular matrix structural constituent;protein binding;protein binding, bridging;structural molecule activity" cell part;collagen;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix;extracellular matrix part;extracellular region part;extracellular space;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;protein complex;proteinaceous extracellular matrix;sarcolemma ECM-receptor interaction;Focal adhesion;Protein digestion and absorption

P35221;P35221-2;F8W845;G3XAM7;Q8N1C0;E5RIB1;E5RJL0;E5RIE0;E5RHV7;E5RGY7;E5RGY6;E5RG03;E5RIC3;P26232-4;P26232-6;E5RJZ2;E5RIT8;E5RFM3;H0YBB8;E5RJ41;A6NKP0;Q9UI47 Catenin alpha-1 CTNNA1>sp|P35221|CTNA1_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1;>sp|P35221-2|CTNA1_HUMAN Isoform 2 of Catenin alpha-1 OS=Homo sapiens GN=CTNNA1;>tr|F8W845|F8W845_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=2 SV=1;>tr|G3XAM7|G3XAM7_HUMAN C1.06 1.19 1.03 0.84 0.65 0.48 0.97 0.8 5.03E-44 11 14.9 adherens junction organization;aging;anatomical structure development;anatomical structure morphogenesis;apical junction assembly;axon regeneration;axonogenesis;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to indole-3-methanol;cellular response to organic substance;cellular response to stimulus;cellular response to stress;developmental process;developmental process involved in reproduction;establishment or maintenance of cell polarity;gap junction assembly;gonad development;macromolecular complex assembly;macromolecular complex subunit organization;male gonad development;muscle cell differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neural precursor cell proliferation;negative regulation of neuroblast proliferation;negative regulation of neurogenesis;negative regulation of programmed cell death;neuron projection morphogenesis;neuron projection regeneration;odontogenesis;odontogenesis of dentine-containing tooth;organ development;organ morphogenesis;ovarian follicle development;ovulation cycle process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle cell differentiation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smoothened signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regeneration;regulation of apoptosis;regulation of biological process;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of nervous system development;regulation of neural precursor cell proliferation;regulation of neurogenesis;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of smoothened signaling pathway;reproductive process;reproductive structure development;response to axon injury;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to indole-3-methanol;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;rhythmic process binding;cadherin binding;cell adhesion molecule binding;protein binding;structural molecule activity acrosomal vesicle;actin cytoskeleton;adherens junction;anchoring junction;catenin complex;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell contact zone;cell-cell junction;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;cytosol;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;intercalated disc;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;plasma membrane;plasma membrane part;protein complex;stored secretory granule;vesicle;zonula adherens Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Endometrial cancer;Leukocyte transendothelial migration;Pathways in cancer;Tight junction

Q14247-3;Q14247;Q14247-2;B4E358;H0YEV2;H7C314;H0YCD9;E9PP90;E9PKG3 Src substrate cortactin CTTN >sp|Q14247-3|SRC8_HUMAN Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN;>sp|Q14247|SRC8_HUMAN Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2;>sp|Q14247-2|SRC8_HUMAN Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN;>tr|B4 0.81 1.15 0.53 1.43 0.73 0.98 0.71 0.64 2.17E-48 11 27.3 cell cortex;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeleton;dendritic spine;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;neuron projection;neuron spine;non-membrane-bounded organelle;organelle;ruffle Bacterial invasion of epithelial cells;Pathogenic Escherichia coli infection;Shigellosis;Tight junction

Q9UHQ9;H7C0R7 NADH-cytochrome b5 reductase 1CYB5R1 >sp|Q9UHQ9|NB5R1_HUMAN NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1;>tr|H7C0R7|H7C0R7_HUMAN NADH-cytochrome b5 reductase 1 (Fragment) OS=Homo sapiens GN=CYB5R1 PE=4 SV=1 0.84 0.87 1.67 0.7 2.91 1.27 1.01 1.15 4.16E-45 11 36.7 alcohol metabolic process;biosynthetic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "catalytic activity;cytochrome-b5 reductase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor" cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle Amino sugar and nucleotide sugar metabolism

Q16643;A8MV58;Q16643-2;D6R9W4;D6RFI1;F8W9Z3;D6R9Q9;D6RCR4 Drebrin DBN1 >sp|Q16643|DREB_HUMAN Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4;>tr|A8MV58|A8MV58_HUMAN Drebrin OS=Homo sapiens GN=DBN1 PE=2 SV=1;>sp|Q16643-2|DREB_HUMAN Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1;>tr|D6R9W4|D6R9W4_HUMAN Drebrin (Fragment) OS=Homo sapien 0.74 1.08 1.06 1.57 0.71 0.55 0.77 0.89 1.42E-60 11 21.3 actin cytoskeleton organization;actin filament organization;actin filament-based process;biological regulation;cell communication;cell communication by chemical coupling;cell communication by electrical coupling;cell differentiation;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;developmental process;generation of neurons;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;neural precursor cell proliferation;neurogenesis;organelle organization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of dendrite development;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse actin binding;binding;cytoskeletal protein binding;profilin binding;protein binding actin cytoskeleton;actomyosin;cell junction;cell part;cell projection;cell-cell junction;cytoplasm;cytoskeletal part;cytoskeleton;dendrite;gap junction;intracellular;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;neuron projection;non-membrane-bounded organelle;organelle;organelle part;plasma membrane

Q92841-1;Q92841-3;Q92841;H3BLZ8;Q92841-2;C9JMU5;G5E9L5 Probable ATP-dependent RNA helicase DDX17 DDX17 >sp|Q92841-1|DDX17_HUMAN Isoform 2 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17;>sp|Q92841-3|DDX17_HUMAN Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17;>sp|Q92841|DDX17_HUMAN Probable ATP-dependent 1.12 1.11 1.01 1.42 0.67 0.54 1.07 0.78 8.56E-35 11 19.5 "anatomical structure development;biological regulation;biosynthetic process;cardiovascular system development;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of estrogen receptor signaling pathway;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of steroid hormone receptor signaling pathway;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;post-embryonic development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of steroid hormone receptor signaling pathway;regulation of striated muscle cell differentiation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;system development;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;estrogen receptor binding;helicase activity;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part

Q14789;Q14789-2;E7EU81;H0Y867 Golgin subfamily B member 1 GOLGB1 >sp|Q14789|GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2;>sp|Q14789-2|GOGB1_HUMAN Isoform 2 of Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1;>tr|E7EU81|E7EU81_HUMAN Golgin subfamily B member 1 (Fragment) OS=Homo sapien 1.34 1.02 3.99 0.68 0.78 0.7 1.1 1.15 5.09E-31 11 4.6 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;Golgi organization;organelle organization cell part;cytoplasmic part;endoplasmic reticulum-Golgi intermediate compartment;Golgi apparatus;Golgi apparatus part;Golgi membrane;Golgi stack;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part

Q00341;Q00341-2;H0Y394;H7C0A4;C9JZI8;C9J5E5;C9JIZ1;C9JT62;C9JHS7;C9JK79;C9JHZ8;C9JES8;C9JMQ6;C9JQ82;C9JBS3;C9JEJ8;C9JKQ5;C9JHN6;H7C2D1;C9JHS9;C9J739;H7BZC3 Vigilin HDLBP >sp|Q00341|VIGLN_HUMAN Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2;>sp|Q00341-2|VIGLN_HUMAN Isoform 2 of Vigilin OS=Homo sapiens GN=HDLBP;>tr|H0Y394|H0Y394_HUMAN Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=4 SV=1 1.34 0.55 0.85 0.39 6.02 0.77 2.23 1.42 4.29E-44 11 11.8 alcohol metabolic process;cholesterol metabolic process;establishment of localization;lipid metabolic process;lipid transport;metabolic process;organic substance transport;primary metabolic process;small molecule metabolic process;steroid metabolic process;sterol metabolic process;transport binding;lipid binding;nucleic acid binding;RNA binding cell part;cytoplasm;extracellular region part;high-density lipoprotein particle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;plasma lipoprotein particle;plasma membrane;protein-lipid complex

Q5T3Q7;Q9H583;Q6P664 HEAT repeat-containing protein 1 HEATR1 >tr|Q5T3Q7|Q5T3Q7_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=2 SV=1;>sp|Q9H583|HEAT1_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3 1.09 1.21 1.87 2.17 0.48 0.31 0.53 0.56 1.90E-35 11 6 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complexRibosome biogenesis in eukaryotes

P52789;E9PB90 Hexokinase-2 HK2>sp|P52789|HXK2_HUMAN Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2;>tr|E9PB90|E9PB90_HUMAN Hexokinase-2 OS=Homo sapiens GN=HK2 PE=2 SV=1 NaN NaN 0.81 NaN 5.12 NaN NaN NaN 7.67E-22 11 14.3 alcohol catabolic process;alcohol metabolic process;apoptotic mitochondrial changes;biological regulation;body fluid secretion;carbohydrate catabolic process;carbohydrate homeostasis;carbohydrate metabolic process;carbohydrate transport;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular glucose homeostasis;cellular homeostasis;cellular metabolic process;cellular process;chemical homeostasis;establishment of localization;generation of precursor metabolites and energy;glucose catabolic process;glucose homeostasis;glucose metabolic process;glucose transport;glycolysis;hexose catabolic process;hexose metabolic process;hexose transport;homeostatic process;lactation;metabolic process;mitochondrion organization;monosaccharide catabolic process;monosaccharide metabolic process;monosaccharide transport;multicellular organismal process;multicellular organismal reproductive process;organelle organization;organic substance transport;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of glucose import;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;secretion;small molecule catabolic process;small molecule metabolic process;transmembrane transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate binding;carbohydrate kinase activity;catalytic activity;fructokinase activity;glucokinase activity;glucose binding;hexokinase activity;kinase activity;mannokinase activity;monosaccharide binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;sugar binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane Amino sugar and nucleotide sugar metabolism;Butirosin and neomycin biosynthesis;Carbohydrate digestion and absorption;Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Insulin signaling pathway;Starch and sucrose metabolism;Streptomycin biosynthesis;Type II diabetes mellitus

Q92743;H0Y7G9 Serine protease HTRA1 HTRA1 >sp|Q92743|HTRA1_HUMAN Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1 1.02 1.11 1.32 0.96 0.27 0.14 0.34 0.33 6.57E-58 11 26.9 biological regulation;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of BMP signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of BMP signaling pathway;regulation of cell communication;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity" cell part;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular part

CON__Q6IME9;Q14CN4-3;Q14CN4-2;Q14CN4;CON__Q14CN4-1;B4DXK4;H0YIG3 "Keratin, type II cytoskeletal 72" KRT72 ">Q6IME9 TREMBL:Q6IME9 Tax_Id=10090 Gene_Symbol=Krt72 Type-II keratin Kb35;>sp|Q14CN4-3|K2C72_HUMAN Isoform 3 of Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72;>sp|Q14CN4-2|K2C72_HUMAN Isoform 2 of Keratin, type II cytoskeletal 72 OS=Homo sapiens" 0.05 18.8 0.06 18.58 0.84 3.04 0.18 0.88 8.19E-251 11 11.9 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

K7EJE8;K7EKE6;F5GZ27;Q8N8K8;P36776;K7ER27;K7ER56;K7ERR6 "Lon protease homolog, mitochondrial" LONP1 ">tr|K7EJE8|K7EJE8_HUMAN Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=3 SV=1;>tr|K7EKE6|K7EKE6_HUMAN Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=3 SV=1;>tr|F5GZ27|F5GZ27_HUMAN Lon protease homolog, mitochondrial OS=Hom" 1.2 1.07 1.58 0.46 1.31 0.8 1.2 1.06 1.14E-28 11 18.5 aging;catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;misfolded or incompletely synthesized protein catabolic process;mitochondrial DNA metabolic process;mitochondrion organization;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;oxidation-dependent protein catabolic process;primary metabolic process;protein catabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein oligomerization;proteolysis;proteolysis involved in cellular protein catabolic process;response to aluminum ion;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to hypoxia;response to inorganic substance;response to metal ion;response to organic substance;response to oxidative stress;response to oxygen levels;response to stimulus;response to stress "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent peptidase activity;binding;catalytic activity;DNA binding;endopeptidase activity;G-quadruplex DNA binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mitochondrial heavy strand promoter anti-sense binding;mitochondrial light strand promoter anti-sense binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA binding;sequence-specific DNA binding;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity;single-stranded DNA binding;single-stranded RNA binding;structure-specific DNA binding;transcription regulatory region DNA binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle lumen;organelle part

P21589-2;P21589;Q96B60;H0Y7R7 5-nucleotidase NT5E >sp|P21589-2|5NTD_HUMAN Isoform 2 of 5-nucleotidase OS=Homo sapiens GN=NT5E;>sp|P21589|5NTD_HUMAN 5-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1;>tr|Q96B60|Q96B60_HUMAN 5-nucleotidase OS=Homo sapiens GN=NT5E PE=2 SV=1 1.53 2.7 0.95 1.56 0.45 0.41 0.25 0.64 5.22E-101 11 24.2 adenosine biosynthetic process;adenosine metabolic process;AMP catabolic process;AMP metabolic process;biological regulation;biosynthetic process;catabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;DNA metabolic process;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of response to external stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside catabolic process;nucleoside metabolic process;nucleoside monophosphate catabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine base metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine nucleoside monophosphate catabolic process;purine nucleoside monophosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine ribonucleoside monophosphate catabolic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;pyrimidine base metabolic process;pyrimidine nucleoside catabolic process;pyrimidine nucleoside metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of defense response;regulation of inflammatory response;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;ribonucleoside biosynthetic process;ribonucleoside metabolic process;ribonucleoside monophosphate catabolic process;ribonucleoside monophosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "5'-nucleotidase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nucleotidase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity" anchored to membrane;cell part;cytoplasm;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;vesicle Nicotinate and nicotinamide metabolism;Purine metabolism;Pyrimidine metabolism

Q14690 Protein RRP5 homolog PDCD11 >sp|Q14690|RRP5_HUMAN Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 1.09 0.96 1.62 1.75 0.52 0.3 0.82 0.72 1.69E-40 11 8 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part

Q13835-2;Q13835 Plakophilin-1 PKP1 >sp|Q13835-2|PKP1_HUMAN Isoform 1 of Plakophilin-1 OS=Homo sapiens GN=PKP1;>sp|Q13835|PKP1_HUMAN Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2 0.76 1.17 1.13 1.17 0.98 1.36 0.94 0.53 1.79E-57 11 17.2 biological adhesion;cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;multicellular organismal development;multicellular organismal process;organelle organization binding;intermediate filament binding;lamin binding;molecular transducer activity;protein binding;protein complex binding;signal transducer activity;structural constituent of epidermis;structural molecule activity anchoring junction;cell junction;cell part;cell-cell junction;cytoskeletal part;desmosome;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex

P51149;C9J592;C9J8S3;C9J4V0;C9IZZ0;C9J4S4;C9J7D1 Ras-related protein Rab-7a RAB7A >sp|P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1;>tr|C9J592|C9J592_HUMAN Ras-related protein Rab-7a (Fragment) OS=Homo sapiens GN=RAB7A PE=2 SV=1;>tr|C9J8S3|C9J8S3_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7 0.87 1.17 2.26 0.5 3.08 1.32 1.08 1.11 3.52E-283 11 58.9 anatomical structure homeostasis;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;bone resorption;catabolic process;cation homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular monovalent inorganic cation homeostasis;cellular process;cellular protein catabolic process;cellular protein metabolic process;cellular response to

stimulus;chemical homeostasis;early endosome to late endosome transport;endosome to lysosome transport;endosome transport;epidermal growth factor catabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;homeostatic process;immune system process;intracellular pH reduction;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;lysosomal transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monovalent inorganic cation homeostasis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle fusion;organelle organization;pH reduction;phagosome acidification;phagosome-lysosome fusion;primary metabolic process;protein catabolic process;protein metabolic process;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular pH;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of intracellular pH;regulation of pH;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;small GTPase mediated signal transduction;tissue homeostasis;transport;vacuolar transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endosome;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;lysosomal membrane;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;phagocytic vesicle;phagocytic vesicle membrane;pigment granule;vacuolar membrane;vacuolar part;vesicle;vesicle membrane
Amoebiasis;Endocytosis;ko05152;Phagosome

P62269;J3JS69 40S ribosomal protein S18 RPS18 >sp|P62269|RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 1.61 1.03 10.69 0.68 0.96 0.79 1.1 0.71 4.82E-71 11 53.3 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;collagen;cytosolic small ribosomal subunit;extracellular matrix part;extracellular region part;intracellular organelle part;intracellular part;macromolecular complex;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome

P23396;E9PPU1;E9PL09;P23396-2;F2Z2S8;H0YCJ7;E9PL45;H0YF32;E9PQ96;E9PJH4;E9PK82;H0YEU2;E9PQX2;E9PSF4;H0YES8 40S ribosomal protein S3 RPS3 >sp|P23396|RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2;>tr|E9PPU1|E9PPU1_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1;>tr|E9PL09|E9PL09_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1;>sp|P23396 1.37 1.04 0.62 0.66 0.78 0.88 1.15 0.91 5.11E-81 11 49 "activation of caspase activity;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;induction of apoptosis;induction of programmed cell death;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA repair;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of sequence-specific DNA binding transcription factor activity;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;positive regulation of programmed cell death;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of DNA metabolic process;regulation of DNA repair;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" "binding;carbon-oxygen lyase activity;catalytic activity;damaged DNA binding;DNA binding;DNA-(apurinic or apyrimidinic site) lyase activity;endonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;iron-sulfur cluster binding;lyase activity;metal cluster binding;mRNA binding;nuclease activity;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity" cell part;cell projection membrane;cell projection part;cytoplasm;cytoplasmic part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part;ribonucleoprotein complex;ribosome;ruffle membrane;small ribosomal subunit Ribosome

O75533;H7C341 Splicing factor 3B subunit 1 SF3B1 >sp|O75533|SF3B1_HUMAN Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 1.11 0.95 1.26 1.42 1.88 0.43 0.78 0.74 5.30E-31 11 9.8 "anterior/posterior pattern specification;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;pattern specification process;primary metabolic process;regionalization;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;chromatin binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome

Q02880-2;Q02880;E9PCY5;B4DLV2 DNA topoisomerase 2-beta;DNA topoisomerase 2 TOP2B >sp|Q02880-2|TOP2B_HUMAN Isoform Beta-1 of DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B;>sp|Q02880|TOP2B_HUMAN DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3;>tr|E9PCY5|E9PCY5_HUMAN DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B 1.07 1.44 1.19 2.37 0.46 0.57 0.5 0.45 5.10E-62 11 7.8 anatomical structure development;anatomical structure morphogenesis;axonogenesis;biosynthetic process;cell cycle process;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome organization;chromosome segregation;chromosome separation;developmental process;DNA conformation change;DNA metabolic process;DNA recombination;DNA replication;DNA topological change;DNA-dependent DNA replication;forebrain development;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;meiotic chromosome separation;metabolic process;mitotic recombination;neuron migration;neuron projection morphogenesis;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;resolution of meiotic recombination intermediates;sister chromatid segregation "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cation binding;chromatin binding;DNA binding;DNA topoisomerase (ATP-hydrolyzing) activity;DNA topoisomerase activity;DNA-dependent ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;isomerase activity;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromatin remodeling complex;chromosomal part;chromosome;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;SWI/SNF-type complex;synaptonemal complex;WINAC complex

P06753-5;P06753-2;Q5VU59;P06753-4;P06753-3;Q5VU58;Q5VU61;D6R904;K7EP68;H0YL80;Q5VU63;A6NL28-2;A6NL28;D6RFM2 TPM3;TPM4 >sp|P06753-5|TPM3_HUMAN Isoform 5 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3;>sp|P06753-2|TPM3_HUMAN Isoform 2 of Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3;>tr|Q5VU59|Q5VU59_HUMAN Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=2 SV= 0.97 0.51 0.31 0.55 1.08 0.87 1.81 1.29 5.81E-131 11 36.7

actin cytoskeleton;cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P12956;B1AHC9;B1AHC8;F5H1I8 X-ray repair cross-complementing protein 6 XRCC6 >sp|P12956|XRCC6_HUMAN X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2;>tr|B1AHC9|B1AHC9_HUMAN X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=2 SV=1;>tr|B1AHC8|B1AHC8_HUMAN X-ray repair complementing de 1.42 0.36 1.01 0.52 1.07 0.45 2.11 1.04 1.49E-62 11 21.7 "anatomical structure homeostasis;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;DNA ligation;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via nonhomologous end joining;homeostatic process;immune system process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to DNA damage stimulus;response to ionizing radiation;response to radiation;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;telomere maintenance;telomere organization;transcription, DNA-dependent;V(D)J recombination"	"5'-deoxyribose-5-phosphate lyase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;carbon-oxygen lyase activity;catalytic activity;damaged DNA binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;double-stranded DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lyase activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;sequence-specific DNA binding;structure-specific DNA binding;telomeric DNA binding;transcription regulatory region DNA binding"	cell part;chromosomal part;cytoplasm;intracellular organelle part;intracellular part;Ku70:Ku80 complex;macromolecular complex;membrane;nonhomologous end joining complex;nuclear chromosome part;nuclear part;nuclear telomere cap complex;nucleoplasm part;organelle part;protein complex;protein-DNA complex;telomere cap complex;transcription factor complex	Non-homologous end-joining

Q99798;A2A274	"Aconitate hydratase, mitochondrial"	ACO2	">sp|Q99798|ACON_HUMAN Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2;>tr|A2A274|A2A274_HUMAN Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=2 SV=1" 0.21 8.17 0.1	6	0.26 2.05 2.03 1.12 8.63E-55 12	21	acetyl-CoA catabolic process;acetyl-CoA metabolic process;carboxylic acid metabolic process;catabolic process;cell death;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;citrate metabolic process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;death;isocitrate metabolic process;metabolic process;organic acid metabolic process;oxoacid metabolic process;small molecule metabolic process;tricarboxylic acid cycle;tricarboxylic acid metabolic process	"3 iron, 4 sulfur cluster binding;4 iron, 4 sulfur cluster binding;aconitate hydratase activity;binding;carbon-oxygen lyase activity;catalytic activity;cation binding;citrate hydro-lyase (cis-aconitate-forming) activity;hydro-lyase activity;ion binding;iron ion binding;iron-sulfur cluster binding;isocitrate hydro-lyase (cis-aconitate-forming) activity;lyase activity;metal cluster binding;metal ion binding;transition metal ion binding"	cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part	Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism

Q14240;Q14240-2;E7EQG2;J3KSN7;Q9NZE6;J3KT04;J3KS93;E7EMV8;B4E102	Eukaryotic initiation factor 4A-II	EIF4A2	>sp|Q14240|IF4A2_HUMAN Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2;>sp|Q14240-2|IF4A2_HUMAN Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2;>tr|E7EQG2|E7EQG2_HUMAN Eukaryotic initiation factor 4A-II OS=H	0.43 2.8	0.15 1.96 0.56 1.02 0.68 0.99 5.01E-82 12	27.5 biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;signal transduction;viral reproductive process;virus-host interaction	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity"	cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex	RNA transport

P38919;I3L3H2;J3QQP0;E9PBH4;F8WE11;C9JUF0;J3QL52	Eukaryotic initiation factor 4A-III	EIF4A3	>sp|P38919|IF4A3_HUMAN Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	1.12 1.64 1.7	2.23 0.25 0.35 0.46 0.47 2.24E-28 12	24.8 "biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of RNA localization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;mRNA transport;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;rRNA metabolic process;rRNA processing;signal transduction;transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mRNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;single-stranded RNA binding" catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;exon-exon junction complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport;Spliceosome

Q04637-6;Q04637-7;Q04637-5;E7EX73;Q04637-4;E9PGM1;Q04637-3;E7EUU4;Q04637;Q04637-8;Q04637-9;C9J6B6;C9JF13;C9J2Z7;C9K073;H7C0V6;H7C044;F5H8J4;F5H564;Q504Z1;O43432;O43432-3 Eukaryotic translation initiation factor 4 gamma 1EIF4G1 >sp|Q04637-6|IF4G1_HUMAN Isoform E of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1;>sp|Q04637-7|IF4G1_HUMAN Isoform 7 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1;>sp|Q04637-5|IF4G1_HUMAN I 1.09 0.57 0.54 0.29 2.11 1.61 1.76 1.01 4.37E-35 12 10.1 "biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytokine-mediated signaling pathway;death;enzyme linked receptor protein signaling pathway;gamete generation;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;male gamete generation;meiotic prophase I;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;prophase;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of translation;regulation of translational initiation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;signal transduction;spermatogenesis;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproductive process;virus-host interaction" "binding;DNA binding;nucleic acid binding;RNA binding;RNA cap binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex RNA transport;Viral myocarditis

Q9Y6C2;H0Y7A0 EMILIN-1 EMILIN1>sp|Q9Y6C2|EMIL1_HUMAN EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2 NaN NaN 0.81 NaN 47.41 NaN NaN NaN 2.62E-39 12 16.8 biological adhesion;biological regulation;cell adhesion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular structure organization;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;regulation of biological process;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular process extracellular matrix constituent conferring elasticity;extracellular matrix structural constituent;structural molecule activity collagen;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;membrane-bounded organelle;membrane-bounded vesicle;organelle;vesicle

P06396-2;F5H1A8;P06396-3;P06396;CON__Q3SX14;Q5T0H8;Q5T0H9;Q5T0H7;Q5T0I0;Q5T0I1 Gelsolin GSN >sp|P06396-2|GELS_HUMAN Isoform 2 of Gelsolin OS=Homo sapiens GN=GSN;>tr|F5H1A8|F5H1A8_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=2 SV=1;>sp|P06396-3|GELS_HUMAN Isoform 3 of Gelsolin OS=Homo sapiens GN=GSN;>sp|P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GS 0.25 1.4 0.21 0.74 1.43 2.74 0.92 1.35 3.90E-30 12 21.9 actin cytoskeleton organization;actin filament capping;actin filament organization;actin filament polymerization;actin filament severing;actin filament-based process;actin polymerization or depolymerization;aging;anatomical structure development;anatomical structure morphogenesis;apoptosis;barbed-end actin filament capping;biological regulation;cell death;cell development;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to cadmium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;cilium morphogenesis;cytoskeleton organization;death;developmental growth;developmental process;establishment of localization;glial cell development;growth;inositol lipid-mediated signaling;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;oligodendrocyte development;organelle organization;phosphatidylinositol-mediated signaling;programmed cell death;protein complex assembly;protein complex subunit organization;protein polymerization;regeneration;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to acid;response to cadmium ion;response to chemical stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to folic acid;response to inorganic substance;response to metal ion;response to nutrient;response to nutrient levels;response to organic substance;response to stimulus;response to vitamin;signal transduction;tissue development;tissue regeneration;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding actin cytoskeleton;cell part;cell projection;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;protein complex;ruffle;vesicle Fc gamma R-mediated phagocytosis;Regulation of actin cytoskeleton

Q5SSJ5;Q5SSJ5-2;B0QZK4;Q5SSJ5-3;Q5SWC8;B0QZK9;B0QZK8;Q5SSJ5-5 Heterochromatin protein 1-binding protein 3 HP1BP3 >sp|Q5SSJ5|HP1B3_HUMAN Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1;>sp|Q5SSJ5-2|HP1B3_HUMAN Isoform 2 of Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3;>tr|B0QZK4|B0QZK4_HUMAN Heterochromatin prote 1.07 1.17 1.03 2.06 0.71 0.71 0.63 0.7 6.05E-27 12 23.5 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex

Q86YZ3;CON__Q86YZ3 Hornerin HRNR >sp|Q86YZ3|HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2;>Q86YZ3 SWISS-PROT:Q86YZ3 Tax_Id=9606 Gene_Symbol=HRNR Hornerin 0.19 5.28 0.06 4.45 0.55 2.85 0.85 1.44 3.26E-33 12 16.2 developmental process;keratinization binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cornified envelope;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;vesicle

P04792;F8WE04;C9J3N8 Heat shock protein beta-1 HSPB1 >sp|P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 0.55 0.59 0.52 0.21 3.63 2.59 1.39 1.22 9.79E-112 12 71.2 biological regulation;cell death;cell surface receptor linked signaling pathway;cellular component movement;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to vascular endothelial growth factor stimulus;death;enzyme linked receptor protein signaling pathway;gene expression;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;metabolic process;mRNA metabolic process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of angiogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of blood vessel endothelial cell migration;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine biosynthetic process;positive regulation of cytokine production;positive regulation of developmental process;positive regulation of endothelial cell migration;positive regulation of interleukin-1 beta production;positive regulation of interleukin-1 production;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of protein metabolic process;positive regulation of tumor necrosis factor biosynthetic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of blood vessel endothelial cell migration;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of developmental process;regulation of endothelial cell migration;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of interleukin-1 beta production;regulation of interleukin-1 production;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of translation;regulation of translational initiation;regulation of tumor necrosis factor biosynthetic process;regulation of tumor necrosis factor production;response to biotic stimulus;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;response to virus;RNA metabolic process;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;vascular endothelial growth factor receptor signaling pathway;vascular endothelial growth factor receptor signaling pathway involved in endothelial cell chemotaxis binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;kinase binding;kinase inhibitor activity;kinase regulator activity;protein binding;protein kinase binding;protein kinase C binding;protein kinase C inhibitor activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity;small conjugating protein binding;ubiquitin binding cell part;cell surface;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;proteasome complex;protein complex;spindle;Z disc Amoebiasis;MAPK signaling pathway;VEGF signaling pathway

Q13724-2;Q13724;C9J8D4;C9JDQ1 Mannosyl-oligosaccharide glucosidase MOGS >sp|Q13724-2|MOGS_HUMAN Isoform 2 of Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS;>sp|Q13724|MOGS_HUMAN Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS PE=1 SV=5;>tr|C9J8D4|C9J8D4_HUMAN Mannosyl-oligosaccharide glucosidase (Fra 1.07 0.61 1.19 0.48 1.68 1.44 1.32 1.39 1.70E-33 12 20.4 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;oligosaccharide metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine "catalytic activity;glucosidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;mannosyl-oligosaccharide glucosidase activity"cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part N-Glycan biosynthesis;Protein processing in endoplasmic reticulum

P26038;P35241-4;P35241;P35241-5 Moesin MSN >sp|P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 0.55 2 0.31 1.47 0.74 0.65 1.12 1.18 3.03E-71 12 20.1 actin filament capping;apical protein localization;asymmetric protein localization;biological adhesion;biological regulation;cell adhesion;cell migration;cell motility;cell projection assembly;cell projection organization;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;immune system process;leukocyte cell-cell adhesion;leukocyte migration;localization;locomotion;macromolecule localization;membrane docking;membrane to membrane docking;microvillus assembly;microvillus organization;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;protein localization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell migration;regulation of cell motility;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of immune system process;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of lymphocyte migration;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization structural constituent of cytoskeleton;structural molecule activity apical part of cell;apical plasma membrane;basolateral plasma membrane;cell division site part;cell part;cell projection;cell projection membrane;cell projection part;cleavage furrow;cytoplasm;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;extrinsic to membrane;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microvillus;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;plasma membrane part;ruffle;stereocilium;uropod;vesicle Leukocyte transendothelial migration;Measles;Regulation of actin cytoskeleton

Q8WUM4;Q8WUM4-2;F8WDK9 Programmed cell death 6-interacting protein PDCD6IP >sp|Q8WUM4|PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1;>sp|Q8WUM4-2|PDC6I_HUMAN Isoform 2 of Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP0.78 1.33 0.51 0.79 2.47 2.08 0.83 0.93 7.14E-116 12 16.4 apoptosis;cell cycle;cell death;cell division;cellular process;death;establishment of localization;establishment of protein localization;interaction with host;interspecies interaction between organisms;multi-organism process;programmed cell death;protein transport;reproductive process;transport;viral reproductive process;virus-host interaction cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;organelle;organelle part;pigment granule;vesicle Endocytosis

P35232;C9JW96;C9JZ20;E7ESE2;E9PCW0;B4DY47;D6RBK0 Prohibitin PHB>sp|P35232|PHB_HUMAN Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1;>tr|C9JW96|C9JW96_HUMAN Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=2 SV=2;>tr|C9JZ20|C9JZ20_HUMAN Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=2 SV=1;>tr|E7ESE2|E7ESE2_HUMAN Prohibiti 0.94 1.59 1.77 1.22 0.54 0.44 0.69 0.94 5.95E-156 12 51.1 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interleukin-6;cellular response to organic substance;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;DNA biosynthetic process;DNA metabolic process;DNA replication;histone deacetylation;histone modification;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of androgen receptor signaling pathway;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of glucocorticoid receptor signaling pathway;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription by competitive promoter binding;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;progesterone receptor signaling pathway;protein deacetylation;protein deacylation;protein metabolic process;protein modification process;regulation of androgen receptor signaling pathway;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of glucocorticoid receptor signaling pathway;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to cytokine stimulus;response to interleukin-6;response to organic substance;response to stimulus;signal transduction;steroid hormone receptor signaling pathway" binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription regulatory region DNA binding cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;nuclear part;nucleoplasm;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane part

P16435;H0Y4R2;E7EVY7;E7EPN3;E7EMD0;F5H468;E7EWU0 NADPH--cytochrome P450 reductase POR>sp|P16435|NCPR_HUMAN NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2;>tr|H0Y4R2|H0Y4R2_HUMAN NADPH--cytochrome P450 reductase (Fragment) OS=Homo sapiens GN=POR PE=4 SV=1;>tr|E7EVY7|E7EVY7_HUMAN NADPH--cytochrome P450 reductase OS=Homo sa 0.92 0.71 1.94 0.39 1.84 1.34 1.18 0.95 3.26E-38 12 18.6 amine metabolic process;betaine metabolic process;biological regulation;carboxylic acid metabolic process;carnitine metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular organofluorine metabolic process;cellular organohalogen metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to follicle-stimulating hormone stimulus;cellular response to gonadotropin stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;demethylation;fatty acid metabolic process;fatty acid oxidation;flavonoid metabolic process;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;lipid metabolic process;lipid modification;lipid oxidation;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of lipase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;nitrate catabolic process;nitrate metabolic process;nitric oxide catabolic process;nitric oxide metabolic process;nitrogen compound metabolic process;one-carbon metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;phenylpropanoid metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cholesterol biosynthetic process;positive regulation of cholesterol metabolic process;positive regulation of chondrocyte differentiation;positive regulation of developmental process;positive regulation of hormone biosynthetic process;positive regulation of hormone metabolic process;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of monooxygenase activity;positive regulation of oxidoreductase activity;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smoothened signaling pathway;positive regulation of steroid biosynthetic process;positive regulation of steroid hormone biosynthetic process;positive regulation of steroid metabolic process;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cartilage development;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cholesterol biosynthetic process;regulation of cholesterol metabolic process;regulation of chondrocyte differentiation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental growth;regulation of developmental process;regulation of endopeptidase activity;regulation of growth;regulation of growth plate cartilage chondrocyte proliferation;regulation of hormone biosynthetic process;regulation of hormone metabolic process;regulation of hydrolase activity;regulation of lipase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of organ morphogenesis;regulation of oxidoreductase activity;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of smoothened signaling pathway;regulation of steroid biosynthetic process;regulation of steroid hormone biosynthetic process;regulation of steroid metabolic process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to follicle-stimulating hormone stimulus;response to gonadotropin stimulus;response to hormone stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to peptide hormone stimulus;response to stimulus;secondary metabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;cytochrome-b5 reductase activity;electron carrier activity;flavin adenine dinucleotide binding;FMN binding;hydrolase activity;ion binding;iron ion binding;iron-cytochrome-c reductase activity;metal ion binding;monooxygenase activity;NADP binding;NADPH-hemoprotein reductase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;transition metal ion binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part

Q13200;E7EW34;E9PCS3;H7C1H2;F8WBS8;H7C2Q3;C9JPC0 26S proteasome non-ATPase regulatory subunit 2PSMD2 >sp|Q13200|PSMD2_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3;>tr|E7EW34|E7EW34_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1;>tr|E9PCS3|E9PCS3_HUMAN 26S proteasome non-AT 0.93 0.88 0.31 0.84 1.79 1.07 1.49 1.35 3.79E-49 12 17.5 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" enzyme regulator activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome complex;proteasome regulatory particle;protein complex Proteasome

P11216;H0Y4Z6;P11217-2;P06737-2;E9PK47;P11217;P06737;E9PMM6 "Glycogen phosphorylase, brain form" PYGB ">sp|P11216|PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5" 0.81 1 0.32 0.34 1.45 1.57 1.41 1.07 6.73E-73 12 19.2 5-phosphoribose 1-diphosphate biosynthetic process;5-phosphoribose 1-diphosphate metabolic process;alcohol biosynthetic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate homeostasis;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;chemical homeostasis;D-ribose biosynthetic process;D-ribose metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan catabolic process;glucan metabolic process;glucose homeostasis;glucose metabolic process;glycogen catabolic process;glycogen metabolic process;heterocycle metabolic process;hexose metabolic process;homeostatic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;oxidation-reduction process;pentose biosynthetic process;pentose metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;regulation of biological quality;ribose phosphate biosynthetic process;ribose phosphate metabolic process;small molecule biosynthetic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;AMP binding;ATP binding;bile acid binding;binding;carbohydrate binding;carboxylic acid binding;catalytic activity;cofactor binding;drug binding;glucose binding;glycogen phosphorylase activity;identical protein binding;lipid binding;monocarboxylic acid binding;monosaccharide binding;nucleobase binding;nucleotide binding;phosphorylase activity;protein binding;protein dimerization activity;protein homodimerization activity;purine base binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyridoxal phosphate binding;ribonucleotide binding;steroid binding;sugar binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;vitamin B6 binding;vitamin binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Insulin signaling pathway;Starch and sucrose metabolism

P38159;P38159-2;H3BT71;Q96E39;H0Y6E7;B3KRG5;H3BUY5;H3BR27;P38159-3;O75526;H3BNC1;Q8IZ40;Q8N7X1 "RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome, N-terminally processed;RNA binding motif protein, X-linked-like-1" RBMX;RBMXL1 ">sp|P38159|RBMX_HUMAN RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3;>sp|P38159-2|RBMX_HUMAN Isoform 2 of RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX;>tr|H3BT71|H3BT71_HUMAN RNA-binding motif protein, X chromo" 1.06 1.41 1.44 2.49 0.37 0.38 0.42 0.48 6.28E-156 12 27.1 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interleukin-1;cellular response to organic substance;cellular response to stimulus;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;membrane protein ectodomain proteolysis;membrane protein proteolysis;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein oligomerization;proteolysis;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to cytokine stimulus;response to interleukin-1;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;chromatin binding;core promoter binding;DNA binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleotide binding;protein binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;sequence-specific DNA binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding catalytic step 2 spliceosome;cell part;chromatin;chromosomal part;euchromatin;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex;transcription factor complex;vesicle Spliceosome

P62701;C9JEH7;Q8TD47;P22090;A6NH36;C9JQ55 "40S ribosomal protein S4, X isoform;40S ribosomal protein S4, Y isoform 2;40S ribosomal protein S4, Y isoform 1" RPS4X;RPS4Y1;RPS4Y2 ">sp|P62701|RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2;>tr|C9JEH7|C9JEH7_HUMAN 40S ribosomal protein S4, Y isoform 1 (Fragment) OS=Homo sapiens GN=RPS4Y1 PE=2 SV=1;>sp|Q8TD47|RS4Y2_HUMAN 40S ribosomal protein S4, Y iso" 1.53 1.07 1.17 0.65 1.06 0.74 1.01 0.7 2.07E-241 12 43.3 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;multicellular organismal development;multicellular organismal process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;polysome;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome

P46781;B5MCT8;C9JM19;F2Z3C0;A8MXK4 40S ribosomal protein S9 RPS9 >sp|P46781|RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3;>tr|B5MCT8|B5MCT8_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=2 SV=1;>tr|C9JM19|C9JM19_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=2 SV=1 1.33 0.76 0.61 0.63 1.41 0.99 1.35 0.94 3.37E-90 12 49.5 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cell proliferation;regulation of cellular process;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity;translation regulator activity cell part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome

O75746;B3KR64;F8W9J0;H0YFB2;B4DGK6 Calcium-binding mitochondrial carrier protein Aralar1 SLC25A12 >sp|O75746|CMC1_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2;>tr|B3KR64|B3KR64_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=2 SV=1 NaN NaN 1.35 1.94 0.59 0.75 NaN NaN 3.64E-30 12 20.6 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;establishment of localization;establishment of localization in cell;gluconeogenesis;glucose metabolic process;hexose biosynthetic process;hexose metabolic process;intracellular transport;malate-aspartate shuttle;metabolic process;mitochondrial transport;monosaccharide biosynthetic process;monosaccharide metabolic process;primary metabolic process;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;small molecule biosynthetic process;small molecule metabolic process;transmembrane transport;transport acidic amino acid transmembrane transporter activity;active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;binding;calcium ion binding;carboxylic acid transmembrane transporter activity;cation binding;ion binding;L-amino acid transmembrane transporter activity;L-aspartate transmembrane transporter activity;L-glutamate transmembrane transporter activity;metal ion binding;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

P35442;Q5RI53 Thrombospondin-2 THBS2 >sp|P35442|TSP2_HUMAN Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2 0.48 0.64 1.05 0.79 0.48 0.24 0.83 2.05 8.85E-207 12 14.2 biological adhesion;biological regulation;cell adhesion;cellular process;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of developmental process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process binding;calcium ion binding;carbohydrate binding;cation binding;glycosaminoglycan binding;heparin binding;ion binding;metal ion binding;pattern binding;polysaccharide binding basement membrane;extracellular matrix part;extracellular region;extracellular region part ECM-receptor interaction;Focal adhesion;Malaria;Phagosome;TGF-beta signaling pathway

P09493-3;P09493-9;P09493-4;P09493-10;Q6ZN40;H0YL52;P09493;P09493-8;H0YKX5;P09493-2;H7BYY1;P09493-7;F5H7S3;B7Z596;P09493-6;H0YKP3;H0YNC7;P09493-5;H0YK48;H0YK20;H0YL42;K7ELP0;H0YKZ6 Tropomyosin alpha-1 chain TPM1 >sp|P09493-3|TPM1_HUMAN Isoform 3 of Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1;>sp|P09493-9|TPM1_HUMAN Isoform 9 of Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1;>sp|P09493-4|TPM1_HUMAN Isoform 4 of Tropomyosin alpha-1 chain OS=Homo sapiens GN= 0.92 0.51 0.51 0.56 0.84 0.75 1.97 1.59 4.11E-54 12 34.5 actin cytoskeleton organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;actomyosin structure organization;anatomical structure morphogenesis;biological regulation;cardiac muscle contraction;cardiac muscle tissue morphogenesis;cell projection organization;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;chordate embryonic development;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;in utero embryonic development;multicellular organismal process;muscle contraction;muscle filament sliding;muscle system process;muscle tissue morphogenesis;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;organelle organization;positive regulation of actin filament bundle assembly;positive regulation of ATPase activity;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of heart rate by epinephrine;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of organelle organization;positive regulation of stress fiber assembly;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of ATPase activity;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of heart contraction;regulation of heart rate;regulation of heart rate by chemical signal;regulation of hydrolase activity;regulation of localization;regulation of locomotion;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of stress fiber assembly;regulation of system process;response to chemical stimulus;response to inorganic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;response to wounding;ruffle organization;sarcomere organization;striated muscle contraction;system process;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis;wound healing actin binding;binding;cytoskeletal protein binding;protein binding;structural constituent of cytoskeleton;structural constituent of muscle;structural molecule activity actin cytoskeleton;actin filament bundle;actomyosin;bleb;cell part;cell projection;cell projection membrane;cell projection part;contractile fiber;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;muscle thin filament tropomyosin;myofibril;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;protein complex;ruffle membrane;stress fiber Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM)

Q13263;Q13263-2;M0R0K9;M0R2I3 Transcription intermediary factor 1-beta TRIM28 >sp|Q13263|TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5;>sp|Q13263-2|TIF1B_HUMAN Isoform 2 of Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28;>tr|M0R0K9|M0R0K9_HUMAN Transcription intermediary 1.38 0.79 1.3 1 1.02 0.47 1.31 1.03 4.02E-66 12 21.4 "anatomical structure morphogenesis;biological regulation;biosynthetic process;cell morphogenesis;cell morphogenesis involved in differentiation;cellular biosynthetic process;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;convergent extension;convergent extension involved in axis elongation;developmental process;DNA metabolic process;DNA repair;embryonic morphogenesis;embryonic placenta morphogenesis;epithelial to mesenchymal transition;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of an epithelium;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA repair;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein autophosphorylation;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein oligomerization;protein phosphorylation;protein sumoylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;tissue morphogenesis;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent" "acid-amino acid ligase activity;binding;catalytic activity;cation binding;DNA binding;enzyme binding;ion binding;kinase activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;phosphotransferase activity, alcohol group as acceptor;protein binding;protein binding transcription factor activity;protein kinase activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;small conjugating protein ligase activity;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;ubiquitin protein ligase binding;ubiquitin-protein ligase activity;zinc ion binding"cell part;chromatin;chromosomal part;euchromatin;heterochromatin;intracellular;intracellular organelle part;intracellular part;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear heterochromatin;nuclear part;nucleoplasm;organelle part

I3L4N8 ACTG1 ">tr|I3L4N8|I3L4N8_HUMAN Actin, cytoplasmic 2, N-terminally processed (Fragment) OS=Homo sapiens GN=ACTG1 PE=2 SV=1" NaN NaN NaN NaN NaN NaN NaN NaN 9.01E-178 13 59.9 adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P07814 Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase EPRS >sp|P07814|SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 1.28 0.53 0.59 0.44 5.34 1.13 1.6 1.12 6.80E-28 13 11.9 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;glutamyl-tRNA aminoacylation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;prolyl-tRNA aminoacylation;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;glutamate-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;proline-tRNA ligase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;RNA stem-loop binding" cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;ribonucleoprotein complex Aminoacyl-tRNA biosynthesis;Porphyrin and chlorophyll metabolism

P43304;P43304-2;F8W6E4;F5GYK7 "Glycerol-3-phosphate dehydrogenase, mitochondrial" GPD2 ">sp|P43304|GPDM_HUMAN Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2 PE=1 SV=3;>sp|P43304-2|GPDM_HUMAN Isoform 2 of Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2;>tr|F8W6E4|F8W6E4_HUMAN Glycerol-3-phos" 1.53 1.67 2.05 0.74 1.1 0.66 0.78 0.9 6.18E-47 13 20.9 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;alditol catabolic process;alditol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;gluconeogenesis;glucose metabolic process;glycerol catabolic process;glycerol metabolic process;glycerol-3-phosphate metabolic process;hexose biosynthetic process;hexose metabolic process;lipid metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;polyol catabolic process;polyol metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "binding;calcium ion binding;catalytic activity;cation binding;glycerol-3-phosphate dehydrogenase activity;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor;sn-glycerol-3-phosphate:ubiquinone oxidoreductase activity;sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity" cell part;cytoplasmic part;glycerol-3-phosphate dehydrogenase complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex Glycerophospholipid metabolism

P51659;E7ER27;E7EWE5;P51659-3;P51659-2;G5E9S2;E7ET17;E7EPL9 Peroxisomal multifunctional enzyme type 2;(3R)-hydroxyacyl-CoA dehydrogenase;Enoyl-CoA hydratase 2 HSD17B4 >sp|P51659|DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3;>tr|E7ER27|E7ER27_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=2 SV=3;>tr|E7EWE5|E7EWE5_HUMAN Peroxisomal multifunctional 1.01 0.52 0.67 0.29 3.81 2.87 1.61 1.28 1.46E-31 13 26.1 anatomical structure development;androgen metabolic process;bile acid biosynthetic process;bile acid metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell development;cellular biosynthetic process;cellular catabolic process;cellular developmental process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;developmental process;developmental process involved in reproduction;estrogen metabolic process;fatty acid beta-oxidation;fatty acid beta-oxidation using acyl-CoA oxidase;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;hormone metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;regulation of biological quality;regulation of hormone levels;reproductive process;Sertoli cell development;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;very long-chain fatty acid metabolic process "3alpha,7alpha,12alpha-trihydroxy-5beta-cholest-24-enoyl-CoA hydratase activity;3-hydroxyacyl-CoA dehydrogenase activity;binding;carbon-oxygen lyase activity;catalytic activity;hydro-lyase activity;identical protein binding;isomerase activity;lipid binding;long-chain-enoyl-CoA hydratase activity;lyase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;protein binding;protein dimerization activity;protein homodimerization activity;steroid binding;sterol binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part;peroxisome Peroxisome;Primary bile acid biosynthesis

J3KR24;P41252;Q5TCC5;Q5TCC4;Q5TCD2;Q5TCC6;Q5TCD1 "Isoleucine--tRNA ligase, cytoplasmic" IARS ">tr|J3KR24|J3KR24_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=4 SV=1;>sp|P41252|SYIC_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2" 1.06 0.91 0.37 0.56 7.04 1.53 1.44 1.13 1.54E-35 13 13.4 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;isoleucyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;isoleucine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis"

Q8N163-2;Q8N163;G3V119;H0YB24;H0YC69;E5RFJ3;H0YC58;E5RHJ4;E5RGU7 DBIRD complex subunit KIAA1967 KIAA1967 >sp|Q8N163-2|K1967_HUMAN Isoform 2 of DBIRD complex subunit KIAA1967 OS=Homo sapiens GN=KIAA1967;>sp|Q8N163|K1967_HUMAN DBIRD complex subunit KIAA1967 OS=Homo sapiens GN=KIAA1967 PE=1 SV=2 1.26 0.93 1.49 1.22 1.3 0.56 1.22 0.99 1.02E-42 13 20.8 "apoptosis;biological regulation;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription elongation, DNA-dependent;regulation of transcription, DNA-dependent;RNA metabolic process;RNA processing;RNA splicing" basal RNA polymerase II transcription machinery binding;basal transcription machinery binding;binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;protein binding;RNA polymerase binding;RNA polymerase core enzyme binding;RNA polymerase II core binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nucleus;organelle;organelle lumen;organelle part

P13646;K7ERE3;P13646-3;CON__ENSEMBL:ENSP00000377550;CON__P13646-1;P13646-2;K7EMD9;K7EQH6 "Keratin, type I cytoskeletal 13" KRT13 ">sp|P13646|K1C13_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4;>tr|K7ERE3|K7ERE3_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=3 SV=1;>sp|P13646-3|K1C13_HUMAN Isoform 3 of Keratin, type I cytoskeletal 13 OS=Ho" NaN 1.79 0.69 1.36 0.87 0.53 NaN 0.27 5.13E-255 13 23.8 anatomical structure development;anatomical structure morphogenesis;cell communication;cellular process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;developmental process;epidermis development;organ morphogenesis;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to radiation;response to retinoic acid;response to stimulus;response to vitamin;response to vitamin A;tissue development;tongue morphogenesis structural molecule activity cell part;cytoskeletal part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle part;protein complex;vesicle

Q9C075;CON__Q9C075;I3L3Q6;J3QR55;K7EPI0 "Keratin, type I cytoskeletal 23" KRT23 ">sp|Q9C075|K1C23_HUMAN Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2;>Q9C075 SWISS-PROT:Q9C075 Tax_Id=9606 Gene_Symbol=KRT23 Keratin, type I cytoskeletal 23;>tr|I3L3Q6|I3L3Q6_HUMAN Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT" 0.79 0.71 0.9 0.33 3.34 2.75 1.25 0.85 2.37E-104 13 33.4 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex

Q7Z794;CON__Q7Z794;F5GY66;F8VS61 "Keratin, type II cytoskeletal 1b" KRT77 ">sp|Q7Z794|K2C1B_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=3;>Q7Z794 SWISS-PROT:Q7Z794 Tax_Id=9606 Gene_Symbol=KRT77 Keratin 77;>tr|F5GY66|F5GY66_HUMAN Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 SV=1" 0.65 2.34 0.98 3.47 3.07 4.11 1.25 1.13 2.97E-223 13 19.9 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

Q6KB66;CON__Q6KB66-1;Q6KB66-2;Q6KB66-3;CON__Q0VBK2 "Keratin, type II cytoskeletal 80" KRT80 ">sp|Q6KB66|K2C80_HUMAN Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2;>Q6KB66-1 SWISS-PROT:Q6KB66-1 Tax_Id=9606 Gene_Symbol=KRT80 Isoform 1 of Keratin, type II cytoskeletal 80;>sp|Q6KB66-2|K2C80_HUMAN Isoform 2 of Keratin, type II cyto" 0.53 0.81 0.59 0.4 3.62 3.12 1.3 1.17 3.48E-85 13 31.9 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

Q13423;E9PCX7;D6RAI5;D6RHU2;D6RCR6 "NAD(P) transhydrogenase, mitochondrial" NNT ">sp|Q13423|NNTM_HUMAN NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3;>tr|E9PCX7|E9PCX7_HUMAN NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=2 SV=1" 0.73 1.25 1.14 1.59 0.84 0.48 0.62 1.03 3.90E-34 13 16.9 acetyl-CoA catabolic process;acetyl-CoA metabolic process;catabolic process;cation transport;cellular catabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;establishment of localization;hydrogen transport;ion transport;metabolic process;monovalent inorganic cation transport;proton transport;reactive oxygen species metabolic process;small molecule metabolic process;transport;tricarboxylic acid cycle "binding;catalytic activity;cation transmembrane transporter activity;coenzyme binding;cofactor binding;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;NAD binding;NAD(P)+ transhydrogenase (AB-specific) activity;NAD(P)+ transhydrogenase (B-specific) activity;NAD(P)+ transhydrogenase activity;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain;organelle inner membrane;organelle membrane;organelle part;respiratory chain Nicotinate and nicotinamide metabolism

P46087;P46087-4;P46087-2;P46087-3;F5GYR3;F5GWB7;F5H709;F5H5X6;F5H359;F5H8G6 Putative ribosomal RNA methyltransferase NOP2NOP2 >sp|P46087|NOP2_HUMAN Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2;>sp|P46087-4|NOP2_HUMAN Isoform 4 of Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2;>sp|P46087-2|NOP2_HUMAN Isoform 2 of Putative r 1.27 1.11 1.27 1.7 0.63 0.37 0.68 0.59 9.87E-42 13 21.4 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;methylation;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;small molecule metabolic process "binding;catalytic activity;methyltransferase activity;nucleic acid binding;RNA binding;S-adenosylmethionine-dependent methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part

Q9H307;Q9H307-2;G3V5F0;G3V579 Pinin PNN >sp|Q9H307|PININ_HUMAN Pinin OS=Homo sapiens GN=PNN PE=1 SV=4;>sp|Q9H307-2|PININ_HUMAN Isoform 2 of Pinin OS=Homo sapiens GN=PNN 1.29 1.62 0.85 2.26 0.53 0.44 0.49 0.53 6.14E-32 13 20.1 "biological adhesion;biological regulation;biosynthetic process;cell adhesion;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent"binding;DNA binding;nucleic acid binding;structural molecule activity anchoring junction;catalytic step 2 spliceosome;cell junction;cell part;cell-cell junction;cytoplasm;cytoskeletal part;desmosome;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;membrane;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;plasma membrane;protein complex;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport

P36578;H3BM89;H3BU31;H3BTP7 60S ribosomal protein L4 RPL4 >sp|P36578|RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5;>tr|H3BM89|H3BM89_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=2 SV=11.23 0.74 0.61 0.68 1.02 0.98 1.33 0.98 9.77E-60 13 28.8 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein

complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome
F5GZ12;Q9UBC9;B1AN48 Small proline-rich protein 3 SPRR3 >tr|F5GZ12|F5GZ12_HUMAN Small proline-rich protein 3 OS=Homo sapiens GN=SPRR3 PE=2 SV=1;>sp|Q9UBC9|SPRR3_HUMAN Small proline-rich protein 3 OS=Homo sapiens GN=SPRR3 PE=1 SV=2;>tr|B1AN48|B1AN48_HUMAN Small proline-rich protein 3 (Fragment) OS=Homo sapiens G 0.32 0.45 0.66 0.2 3.25 3.6 1.2 0.56 1.37E-36 13 79.5 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process;response to stimulus;response to stress;response to wounding;wound healing structural molecule activity cell part;cytoplasm;intracellular part
Q9BUF5;K7ESM5;K7ESQ3;K7EQT3;K7EJ64;K7ERA8;K7EJZ4;K7EL29;K7EN98;K7EPE5 Tubulin beta-6 chain TUBB6 >sp|Q9BUF5|TBB6_HUMAN Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1;>tr|K7ESM5|K7ESM5_HUMAN Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=3 SV=1 1.13 0.82 0.76 0.44 2.72 1.82 1.79 1.37 3.81E-109 13 35.7 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;organelle part;plasma membrane;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome
Q05682-5;E9PGZ1;Q05682-4;F5H1Z9;E7EX44;Q05682-3;Q05682-6;Q05682-2;Q05682;C9J813;C9JEK3;C9JE79;F8WE61 Caldesmon CALD1 >sp|Q05682-5|CALD1_HUMAN Isoform 5 of Caldesmon OS=Homo sapiens GN=CALD1;>tr|E9PGZ1|E9PGZ1_HUMAN Caldesmon OS=Homo sapiens GN=CALD1 PE=2 SV=1;>sp|Q05682-4|CALD1_HUMAN Isoform 4 of Caldesmon OS=Homo sapiens GN=CALD1;>tr|F5H1Z9|F5H1Z9_HUMAN Caldesmon OS=Homo 0.9 0.44 0.9 0.97 0.67 0.45 1.69 1.02 2.79E-122 14 32.3 cellular component movement;cellular process;multicellular organismal process;muscle contraction;muscle system process;system process actin binding;binding;calmodulin binding;cytoskeletal protein binding;protein binding;tropomyosin binding actin cap;actin cytoskeleton;cell cortex part;cell part;contractile fiber;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;myofibril;non-membrane-bounded organelle;organelle;organelle part;plasma membrane Vascular smooth muscle contraction
P53621;P53621-2 Coatomer subunit alpha;Xenin;Proxenin COPA >sp|P53621|COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2;>sp|P53621-2|COPA_HUMAN Isoform 2 of Coatomer subunit alpha OS=Homo sapiens GN=COPA 0.68 1.23 0.37 0.75 4.95 1.48 1.19 1.34 5.88E-36 14 14.4 "biological regulation;body fluid secretion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;digestive system process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;multicellular organismal process;organelle organization;pancreatic juice secretion;protein transport;regulation of biological quality;regulation of body fluid levels;retrograde vesicle-mediated transport, Golgi to ER;secretion;system process;transport;vesicle coating;vesicle organization;vesicle-mediated transport" structural molecule activity cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;extracellular region part;extracellular space;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;protein complex;vesicle coat Neuroactive ligand-receptor interaction
P32926 Desmoglein-3 DSG3 >sp|P32926|DSG3_HUMAN Desmoglein-3 OS=Homo sapiens GN=DSG3 PE=1 SV=2 1.13 1.59 0.68 0.82 1.11 1.12 0.83 1.14 1.11E-110 14 17 biological adhesion;cell adhesion;cell-cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;desmosome;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;plasma membrane
G3V4C1;P07910-2;G3V2Q1;P07910;P07910-4;G3V4W0;B4DY08;P07910-3;G3V576;G3V555;G3V575;G3V2D6;G3V5X6;G3V3K6;G3V251;B4DSU6;G3V4M8;G3V2H6 Heterogeneous nuclear ribonucleoproteins C1/C2 HNRNPC >tr|G3V4C1|G3V4C1_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=2 SV=1;>sp|P07910-2|HNRPC_HUMAN Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC;>tr|G3V2Q1|G3V2Q1_HUMAN Heterogeneous 1.05 1.31 1.47 2.43 0.37 0.34 0.45 0.48 3.91E-227 14 43.8 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome
K7EMS3 KRT19 ">tr|K7EMS3|K7EMS3_HUMAN Keratin, type I cytoskeletal 19 (Fragment) OS=Homo sapiens GN=KRT19 PE=4 SV=1" 0.83 1.09 1.1 1.45 0.79 0.92 0.71 0.78 0 14 68 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle

part;protein complex

Q6P2Q9;I3L0J9;I3L3Z8	Pre-mRNA-processing-splicing factor 8	PRPF8	>sp|Q6P2Q9|PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	1.08	1.02	1.35	1.78	0.49	0.46	0.72	0.63	2.78E-141	14	8.2	"cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile"	binding;nucleic acid binding;RNA binding	catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U5 snRNP	Spliceosome

O43242;B4DT72;H0YGV8	26S proteasome non-ATPase regulatory subunit 3	PSMD3	>sp|O43242|PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2;>tr|B4DT72|B4DT72_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=2 SV=1	0.82	1.67	0.44	1.19	1.56	1.37	1.13	1.3	4.22E-57	14	30.3	"anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction"	enzyme regulator activity	cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;proteasome complex;protein complex	Proteasome

Q13509;A8K854	Tubulin beta-3 chain	TUBB3	">sp|Q13509|TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2;>tr|A8K854|A8K854_HUMAN HCG1983504, isoform CRA_f OS=Homo sapiens GN=TUBB3 PE=2 SV=1"	0.87	0.84	0.58	0.4	1.75	2.05	1.26	1.31	5.48E-190	14	35.8	axon guidance;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chemotaxis;'de novo' posttranslational protein folding;'de novo' protein folding;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;mitosis;nuclear division;organelle fission;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;taxis	"binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;peptide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity"	axon;cell part;cell projection;cytoplasm;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule cytoskeleton;neuron projection;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome

P26640;B0V043;B4DZ61;Q5SP20;B0V044;A2ABF4 Valine--tRNA ligase VARS >sp|P26640|SYVC_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4;>tr|B0V043|B0V043_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=2 SV=1 0.74 1.2 0.69 0.72 3.95 1 1.52 1.11 5.41E-38 14 14.2 amine metabolic process;amino acid activation;biological regulation;biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;translational elongation;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;valyl-tRNA aminoacylation "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;valine-tRNA ligase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis"

P21796;C9JI87 Voltage-dependent anion-selective channel protein 1 VDAC1 >sp|P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2;>tr|C9JI87|C9JI87_HUMAN Voltage-dependent anion-selective channel protein 1 (Fragment) OS=Homo sapiens GN=VDAC1 PE=2 SV=1 1.01 1.35 1.05 1.47 1.37 0.71 0.72 1.02 0 14 59.4 apoptosis;behavior;behavioral defense response;behavioral fear response;cell communication;cell death;cell-cell signaling;cellular process;cognition;death;defense response;fear response;interaction with host;interspecies interaction between organisms;learning;learning or memory;multicellular organismal process;multicellular organismal response to stress;multi-organism process;neurological system process;neuron-neuron synaptic transmission;programmed cell death;reproductive process;response to stimulus;response to stress;signaling;synaptic transmission;system process;viral reproductive process;virus-host interaction anion channel activity;anion transmembrane transporter activity;channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;passive transmembrane transporter activity;porin activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated ion channel activity;wide pore channel activity cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial outer membrane;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;plasma membrane;pore complex;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease

Q9UMD9-2;Q9UMD9;A2A2Y8 Collagen alpha-1(XVII) chain;120 kDa linear IgA disease antigen;97 kDa linear IgA disease antigen COL17A1 >sp|Q9UMD9-2|COHA1_HUMAN Isoform 2 of Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1;>sp|Q9UMD9|COHA1_HUMAN Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1 PE=1 SV=3;>tr|A2A2Y8|A2A2Y8_HUMAN Collagen alpha-1(XVII) chain OS=Homo sapiens GN=C 0.92 1.51 1.17 1.15 0.23 0.16 0.39 0.43 7.55E-93 15 12 anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;developmental process;epidermis development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;tissue development basement membrane;cell junction;cell part;cell-cell junction;cell-substrate junction;collagen;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region;extracellular region part;hemidesmosome;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane part Protein digestion and absorption

B4DLW8;P17844;J3KTA4;J3QSF1;J3KRZ1;J3QR02;J3KRX8;J3QRQ7 Probable ATP-dependent RNA helicase DDX5 DDX5 >tr|B4DLW8|B4DLW8_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=2 SV=1;>sp|P17844|DDX5_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1;>tr|J3KTA4|J3KTA4_HUMAN Probable ATP-dependent RNA helicase 1.51 1.15 1.08 1.37 0.47 0.29 0.94 0.74 7.37E-59 15 28.2 "biological regulation;biosynthetic process;cell growth;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chordate embryonic development;circadian rhythm;developmental process;embryo development;embryo development ending in birth or egg hatching;growth;in utero embryonic development;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA damage response, signal transduction by p53 class mediator;positive regulation of estrogen receptor signaling pathway;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of steroid hormone receptor signaling pathway;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of androgen receptor signaling pathway;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of developmental process;regulation of DNA damage response, signal transduction by p53 class mediator;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of ossification;regulation of osteoblast differentiation;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA splicing;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of steroid hormone receptor signaling pathway;regulation of striated muscle cell differentiation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral genome replication;regulation of viral reproduction;response to stimulus;rhythmic process;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;androgen receptor binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;estrogen receptor binding;helicase activity;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;pre-mRNA binding;protein binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

Q15029-2;K7EJ81;Q15029;K7EP67;K7EJ74 116 kDa U5 small nuclear ribonucleoprotein component EFTUD2 >sp|Q15029-2|U5S1_HUMAN Isoform 2 of 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2;>tr|K7EJ81|K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=4 SV=1;>sp|Q15029|U5S1_HUMAN 116 k 1.1 1.21 1.32 2.06 0.75 0.42 0.68 0.68 4.91E-42 15 20.4 "catabolic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;small molecule metabolic process" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" Cajal body;catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

P54652 Heat shock-related 70 kDa protein 2 HSPA2 >sp|P54652|HSP72_HUMAN Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 NaN 4.19 0.09 0.33 0.15 0.11 NaN 1.38 4.29E-139 15 20 anatomical structure development;biological regulation;cell cycle phase;cell cycle process;cell development;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular process involved in reproduction;chromosome organization;developmental process;developmental process involved in reproduction;germ cell development;male meiosis;male meiosis I;meiosis;meiosis I;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle;positive regulation of cellular process;positive regulation of cyclin-dependent protein kinase activity;positive regulation of cyclin-dependent protein kinase activity involved in G2/M;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of cyclin-dependent protein kinase activity involved in G2/M;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of transferase activity;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;spermatid development;synaptonemal complex disassembly;synaptonemal complex organization adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;glycolipid binding;lipid binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;cell surface;chromosomal part;cytoplasmic part;germ cell nucleus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;male germ cell nucleus;membrane-bounded organelle;mitochondrion;nuclear chromosome part;nuclear part;nucleus;organelle;organelle part;synaptonemal complex Antigen processing and presentation;Endocytosis;MAPK signaling pathway;Measles;Protein processing in endoplasmic reticulum;Spliceosome;Toxoplasmosis

F5H8K9;P19013;CON__P19013 "Keratin, type II cytoskeletal 4" KRT4 ">tr|F5H8K9|F5H8K9_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=2 SV=1;>sp|P19013|K2C4_HUMAN Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4;>P19013 SWISS-PROT:P19013 Tax_Id=9606 Gene_Symbol=KRT4 keratin 4" 1.58 1.48 0.42 0.45 4.66 2.36 0.97 0.99 1.94E-272 15 26.4 biological regulation;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;developmental process;epithelial cell differentiation;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epithelial cell proliferation;organelle organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of epithelial cell proliferation structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P28331-4;P28331-5;P28331;P28331-2;B4DJ81;P28331-3;C9JPQ5 "NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial" NDUFS1 ">sp|P28331-4|NDUS1_HUMAN Isoform 4 of NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1;>sp|P28331-5|NDUS1_HUMAN Isoform 5 of NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1;>sp|P2" 1.16 1.74 1.34 1.96 0.54 0.44 0.5 0.89 1.04E-82 15 31.6 "apoptosis;ATP metabolic process;ATP synthesis coupled electron transport;biological regulation;cell death;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;death;electron transport chain;generation of precursor metabolites and energy;heterocycle metabolic process;homeostatic process;ion homeostasis;metabolic process;mitochondrial electron transport, NADH to ubiquinone;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;programmed cell death;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;reactive oxygen species metabolic process;regulation of biological quality;regulation of membrane potential;regulation of mitochondrial membrane potential;respiratory electron transport chain;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;small molecule metabolic process" "2 iron, 2 sulfur cluster binding;4 iron, 4 sulfur cluster binding;binding;catalytic activity;cation binding;electron carrier activity;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor"cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial intermembrane space;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;mitochondrion;NADH dehydrogenase complex;organelle;organelle envelope lumen;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

Q99623;J3KPX7;Q99623-2;F5GY37;B4DW05;F5H3X6;F5GWA7;F5H2D2;F5H0C5;F5H0S4 Prohibitin-2 PHB2 >sp|Q99623|PHB2_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2;>tr|J3KPX7|J3KPX7_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=4 SV=1;>sp|Q99623-2|PHB2_HUMAN Isoform 2 of Prohibitin-2 OS=Homo sapiens GN=PHB2;>tr|F5GY37|F5GY37_HUMAN Prohibitin-2 OS=Ho 0.96 1.53 1.83 1.29 0.57 0.47 0.72 0.93 2.84E-188 15 53.8 "anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a tube;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;developmental process involved in reproduction;macromolecule biosynthetic process;macromolecule metabolic process;mammary gland alveolus development;mammary gland branching involved in thelarche;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of epithelial cell proliferation;negative regulation of estrogen receptor signaling pathway;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of mammary gland epithelial cell proliferation;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biosynthetic process;regulation of branching involved in mammary gland duct morphogenesis;regulation of cell communication;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of epithelial cell proliferation;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of mammary gland epithelial cell proliferation;regulation of metabolic process;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;tissue morphogenesis;transcription, DNA-dependent;tube morphogenesis" binding;estrogen receptor binding;hormone receptor binding;nuclear hormone receptor binding;protein binding;receptor binding;steroid hormone receptor binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part

Q7KZF4;H7C597 Staphylococcal nuclease domain-containing protein 1 SND1 >sp|Q7KZF4|SND1_HUMAN Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 1.26 0.43 0.74 0.39 1.24 0.89 1.92 1.19 3.14E-48 15 20.2 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;gene silencing;gene silencing by RNA;interaction with host;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism process;negative regulation of biological process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;viral reproductive process;virus-host interaction" "binding;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding;protein binding transcription factor activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;melanosome;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;nucleus;organelle;pigment granule;ribonucleoprotein complex;RNAi effector complex;RNA-induced silencing complex;vesicle

Q15582;G8JLA8;H0Y8L3;H0Y9D7;H0YAB8;D6RBX4;H0YAH8 Transforming growth factor-beta-induced protein ig-h3 TGFBI >sp|Q15582|BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1;>tr|G8JLA8|G8JLA8_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=2 SV=1;>tr|H0Y8L3|H0Y8L3_HUMAN Transfor 0.65 0.75 0.89 0.72 0.42 0.68 0.95 2.74 8.46E-89 15 22.8 anatomical structure formation involved in morphogenesis;angiogenesis;biological adhesion;biological regulation;cell adhesion;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;extracellular matrix organization;extracellular structure organization;multicellular organismal process;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;neurological system process;regulation of biological process;regulation of cell adhesion;regulation of cellular process;response to stimulus;sensory perception;sensory perception of light stimulus;system process;visual perception binding;extracellular matrix binding;integrin binding;protein binding;protein complex binding;receptor binding cell part;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;proteinaceous extracellular matrix;vesicle

P22314;Q5JRR6;Q5JRS1;Q5JRS3;Q5JRS2;Q5JRR9;Q5JRS0 Ubiquitin-like modifier-activating enzyme 1 UBA1 >sp|P22314|UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 0.2 4.61 0.16 2.77 0.48 1.26 0.63 1.35 1.17E-110 15 20.5 cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small protein activating enzyme activity Parkinson's disease;Ubiquitin mediated proteolysis

A8K2U0;F5H2Z2;H0YGG5;H0YH14;F5GXP1 Alpha-2-macroglobulin-like protein 1 A2ML1 >sp|A8K2U0|A2ML1_HUMAN Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens GN=A2ML1 PE=1 SV=3;>tr|F5H2Z2|F5H2Z2_HUMAN Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens GN=A2ML1 PE=2 SV=1;>tr|H0YGG5|H0YGG5_HUMAN Alpha-2-macroglobulin-like protein 1 (Fra 0.58 0.55 0.52 0.24 4.09 2.6 1.24 1.14 1.31E-50 16 15.3 biological regulation;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity extracellular region;extracellular region part;extracellular space

P49748-3;P49748-2;P49748;G3V1M7;K7EQP4;J3QRJ8;J3KS89;J3KSR4;K7EMF8;J3QKU9;K7EJW8 "Very long-chain specific acyl-CoA dehydrogenase, mitochondrial" ACADVL ">sp|P49748-3|ACADV_HUMAN Isoform 3 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL;>sp|P49748-2|ACADV_HUMAN Isoform 2 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL;>s" 0.61 0.85 0.63 0.49 2.84 1.97 1.43 1.21 5.86E-99 16 31.1 activation of signaling protein activity involved in unfolded protein response;biological regulation;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;energy derivation by oxidation of organic compounds;fatty acid beta-oxidation;fatty acid beta-oxidation using acyl-CoA dehydrogenase;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;generation of precursor metabolites and energy;homeostatic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;macromolecule metabolic process;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;multicellular organismal homeostasis;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of fatty acid biosynthetic process;negative regulation of fatty acid metabolic process;negative regulation of fatty acid oxidation;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cholesterol metabolic process;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of fatty acid oxidation;regulation of hydrolase activity;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of steroid metabolic process;regulation of transferase activity;small molecule catabolic process;small molecule metabolic process;temperature homeostasis "acyl-CoA dehydrogenase activity;binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;long-chain-acyl-CoA dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors" cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle part Fatty acid metabolism

P53396-2;P53396;B4E3P0;K7ESG8;K7EIE7 ATP-citrate synthase ACLY >sp|P53396-2|ACLY_HUMAN Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY;>sp|P53396|ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3;>tr|B4E3P0|B4E3P0_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1 0.69 1.07 0.39 0.81 1.66 1.53 1.31 1.41 9.33E-43 16 19.9 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;ATP catabolic process;ATP metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;citrate metabolic process;coenzyme A metabolic process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;generation of precursor metabolites and energy;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;heterocycle catabolic process;heterocycle metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;primary metabolic process;purine nucleoside metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;ribonucleoside metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;tricarboxylic acid metabolic process;triglyceride biosynthetic process;triglyceride metabolic process "acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATP citrate synthase activity;binding;catalytic activity;cation binding;CoA-ligase activity;cofactor binding;ion binding;ligase activity;ligase activity, forming carbon-sulfur bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;succinate-CoA ligase (ADP-forming) activity;succinate-CoA ligase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer" cell part;citrate lyase complex;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;nucleus;organelle;plasma membrane;protein complex Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle)

P80723;P80723-2 Brain acid soluble protein 1 BASP1 >sp|P80723|BASP1_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2;>sp|P80723-2|BASP1_HUMAN Isoform 2 of Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 0.92 1.63 1.31 0.91 0.73 0.6 0.84 1.18 1.54E-115 16 76.7 "anatomical structure development;anatomical structure morphogenesis;anterior/posterior pattern specification;biological regulation;cell differentiation;cell differentiation involved in kidney development;cell morphogenesis;cell morphogenesis involved in differentiation;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;developmental process;developmental process involved in reproduction;diaphragm development;epithelial cell differentiation;epithelial cell differentiation involved in kidney development;epithelial cell morphogenesis;glomerular epithelial cell differentiation;glomerular visceral epithelial cell differentiation;gonad development;kidney mesenchyme development;mesenchymal to epithelial transition;mesenchyme development;metanephric mesenchyme development;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;organ development;pattern specification process;positive regulation of biological process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of heart growth;positive regulation of metanephric ureteric bud development;positive regulation of organ growth;regionalization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of gene expression;regulation of growth;regulation of heart growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metanephric ureteric bud development;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ growth;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;renal filtration cell differentiation;reproductive process;reproductive structure development;skeletal muscle organ development;thorax and anterior abdomen determination;tissue development" binding;DNA binding;nucleic acid binding;protein binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding cell part;cell projection part;cytoplasm;cytoskeleton;growth cone;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part;plasma membrane;site of polarized growth

Q02413;B7Z845 Desmoglein-1 DSG1 >sp|Q02413|DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2 0.56 1.14 0.31 0.55 2.86 2.28 1.5 1.04 9.17E-104 16 21.7 biological adhesion;biological regulation;calcium-dependent cell-cell adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion;maternal process involved in female pregnancy;multicellular organismal process;multicellular organismal reproductive process;posttranscriptional regulation of gene expression;protein stabilization;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to progesterone stimulus;response to steroid hormone stimulus;response to stimulus binding;calcium ion binding;cation binding;ion binding;metal ion binding;toxin binding anchoring junction;apical plasma membrane;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;desmosome;integral to membrane;internal side of plasma membrane;intracellular part;intrinsic to membrane;lateral plasma membrane;membrane part;plasma membrane part Staphylococcus aureus infection

Q5VTE0;P68104;A6PW80;Q5JR01 Putative elongation factor 1-alpha-like 3;Elongation factor 1-alpha 1 EEF1A1P5;EEF1A1 >sp|Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1;>sp|P68104|EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 0.57 0.87 0.3 0.54 1.58 1.8 1.22 0.99 9.82E-60 16 30.3 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;transcription, DNA-dependent" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex RNA transport

Q9BSJ8;Q9BSJ8-2;F8VZB1 Extended synaptotagmin-1 ESYT1 >sp|Q9BSJ8|ESYT1_HUMAN Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1;>sp|Q9BSJ8-2|ESYT1_HUMAN Isoform 2 of Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 0.77 0.66 0.9 0.39 5.36 1.59 1.48 1.23 5.63E-89 16 22.3 cell part;integral to membrane;intrinsic to membrane;membrane part

P22626;P22626-2 Heterogeneous nuclear ribonucleoproteins A2/B1 HNRNPA2B1 >sp|P22626|ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2;>sp|P22626-2|ROA2_HUMAN Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 1.27 1.09 1.5 2.01 0.33 0.23 0.75 0.63 1.75E-273 16 48.7 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of RNA localization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;transport" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;sequence-specific DNA binding;single-stranded DNA binding;single-stranded telomeric DNA binding;structure-specific DNA binding;telomeric DNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex

P61978-3;Q5T6W5;P61978;P61978-2;Q5T6W2;Q5T6W1 Heterogeneous nuclear ribonucleoprotein K HNRNPK >sp|P61978-3|HNRPK_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK;>tr|Q5T6W5|Q5T6W5_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1;>sp|P61978|HNRPK_HUMAN Heterogeneous nuclear rib1.24 1.16 1.81 1.72 0.42 0.37 0.84 0.79 0 16 42.3 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of gene expression;positive regulation of low-density lipoprotein particle receptor biosynthetic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of receptor biosynthetic process;positive regulation of receptor-mediated endocytosis;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of endocytosis;regulation of gene expression;regulation of lipid transport;regulation of lipid transport by positive regulation of transcription from RNA polymerase II promoter;regulation of lipid transport by regulation of transcription from RNA polymerase II promoter;regulation of lipoprotein particle clearance;regulation of localization;regulation of low-density lipoprotein particle clearance;regulation of low-density lipoprotein particle receptor biosynthetic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of receptor biosynthetic process;regulation of receptor-mediated endocytosis;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to stimulus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;signal transduction;viral reproductive process;virus-host interaction" binding;core promoter proximal region DNA binding;core promoter proximal region sequence-specific DNA binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding catalytic step 2 spliceosome;cell part;chromatin;chromosomal part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome

O43390;O43390-2;O43390-3;E7ETM7 Heterogeneous nuclear ribonucleoprotein R HNRNPR >sp|O43390|HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1;>sp|O43390-2|HNRPR_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR;>sp|O43390-3|HNRPR_HUMAN Isoform 3 of Heterogeneo 1.06 1.36 1.2 2.64 0.44 0.36 0.48 0.56 2.09E-294 16 30.6 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex

E9PL22;Q9Y4L1;E9PJ21;B7Z909;J3KTF1;J3QL06;J3QQH7;J3QLE9;J3KSJ2;J3KT27 Hypoxia up-regulated protein 1 HYOU1 >tr|E9PL22|E9PL22_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=2 SV=1;>sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1;>tr|E9PJ21|E9PJ21_HUMAN Hypoxia up-regulated protein 1 (Fragment) OS=Homo sap 0.74 1.15 0.3 0.78 4.05 1.42 1.64 1.44 1.98E-163 16 23.3 activation of signaling protein activity involved in unfolded protein response;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle partProtein processing in endoplasmic reticulum

Q5JPE7-2;P69849;Q5JPE7;J3KN36;Q15155;Q4G177;F5H826;H3BUC9;I3L0Q6;H3BTW1;H3BPS9 Nodal modulator 3;Nodal modulator 2;Nodal modulator 1 NOMO3;NOMO2;NOMO1 >sp|Q5JPE7-2|NOMO2_HUMAN Isoform 2 of Nodal modulator 2 OS=Homo sapiens GN=NOMO2;>sp|P69849|NOMO3_HUMAN Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=2;>sp|Q5JPE7|NOMO2_HUMAN Nodal modulator 2 OS=Homo sapiens GN=NOMO2 PE=1 SV=1;>tr|J3KN36|J3KN36_HUMAN 0.93 0.92 1.4 0.27 7.81 1.06 1.23 1.17 8.34E-87 16 19.6 binding;carbohydrate binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part

P11940-2;P11940;E7EQV3;E7ERJ7;H0YAR2;H0YBN4;Q9H361;H0YAP2;H3BNY3;E5RGH3;E5RH24;E5RJB9;H0YB86;H3BPI5;E5RHG7;Q4VY17;Q4VXU2;H0YC10;E5RGC4;E5RFD8;H0YAS7;H0YAS6;H0YB75;Q5JQF8;Q96DU9-2;Q96DU9 Polyadenylate-binding protein 1 PABPC1 >sp|P11940-2|PABP1_HUMAN Isoform 2 of Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1;>sp|P11940|PABP1_HUMAN Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2;>tr|E7EQV3|E7EQV3_HUMAN Polyadenylate-binding protein 1 OS=Homo sapie 1.97 0.71 0.91 0.59 1.18 0.72 1.72 1.13 3.26E-39 16 30 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;gene silencing;gene silencing by RNA;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA polyadenylation;mRNA processing;mRNA stabilization;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA 3'-end processing;positive regulation of mRNA catabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear-transcribed mRNA poly(A) tail shortening;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA 3'-end processing;regulation of mRNA catabolic process;regulation of mRNA processing;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;regulation of nuclear-transcribed mRNA poly(A) tail shortening;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA polyadenylation;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization;translational initiation" "binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;RNA binding;single-stranded RNA binding;translation activator activity;translation regulator activity;translation regulator activity, nucleic acid binding" catalytic step 2 spliceosome;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;organelle;organelle part;ribonucleoprotein complex;RNA granule;spliceosomal complex;stress granule mRNA surveillance pathway;RNA degradation;RNA transport

P12270;Q5SWX9 Nucleoprotein TPR TPR >sp|P12270|TPR_HUMAN Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 1.43 0.6 1.76 0.73 1.01 0.64 1.36 1.12 9.84E-59 16 8.8 "amine metabolic process;amino acid activation;biological regulation;carbohydrate metabolic process;carbohydrate transport;carboxylic acid metabolic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular amine metabolic process;cellular amino acid metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to heat;cellular response to interferon-alpha;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular protein transport;intracellular transport;macromolecular complex subunit organization;macromolecule metabolic process;MAPK import into nucleus;metabolic process;mitosis;mitotic cell cycle checkpoint;mitotic cell cycle spindle assembly checkpoint;mitotic cell cycle spindle checkpoint;monosaccharide transport;mRNA export from nucleus;mRNA export from nucleus in response to heat stress;mRNA transport;ncRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of intracellular transport;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitosis;negative regulation of mitotic metaphase/anaphase transition;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear division;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleobase-containing compound transport;negative regulation of nucleocytoplasmic transport;negative regulation of organelle organization;negative regulation of protein metabolic process;negative regulation of RNA export from nucleus;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;negative regulation of translational initiation;negative regulation of transport;nitrogen compound metabolic process;nuclear division;nuclear export;nuclear import;nuclear pore organization;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;nucleus organization;organelle fission;organelle organization;organic acid metabolic process;organic substance transport;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of chromatin assembly or disassembly;positive regulation of heterochromatin formation;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of mitotic cell cycle spindle assembly checkpoint;positive regulation of nucleocytoplasmic transport;positive regulation of organelle organization;positive regulation of protein export from nucleus;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of spindle checkpoint;positive regulation of transmembrane transport;positive regulation of transport;posttranscriptional regulation of gene expression;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromatin assembly;regulation of chromatin assembly or disassembly;regulation of chromosome organization;regulation of chromosome segregation;regulation of establishment of protein localization;regulation of gene expression;regulation of glucose transport;regulation of heterochromatin formation;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic cell cycle spindle assembly checkpoint;regulation of mitotic metaphase/anaphase transition;regulation of mitotic sister chromatid segregation;regulation of mitotic sister chromatid separation;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of nucleobase-containing compound transport;regulation of nucleocytoplasmic transport;regulation of organelle organization;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of RNA export from nucleus;regulation of RNA metabolic process;regulation of sister chromatid segregation;regulation of spindle checkpoint;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;regulation of transmembrane transport;regulation of transport;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to epidermal growth factor stimulus;response to growth factor stimulus;response to heat;response to interferon-alpha;response to organic substance;response to stimulus;response to stress;response to temperature stimulus;RNA export from nucleus;RNA import into nucleus;RNA metabolic process;RNA transport;seryl-tRNA aminoacylation;signal transduction;small molecule metabolic process;spindle assembly checkpoint;spindle checkpoint;transmembrane transport;transport;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;viral reproductive process" "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;chromatin binding;cytoskeletal protein binding;dynein complex binding;enzyme binding;heat shock protein binding;identical protein binding;kinase binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;mitogen-activated protein kinase binding;mRNA binding;nucleic acid binding;nucleocytoplasmic transporter activity;nucleotide binding;protein binding;protein complex binding;protein dimerization activity;protein homodimerization activity;protein kinase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;serine-tRNA ligase activity;transporter activity;tubulin binding" cell part;chromosomal part;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;dynein complex;extrinsic to membrane;inclusion body;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane part;microtubule associated complex;mitotic spindle;non-membrane-bounded organelle;nuclear inclusion body;nuclear membrane;nuclear part;nuclear periphery;nucleoplasm;organelle;organelle membrane;organelle part;protein complex;spindle MAPK signaling pathway - yeast;Pathways in cancer;RNA transport;Thyroid cancer

A8MUB1;P68366;Q9NY65-2;Q9NY65;C9J2C0;C9JEV8;C9JQ00;C9JJQ8;C9JDL2;C9JDS9;C9K0S6;Q9H853 Tubulin alpha-4A chain;Tubulin alpha-8 chain TUBA4A;TUBA8 >tr|A8MUB1|A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1;>sp|P68366|TBA4A_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1;>sp|Q9NY65-2|TBA8_HUMAN Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8;>sp|Q9N 0.63 0.38 0.48 0.15 2.96 2.56 1.67 1.38 1.20E-170 16 39.5 cell activation;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cytoskeleton organization;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;exocytosis;G2/M transition of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;organelle organization;platelet activation;platelet degranulation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;secretion;secretion by cell;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;protein complex "Aminobenzoate degradation;Benzoate degradation;beta-Alanine metabolism;Butanoate metabolism;Caprolactam degradation;Fatty acid metabolism;Gap junction;Lysine degradation;Pathogenic Escherichia coli infection;Peroxisome;Phagosome;PPAR signaling pathway;Propanoate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation"

Q5T9A4;Q5T9A4-3;J3QSF3 ATPase family AAA domain-containing protein 3B ATAD3B>sp|Q5T9A4|ATD3B_HUMAN ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1;>sp|Q5T9A4-3|ATD3B_HUMAN Isoform 3 of ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B 1.45 1.35 1.34 1.97 0.67 0.54 0.55 0.94 2.64E-79 17 25.8 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

P05023-4;P05023;P05023-3;P05023-2;M0R116;P13637;P13637-2;P13637-3;B1AKY9;P50993;Q5TC01;H0Y7C1;Q5TC02;Q13733;P20648;P54707;P54707-2;M0QXF2;E9PRA5;REV__Q15772-1;REV__Q15772 Sodium/potassium-transporting ATPase subunit alpha-1 ATP1A1 >sp|P05023-4|AT1A1_HUMAN Isoform 4 of Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1;>sp|P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1;>sp|P05023-3|AT1A1_HUMAN Is 0.83 1.29 1.19 0.78 0.71 0.62 0.83 1.02 5.37E-288 17 20.5 "adult behavior;adult locomotory behavior;associative learning;ATP biosynthetic process;ATP hydrolysis coupled proton transport;ATP metabolic process;behavior;biological regulation;biosynthetic process;calcium ion homeostasis;cation homeostasis;cation transport;cell motility;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component movement;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular monovalent inorganic cation homeostasis;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular potassium ion transport;cellular process;cellular response to abiotic stimulus;cellular response to external stimulus;cellular response to mechanical stimulus;cellular response to stimulus;chemical homeostasis;cognition;cytosolic calcium ion homeostasis;divalent inorganic cation homeostasis;energy coupled proton transport, against electrochemical gradient;establishment of localization;fertilization;gamete generation;glutamate signaling pathway;heterocycle biosynthetic process;heterocycle metabolic process;homeostatic process;hydrogen transport;ion homeostasis;ion transmembrane transport;ion transport;ionotropic glutamate receptor signaling pathway;learning;learning or memory;locomotion;locomotory behavior;male gamete generation;membrane hyperpolarization;memory;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of glucocorticoid biosynthetic process;negative regulation of glucocorticoid metabolic process;negative regulation of heart contraction;negative regulation of hormone biosynthetic process;negative regulation of hormone metabolic process;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of metabolic process;negative regulation of multicellular organismal process;negative regulation of muscle contraction;negative regulation of steroid biosynthetic process;negative regulation of steroid hormone biosynthetic process;negative regulation of steroid metabolic process;negative regulation of striated muscle contraction;neurological system process;neurotransmitter transport;neurotransmitter uptake;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;pH reduction;positive regulation of biological process;positive regulation of heart contraction;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of striated muscle contraction;potassium ion homeostasis;potassium ion import;potassium ion transmembrane transport;potassium ion transport;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;reduction of cytosolic calcium ion concentration;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular pH;regulation of cellular process;regulation of glucocorticoid biosynthetic process;regulation of glucocorticoid metabolic process;regulation of heart contraction;regulation of hormone biosynthetic process;regulation of hormone metabolic process;regulation of ion transport;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of membrane potential;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of neurotransmitter levels;regulation of pH;regulation of primary metabolic process;regulation of proton transport;regulation of respiratory gaseous exchange;regulation of respiratory gaseous exchange by neurological system process;regulation of respiratory system process;regulation of smooth muscle contraction;regulation of sodium ion transport;regulation of steroid biosynthetic process;regulation of steroid hormone biosynthetic process;regulation of steroid metabolic process;regulation of striated muscle contraction;regulation of system process;regulation of the force of heart contraction;regulation of transport;regulation of vasoconstriction;reproductive process;response to abiotic stimulus;response to alkaloid;response to chemical stimulus;response to drug;response to external stimulus;response to light stimulus;response to mechanical stimulus;response to nicotine;response to organic cyclic compound;response to organic substance;response to radiation;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;sperm motility;spermatogenesis;system process;transmembrane transport;transport;visual behavior;visual learning" "4-nitrophenylphosphatase activity;active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;alkali metal ion binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;chaperone binding;hydrogen ion transmembrane transporter activity;hydrogen:potassium-exchanging ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;hydrolase activity, acting on ester bonds;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;magnesium ion binding;metal ion binding;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity;potassium ion binding;potassium ion transmembrane transporter activity;potassium-transporting ATPase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;sodium ion binding;sodium ion transmembrane transporter activity;sodium:potassium-exchanging ATPase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" axon;basolateral plasma membrane;caveola;cell part;cell projection;cell projection part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;dendritic spine;endoplasmic reticulum;endosome;Golgi apparatus;hydrogen:potassium-exchanging ATPase complex;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;melanosome;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;myelin sheath;neuron projection;neuron spine;nucleus;organelle;pigment granule;plasma membrane part;protein complex;sodium:potassium-exchanging ATPase complex;synapse;T-tubule;vesicle Aldosterone-regulated sodium reabsorption;Bile secretion;Carbohydrate digestion and absorption;Cardiac muscle contraction;Collecting duct acid secretion;Endocrine and other factor-regulated calcium reabsorption;Gastric acid secretion;Mineral absorption;Oxidative phosphorylation;Pancreatic secretion;Protein digestion and absorption;Proximal tubule bicarbonate reclamation;Salivary secretion

P19012;CON__P19012;B3KRA2;A8MT21;C9JTG5 "Keratin, type I cytoskeletal 15" KRT15 ">sp|P19012|K1C15_HUMAN Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3;>P19012 SWISS-PROT:P19012 Tax_Id=9606 Gene_Symbol=KRT15 Keratin, type I cytoskeletal 15" 1.16 1.25 1.07 1.64 0.59 0.79 0.83 0.99 0 17 34.9

anatomical structure development;developmental process;epidermis development;tissue development structural constituent of cytoskeleton;structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex

Q9UM54-6;E7EW20;Q9UM54-5;Q9UM54-2;Q9UM54-4;Q9UM54-1;Q9UM54;Q5JVM0 Unconventional myosin-VI MYO6 >sp|Q9UM54-6|MYO6_HUMAN Isoform 6 of Unconventional myosin-VI OS=Homo sapiens GN=MYO6;>tr|E7EW20|E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1;>sp|Q9UM54-5|MYO6_HUMAN Isoform 5 of Unconventional myosin-VI OS=Homo sapiens GN=MYO6;> 0.81 1.19 0.64 0.79 5.15 2.25 0.93 1.1 4.47E-103 17 16.7 "actin filament-based movement;actin filament-based process;anatomical structure development;anatomical structure morphogenesis;auditory receptor cell differentiation;behavior;biological regulation;cell communication;cell differentiation;cell projection organization;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to abiotic stimulus;cellular response to electrical stimulus;cellular response to stimulus;cellular response to stress;dendrite development;developmental process;DNA damage response, signal transduction by p53 class mediator;embryonic morphogenesis;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;glutamate secretion;inner ear morphogenesis;inner ear receptor cell differentiation;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotory behavior;mechanoreceptor differentiation;membrane invagination;membrane organization;multicellular organismal process;neurological system process;neuron differentiation;neuron projection development;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;protein targeting;protein transport;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of secretion;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmission of nerve impulse;regulation of transport;response to abiotic stimulus;response to DNA damage stimulus;response to electrical stimulus;response to stimulus;response to stress;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal release;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signaling;synapse assembly;synapse organization;synaptic transmission;system process;transport;vesicle-mediated transport" "actin binding;actin filament binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;binding;calmodulin binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microfilament motor activity;minus-end directed microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" "axon;cell body;cell cortex;cell part;cell projection;cell projection membrane;cell projection part;clathrin coated vesicle membrane;coated pit;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;DNA-directed RNA polymerase II, holoenzyme;filamentous actin;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;lysosomal membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;myosin complex;neuron projection;neuronal cell body;nuclear membrane;nuclear part;nucleoplasm part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;ruffle;ruffle membrane;unconventional myosin complex;vacuolar membrane;vacuolar part;vesicle;vesicle membrane"

E7EUY0;P78527-2;P78527 DNA-dependent protein kinase catalytic subunit PRKDC >tr|E7EUY0|E7EUY0_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=2 SV=1;>sp|P78527-2|PRKDC_HUMAN Isoform 2 of DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC;>sp|P78527|PRKDC_HUMAN DNA-dependent pro 1.19 0.61 0.78 0.87 0.8 0.63 1.35 1.09 1.13E-36 17 5 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;anterior/posterior pattern specification;apoptosis;B cell lineage commitment;biological regulation;brain development;cell activation;cell death;cell differentiation;cell fate commitment;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chromosome organization;death;developmental process;developmental process involved in reproduction;developmental programmed cell death;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via nonhomologous end joining;germ cell programmed cell death;heart development;hemopoietic progenitor cell differentiation;homeostatic process;immune system process;immunoglobulin V(D)J recombination;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;lymphoid progenitor cell differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle organization;pattern specification process;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;pro-B cell differentiation;programmed cell death;protein destabilization;protein metabolic process;protein modification process;protein phosphorylation;regionalization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein stability;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to gamma radiation;response to hormone stimulus;response to insulin stimulus;response to ionizing radiation;response to organic substance;response to peptide hormone stimulus;response to radiation;response to stimulus;response to stress;segmentation;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of T cell receptor genes;somatic recombination of immunoglobulin gene segments;somatic recombination of T cell receptor gene segments;somitogenesis;T cell activation;T cell differentiation;T cell differentiation in thymus;T cell lineage commitment;T cell receptor V(D)J recombination;telomere maintenance;telomere organization;V(D)J recombination" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;DNA-dependent protein kinase activity;kinase activity;nucleic acid binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;DNA-dependent protein kinase-DNA ligase 4 complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nonhomologous end joining complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;nucleus;organelle;organelle part;protein complex;transcription factor complex Cell cycle;Non-homologous end-joining

P04844-2;P04844;Q5JYR4;Q5JYR7;Q5JYR3;H0Y5M1;F2Z3K5 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 RPN2 >sp|P04844-2|RPN2_HUMAN Isoform 2 of Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2;>sp|P04844|RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE= 1.1 1.31 1.53 1 0.91 0.73 0.87 1.01 3.58E-174 17 37.4 aging;biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glycosylation;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to drug;response to stimulus;SRP-dependent cotranslational protein targeting to membrane;translation;transport "binding;catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;ribonucleoprotein binding;ribosome binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" autophagic vacuole membrane;cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;oligosaccharyltransferase complex;organelle;organelle membrane;organelle part;protein complex;rough endoplasmic reticulum;vacuolar membrane;vacuolar part N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis

O60506-2;O60506 Heterogeneous nuclear ribonucleoprotein Q SYNCRIP >sp|O60506-2|HNRPQ_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP;>sp|O60506|HNRPQ_HUMAN Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 1.23 1.1 1.23 1.77 0.49 0.39 0.79 0.71 0 17 35.2 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;CRD-mediated mRNA stabilization;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of translation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization;viral reproductive process;virus-host interaction" binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;RNA binding;single-stranded RNA binding catalytic step 2 spliceosome;cell part;CRD-mediated mRNA stability complex;cytoplasmic part;endoplasmic reticulum;histone pre-mRNA 3'end processing complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex

Q9Y4K1;B4DU04;Q96QW7 Absent in melanoma 1 protein AIM1 >sp|Q9Y4K1|AIM1_HUMAN Absent in melanoma 1 protein OS=Homo sapiens GN=AIM1 PE=1 SV=3 1.17

1.13 1.2 1.16 0.85 0.82 0.9 0.69 6.99E-62 18 15.5
O00571;O00571-2;B4DXX7;O15523;B4E132;C9J8G5;C9J081;B4E3C4;B4DLA0;D6RCM4;Q9NQI0-3;Q9NQI0-2;Q9NQI0-4;Q9NQI0 ATP-dependent RNA helicase DDX3X;ATP-dependent RNA helicase DDX3Y DDX3X;DDX3Y >sp|O00571|DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3;>sp|O00571-2|DDX3X_HUMAN Isoform 2 of ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X;>tr|B4DXX7|B4DXX7_HUMAN Uncharacterized protein OS=Homo sapiens GN=DD 1.07 0.76 0.8 0.65 1.78 1.72 1.29 0.86 2.49E-93 18 31 "biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell motility;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to arsenic-containing substance;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to osmotic stress;cellular response to stimulus;cellular response to stress;chromosome segregation;defense response;developmental process;gamete generation;immune response;immune system process;induction of apoptosis;induction of apoptosis by extracellular signals;induction of apoptosis via death domain receptors;induction of programmed cell death;innate immune response;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;leptotene;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;male gamete generation;male meiosis I;mature ribosome assembly;meiosis I;metabolic process;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of growth;negative regulation of hydrolase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of protein complex assembly;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle assembly;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemokine (C-C motif) ligand 5 production;positive regulation of chemokine production;positive regulation of cytokine production;positive regulation of gene expression;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of interferon-beta production;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of translation;positive regulation of translational initiation;positive regulation of type I interferon production;posttranscriptional regulation of gene expression;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemokine (C-C motif) ligand 5 production;regulation of chemokine production;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of interferon-beta production;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein localization;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;regulation of type I interferon production;reproductive process;response to abiotic stimulus;response to arsenic-containing substance;response to biotic stimulus;response to chemical stimulus;response to inorganic substance;response to osmotic stress;response to other organism;response to stimulus;response to stress;response to virus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;RNA biosynthetic process;RNA metabolic process;RNA secondary structure unwinding;signal transduction;sperm motility;spermatogenesis;stress granule assembly;transcription, DNA-dependent;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;eukaryotic initiation factor 4E binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;protein binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleoprotein binding;ribonucleotide binding;ribosomal small subunit binding;RNA binding;RNA helicase activity;RNA stem-loop binding;RNA-dependent ATPase activity;single-stranded RNA binding;transcription factor binding;translation initiation factor binding" cell part;chromatoid body;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;P granule;perinuclear region of cytoplasm;pi-body;piP-body;ribonucleoprotein complex;RNA granule;stress granule RIG-I-like receptor signaling pathway
Q1KMD3;H3BQZ7 Heterogeneous nuclear ribonucleoprotein U-like protein 2 HNRNPUL2;hCG_2044799 >sp|Q1KMD3|HNRL2_HUMAN Heterogeneous nuclear

ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1;>tr|H3BQZ7|H3BQZ7_HUMAN HCG2044799 OS=Homo sapiens GN=hCG_2044799 PE=4 SV=1 0.94 1.11 1.22 1.95 0.76 0.53 0.66 0.68 8.53E-81 18 25.6 binding;nucleic acid binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q8N1N4;CON__Q8N1N4-2;CON__Q7RTT2;Q8N1N4-2;F8VS93 "Keratin, type II cytoskeletal 78" KRT78 ">sp|Q8N1N4|K2C78_HUMAN Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2;>Q8N1N4-2 SWISS-PROT:Q8N1N4-2 Tax_Id=9606 Gene_Symbol=KRT78 Isoform 2 of Keratin, type II cytoskeletal 78;>Q7RTT2 TREMBL:Q7RTT2 Tax_Id=9606 Gene_Symbol=KRT78 Keratin" 0.52 1.19 0.36 0.89 3.18 3.08 1.07 1.13 7.28E-106 18 33.8 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

Q9BQE3;F5H5D3;Q13748;Q13748-2;Q6PEY2;F8VX09;F8VRK0;F8VXZ7;F8W0F6 Tubulin alpha-1C chain;Tubulin alpha-3C/D chain;Tubulin alpha-3E chain TUBA1C;TUBA3C;TUBA3E >sp|Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1;>tr|F5H5D3|F5H5D3_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1;>sp|Q13748|TBA3C_HUMAN Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3;>sp|Q13 0.71 0.66 0.35 0.4 1.74 1.43 1.55 1.27 1.58E-274 18 46.8 cell division;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome

B7Z1R5;P38606;C9JA17;C9JVW8 V-type proton ATPase catalytic subunit A ATP6V1A >tr|B7Z1R5|B7Z1R5_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=2 SV=1;>sp|P38606|VATA_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 0.48 2.46 0.45 1.93 0.66 1.35 0.56 1.12 1.66E-144 19 38.7 "ATP hydrolysis coupled proton transport;ATP metabolic process;biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;heterocycle metabolic process;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;organelle organization;phagosome maturation;primary metabolic process;protein transport;proton transport;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "apical plasma membrane;cell part;cell projection;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;membrane-bounded organelle;microvillus;mitochondrion;organelle;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain;proton-transporting V-type ATPase, V1 domain" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection

Q14980-2;Q14980;Q14980-4;Q14980-3;H0YFY6;F5H6Y5;F5H4J1;Q9BTE9;K4DIE0;F5H1L0;F5GZW1;F5H2F3;F5H3L6;F5H0Z7;F5H763 Nuclear mitotic apparatus protein 1 NUMA1 >sp|Q14980-2|NUMA1_HUMAN Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1;>sp|Q14980|NUMA1_HUMAN Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2;>sp|Q14980-4|NUMA1_HUMAN Isoform Numa-s of Nuclear mitotic appa 1.19 1.19 1.27 2.45 0.7 0.4 0.37 0.36 1.19E-62 19 10.9 anaphase;cell cycle phase;cell cycle process;cell differentiation;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;developmental process;epithelial cell differentiation;establishment of localization;establishment of localization in cell;establishment of mitotic spindle localization;establishment of mitotic spindle orientation;establishment of organelle localization;establishment of spindle localization;establishment of spindle orientation;G2/M transition of mitotic cell cycle;lung cell differentiation;lung epithelial cell differentiation;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;nucleus organization;organelle organization structural molecule activity apical part of cell;cell part;chromosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;non-membrane-bounded organelle;nuclear matrix;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;spindle microtubule;spindle pole

Q9UQ35;Q9UQ35-2;I3L4D8;I3L1I8;Q9UQ35-3;I3L182;I3L1C0;I3L4U6;I3L0N7 Serine/arginine repetitive matrix protein 2 SRRM2 >sp|Q9UQ35|SRRM2_HUMAN Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2;>sp|Q9UQ35-2|SRRM2_HUMAN Isoform 2 of Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 1.78 1.37 0.54 0.95 0.33 0.28 0.75 0.72 1.84E-101 19 9.7 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;C2H2 zinc finger domain binding;nucleic acid binding;protein binding;protein domain specific binding;RNA binding Cajal body;catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex

P07437;Q5JP53;Q5ST81;E9PBJ4;G3V5W4;G3V2R8;G3V3R4;G3V2N6 Tubulin beta chain TUBB >sp|P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2;>tr|Q5JP53|Q5JP53_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=2 SV=1;>tr|Q5ST81|Q5ST81_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=2 SV=1;>tr|E9PBJ4|E9PBJ4_HUMAN Tub 0.62 0.44 0.49 0.28 2.64 1.56 1.67 1.15 4.70E-262 19 55.9 biological regulation;cell cycle process;cell division;cell killing;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytoskeleton organization;cytoskeleton-dependent intracellular transport;defense response;establishment of localization;establishment of localization in cell;G2/M transition of mitotic cell cycle;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;intracellular transport;leukocyte mediated cytotoxicity;leukocyte mediated immunity;lymphocyte mediated immunity;macromolecular complex assembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule-based process;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;organelle assembly;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;protein complex assembly;protein complex subunit organization;protein polymerization;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to stimulus;response to stress;spindle assembly;spindle organization;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;MHC class I protein binding;MHC protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell body;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;nuclear envelope lumen;nuclear part;nucleus;organelle;organelle envelope lumen;organelle part;plasma membrane;protein complex;vesicle Gap junction;Pathogenic Escherichia coli infection;Phagosome

P68371;P04350;Q3ZCM7;G3V2A3;F5H0I4;A6NKZ8;Q5SQY0;I3L2F9;A6NNZ2;M0R2D3;Q9H4B7;CON__ENSEMBL:ENSBTAP00000025008;M0QY85;M0QZL7;M0R278;M0R0X0;M0QY37;M0QX14;M0R042;M0QYM7;G3V4U2;G3V3J6;M0R1I1;G3V3W7;M0R2T4 Tubulin beta-4B chain;Tubulin beta-4A chain TUBB4B;TUBB4A >sp|P68371|TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1;>sp|P04350|TBB4A_HUMAN Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 0.91 0.76 0.43 0.46 1.85 2.04 1.49 1.25 3.65E-220 19 49.9 axon guidance;biological regulation;cell cycle phase;cell cycle process;cell killing;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;centrosome organization;chemotaxis;cytoskeleton organization;'de novo' posttranslational protein folding;'de novo' protein folding;defense response;G2/M transition of mitotic cell cycle;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;leukocyte mediated cytotoxicity;leukocyte mediated immunity;locomotion;lymphocyte mediated immunity;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based process;mitosis;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;nuclear division;organelle assembly;organelle fission;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;spindle assembly;spindle organization;taxis "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;MHC class I protein binding;MHC protein binding;nucleoside-triphosphatase activity;nucleotide binding;peptide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity;unfolded protein binding" axon;axon part;cell body;cell part;cell projection;cell projection part;cilium;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;internode region of axon;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule cytoskeleton;microtubule organizing center part;myelin sheath;neuron projection;neuronal cell body;non-membrane-bounded organelle;organelle;organelle part;pericentriolar material;plasma membrane;protein complexGap junction;Pathogenic Escherichia coli infection;Phagosome

P04083;Q5T3N1;Q5T3N0 Annexin A1 ANXA1 >sp|P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2;>tr|Q5T3N1|Q5T3N1_HUMAN Annexin A1 (Fragment) OS=Homo sapiens GN=ANXA1 PE=2 SV=1 1.27 1.28 0.41 0.11 2.42 2.23 1.26 0.47 0 20 53.5 acid secretion;alpha-beta T cell activation;alpha-beta T cell differentiation;anatomical structure development;arachidonic acid secretion;biological regulation;carboxylic acid transport;cell activation;cell cycle;cell differentiation;cell surface receptor linked signaling pathway;cellular component movement;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to corticosteroid stimulus;cellular response to endogenous stimulus;cellular response to glucocorticoid stimulus;cellular response to hormone stimulus;cellular response to hydrogen peroxide;cellular response to organic substance;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to stress;defense response;developmental process;endocrine pancreas development;epidermal cell differentiation;epithelial cell differentiation;establishment of localization;establishment of localization in cell;estrous cycle phase;fatty acid transport;gliogenesis;hepatocyte differentiation;homeostasis of number of cells;homeostatic process;hormone secretion;hormone transport;icosanoid secretion;icosanoid transport;immune system process;inflammatory response;insulin secretion;keratinocyte differentiation;leukocyte activation;leukocyte differentiation;lipid transport;long-chain fatty acid transport;lymphocyte activation;lymphocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid transport;myeloid cell homeostasis;negative regulation of acute inflammatory response;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of programmed cell death;negative regulation of protein secretion;negative regulation of protein transport;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of transport;neurogenesis;neutrophil homeostasis;organic acid transport;organic substance transport;ovulation cycle process;peptide cross-linking;peptide hormone secretion;peptide secretion;peptide transport;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of fatty acid biosynthetic process;positive regulation of fatty acid metabolic process;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of myeloid cell apoptosis;positive regulation of neutrophil apoptosis;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of prostaglandin biosynthetic process;positive regulation of transport;positive regulation of vesicle fusion;primary metabolic process;protein metabolic process;protein modification process;regulation of acute inflammatory response;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of defense response;regulation of establishment of protein localization;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of homeostatic process;regulation of hormone levels;regulation of immune system process;regulation of inflammatory response;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of metabolic process;regulation of myeloid cell apoptosis;regulation of neutrophil apoptosis;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of prostaglandin biosynthetic process;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of transport;regulation of vesicle fusion;regulation of vesicle-mediated transport;response to abiotic stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to interleukin-1;response to ionizing radiation;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to radiation;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;response to X-ray;rhythmic process;secretion;secretion by cell;signal release;signal transduction;T cell activation;T cell differentiation;transport "binding;binding, bridging;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phospholipase A2 inhibitor activity;phospholipase inhibitor activity;phospholipid binding;protein binding;protein binding, bridging;receptor binding;structural molecule activity" basolateral plasma membrane;cell part;cell projection;cilium;cornified envelope;cytoplasm;cytoplasmic part;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;sarcolemma;vesicle

P08195-2;P08195-3;F5GZS6;P08195;J3KPF3;P08195-4;F5H0E2;H0YFS2;F5GZI0;F5GZR9;H0YFX4 4F2 cell-surface antigen heavy chain SLC3A2 >sp|P08195-2|4F2_HUMAN Isoform 2 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2;>sp|P08195-3|4F2_HUMAN Isoform 3 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2;>tr|F5GZS6|F5GZS6_HUMAN 4F2 cell-surface antigen heavy cha 0.73 1.43 1.1 1.1 0.29 0.15 0.62 0.77 2.58E-302 20 41.4 amine transport;amino acid import;amino acid transport;aromatic amino acid transport;biological regulation;blood coagulation;branched-chain aliphatic amino acid transport;carbohydrate metabolic process;carboxylic acid transport;cell growth;cell migration;cell motility;cellular component movement;cellular process;coagulation;establishment of localization;growth;hemostasis;immune system process;leucine import;leucine transport;leukocyte migration;locomotion;metabolic process;multicellular organismal process;neutral amino acid transport;nitrogen compound transport;organic acid transport;organic substance transport;primary metabolic process;regulation of biological quality;regulation of body fluid levels;transport;tryptophan transportactive transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;antiporter activity;binding;calcium ion transmembrane transporter activity;calcium:cation antiporter activity;calcium:sodium antiporter activity;carboxylic acid transmembrane transporter activity;catalytic activity;cation binding;cation transmembrane transporter activity;cation:cation antiporter activity;divalent inorganic cation transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;neutral amino acid transmembrane transporter activity;organic acid transmembrane transporter activity;secondary active transmembrane transporter activity;sodium ion transmembrane transporter activity;solute:cation antiporter activity;solute:solute antiporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity apical plasma membrane;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;plasma membrane;plasma membrane part;vesicle Protein digestion and absorption

O75643;O75643-2;C9JAQ9;B4E0P5 U5 small nuclear ribonucleoprotein 200 kDa helicase SNRNP200 >sp|O75643|U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 1.21 1.05 1.54 1.41 0.57 0.39 0.71 0.66 9.53E-149 20 11.5 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cis assembly of pre-catalytic spliceosome;macromolecular complex assembly;macromolecular complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA helicase activity;RNA-dependent ATPase activity" catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U5 snRNP Spliceosome

Q13885;Q9BVA1;K7ES63 Tubulin beta-2A chain;Tubulin beta-2B chain TUBB2A;TUBB2B >sp|Q13885|TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1;>sp|Q9BVA1|TBB2B_HUMAN Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1 0.66 0.6 0.4 0.34 1.87 1.91 1.44 1.2 0 20 54.8 cell migration;cell motility;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;neuron migration;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;organelle part;plasma membrane;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome

P68133;P68032;P62736;P63267;Q5T8M8;A6NL76;Q5T8M7;P63267-2;C9JFL5;F6UVQ4;F6QUT6;F8WB63;B8ZZJ2"Actin, alpha skeletal muscle;Actin, alpha cardiac muscle 1;Actin, aortic smooth muscle;Actin, gamma-enteric smooth muscle" ACTA1;ACTC1;ACTA2;ACTG2 ">sp|P68133|ACTS_HUMAN Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1;>sp|P68032|ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1;>sp|P62736|ACTA_HUMAN Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=" 0.89 1.12 0.86 1.31 0.5 0.89 0.76 1.27 0 21 45.6 actin cytoskeleton organization;actin filament organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;actomyosin structure organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptosis;biological regulation;cardiac muscle contraction;cardiac muscle tissue morphogenesis;cardiac myofibril assembly;cell death;cell development;cell growth;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;circulatory system process;cytoskeleton organization;death;developmental process;glomerular mesangial cell development;growth;heart contraction;heart process;mesangial cell development;multicellular organismal process;multi-organism process;muscle adaptation;muscle cell development;muscle contraction;muscle fiber development;muscle filament sliding;muscle system process;muscle tissue morphogenesis;myofibril assembly;organelle organization;programmed cell death;regulation of anatomical structure size;regulation of biological quality;regulation of blood pressure;regulation of blood vessel size;regulation of tube size;response to abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to inorganic substance;response to lithium ion;response to mechanical stimulus;response to metal ion;response to organic substance;response to other organism;response to steroid hormone stimulus;response to stimulus;response to virus;skeletal muscle adaptation;skeletal muscle fiber adaptation;skeletal muscle fiber development;skeletal muscle thin filament assembly;smooth muscle contraction;striated muscle adaptation;striated muscle cell development;striated muscle contraction;system process;tissue morphogenesis;vascular process in circulatory system;vascular smooth muscle contraction;vasoconstriction "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;myosin binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" "actin cytoskeleton;actin filament;actin filament bundle;actomyosin;actomyosin, actin part;cell part;cell periphery;contractile fiber;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;I band;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle part;protein complex;smooth muscle contractile fiber;stress fiber;striated muscle thin filament;vesicle" Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM);Vascular smooth muscle contraction

O00468-6;O00468-3;O00468-7;O00468-2;O00468-5;O00468-4;O00468;H0Y5U1 Agrin;Agrin N-terminal 110 kDa subunit;Agrin C-terminal 110 kDa subunit;Agrin C-terminal 90 kDa fragment;Agrin C-terminal 22 kDa fragment AGRN >sp|O00468-6|AGRIN_HUMAN Isoform 6 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-3|AGRIN_HUMAN Isoform 3 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-7|AGRIN_HUMAN Isoform 7 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-2|AGRIN_HUMAN Isoform 2 of Agrin OS=Homo 1.21 1.24 1.44 0.89 0.16 0.23 0.5 0.62 4.57E-83 21 11.6 "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;axon guidance;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular response to stimulus;chemotaxis;chondroitin sulfate metabolic process;clustering of voltage-gated sodium channels;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;G-protein coupled receptor protein signaling pathway;isoprenoid metabolic process;lipid metabolic process;localization;locomotion;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;muscarinic acetylcholine receptor signaling pathway;neuronal ion channel clustering;nitrogen compound metabolic process;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell projection organization;positive regulation of cellular biosynthetic process;positive regulation of cellular component biogenesis;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of filopodium assembly;positive regulation of gene expression;positive regulation of growth;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nervous system development;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;positive regulation of RNA metabolic process;positive regulation of synapse assembly;positive regulation of synaptic growth at neuromuscular junction;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein localization;protein localization in membrane;receptor clustering;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell development;regulation of cell differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of filopodium assembly;regulation of gene expression;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of nervous system development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;regulation of synapse assembly;regulation of synapse organization;regulation of synaptic growth at neuromuscular junction;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;sulfur compound metabolic process;synapse organization;taxis;terpenoid metabolic process" binding;calcium ion binding;carbohydrate binding;cation binding;chondroitin sulfate binding;dystroglycan binding;extracellular matrix binding;glycoprotein binding;glycosaminoglycan binding;heparan sulfate proteoglycan binding;ion binding;laminin binding;metal ion binding;monosaccharide binding;pattern binding;polysaccharide binding;protein binding;proteoglycan binding;sialic acid binding;structural constituent of cytoskeleton;structural molecule activity;sugar binding basal lamina;cell junction;cell part;cytoplasmic part;extracellular matrix part;extracellular region part;Golgi apparatus part;Golgi lumen;integral to membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal lumen;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;synapse;vacuolar lumen;vacuolar part ECM-receptor interaction

Q9NVI7-2;Q9NVI7;Q9NVI7-3;H0Y2W2;Q5T9A4-2;Q5SV16;A6NFL3 ATPase family AAA domain-containing protein 3A ATAD3A>sp|Q9NVI7-2|ATD3A_HUMAN Isoform 2 of ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A;>sp|Q9NVI7|ATD3A_HUMAN ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2;>sp|Q9NVI7-3|ATD3A_HUMAN Isoform 3 of A 1.28 1.44 1.19 1.66 0.61 0.58 0.59 0.9 7.91E-70 21 34.5 biological regulation;cell growth;cellular process;growth;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle part

P40939;H0YFD6;B4DYP2 "Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydratase;Long chain 3-hydroxyacyl-CoA dehydrogenase" HADHA ">sp|P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2" 0.79 0.89 1.36 0.42 1.16 1.07 1.36 1.37 4.40E-191 21 30.5 biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;cardiolipin acyl-chain remodeling;cardiolipin metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;organophosphate metabolic process;oxidation-reduction process;oxoacid metabolic process;phosphatidylglycerol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;small molecule catabolic process;small molecule metabolic process "3-hydroxyacyl-CoA dehydrogenase activity;acetyl-CoA C-acetyltransferase activity;acetyl-CoA C-acyltransferase activity;acetyltransferase activity;binding;C-acetyltransferase activity;C-acyltransferase activity;carbon-oxygen lyase activity;carboxylic acid binding;catalytic activity;coenzyme binding;cofactor binding;enoyl-CoA hydratase activity;fatty acid binding;fatty-acyl-CoA binding;hydro-lyase activity;lipid binding;long-chain-3-hydroxyacyl-CoA dehydrogenase activity;long-chain-enoyl-CoA hydratase activity;lyase activity;monocarboxylic acid binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;fatty acid beta-oxidation multienzyme complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nuclear part;nucleoid;nucleolus;organelle;organelle inner membrane;organelle membrane;organelle part;protein complex "Aminobenzoate degradation;Benzoate degradation;beta-Alanine metabolism;Biosynthesis of unsaturated fatty acids;Butanoate metabolism;Caprolactam degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Lysine degradation;Propanoate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation"

P08107;P08107-2;E7EP94;Q5SP16;P48741 Heat shock 70 kDa protein 1A/1B HSPA1A >sp|P08107|HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5;>sp|P08107-2|HSP71_HUMAN Isoform 2 of Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A;>tr|E7EP94|E7EP94_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapie 0.79 1.49 0.76 1.5 0.48 0.76 0.93 0.88 7.58E-142 21 33.9 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;gene expression;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of growth;negative regulation of inclusion body assembly;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of erythrocyte differentiation;positive regulation of myeloid cell differentiation;primary metabolic process;protein folding;protein metabolic process;protein refolding;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of erythrocyte differentiation;regulation of growth;regulation of homeostatic process;regulation of immune system process;regulation of inclusion body assembly;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of programmed cell death;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;RNA catabolic process;RNA metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;protein binding involved in protein folding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding aggresome;cell part;cytoplasmic part;cytosol;endoplasmic reticulum;inclusion body;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part;perinuclear region of cytoplasm;ribonucleoprotein complex Antigen processing and presentation;Endocytosis;MAPK signaling pathway;Measles;Protein processing in endoplasmic reticulum;Spliceosome;Toxoplasmosis

Q9NZM1-6;Q9NZM1-3;C9JCN0;Q9NZM1;F8W8J4;Q9NZM1-2;Q9NZM1-5;H0YD14;Q9NZM1-7;Q9NZM1-8;Q9NZM1-4;O75923-15;O75923-3;O75923-9;O75923;O75923-14;O75923-6;O75923-12;O75923-5;O75923-11;O75923-4;O75923-10;O75923-2;O75923-8;O75923-7;O75923-13 Myoferlin MYOF >sp|Q9NZM1-6|MYOF_HUMAN Isoform 6 of Myoferlin OS=Homo sapiens GN=MYOF;>sp|Q9NZM1-3|MYOF_HUMAN Isoform 3 of Myoferlin OS=Homo sapiens GN=MYOF;>tr|C9JCN0|C9JCN0_HUMAN Myoferlin OS=Homo sapiens GN=MYOF PE=2 SV=2;>sp|Q9NZM1|MYOF_HUMAN Myoferlin OS=Homo sapien 0.96 0.79 0.84 0.47 0.71 0.66 1.6 1.93 2.71E-134 21 13.1 biological regulation;blood circulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;circulatory system process;membrane fusion;membrane organization;multicellular organismal process;muscle contraction;muscle system process;organelle fusion;organelle organization;plasma membrane organization;plasma membrane repair;regulation of biological process;regulation of cellular process;regulation of cellular response to growth factor stimulus;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of vascular endothelial growth factor receptor signaling pathway;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus;system process;vesicle fusion;vesicle organization binding;calcium-dependent phospholipid binding;lipid binding;phospholipid binding caveola;cell part;cell projection;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;envelope;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lamellipodium;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;nuclear envelope;nuclear membrane;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;plasma membrane;plasma membrane part;T-tubule;vesicle;vesicle membrane

P48681 Nestin NES >sp|P48681|NEST_HUMAN Nestin OS=Homo sapiens GN=NES PE=1 SV=2 NaN NaN 1.61 NaN 3.6 NaN NaN NaN 6.35E-60 21 19.4 anatomical structure development;anatomical structure morphogenesis;biological regulation;brain development;camera-type eye development;cell cycle process;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;developmental process;embryonic camera-type eye development;embryonic organ development;eye development;G2/M transition of mitotic cell cycle;negative regulation of apoptosis;negative regulation of binding;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of molecular function;negative regulation of programmed cell death;negative regulation of protein binding;organ development;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of intermediate filament depolymerization;positive regulation of neural precursor cell proliferation;positive regulation of organelle organization;positive regulation of protein complex disassembly;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of intermediate filament depolymerization;regulation of intermediate filament polymerization or depolymerization;regulation of metabolic process;regulation of molecular function;regulation of neural precursor cell proliferation;regulation of organelle organization;regulation of programmed cell death;regulation of protein binding;regulation of protein complex disassembly;sensory organ development;stem cell proliferation binding;intermediate filament binding;protein binding;protein complex binding;structural molecule activity cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex

Q8WVV4;Q8WVV4-1;F2Z2D5;Q8WVV4-3 Protein POF1B POF1B >sp|Q8WVV4|POF1B_HUMAN Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3;>sp|Q8WVV4-1|POF1B_HUMAN Isoform 1 of Protein POF1B OS=Homo sapiens GN=POF1B 0.65 0.67 0.56 0.26 4.1 2.8 1.45 1.12 1.81E-140 21 38.7

Q9UJS0;Q9UJS0-2;F5GX33;R4GN64 Calcium-binding mitochondrial carrier protein Aralar2 SLC25A13 >sp|Q9UJS0|CMC2_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2;>sp|Q9UJS0-2|CMC2_HUMAN Isoform 2 of Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13;>tr|F5GX33|F5GX33_HUMAN 0.93 1.23 1.07 1.44 0.76 0.71 0.85 1.27 1.67E-104 21 37.8 alcohol biosynthetic process;alcohol metabolic process;ATP biosynthetic process;ATP metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;gluconeogenesis;glucose metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;hexose biosynthetic process;hexose metabolic process;intracellular transport;malate-aspartate shuttle;metabolic process;mitochondrial transport;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule biosynthetic process;small molecule metabolic process;transmembrane transport;transport acidic amino acid transmembrane transporter activity;active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;binding;calcium ion binding;carboxylic acid transmembrane transporter activity;cation binding;ion binding;L-amino acid transmembrane transporter activity;L-aspartate transmembrane transporter activity;L-glutamate transmembrane transporter activity;metal ion binding;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;plasma membrane part

P07355;P07355-2;H0YN42;H0YMD0;H0YMU9;A6NMY6;H0YKS4;H0YM50;H0YMM1;H0YNP5;H0YKZ7;H0YLV6;H0YMT9;H0YKX9;H0YN28;H0YL33;H0YKV8;H0YKL9;H0YMW4;H0YMD9;H0YNA0;H0YNB8;H0YN52;H0YKN4;H0YLE2 Annexin A2;Annexin;Putative annexin A2-like protein ANXA2;ANXA2P2 >sp|P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2;>sp|P07355-2|ANXA2_HUMAN Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2;>tr|H0YN42|H0YN42_HUMAN Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1;>tr|H0YMD0|H0YMD0_HUMAN Annexin (Fr 1.02 0.65 0.5 0.16 3.37 1.91 1.64 0.93 0 22 52.2 anatomical structure development;anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;body fluid secretion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to chemical stimulus;cellular response to stimulus;collagen fibril organization;developmental process;establishment of localization;extracellular matrix organization;extracellular structure organization;fibrinolysis;multicellular organismal process;negative regulation of biological process;negative regulation of blood coagulation;negative regulation of coagulation;negative regulation of multicellular organismal process;positive regulation of binding;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of transport;positive regulation of vesicle fusion;regulation of binding;regulation of biological process;regulation of biological quality;regulation of blood coagulation;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular process;regulation of coagulation;regulation of localization;regulation of molecular function;regulation of multicellular organismal process;regulation of organelle organization;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of transport;regulation of vesicle fusion;regulation of vesicle-mediated transport;regulation of wound healing;response to acid;response to chemical stimulus;response to stimulus;secretion;skeletal system development;system development;transport "binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipase inhibitor activity;phospholipid binding" basement membrane;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome;endosome;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;extrinsic to membrane;extrinsic to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lipid particle;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;midbody;myelin sheath adaxonal region;organelle;perinuclear region of cytoplasm;pigment granule;plasma membrane;plasma membrane part;protein complex;sarcolemma;Schmidt-Lanterman incisure;vesicle

Q08211;Q08211-2 ATP-dependent RNA helicase A DHX9 >sp|Q08211|DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 1.63 0.68 0.85 1.38 3.72 0.44 1.06 0.73 8.08E-212 22 21 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;circadian rhythm;CRD-mediated mRNA stabilization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus;rhythmic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization""adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;double-stranded RNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;centrosome;CRD-mediated mRNA stability complex;cytoplasmic part;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;protein complex;ribonucleoprotein complex

Q12906;Q12906-5;Q12906-2;Q12906-3;K7EKJ9;K7ER69;K7ERM6;K7ENK6;K7EM82;K7EJ09;K7EQR9;Q96SI9-2;Q96SI9;K7EKY0;K7EQ75 Interleukin enhancer-binding factor 3 ILF3 >sp|Q12906|ILF3_HUMAN Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3;>sp|Q12906-5|ILF3_HUMAN Isoform 5 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3;>sp|Q12906-2|ILF3_HUMAN Isoform 2 of Interleukin enhancer-bindi 1.24 0.88 1.13 1.63 0.57 0.35 0.97 0.92 7.19E-290 22 29.3 "anatomical structure development;behavior;biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell development;cellular biosynthetic process;cellular component movement;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;developmental process;developmental process involved in reproduction;germ cell development;M phase;macromolecule biosynthetic process;macromolecule metabolic process;mechanosensory behavior;metabolic process;multicellular organismal development;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to abiotic stimulus;response to external stimulus;response to mechanical stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;spermatid development;transcription, DNA-dependent" binding;DNA binding;double-stranded RNA binding;nucleic acid binding;RNA binding;single-stranded RNA binding cell part;cytoplasm;cytoplasmic part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule cytoskeleton;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;ribonucleoprotein complex

O95202;O95202-2;O95202-3"LETM1 and EF-hand domain-containing protein 1, mitochondrial" LETM1 ">sp|O95202|LETM1_HUMAN LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1" 0.95 1.33 1.36 1.15 0.74 0.62 0.76 1.14 3.92E-186 22 29.5 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cristae formation;inner mitochondrial membrane organization;membrane organization;mitochondrial membrane organization;mitochondrion organization;organelle organization binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

Q12906-7;Q12906-4;Q12906-6 >sp|Q12906-7|ILF3_HUMAN Isoform 7 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3;>sp|Q12906-4|ILF3_HUMAN Isoform 4 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3;>sp|Q12906-6|ILF3_HUMAN Isoform 6 of Interleukin enhancer- 1.18 0.89 1.23 1.5 0.71 0.36 0.85 1.07 1.84E-287 22 28.7

P06576;F8VPV9;H0YH81;F8W079;F8W0P7;H0YI37;F8VQY0 "ATP synthase subunit beta, mitochondrial;ATP synthase subunit beta" ATP5B ">sp|P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3;>tr|F8VPV9|F8VPV9_HUMAN ATP synthase subunit beta OS=Homo sapiens GN=ATP5B PE=2 SV=1;>tr|H0YH81|H0YH81_HUMAN ATP synthase subunit beta (Fragment) OS=Homo sapi" 1.05 1.84 1.39 1.35 0.56 0.59 0.65 0.89 0 23 52.9 "anatomical structure formation involved in morphogenesis;angiogenesis;ATP biosynthetic process;ATP hydrolysis coupled proton transport;ATP metabolic process;ATP synthesis coupled proton transport;biological regulation;biosynthetic process;cation homeostasis;cation transport;cellular biosynthetic process;cellular cation homeostasis;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular monovalent inorganic cation homeostasis;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;developmental process;electron transport chain;energy coupled proton transport, against electrochemical gradient;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;homeostatic process;hydrogen transport;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;lipid metabolic process;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell adhesion involved in substrate-bound cell migration;negative regulation of cellular process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cellular pH;regulation of cellular process;regulation of intracellular pH;regulation of pH;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;cell surface binding;eukaryotic cell surface binding;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;MHC class I protein binding;MHC protein binding;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cell surface;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial nucleoid;mitochondrial part;mitochondrial proton-transporting ATP synthase, catalytic core;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle part;plasma membrane;protein complex;proton-transporting ATP synthase complex, catalytic core F(1);proton-transporting ATP synthase, catalytic core;proton-transporting two-sector ATPase complex, catalytic domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P13639 Elongation factor 2 EEF2 >sp|P13639|EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 0.46 2.07 0.2 1.4 0.91 1.64 0.81 0.95 2.37E-82 23 31.8 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;translational elongation "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;polysome;ribonucleoprotein complex

P07900;P07900-2;Q86U12;G3V2J8;Q14568;Q58FG0;Q9NQH7-3;Q9NQH7-5;Q9NQH7-2;Q9NQH7-4;Q9NQH7Heat shock protein HSP 90-alpha HSP90AA1 >sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5;>sp|P07900-2|HS90A_HUMAN Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1;>tr|Q86U12|Q86U12_HUMAN Full-length cDNA clone CS0CAP007YF18 of T 0.56 2.94 0.22 2.12 0.52 0.63 0.79 0.9 7.80E-300 23 32.5 axon guidance;biological regulation;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chaperone-mediated protein complex assembly;chemotaxis;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;G2/M transition of mitotic cell cycle;glomerular filtration;immune response;immune system process;innate immune response;intracellular protein transport;intracellular transport;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;multicellular organismal process;nitric oxide metabolic process;nitrogen compound metabolic process;organelle organization;outer mitochondrial membrane organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein import;protein import into mitochondrial outer membrane;protein maturation;protein metabolic process;protein processing;protein refolding;protein targeting;protein targeting to membrane;protein targeting to mitochondrion;protein transport;proteolysis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of oxidoreductase activity;renal system process;response to chemical stimulus;response to external stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;system process;taxis;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;aminopeptidase activity;ATP binding;ATPase activity;binding;catalytic activity;cation binding;enzyme regulator activity;exopeptidase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;ion binding;manganese ion binding;metal ion binding;metallopeptidase activity;nitric-oxide synthase regulator activity;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;protein dimerization activity;protein domain specific binding;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;TPR domain binding;transition metal ion binding" cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;pigment granule;plasma membrane;vesicle Antigen processing and presentation;NOD-like receptor signaling pathway;Pathways in cancer;Plant-pathogen interaction;Progesterone-mediated oocyte maturation;Prostate cancer;Protein processing in endoplasmic reticulum

P43243;A8MXP9;D6REM6;D6R991;B3KM87;P43243-2;H0Y8T4;D6RBK5;D6RB45;D6R9F3;D6RAM9;D6RAY2;D6RBS2;D6RCM3;D6REK4;D6R8Z5;D6RBI2;D6RE02;D6RIA2 Matrin-3 MATR3 >sp|P43243|MATR3_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2;>tr|A8MXP9|A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1;>tr|D6REM6|D6REM6_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1;>tr|D6R991|D6R991_HUMAN Matrin-3 (Fragment) OS=Homo s 1.23 0.96 1.41 1.4 0.86 0.52 0.9 0.99 1.89E-195 23 26.8 binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;structural molecule activity;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nuclear inner membrane;nuclear matrix;nuclear membrane;nuclear part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part

Q02218;E9PCR7;F5H801;Q02218-2;E9PDF2;E9PFG7;Q02218-3;Q9ULD0;C9J4G7;Q9ULD0-3;Q9ULD0-2 "2-oxoglutarate dehydrogenase, mitochondrial" OGDH ">sp|Q02218|ODO1_HUMAN 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3;>tr|E9PCR7|E9PCR7_HUMAN 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=2 SV=1;>tr|F5H801|F5H801_HUMAN 2-oxoglutarate dehydrogenase," 0.83 1.35 1.12 0.86 1.16 1.12 0.9 1.34 9.13E-97 23 28 2-oxoglutarate metabolic process;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol catabolic process;alcohol metabolic process;amine catabolic process;amine metabolic process;anatomical structure development;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell development;cell migration;cell motility;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular component movement;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;central nervous system neuron development;cerebellar cortex development;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental process;dicarboxylic acid metabolic process;forebrain cell migration;forebrain neuron development;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;hippocampus development;locomotion;lysine catabolic process;lysine metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;NAD metabolic process;NADH metabolic process;neuron development;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;olfactory bulb mitral cell layer development;organic acid catabolic process;organic acid metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;pyramidal neuron development;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule catabolic process;small molecule metabolic process;striatum development;succinyl-CoA metabolic process;tangential migration from the subventricular zone to the olfactory bulb;telencephalon cell migration;thalamus development;tricarboxylic acid cycle "binding;catalytic activity;coenzyme binding;cofactor binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxoglutarate dehydrogenase (NAD+) activity;oxoglutarate dehydrogenase (succinyl-transferring) activity;thiamine pyrophosphate binding;vitamin binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;oxoglutarate dehydrogenase complex;protein complex Citrate cycle (TCA cycle);Lysine degradation;Tryptophan metabolism

Q9Y446;E9PKC4;E9PK71;E9PRW6;E9PJR7;E9PQ15;H0YEY5 Plakophilin-3 PKP3 >sp|Q9Y446|PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1 0.94 1.23 1.07 0.98 1.22 1.4 0.72 0.68 2.08E-124 23 33.6 biological adhesion;cell adhesion;cellular process anchoring junction;cell junction;cell part;cell-cell junction;desmosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

Q6UWP8;Q6UWP8-2;K7ESC4 Suprabasin SBSN >sp|Q6UWP8|SBSN_HUMAN Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2 1.07 0.95 0.45 0.19 3.27 1.89 1.6 1.06 7.60E-241 23 67.5 extracellular region

P23246;P23246-2;H0Y9K7;H0Y9U2;REV__F8WBD4;REV__B4DSY9;REV__E7EVD1;REV__O43395;C9JHW1;E7ESB6;REV__Q9Y2L8;E9PC50;REV__E9PFQ4;REV__Q86SQ0-2;REV__Q86SQ0-3;REV__Q86SQ0;Q6Y7W6-4;Q6Y7W6;Q6Y7W6-3;I1E4Y6 "Splicing factor, proline- and glutamine-rich" SFPQ ">sp|P23246|SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2;>sp|P23246-2|SFPQ_HUMAN Isoform Short of Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ" 1.34 1.07 0.96 1.57 0.55 0.47 0.87 0.84 4.77E-189 23 39.3 "adult behavior;adult locomotory behavior;alternative nuclear mRNA splicing, via spliceosome;anatomical structure homeostasis;behavior;biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell death;cell differentiation;cell differentiation in spinal cord;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;central nervous system neuron differentiation;death;developmental process;DNA metabolic process;DNA recombination;DNA repair;enzyme linked receptor protein signaling pathway;feeding behavior;growth;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;insulin-like growth factor receptor signaling pathway;locomotory behavior;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;multicellular organism growth;multicellular organismal movement;multicellular organismal process;musculoskeletal movement;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;post-embryonic development;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;S phase;S phase of mitotic cell cycle;signal transduction;spinal cord motor neuron differentiation;system process;tissue homeostasis;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway"	binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding	cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear body;nuclear matrix;nuclear part;nucleoplasm part;organelle part;paraspeckles

Q6ZRV2;J3KPS2	Protein FAM83H	FAM83H	>sp|Q6ZRV2|FA83H_HUMAN Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3;>tr|J3KPS2|J3KPS2_HUMAN Protein FAM83H (Fragment) OS=Homo sapiens GN=FAM83H PE=4 SV=1	1.15	1.68	1.06	1.82	2.25	0.69	0.63	0.66	1.71E-141	24	31.2	anatomical structure development;biomineral tissue development;developmental process;tissue development

Q9UPN3;H3BPE1;H3BQK9;Q9UPN3-4;F5GZL7;Q9UPN3-3;Q9UPN3-2;F8W8Q1;H0Y390;Q9UPN3-5;E9PNZ4;E9PLY0;H0YD69;REV__Q8WXU2-3;REV__Q8WXU2-2;REV__Q8WXU2;O15169-2;O15169	"Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5"	MACF1	">sp|Q9UPN3|MACF1_HUMAN Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4;>tr|H3BPE1|H3BPE1_HUMAN Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=2 SV=1;>tr|H3BQK9|H3BQK9_HUM"	1.32	0.85	1.46	0.62	1.02	1.24	1.31	1.07	9.91E-55	24	4.4	"activation of JUN kinase activity;activation of MAPK activity;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;anterior/posterior pattern specification;apoptosis;axial mesoderm formation;axis specification;biological regulation;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling pathway involved in neural plate anterior/posterior pattern formation;catabolic process;cell cycle arrest;cell cycle process;cell death;cell development;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;chordate embryonic development;cytoplasmic microtubule organization;cytoskeleton organization;death;determination of bilateral symmetry;determination of left/right symmetry;developmental process;dorsal/ventral axis specification;ectodermal placode formation;embryo development;embryo development ending in birth or egg hatching;embryonic eye morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;embryonic skeletal joint morphogenesis;embryonic skeletal system morphogenesis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;establishment or maintenance of cell polarity;eye morphogenesis;forebrain anterior/posterior pattern specification;formation of primary germ layer;genetic imprinting;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;in utero embryonic development;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;mesoderm formation;metabolic process;microtubule cytoskeleton organization;microtubule-based process;multicellular organismal process;muscle cell development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of fat cell differentiation;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription elongation from RNA polymerase II promoter;negative regulation of transcription elongation, DNA-dependent;negative regulation of Wnt receptor signaling pathway;neurological system process;nitrogen compound metabolic process;nuclear transport;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;olfactory placode formation;optic placode formation;organ morphogenesis;organelle organization;pattern specification process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of intracellular protein kinase cascade;positive regulation of JNK cascade;positive regulation of JUN kinase activity;positive regulation of kinase activity;positive regulation of ligase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidyl-serine phosphorylation;positive regulation of peptidyl-threonine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of protein ubiquitination;positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;positive regulation of proteolysis;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transforming growth factor beta receptor signaling pathway;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;positive regulation of ubiquitin-protein ligase activity;positive regulation of Wnt receptor signaling pathway;post-Golgi vesicle-mediated transport;posttranslational protein targeting to membrane;primary metabolic process;programmed cell death;protein catabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein oligomerization;protein phosphorylation;protein polyubiquitination;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;protein ubiquitination;regionalization;regulation of biological process;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of catabolic process;regulation of catalytic activity;regulation of catenin import into nucleus;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of developmental process;regulation of epithelial cell migration;regulation of establishment of protein localization;regulation of fat cell differentiation;regulation of focal adhesion assembly;regulation of gene expression;regulation of G-protein coupled receptor protein signaling pathway;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of ligase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of microtubule-based process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of peptidyl-serine phosphorylation;regulation of peptidyl-threonine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of protein ubiquitination;regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of proteolysis;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transcription elongation from RNA polymerase II promoter;regulation of transcription elongation, DNA-dependent;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmembrane transport;regulation of transport;regulation of ubiquitin-protein ligase activity;regulation of Wnt receptor signaling pathway;response to chemical stimulus;response to organic cyclic compound;response to organic substance;response to stimulus;response to stress;response to wounding;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal transduction;skeletal system morphogenesis;specification of symmetry;system process;termination of G-protein coupled receptor signaling pathway;termination of signal transduction;transport;vesicle-mediated transport;Wnt receptor signaling pathway;Wnt receptor signaling pathway involved in forebrain neuron fate commitment;Wnt receptor signaling pathway involved in somitogenesis;wound healing" "actin binding;actin filament binding;armadillo repeat domain binding;ATPase activity;beta-catenin binding;binding;calcium ion binding;catalytic activity;cation binding;cytoskeletal protein binding;enzyme activator activity;enzyme binding;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;ion binding;kinase binding;metal ion binding;microtubule binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleoside-triphosphatase regulator activity;p53 binding;protein binding;protein complex scaffold;protein dimerization activity;protein domain specific binding;protein homodimerization activity;protein kinase binding;pyrophosphatase activity;signal transducer activity;structural molecule activity;tubulin binding" actin cytoskeleton;beta-catenin destruction complex;cell cortex;cell part;cell projection membrane;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic microtubule;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microtubule;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane part;postsynaptic density;protein complex;ruffle membrane;synapse part;vesicle Basal cell carcinoma;Colorectal cancer;Endometrial cancer;Pathways in cancer;Wnt signaling pathway

Q6XPR3 Repetin RPTN >sp|Q6XPR3|RPTN_HUMAN Repetin OS=Homo sapiens GN=RPTN PE=1 SV=1 0.23 0.28 0.45 0.18 3.52 2.5 1.75 1.08 7.32E-102 24 46.9 binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cornified envelope;cytoskeleton;extracellular matrix;extracellular region part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle;proteinaceous extracellular matrix

P19367-4;P19367-2;P19367;P19367-3;E7ENR4;B1AR63;B1AR62;B1AR61;Q2TB90 Hexokinase-1 HK1>sp|P19367-4|HXK1_HUMAN Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1;>sp|P19367-2|HXK1_HUMAN Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1;>sp|P19367|HXK1_HUMAN Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3;>sp|P19367-3|HXK1_HUMAN Isoform 3 of Hexok 0.7 0.76 0.69 0.43 2.51 1.54 1.51 1.34 9.53E-176 25 30.9 alcohol catabolic process;alcohol metabolic process;biological regulation;carbohydrate catabolic process;carbohydrate homeostasis;carbohydrate metabolic process;carbohydrate transport;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular chemical homeostasis;cellular glucose homeostasis;cellular homeostasis;cellular metabolic process;cellular process;chemical homeostasis;establishment of localization;generation of precursor metabolites and energy;glucose catabolic process;glucose homeostasis;glucose metabolic process;glucose transport;glycolysis;hexose catabolic process;hexose metabolic process;hexose transport;homeostatic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;monosaccharide transport;organic substance transport;primary metabolic process;regulation of biological quality;small molecule catabolic process;small molecule metabolic process;transmembrane transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate kinase activity;catalytic activity;fructokinase activity;glucokinase activity;hexokinase activity;kinase activity;mannokinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane Amino sugar and nucleotide sugar metabolism;Butirosin and neomycin biosynthesis;Carbohydrate digestion and absorption;Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Insulin signaling pathway;Starch and sucrose metabolism;Streptomycin biosynthesis;Type II diabetes mellitus

P33176;J3KNA1;Q12840 Kinesin-1 heavy chain KIF5B >sp|P33176|KINH_HUMAN Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 1.14 1.13 0.41 0.54 2.21 1.95 1.17 1.01 4.52E-213 25 32.2 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;blood coagulation;cell communication;cell death;cell-cell signaling;cellular chemical homeostasis;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chemical homeostasis;coagulation;cytoplasm organization;cytoskeleton-dependent intracellular transport;death;establishment of localization;establishment of localization in cell;hemostasis;homeostatic process;immune system process;intracellular transport;ion homeostasis;localization;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;multicellular organismal process;organelle localization;organelle transport along microtubule;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of establishment of protein localization in plasma membrane;positive regulation of ion transport;positive regulation of potassium ion transport;positive regulation of transport;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of ion transport;regulation of localization;regulation of membrane potential;regulation of metal ion transport;regulation of potassium ion transport;regulation of protein localization;regulation of transport;ribonucleoprotein complex disassembly;ribonucleoprotein complex subunit organization;signaling;stress granule disassembly;synaptic transmission;transport;vesicle localization;vesicle transport along microtubule "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule binding;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;tubulin binding" cell part;cell projection;cell projection part;ciliary rootlet;cilium part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;kinesin complex;macromolecular complex;membrane;microtubule;microtubule associated complex;neuron projection;organelle;organelle part;perinuclear region of cytoplasm;protein complex;vesicle

O43795-2;E9PDF6;O43795;E7EPB4;H7C2Y7;E7EQD9;C9JYW1;C9JUP5;F5H3C6;Q8N1T3 Unconventional myosin-Ib MYO1B >sp|O43795-2|MYO1B_HUMAN Isoform 2 of Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B;>tr|E9PDF6|E9PDF6_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=2 SV=1;>sp|O43795|MYO1B_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3 0.81 1.23 0.65 1.5 1.41 0.68 0.67 1.1 1.19E-185 25 26 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based movement;actin filament-based process;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-3,4,5-trisphosphate binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" brush border;cell part;cell projection;cytoplasm;cytoskeletal part;filopodium;intracellular organelle part;intracellular part;macromolecular complex;membrane;myosin complex;organelle part;plasma membrane;protein complex

Q00839-2;Q5RI18 >sp|Q00839-2|HNRPU_HUMAN Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU 1 1.28 1.55 2 0.32 0.29 0.56 0.49 0 25 27.9 cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

O95171-2;F2Z2X8 >sp|O95171-2|SCEL_HUMAN Isoform 2 of Sciellin OS=Homo sapiens GN=SCEL NaN 1.36 0.25 0.17 2.44 2.61 NaN 0.79 1.15E-97 25 39.7 cell part;membrane;plasma membrane

P16615-5;P16615-2;P16615-3;P16615;P16615-4;H7C5W9;O14983-2;O14983;B3KY17;Q93084-4;Q93084-2;Q93084-3;Q93084-7;Q93084;Q93084-6;Q93084-5;F8VSH0;H3BVB2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 ATP2A2 >sp|P16615-5|AT2A2_HUMAN Isoform 5 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2;>sp|P16615-2|AT2A2_HUMAN Isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2;>sp|P16615-3|AT2A2_HUMAN 1.05 1.14 1.34 0.73 1.48 0.77 0.96 1.07 6.57E-154 26 28.4 anatomical structure development;apoptosis;apoptosis in response to endoplasmic reticulum stress;apoptotic mitochondrial changes;biological adhesion;biological regulation;blood coagulation;calcium ion homeostasis;calcium ion import;calcium ion transmembrane transport;calcium ion transport;cation homeostasis;cation transport;cell adhesion;cell death;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;coagulation;death;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of endoplasmic reticulum calcium ion concentration;elevation of mitochondrial calcium ion concentration;endoplasmic reticulum calcium ion homeostasis;epidermis development;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;hemostasis;homeostatic process;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;maintenance of location;maintenance of location in cell;maintenance of mitochondrion location;maintenance of organelle location;metal ion homeostasis;metal ion transport;mitochondrial calcium ion homeostasis;mitochondrion organization;multicellular organismal process;muscle system process;negative regulation of biological process;negative regulation of cardiac muscle contraction;negative regulation of heart contraction;negative regulation of multicellular organismal process;negative regulation of muscle contraction;negative regulation of striated muscle contraction;organelle organization;positive regulation of biological process;positive regulation of fast-twitch skeletal muscle fiber contraction;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of striated muscle contraction;programmed cell death;reduction of endoplasmic reticulum calcium ion concentration;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cardiac muscle contraction;regulation of cellular process;regulation of fast-twitch skeletal muscle fiber contraction;regulation of heart contraction;regulation of heart rate;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of skeletal muscle contraction;regulation of striated muscle contraction;regulation of system process;regulation of the force of heart contraction;regulation of twitch skeletal muscle contraction;relaxation of cardiac muscle;relaxation of muscle;relaxation of skeletal muscle;response to stimulus;sarcoplasmic reticulum calcium ion transport;signal transduction;system process;tissue development;transmembrane transport;transport "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;calcium ion binding;calcium ion transmembrane transporter activity;calcium-transporting ATPase activity;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;divalent inorganic cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;metal ion transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" calcium channel complex;cation channel complex;cell part;contractile fiber part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;H zone;I band;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nuclear membrane;nuclear part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;platelet dense tubular network membrane;protein complex;sarcoplasmic reticulum;sarcoplasmic reticulum membrane Alzheimer's disease;Calcium signaling pathway;Pancreatic secretion

P52272-2;P52272;M0QZM1;M0R2T0;M0R019;M0R2I7;M0QYQ7;M0R0N3;M0R0Y6;M0QY96;M0QYL3 Heterogeneous nuclear ribonucleoprotein M HNRNPM >sp|P52272-2|HNRPM_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM;>sp|P52272|HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3;>tr|M0QZM1|M0QZM1_HUMAN Heterogeneous nuclear rib 1.26 0.97 1.09 1.13 0.86 0.59 0.98 0.88 1.36E-157 26 43.8 "alternative nuclear mRNA splicing, via spliceosome;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;nuclear body;nuclear matrix;nuclear part;nucleoplasm part;organelle part;paraspeckles;plasma membrane part;ribonucleoprotein complex;spliceosomal complex Spliceosome

Q00839 Heterogeneous nuclear ribonucleoprotein U HNRNPU >sp|Q00839|HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 1.16 1.4 1.22 2.04 0.7 0.38 0.55 0.53 0 26 29.3 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;CRD-mediated mRNA stabilization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;DNA binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;cell surface;CRD-mediated mRNA stability complex;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex Spliceosome

P08238;Q58FF7;Q58FF8;Q5T9W8;Q58FG1 Heat shock protein HSP 90-beta HSP90AB1 >sp|P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 0.68 1.86 0.29 1.23 0.65 0.66 1.02 0.99 0 26 36.5 "anatomical structure development;axon guidance;biological regulation;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;chemotaxis;defense response;developmental process;immune response;immune system process;innate immune response;intracellular receptor mediated signaling pathway;locomotion;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cell death;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of proteasomal ubiquitin-dependent protein catabolic process;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;organ development;placenta development;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell size;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;positive regulation of protein binding;positive regulation of protein import into nucleus, translocation;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of protein transport;positive regulation of transferase activity;positive regulation of transport;primary metabolic process;protein folding;protein metabolic process;regulation of anatomical structure size;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell death;regulation of cell size;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component size;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of establishment of protein localization;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-gamma-mediated signaling pathway;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of nitric oxide biosynthetic process;regulation of nitrogen compound metabolic process;regulation of nucleocytoplasmic transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein binding;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of proteolysis;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of transmembrane transport;regulation of transport;regulation of type I interferon-mediated signaling pathway;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to organic cyclic compound;response to organic substance;response to osmotic stress;response to salt stress;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;signal transduction;taxis" adenyl deoxyribonucleotide binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;CTP binding;dATP binding;deoxyribonucleotide binding;enzyme regulator activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nitric-oxide synthase regulator activity;nucleotide binding;protein binding;protein domain specific binding;purine deoxyribonucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrimidine nucleotide binding;pyrimidine ribonucleotide binding;ribonucleotide binding;TPR domain binding;UTP binding apical plasma membrane;basolateral plasma membrane;brush border membrane;cell part;cell projection membrane;cell projection part;cell surface;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;inclusion body;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;pigment granule;plasma membrane part;vesicle Antigen processing and presentation;NOD-like receptor signaling pathway;Pathways in cancer;Plant-pathogen interaction;Progesterone-mediated oocyte maturation;Prostate cancer;Protein processing in endoplasmic reticulum

O00515;E9PDI4;H0Y901 Ladinin-1LAD1 >sp|O00515|LAD1_HUMAN Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2;>tr|E9PDI4|E9PDI4_HUMAN Ladinin-1 OS=Homo sapiens GN=LAD1 PE=2 SV=1 1 0.78 0.86 1.04 1.03 0.93 1.1 0.93 0 26 48.9 structural molecule activity actin cytoskeleton;basement membrane;cell part;cytoskeleton;extracellular matrix part;extracellular region part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P04843;B7Z4L4;F8WF32 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 RPN1 >sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1;>tr|B7Z4L4|B7Z4L4_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=2 S 1.15 1.23 1.54 0.92 0.98 0.64 0.93 0.95 2.66E-200 26 46.8 biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glycosylation;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;SRP-dependent cotranslational protein targeting to membrane;translation;transport "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;oligosaccharyltransferase complex;organelle;organelle membrane;organelle part;pigment granule;protein complex;rough endoplasmic reticulum;vesicle N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis

P55072;C9JUP7;C9IZA5;K7EM02;K7EIJ8;Q8IYT4-2;Q8IYT4 Transitional endoplasmic reticulum ATPase VCP>sp|P55072|TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 0.8 1.35 0.39 0.97 1.05 0.82 1.31 1.45 4.81E-198 26 36.7 "activation of caspase activity;aggresome assembly;biological regulation;biosynthetic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cellular response to topologically incorrect protein;cellular response to unfolded protein;DNA biosynthetic process;DNA metabolic process;DNA repair;double-strand break repair;endoplasmic reticulum unfolded protein response;ER to Golgi vesicle-mediated transport;ER-associated protein catabolic process;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi vesicle transport;inclusion body assembly;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cellular catabolic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of peptidase activity;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein complex assembly;positive regulation of protein metabolic process;positive regulation of proteolysis;postreplication repair;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex assembly;protein complex subunit organization;protein glycosylation;protein homooligomerization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein oligomerization;protein transport;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein metabolic process;regulation of proteolysis;response to chemical stimulus;response to DNA damage stimulus;response to endoplasmic reticulum stress;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;retrograde protein transport, ER to cytosol;signal transduction;translesion synthesis;transport;ubiquitin-dependent protein catabolic process;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;microtubule-severing ATPase activity;nucleoside-triphosphatase activity;nucleotide binding;polyubiquitin binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;small conjugating protein binding;ubiquitin binding" cell part;chromosomal part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;nucleus;organelle;organelle part;proteasome complex;protein complex;site of double-strand break Protein processing in endoplasmic reticulum

P60709;CON__P60712;G5E9R0;E7EVS6;C9JZR7;C9JTX5;C9JUM1;Q6S8J3;A5A3E0;P0CG38;P0CG39;Q9BYX7;F8WCH0 "Actin, cytoplasmic 1;Actin, cytoplasmic 1, N-terminally processed" ACTB ">sp|P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1;>P60712 SWISS-PROT:P60712 (Bos taurus) Actin, cytoplasmic 1" 0.99 1.13 0.79 1.31 0.68 0.78 0.84 1.15 0 27 62.9 adherens junction organization;anatomical structure morphogenesis;axon guidance;axonogenesis;biological regulation;blood coagulation;cell activation;cell junction assembly;cell junction organization;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;coagulation;'de novo' posttranslational protein folding;'de novo' protein folding;defense response;developmental process;establishment of localization;establishment of localization in cell;exocytosis;hemostasis;immune response;immune system process;innate immune response;locomotion;macromolecule metabolic process;membrane organization;metabolic process;multicellular organismal process;neuron projection morphogenesis;platelet activation;platelet degranulation;primary metabolic process;protein folding;protein metabolic process;regulation of biological quality;regulation of body fluid levels;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;secretion;secretion by cell;taxis;transport;vesicle-mediated transport adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity axon;cell cortex;cell cortex part;cell part;cell projection;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region;extracellular region part;extracellular vesicular exosome;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;histone methyltransferase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;methyltransferase complex;MLL5-L complex;neuron projection;non-membrane-bounded organelle;NuA4 histone acetyltransferase complex;nuclear part;nucleoplasm part;organelle;organelle part;postsynaptic density;protein complex;ribonucleoprotein complex;synapse part;vesicle Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Dilated cardiomyopathy;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Phagosome;Phototransduction - fly;Regulation of actin cytoskeleton;Shigellosis;Tight junction;Vibrio cholerae infection;Viral myocarditis

P63261;I3L3I0;I3L1U9;K7EM38;I3L3R2;J3KT65 "Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed" ACTG1 ">sp|P63261|ACTG_HUMAN Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1;>tr|I3L3I0|I3L3I0_HUMAN Actin, cytoplasmic 2, N-terminally processed (Fragment) OS=Homo sapiens GN=ACTG1 PE=2 SV=1;>tr|I3L1U9|I3L1U9_HUMAN Actin, cytoplasmic 2, N-terminally proc" 1.3 NaN 0.83 1.22 0.63 0.86 0.93 NaN 0 27 62.9 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;adherens junction organization;axon guidance;cell junction assembly;cell junction organization;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;chemotaxis;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;locomotion;membrane organization;organelle organization;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;sarcomere organization;taxis adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity cell part;contractile fiber;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;myofibril;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Dilated cardiomyopathy;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Phagosome;Phototransduction - fly;Regulation of actin cytoskeleton;Shigellosis;Tight junction;Vibrio cholerae infection;Viral myocarditis

P15144;H0YLZ8;H0YMC1 Aminopeptidase N ANPEP >sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 0.27 0.46 0.74 0.94 7.98 1.17 0.55 1.39 1.11E-173 27 27.8 anatomical structure formation involved in morphogenesis;angiogenesis;angiotensin maturation;biological regulation;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;hormone metabolic process;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;metabolic process;multi-organism process;peptide hormone processing;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;regulation of biological quality;regulation of hormone levels;reproductive process;viral reproductive process;virus-host interaction "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;receptor activity;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum-Golgi intermediate compartment;external side of plasma membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;organelle;plasma membrane part Glutathione metabolism;Hematopoietic cell lineage;Renin-angiotensin system

P27824;B4DGP8;B4E2T8;D6RGY2;H0Y9Q7;D6RFL1;D6RB85;D6RDP7;D6RAU8;H0Y9H1;D6RAQ8;D6RHJ3;D6RD16 Calnexin CANX >sp|P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2;>tr|B4DGP8|B4DGP8_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1;>tr|B4E2T8|B4E2T8_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1 0.87 0.88 1.69 0.37 1.5 0.96 1.22 1.07 1.15E-268 27 40.5 aging;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;clathrin-mediated endocytosis;developmental process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;immune system process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein secretion;protein transport;receptor-mediated endocytosis;secretion;secretion by cell;synaptic vesicle endocytosis;synaptic vesicle transport;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding;protein binding;unfolded protein binding axon;cell body;cell part;cell projection;cell projection cytoplasm;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;dendrite cytoplasm;dendritic spine;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;neuron projection;neuron spine;neuronal cell body;non-membrane-bounded organelle;organelle;organelle lumen;organelle part;pigment granule;ribonucleoprotein complex;ribosome;vesicle Antigen processing and presentation;Phagosome;Protein processing in endoplasmic reticulum

P12035;J3QST3;CON__P12035 "Keratin, type II cytoskeletal 3" KRT3 ">sp|P12035|K2C3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=1 SV=3;>tr|J3QST3|J3QST3_HUMAN Keratin, type II cytoskeletal 3 OS=Homo sapiens GN=KRT3 PE=3 SV=1;>P12035 SWISS-PROT:P12035 Tax_Id=9606 Gene_Symbol=KRT3 Keratin, type II cytosk" 0.99 1.49 1.07 1.42 1.62 1.71 0.77 0.8 1.09E-232 27 23.9 cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;developmental process;epithelial cell differentiation;intermediate filament cytoskeleton organization;intermediate filament-based process;organelle organization structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

Q9UHB6;F8VQE1;Q9UHB6-2;F8VS07;Q9UHB6-3;F8VRN8 LIM domain and actin-binding protein 1 LIMA1 >sp|Q9UHB6|LIMA1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1;>tr|F8VQE1|F8VQE1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=2 SV=1;>sp|Q9UHB6-2|LIMA1_HUMAN Isoform Alpha of LIM domain and acti0.99 1.23 0.88 1.65 0.33 0.35 0.7 0.86 1.43E-241 27 37.8 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;biological regulation;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;negative regulation of actin filament depolymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex disassembly;organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex disassembly;ruffle organization actin binding;actin filament binding;actin monomer binding;binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding;transition metal ion binding;zinc ion binding actin cytoskeleton;actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeletal part;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;stress fiber

O95171;O95171-3 Sciellin SCEL >sp|O95171|SCEL_HUMAN Sciellin OS=Homo sapiens GN=SCEL PE=1 SV=2;>sp|O95171-3|SCEL_HUMAN Isoform 3 of Sciellin OS=Homo sapiens GN=SCEL 0.78 1.12 0.49 0.22 2.5 2.2 1.22 0.81 2.14E-98 27 40 cell differentiation;cellular developmental process;cellular process;developmental process;embryo development;epidermal cell differentiation;epithelial cell differentiation;keratinocyte differentiationbinding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;non-membrane-bounded organelle;organelle;plasma membrane

Q14134-2;Q14134;B7Z8U9;E9PRL4;E9PI31;E9PLI4;E9PJ94;E9PJ25;H0YCT2;H0YD78;E9PIQ2;E9PM74;E9PPX1;H0YCK2;E9PJD4 Tripartite motif-containing protein 29 TRIM29 >sp|Q14134-2|TRI29_HUMAN Isoform Beta of Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29;>sp|Q14134|TRI29_HUMAN Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2 1.14 1.18 1.1 1.08 0.91 0.82 0.89 0.49 3.87E-105 27 42.1 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;cation binding;ion binding;metal ion binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular part

Q9NR30;Q9NR30-2;Q9BQ39 Nucleolar RNA helicase 2 DDX21 >sp|Q9NR30|DDX21_HUMAN Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5;>sp|Q9NR30-2|DDX21_HUMAN Isoform 2 of Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 1.12 1.36 1.16 2.66 0.39 0.25 0.45 0.46 4.92E-254 28 39.1 multi-organism process;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to virus "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;double-stranded RNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane

P05783;F8VZY9;CON__H-INV:HIT000015463;CON__Q497I4 "Keratin, type I cytoskeletal 18" KRT18 ">sp|P05783|K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2;>tr|F8VZY9|F8VZY9_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=2 SV=1" 1.16 1.22 1.09 1.48 0.54 0.7 0.76 0.97 0 28 59.8 anatomical structure morphogenesis;apoptosis;biological regulation;cell cycle;cell death;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to tumor necrosis factor;cytokine-mediated signaling pathway;death;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi to plasma membrane CFTR protein transport;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;post-Golgi vesicle-mediated transport;programmed cell death;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;response to tumor necrosis factor;signal transduction;transport;tumor necrosis factor-mediated signaling pathway;vesicle-mediated transport;viral reproductive process;virus-host interaction structural molecule activity cell part;centriolar satellite;cytoplasm;cytoplasmic part;cytoskeletal part;intermediate filament;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;microtubule organizing center part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;perinuclear region of cytoplasm;protein complex

Q86UP2;Q86UP2-2;Q86UP2-3;G3V4Y7;B7Z6P3;G3V5G2;H0YJZ8;H0YJP2;H0YJV5;G3V5P0 Kinectin KTN1 >sp|Q86UP2|KTN1_HUMAN Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1;>sp|Q86UP2-2|KTN1_HUMAN Isoform 2 of Kinectin OS=Homo sapiens GN=KTN1;>sp|Q86UP2-3|KTN1_HUMAN Isoform 3 of Kinectin OS=Homo sapiens GN=KTN1;>tr|G3V4Y7|G3V4Y7_HUMAN Kinectin OS=Homo sapiens GN 1.21 1.29 1.37 1.03 1.48 0.45 0.97 1.03 5.79E-221 28 24.2 cellular component movement;cellular process;microtubule-based movement;microtubule-based process cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part

P20700;E9PBF6 Lamin-B1 LMNB1 >sp|P20700|LMNB1_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2;>tr|E9PBF6|E9PBF6_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=2 SV=1 0.88 1.39 1.45 2.68 0.55 0.33 0.32 0.32 1.22E-207 28 45.1 cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process structural molecule activity cell part;cytoskeletal part;envelope;intermediate filament;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane;nuclear envelope;nuclear inner membrane;nuclear membrane;nuclear part;nucleoplasm;organelle envelope;organelle inner membrane;organelle membrane;organelle part;protein complex

P22735;B4DWR7;H0YMQ8;H0YN27;H0YNM4;H0YLJ6;H0YKI6;H0YLT9 Protein-glutamine gamma-glutamyltransferase K TGM1 >sp|P22735|TGM1_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4;>tr|B4DWR7|B4DWR7_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=2 SV=1 1.07 1.41 1.31 0.59 2.3 1.74 0.88 0.41 1.85E-293 28 37.8 anatomical structure morphogenesis;cell differentiation;cell envelope organization;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;external encapsulating structure organization;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;organ morphogenesis;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process"binding;catalytic activity;cation binding;ion binding;metal ion binding;protein-glutamine gamma-glutamyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring amino-acyl groups" adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cornified envelope;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;non-membrane-bounded organelle;organelle

O15231-3;H0Y704;O15231-5;O15231-2;J3KNL4;H7C3U6;H7BZT5;H0Y4M8 ZNF185 >sp|O15231-3|ZN185_HUMAN Isoform 3 of Zinc finger protein 185 OS=Homo sapiens GN=ZNF185;>tr|H0Y704|H0Y704_HUMAN Zinc finger protein 185 (Fragment) OS=Homo sapiens GN=ZNF185 PE=4 SV=1;>sp|O15231-5|ZN185_HUMAN Isoform 5 of Zinc finger protein 185 OS=Homo sap 1.59 1.22 1.37 0.5 2.21 1.73 1.01 0.69 2.02E-134 28 49.7 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding

CON__P08727;P08727;C9JM50 "Keratin, type I cytoskeletal 19" KRT19 ">P08727 SWISS-PROT:P08727 Tax_Id=9606 Gene_Symbol=KRT19 Keratin, type I cytoskeletal 19;>sp|P08727|K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4;>tr|C9JM50|C9JM50_HUMAN Keratin, type I cytoskeletal 19 (Fragment) OS=Homo sap" 2.43 2.43 1.85 2.04 0.28 0.51 0.4 0.69 0 29 73.5 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;cell differentiation;cell differentiation involved in embryonic placenta development;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;developmental process;interaction with host;interspecies interaction between organisms;multi-organism process;organelle organization;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus;sarcomere organization;viral reproductive process;virus-host interaction structural constituent of cytoskeleton;structural constituent of muscle;structural molecule activity cell part;cell periphery;contractile fiber part;costamere;cytoplasmic part;cytoskeletal part;dystrophin-associated glycoprotein complex;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;organelle part;plasma membrane;plasma membrane part;protein complex;sarcolemma;Z disc

P35527;CON__P35527;K7EQQ3 "Keratin, type I cytoskeletal 9" KRT9 ">sp|P35527|K1C9_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3;>P35527 SWISS-PROT:P35527 Tax_Id=9606 Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9;>tr|K7EQQ3|K7EQQ3_HUMAN Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=3" 0.04 122.54 0.08 36.12 0.03 0.94 0.02 1 0 29 61.5 anatomical structure development;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;epidermis development;gamete generation;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;male gamete generation;multicellular organismal process;multicellular organismal reproductive process;organelle organization;reproductive process;skin development;spermatogenesis;tissue development structural constituent of cytoskeleton;structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex

P27816;E7EVA0;P27816-6;P27816-2;B9ZVR1;P27816-4;E9PGM5;B5MEG9;H0Y2V1;F8W9U4;B4DSQ1;P27816-7;H7C456;P27816-3 Microtubule-associated protein 4;Microtubule-associated protein MAP4 >sp|P27816|MAP4_HUMAN Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3;>tr|E7EVA0|E7EVA0_HUMAN Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=2 SV=1;>sp|P27816-6|MAP4_HUMAN Isoform 6 of Microtubule-associated protein 4 OS=Homo 1.15 0.36 0.52 0.31 4.86 0.79 2.58 1.35 7.84E-144 29 33.9 cell cycle process;cell division;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of spindle localization;establishment of spindle orientation;microtubule cytoskeleton organization;microtubule sliding;microtubule-based movement;microtubule-based process;mitotic spindle organization;organelle organization;spindle organization structural molecule activity cell part;cytoplasm;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule associated complex;microtubule cytoskeleton;mitotic spindle;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;spindle

P19338;H7BY16;C9JYW2;C9JLB1;C9J1H7;C9JWL1 Nucleolin NCL >sp|P19338|NUCL_HUMAN Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3;>tr|H7BY16|H7BY16_HUMAN Nucleolin (Fragment) OS=Homo sapiens GN=NCL PE=2 SV=1 1.57 0.75 1.29 0.95 0.58 0.25 1.26 0.85 0 29 36.1 anatomical structure formation involved in morphogenesis;angiogenesis;developmental process binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;sequence-specific DNA binding;telomeric DNA binding cell cortex;cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex Pathogenic Escherichia coli infection

P25705;P25705-2;K7ENP3;K7EK77;K7ERX7;K7ENJ4;K7EJP1;K7EQH4;K7ESA0;REV__C9JJM9;REV__C9JD81;REV__C9J3W7;REV__C9JBN7;REV__C9JEW7;REV__F8WDL9;REV__C9J7X7;REV__C9J718;REV__C9JF32;REV__C9JRT6;REV__F8WDB6;REV__Q8TBF8;Q32P41;REV__Q9Y5A7-2;REV__Q9Y5A7;REV__H3BM14;REV__H3BM74;REV__O00522-3;REV__O00522 "ATP synthase subunit alpha, mitochondrial;ATP synthase subunit alpha" ATP5A1 ">sp|P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1;>sp|P25705-2|ATPA_HUMAN Isoform 2 of ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1;>tr|K7ENP3|K7ENP3_HUMAN ATP synthase subunit alpha" 1.12 1.53 1.47 1.23 0.62 0.58 0.72 0.85 0 30 53.5 "ATP biosynthetic process;ATP hydrolysis coupled proton transport;ATP metabolic process;ATP synthesis coupled proton transport;biological regulation;biosynthetic process;cation transport;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;developmental process;electron transport chain;embryo development;energy coupled proton transport, against electrochemical gradient;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;lipid metabolic process;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;cell surface binding;eukaryotic cell surface binding;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;MHC class I protein binding;MHC protein binding;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;nucleus;organelle;organelle lumen;organelle part;plasma membrane;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, catalytic core F(1);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease

P38646;D6RJI2;H0YBG6;D6RA73;H0Y8S0 "Stress-70 protein, mitochondrial" HSPA9 ">sp|P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2" 1.14 1.08 1.35 0.59 1.2 0.86 1.17 1.27 1.10E-267 30 44.3 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nuclear export;nuclear transport;nucleocytoplasmic transport;primary metabolic process;protein export from nucleus;protein folding;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;transport adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;cell surface;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleoid;nucleolus;organelle;organelle part ko05152;RNA degradation

P14923 Junction plakoglobin JUP >sp|P14923|PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 0.79 1.11 0.48 0.6 1.87 1.91 1.18 0.93 3.09E-205 30 41.6 "adherens junction organization;anatomical structure development;anatomical structure morphogenesis;atrioventricular valve morphogenesis;biological adhesion;biological regulation;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling pathway involved in heart development;cell adhesion;cell development;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell motility;cell surface receptor linked signaling pathway;cell surface receptor linked signaling pathway involved in heart development;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular process involved in reproduction;cellular response to chemical stimulus;cellular response to indole-3-methanol;cellular response to organic substance;cellular response to stimulus;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;desmosome assembly;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection of stimulus;developmental process;developmental process involved in reproduction;ectoderm development;embryonic morphogenesis;endothelial cell-cell adhesion;epidermis development;epithelial cell-cell adhesion;gastrulation;germ cell development;heart valve morphogenesis;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;negative regulation of biological process;negative regulation of cardiac cell fate specification;negative regulation of cardioblast cell fate specification;negative regulation of cell communication;negative regulation of cell differentiation;negative regulation of cell fate commitment;negative regulation of cell fate specification;negative regulation of cellular process;negative regulation of developmental process;negative regulation of heart induction by canonical Wnt receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;negative regulation of Wnt receptor signaling pathway involved in heart development;nervous system development;oocyte development;organelle organization;positive regulation of biological process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cell communication;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of molecular function;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of Wnt receptor signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac cell fate specification;regulation of cardioblast cell fate specification;regulation of cardioblast differentiation;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell fate commitment;regulation of cell fate specification;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of establishment of protein localization;regulation of gene expression;regulation of heart induction;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of Wnt receptor signaling pathway;regulation of Wnt receptor signaling pathway involved in heart development;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to indole-3-methanol;response to mechanical stimulus;response to organic substance;response to stimulus;signal transduction;skin development;system development;tissue development;tissue morphogenesis;Wnt receptor signaling pathway;Wnt receptor signaling pathway involved in heart development" binding;enzyme binding;identical protein binding;kinase binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein homodimerization activity;protein kinase binding;structural constituent of cell wall;structural molecule activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity actin cytoskeleton;adherens junction;anchoring junction;apicolateral plasma membrane;basolateral plasma membrane;catenin complex;catenin-TCF7L2 complex;cell junction;cell part;cell-cell adherens junction;cell-cell junction;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;cytosolic part;desmosome;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;gamma-catenin-TCF7L2 complex;intermediate filament;internal side of plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;protein complex;protein-DNA complex;Z disc;zonula adherens Acute myeloid leukemia;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Pathways in cancer

Q14764;H3BQK6;H3BRL2;H3BUK7;H3BNF6;H3BP76;H3BPZ2;H3BNF2;H3BUP3;H3BQE7 Major vault protein MVP >sp|Q14764|MVP_HUMAN Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 0.83 0.4 0.46 0.3 2.35 1.24 2.05 1.59 2.54E-189 30 43.1 biological regulation;establishment of localization;establishment of protein localization;establishment of RNA localization;mRNA transport;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of kinase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein autophosphorylation;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of protein tyrosine kinase activity;negative regulation of signaling;negative regulation of transferase activity;nucleic acid transport;nucleobase-containing compound transport;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein autophosphorylation;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein tyrosine kinase activity;regulation of signaling;regulation of transferase activity;RNA transport;transport binding;enzyme binding;phosphatase binding;protein binding;protein phosphatase binding cell part;cytoplasmic part;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleus;organelle;organelle part;perinuclear region of cytoplasm;pore complex;protein complex;ribonucleoprotein complex;vesicle

O00159-3;F5H6E2;O00159;O00159-2;I3L501;I3L204;I3L4D4;I3L3Y6;I3L168;I3L3F5 Unconventional myosin-Ic MYO1C >sp|O00159-3|MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C;>tr|F5H6E2|F5H6E2_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=2 SV=1;>sp|O00159|MYO1C_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4;> 0.92 1.5 1.14 1.45 0.67 0.64 0.55 0.79 2.27E-176 30 31 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;immune response;immune system process;innate immune response;intracellular protein transport;intracellular transport;membrane organization;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;positive regulation of biological process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of protein targeting to membrane;positive regulation of protein transport;positive regulation of transport;protein targeting;protein targeting to membrane;protein transport;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of protein localization;regulation of protein targeting to membrane;regulation of protein transport;regulation of tight junction assembly;regulation of transport;response to stimulus;response to stress;RNA transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" basal plasma membrane;brush border;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;filamentous actin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;microvillus;microvillus membrane;myosin complex;myosin I complex;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleolus;nucleoplasm;nucleus;organelle;organelle part;plasma membrane part;pore complex;protein complex;stereocilium;stereocilium membrane;unconventional myosin complex;vesicle

Q5XKE5;CON__Q5XKE5;H0YID6 "Keratin, type II cytoskeletal 79" KRT79 ">sp|Q5XKE5|K2C79_HUMAN Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2;>Q5XKE5 SWISS-PROT:Q5XKE5 Tax_Id=9606 Gene_Symbol=KRT79 Keratin, type II cytoskeletal 79" 0.57 0.78 0.67 0.32 5.39 3.48 0.97 0.93 0 31 46.7 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P14618;P14618-3;H3BQ34;H3BUW1;H3BTJ2;H3BT25;H3BU13;H3BN34;H3BQZ3;P30613-2;P30613 Pyruvate kinase isozymes M1/M2;Pyruvate kinase PKM >sp|P14618|KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4;>sp|P14618-3|KPYM_HUMAN Isoform 3 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM;>tr|H3BQ34|H3BQ34_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM PE=2 SV=1 0.23 4.03 0.13 2.83 0.48 1.6 0.51 1.07 0 32 63.1 alcohol catabolic process;alcohol metabolic process;anatomical structure development;ATP biosynthetic process;ATP metabolic process;biological regulation;biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;catabolic process;cell death;cellular biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;death;developmental process;endocrine pancreas development;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle biosynthetic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;primary metabolic process;programmed cell death;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyruvate biosynthetic process;pyruvate metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;response to abiotic stimulus;response to ATP;response to biotic stimulus;response to cAMP;response to carbohydrate stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to glucose stimulus;response to heat;response to hexose stimulus;response to hormone stimulus;response to hypoxia;response to inorganic substance;response to insulin stimulus;response to lithium ion;response to metal ion;response to monosaccharide stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to other organism;response to oxygen levels;response to peptide hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;alkali metal ion binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;potassium ion binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyruvate kinase activity;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;nucleus;organelle;plasma membrane;vesicle Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis;Insulin signaling pathway;Maturity onset diabetes of the young;Purine metabolism;Pyruvate metabolism;Type II diabetes mellitus

P14625;F8W026;H0YIV0;Q58FF3;F8VPC7 Endoplasmin HSP90B1 >sp|P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 1 1.28 0.53 0.62 0.76 0.37 1.46 1.22 7.13E-288 33 41.7 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin rod assembly;activation of immune response;activation of innate immune response;activation of signaling protein activity involved in unfolded protein response;biological regulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to ATP;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;defense response;ER-associated protein catabolic process;establishment of localization;establishment of protein localization;immune response;immune

response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;macromolecule catabolic process;macromolecule metabolic process;maintenance of location;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organelle organization;pattern recognition receptor signaling pathway;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of defense response;positive regulation of hydrolase activity;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of response to stimulus;positive regulation of transferase activity;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein folding;protein metabolic process;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of dephosphorylation;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of response to stress;regulation of transferase activity;response to ATP;response to chemical stimulus;response to hypoxia;response to organic substance;response to oxygen levels;response to stimulus;response to stress;sequestering of calcium ion;sequestering of metal ion;signal transduction;toll-like receptor signaling pathway;transport;ubiquitin-dependent protein catabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;cation binding;enzyme binding;ion binding;lipoprotein particle receptor binding;low-density lipoprotein particle receptor binding;metal ion binding;nucleic acid binding;nucleotide binding;phosphatase binding;protein binding;protein phosphatase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;RNA binding;virion binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;midbody;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;pigment granule;plasma membrane part;vesicle NOD-like receptor signaling pathway;Pathways in cancer;Plant-pathogen interaction;Prostate cancer;Protein processing in endoplasmic reticulum
P10809;E7ESH4;E7EXB4;B7Z712;C9JL25;C9JL19;C9JCQ4;C9J0S9 "60 kDa heat shock protein, mitochondrial" HSPD1 ">sp|P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2" 1.14 1.15 1.67 0.51 1.21 0.77 1.24 1.27 0 33 66.7 activation of caspase activity;activation of immune response;activation of innate immune response;adaptive immune response;adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;B cell activation;B cell activation involved in immune response;B cell cytokine production;B cell mediated immunity;B cell proliferation;biological regulation;cell activation;cell activation involved in immune response;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;chaperone-mediated protein complex assembly;cytokine production;cytokine production involved in immune response;'de novo' protein folding;DNA metabolic process;DNA recombination;immune effector process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response-activating signal transduction;interaction with host;interspecies interaction between organisms;isotype switching;isotype switching to IgG isotypes;leukocyte activation;leukocyte activation involved in immune response;leukocyte mediated immunity;leukocyte proliferation;lymphocyte activation;lymphocyte activation involved in immune response;lymphocyte mediated immunity;lymphocyte proliferation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mononuclear cell proliferation;multicellular organismal process;multi-organism process;MyD88-dependent toll-like receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;pattern recognition receptor signaling pathway;positive regulation of adaptive immune response;positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell death;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of hydrolase activity;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune response to tumor cell;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of interferon-alpha production;positive regulation of interferon-gamma production;positive regulation of interleukin-10 production;positive regulation of interleukin-12 production;positive regulation of interleukin-6 production;positive regulation of leukocyte activation;positive regulation of leukocyte mediated immunity;positive regulation of lymphocyte activation;positive regulation of lymphocyte mediated immunity;positive regulation of macrophage activation;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of response to biotic stimulus;positive regulation of response to stimulus;positive regulation of response to tumor cell;positive regulation of T cell activation;positive regulation of T cell mediated immune response to tumor cell;positive regulation of T cell mediated immunity;positive regulation of type I interferon production;posttranscriptional regulation of gene expression;primary metabolic process;production of molecular mediator of immune response;protein complex assembly;protein complex subunit organization;protein folding;protein maturation;protein metabolic process;protein refolding;protein stabilization;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell activation;regulation of cell death;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of immune effector process;regulation of immune

response;regulation of immune response to tumor cell;regulation of immune system process;regulation of innate immune response;regulation of interferon-alpha production;regulation of interferon-gamma production;regulation of interleukin-10 production;regulation of interleukin-12 production;regulation of interleukin-6 production;regulation of leukocyte activation;regulation of leukocyte mediated immunity;regulation of lymphocyte activation;regulation of lymphocyte mediated immunity;regulation of macromolecule metabolic process;regulation of macrophage activation;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of peptidase activity;regulation of programmed cell death;regulation of protein stability;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of response to tumor cell;regulation of T cell activation;regulation of T cell mediated immune response to tumor cell;regulation of T cell mediated immunity;regulation of type I interferon production;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;signal transduction;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response;T cell activation;toll-like receptor signaling pathway;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cell surface binding;DNA binding;DNA replication origin binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipopolysaccharide binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;sequence-specific DNA binding;single-stranded DNA binding;structure-specific DNA binding;unfolded protein binding" cell part;cell surface;coated pit;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;early endosome;endosome;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lipopolysaccharide receptor complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane part;protein complex;receptor complex;stored secretory granule;vesicle ko05152;RNA degradation;Type I diabetes mellitus

C9J406;H7C463 IMMT >tr|C9J406|C9J406_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=2 SV=1;>tr|H7C463|H7C463_HUMAN Mitochondrial inner membrane protein (Fragment) OS=Homo sapiens GN=IMMT PE=4 SV=1 0.78 1.38 1.61 2.04 0.73 0.65 0.7 0.98 9.29E-130 33 52.2 cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

P11142;E9PKE3;P11142-2;E9PNE6;E9PN89;A8K7Q2;E9PLF4;E9PQQ4;E9PQK7;E9PK54;E9PPY6;E9PS65;E9PI65;E9PN25;E9PM13 Heat shock cognate 71 kDa protein HSPA8 >sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1;>tr|E9PKE3|E9PKE3_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=2 SV=1;>sp|P11142-2|HSP7C_HUMAN Isoform 2 of Heat shock cognate 71 kDa protein 1.05 1.33 0.91 1.34 0.41 0.43 0.95 0.98 0 34 50.2 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chaperone mediated protein folding requiring cofactor;chaperone-mediated protein folding;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;gene expression;Golgi vesicle transport;interaction with host;interspecies interaction between organisms;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;membrane organization;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;post-Golgi vesicle-mediated transport;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of neurotransmitter levels;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;secretion;secretion by cell;signal release;transcription, DNA-dependent;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cell surface;clathrin coated vesicle membrane;clathrin sculpted gamma-aminobutyric acid transport vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;protein complex;Prp19 complex;ribonucleoprotein complex;spliceosomal complex;vesicle;vesicle membrane Antigen processing and presentation;Endocytosis;MAPK signaling pathway;Measles;Protein processing in endoplasmic reticulum;Spliceosome;Toxoplasmosis

P23229-7;C9JXX7 >sp|P23229-7|ITA6_HUMAN Isoform 7 of Integrin alpha-6 OS=Homo sapiens GN=ITGA6 NaN 1.75 NaN NaN NaN NaN NaN 0.35 0 34 41.4 anatomical structure morphogenesis;biological adhesion;biological regulation;brown fat cell differentiation;cell adhesion;cell adhesion mediated by integrin;cell communication;cell differentiation;cell migration;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to stimulus;developmental process;fat cell differentiation;filopodium assembly;immune system process;integrin-mediated signaling pathway;leukocyte migration;locomotion;microspike assembly;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-cell adhesion;positive regulation of cellular process;regulation of biological process;regulation of cell adhesion;regulation of cell-cell adhesion;regulation of cellular process;response to external stimulus;response to extracellular stimulus;response to stimulus;signal transduction

basal plasma membrane;basement membrane;cell junction;cell part;cell-substrate junction;external side of plasma membrane;extracellular matrix part;extracellular region part;hemidesmosome;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex

P11021;O95399;Q5H8X8;O95399-2 78 kDa glucose-regulated protein HSPA5 >sp|P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 1.42 0.87 0.62 0.39 0.86 0.42 1.73 1.42 0 36 51.2 "activation of signaling protein activity involved in unfolded protein response;anatomical structure arrangement;anatomical structure development;behavior;biological regulation;calcium ion homeostasis;catabolic process;cation homeostasis;cell activation;cell communication;cell-cell signaling;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to biotic stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;cerebellar Purkinje cell layer development;cerebellum structural organization;chemical homeostasis;circadian behavior;circadian rhythm;circadian sleep/wake cycle process;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion concentration;ER overload response;ER-associated protein catabolic process;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;homeostatic process;ion homeostasis;macromolecule catabolic process;macromolecule metabolic process;metabolic process;metal ion homeostasis;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multicellular organismal process;muscle contraction;muscle system process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood pressure;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular process;negative regulation of glomerular filtration;negative regulation of heart contraction;negative regulation of heart rate;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of multicellular organismal process;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of programmed cell death;negative regulation of renal sodium excretion;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of transport;negative regulation of urine volume;platelet activation;platelet degranulation;positive regulation of angiogenesis;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of blood pressure;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of circadian rhythm;positive regulation of circadian sleep/wake cycle, REM sleep;positive regulation of circadian sleep/wake cycle, sleep;positive regulation of circadian sleep/wake cycle, wakefulness;positive regulation of collagen biosynthetic process;positive regulation of collagen metabolic process;positive regulation of developmental process;positive regulation of fibroblast migration;positive regulation of fibroblast proliferation;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal metabolic process;positive regulation of multicellular organismal process;positive regulation of neurological system process;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of response to stimulus;positive regulation of signaling;positive regulation of synaptic transmission;positive regulation of synaptic transmission, cholinergic;positive regulation of transferase activity;positive regulation of transmission of nerve impulse;positive regulation of vasodilation;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of body fluid levels;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of circadian rhythm;regulation of circadian sleep/wake cycle;regulation of circadian sleep/wake cycle, REM sleep;regulation of circadian sleep/wake cycle, sleep;regulation of circadian sleep/wake cycle, wakefulness;regulation of collagen biosynthetic process;regulation of collagen metabolic process;regulation of developmental process;regulation of excretion;regulation of fibroblast migration;regulation of fibroblast proliferation;regulation of glomerular filtration;regulation of heart contraction;regulation of heart rate;regulation of homeostatic process;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of ion homeostasis;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of nuclease activity;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein folding in endoplasmic reticulum;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein ubiquitination;regulation of renal sodium excretion;regulation of response to stimulus;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of synaptic transmission;regulation of synaptic transmission, cholinergic;regulation of system process;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmission of nerve impulse;regulation of transport;regulation of urine volume;regulation of vasodilation;renal system process;renal system process involved in regulation of blood volume;renal system process involved in regulation of systemic arterial blood pressure;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to endoplasmic reticulum stress;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to hypoxia;response to nutrient levels;response to organic substance;response to oxygen levels;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;rhythmic behavior;rhythmic process;secretion;secretion by cell;signal transduction;signaling;synaptic transmission;system process;transport;ubiquitin-dependent protein catabolic process;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;binding, bridging;calcium ion binding;catalytic activity;cation binding;chaperone binding;hormone activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;misfolded protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleoprotein binding;ribonucleotide binding;ribosome binding;unfolded protein binding" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum chaperone complex;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;extracellular region part;extracellular space;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;midbody;nucleus;organelle;organelle lumen;organelle part;pigment granule;protein complex;vesicle Neuroactive ligand-receptor interaction;Prion diseases;Protein export;Protein processing in endoplasmic reticulum

Q16891-2;Q16891;B9A067;Q16891-4;Q16891-3;D6RAW4 Mitochondrial inner membrane protein IMMT >sp|Q16891-2|IMMT_HUMAN Isoform 2 of Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT;>sp|Q16891|IMMT_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=1 SV=1;>tr|B9A067|B9A067_HUMAN Mitochondrial inner membrane protein OS=H 0.92 1.18 1.13 1.73 0.82 0.7 0.65 1.02 3.80E-136 36 52.6 biological regulation;calcium ion homeostasis;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;chemical homeostasis;divalent inorganic cation homeostasis;homeostatic process;ion homeostasis;metal ion homeostasis;mitochondrial calcium ion homeostasis;regulation of biological quality;response to abiotic stimulus;response to cold;response to stimulus;response to stress;response to temperature stimulus cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part

P24821-4;J3QSU6;P24821-2;E9PC84;F5H7V9;P24821-5;P24821-6;H0YGZ3 TNC >sp|P24821-4|TENA_HUMAN Isoform 4 of Tenascin OS=Homo sapiens GN=TNC;>tr|J3QSU6|J3QSU6_HUMAN Tenascin OS=Homo sapiens GN=TNC PE=4 SV=1;>sp|P24821-2|TENA_HUMAN Isoform 2 of Tenascin OS=Homo sapiens GN=TNC;>tr|E9PC84|E9PC84_HUMAN Tenascin OS=Homo sapiens GN= NaN NaN NaN NaN NaN NaN NaN NaN 6.75E-173 36 25.5

Q00610-2;Q00610;J3KS13;K7EJJ5;J3KSQ2;J3KRF5;F5H5N6 Clathrin heavy chain 1 CLTC >sp|Q00610-2|CLH1_HUMAN Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC;>sp|Q00610|CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 0.96 0.94 0.37 0.7 1.05 1.05 1.57 1.38 0 37 28.4 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cation transport;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;ferric iron transport;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;ion transport;iron ion transport;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;metal ion transport;mitosis;nuclear division;organelle fission;organelle organization;post-Golgi vesicle-mediated transport;protein transport;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;transferrin transport;transition metal ion transport;transport;vesicle-mediated transport structural molecule activity cell part;clathrin coat;clathrin coat of coated pit;clathrin coat of trans-Golgi network vesicle;clathrin coated vesicle membrane;clathrin vesicle coat;clathrin-coated endocytic vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endocytic vesicle membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane coat;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;protein complex;spindle;trans-Golgi network membrane;vesicle;vesicle coat;vesicle membrane Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease;Lysosome

P23229-4;P23229-2;P23229-9;P23229-6;P23229-5;P23229-3;P23229;H7BZ97 Integrin alpha-6;Integrin alpha-6 heavy chain;Integrin alpha-6 light chain ITGA6 >sp|P23229-4|ITA6_HUMAN Isoform Alpha-6X2A of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;>sp|P23229-2|ITA6_HUMAN Isoform Alpha-6X1A of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;>sp|P23229-9|ITA6_HUMAN Isoform 9 of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;> 1.4 1.45 0.93 0.9 0.51 0.14 0.33 0.39 0 37 39.8 "biological adhesion;biological regulation;blood coagulation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;coagulation;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;hemostasis;immune system process;integrin-mediated signaling pathway;leukocyte migration;locomotion;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;signal transduction" binding;cation binding;ion binding;metal ion binding cell part;integrin complex;macromolecular complex;membrane;membrane part;plasma membrane;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer;Toxoplasmosis

P13645;CON__P13645;Q7Z3Y7;CON__Q7Z3Y7;Q7Z3Y8;CON__Q7Z3Y8;Q7Z3Z0;CON__Q7Z3Z0 "Keratin, type I cytoskeletal 10" KRT10 ">sp|P13645|K1C10_HUMAN Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6;>P13645 SWISS-PROT:P13645 Tax_Id=9606 Gene_Symbol=KRT10 Keratin, type I cytoskeletal 10" 0.32 3.11 0.13 2.56 1.6 2.86 0.83 1.16 0 37 61.5 anatomical structure morphogenesis;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;cytoskeleton organization;developmental process;epidermal cell differentiation;epithelial cell differentiation;hair cycle process;hair follicle morphogenesis;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;keratinocyte differentiation;molting cycle;molting cycle process;multicellular organismal process;organelle organization;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus structural constituent of epidermis;structural molecule activity cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P24821;P24821-3 Tenascin TNC >sp|P24821|TENA_HUMAN Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3;>sp|P24821-3|TENA_HUMAN Isoform 3 of Tenascin OS=Homo sapiens GN=TNC 0.25 0.42 0.66 0.53 0.96 1.26 1.15 3.46 3.11E-178 37 25 anatomical structure morphogenesis;axon regeneration;axonogenesis;biological adhesion;biological regulation;cell adhesion;cell communication;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell signaling;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular process involved in reproduction;cellular response to stimulus;cellular response to stress;developmental process;developmental process involved in reproduction;mesenchymal-epithelial cell signaling;mesenchymal-epithelial cell signaling involved in prostate gland development;morphogenesis of an epithelium;neuromuscular junction development;neuron projection morphogenesis;neuron projection regeneration;peripheral nervous system axon regeneration;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;prostate gland epithelium morphogenesis;regeneration;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;reproductive process;response to axon injury;response to stimulus;response to stress;response to wounding;signaling;synapse organization;tissue morphogenesis basement membrane;extracellular matrix;extracellular matrix part;extracellular region part;extracellular space;interstitial matrix;proteinaceous extracellular matrix ECM-receptor interaction;Focal adhesion

P46940;H0YLE8;F2Z2E2;Q86VI3;H0YKA5;E9PDT6;Q13576-2;J3KR91;F5H7S7;E7EWC2;Q13576 Ras GTPase-activating-like protein IQGAP1 IQGAP1 >sp|P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1;>tr|H0YLE8|H0YLE8_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=2 SV=1 1.07 1.12 1.21 0.64 1.31 1.45 1.18 0.88 0 38 30 activation of MAPK activity;anatomical structure development;biological regulation;cell cycle process;cell development;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to organic substance;cellular response to stimulus;developmental process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;epithelial cell development;ERK1 and ERK2 cascade;G1/S transition of mitotic cell cycle;generation of precursor metabolites and energy;glomerular epithelial cell development;glomerular visceral epithelial cell development;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of dephosphorylation;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of epithelial cell proliferation;positive regulation of gene expression;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of macromolecule metabolic process;positive regulation of mammary gland epithelial cell proliferation;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of Ras GTPase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell proliferation;regulation of cell size;regulation of cellular catabolic process;regulation of cellular component size;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of dephosphorylation;regulation of developmental process;regulation of epithelial cell proliferation;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of mammary gland epithelial cell proliferation;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of transport;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to stimulus;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process   actin binding;binding;calcium ion binding;calmodulin binding;cation binding;cytoskeletal protein binding;enzyme activator activity;enzyme inhibitor activity;enzyme regulator activity;GTPase activator activity;GTPase inhibitor activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;protein binding;Ras GTPase activator activity;small GTPase regulator activity   actin cytoskeleton;actin filament;cell junction;cell leading edge;cell part;cell projection;cell-cell junction;cytoplasm;cytoskeletal part;cytoskeleton;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;microvillus;midbody;neuron projection;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ribonucleoprotein complex   Regulation of actin cytoskeleton

P49327 Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-oxoacyl-[acyl-carrier-protein] synthase;3-oxoacyl-[acyl-carrier-protein] reductase;3-hydroxyacyl-[acyl-carrier-protein] dehydratase;Enoyl-[acyl-carrier-protein] reductase;Oleoyl-[acyl-carrier-protein] hydrolase FASN   >sp|P49327|FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3   0.95   0.53   0.7   0.37   2.04   1.46   1.57   1.09   1.09E-191   39   22.8   acetyl-CoA metabolic process;acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;fatty acid biosynthetic process;fatty acid metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;generation of precursor metabolites and energy;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;pantothenate metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;small molecule biosynthetic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process   "[acyl-carrier-protein] S-acetyltransferase activity;[acyl-carrier-protein] S-malonyltransferase activity;3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity;3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase activity;3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity;3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity;3-oxoacyl-[acyl-carrier-protein] synthase activity;acetyltransferase activity;acyl-[acyl-carrier-protein] hydrolase activity;binding;carbon-oxygen lyase activity;catalytic activity;cation binding;coenzyme binding;cofactor binding;drug binding;enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity;fatty acid synthase activity;hydrolase activity;hydrolase activity, acting on ester bonds;hydro-lyase activity;ion binding;lyase activity;malonyltransferase activity;metal ion binding;myristoyl-[acyl-carrier-protein] hydrolase activity;NADP binding;NADPH binding;nucleotide binding;oleoyl-[acyl-carrier-protein] hydrolase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;palmitoyl-[acyl-carrier-protein] hydrolase activity;S-acetyltransferase activity;S-acyltransferase activity;S-malonyltransferase activity;thiolester hydrolase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups;transition metal ion binding;zinc ion binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;glycogen granule;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;pigment granule;plasma membrane;vesicle   Fatty acid biosynthesis;Insulin signaling pathway

P07476;J3KPN6   Involucrin   IVL   >sp|P07476|INVO_HUMAN Involucrin OS=Homo sapiens GN=IVL PE=1 SV=2;>tr|J3KPN6|J3KPN6_HUMAN Involucrin OS=Homo sapiens GN=IVL PE=4 SV=1   0.41   0.59   0.25   0.07   3.18   2.26   1.34   0.76   0   39   73.2   cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;isopeptide cross-linking;isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;peptidyl-amino acid modification;peptidyl-glutamine modification;peptidyl-lysine modification;primary metabolic process;protein metabolic process;protein modification process;response to abiotic stimulus;response to light stimulus;response to radiation;response to stimulus;response to UV;response to UV-B   "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity"   cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

Q03252;J9JID7   Lamin-B2   LMNB2   ">sp|Q03252|LMNB2_HUMAN Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=3;>tr|J9JID7|J9JID7_HUMAN Lamin B2, isoform CRA_a OS=Homo sapiens GN=LMNB2 PE=3 SV=1" 0.96   1.24   1.43   2.02   0.67   0.53   0.5   0.55   2.22E-141   39   49.3   structural molecule activity   cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane;nuclear inner membrane;nuclear lamina;nuclear membrane;nuclear part;organelle inner membrane;organelle membrane;organelle part;protein complex

P42704;B8ZZ38;C9JCA9;H7C3W8   "Leucine-rich PPR motif-containing protein, mitochondrial"   LRPPRC   ">sp|P42704|LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3"   1   1.19   1.74   0.85   1.63   0.46   1.01   1.14   8.66E-249   39   32.8   "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component movement;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoskeleton-dependent intracellular transport;establishment of localization;establishment of localization in cell;establishment of mitochondrion localization;establishment of mitochondrion localization, microtubule-mediated;establishment of organelle localization;establishment of RNA localization;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrion transport along microtubule;mRNA transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;organelle transport along microtubule;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA transport;transcription, DNA-dependent;transport" beta-tubulin binding;binding;cytoskeletal protein binding;DNA binding;microtubule binding;nucleic acid binding;protein binding;RNA binding;single-stranded DNA binding;structure-specific DNA binding;tubulin binding cell part;chromosome;condensed chromosome;condensed nuclear chromosome;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear chromosome;nuclear inner membrane;nuclear membrane;nuclear outer membrane;nuclear part;nucleoid;nucleoplasm;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;perinuclear region of cytoplasm;protein complex

Q01082;Q01082-3;Q01082-2;F8W6C1 "Spectrin beta chain, non-erythrocytic 1" SPTBN1 ">sp|Q01082|SPTB2_HUMAN Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2;>sp|Q01082-3|SPTB2_HUMAN Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1;>sp|Q01082-2|SPTB2_HUMAN Isoform Short of Spectrin be" 1.16 0.83 1.01 1.07 0.72 0.72 1.32 1.06 8.17E-217 39 20.6 actin filament capping;axon guidance;biological regulation;cell cycle cytokinesis;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;common-partner SMAD protein phosphorylation;cytokinesis;cytokinesis after mitosis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;intracellular protein transport;intracellular transport;locomotion;macromolecule metabolic process;macromolecule modification;membrane assembly;membrane organization;metabolic process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;nuclear import;nuclear transport;nucleocytoplasmic transport;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;post-Golgi vesicle-mediated transport;primary metabolic process;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein targeting to plasma membrane;protein transport;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;SMAD protein import into nucleus;taxis;transport;vesicle-mediated transport actin binding;ankyrin binding;binding;cytoskeletal protein binding;lipid binding;phospholipid binding;protein binding;structural constituent of cytoskeleton;structural molecule activity axolemma;axon part;cell cortex part;cell part;cell projection membrane;cell projection part;contractile fiber part;cuticular plate;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;M band;membrane;membrane part;membrane-bounded organelle;neuron projection membrane;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;spectrin;spectrin-associated cytoskeleton

Q07065;H3BUW6;H3BRM1;Q96K21-3 Cytoskeleton-associated protein 4 CKAP4 >sp|Q07065|CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 0.8 0.94 1.19 0.94 1.01 0.9 1.03 1.29 0 40 70.6 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;cytoskeleton;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lipid particle;membrane;membrane part;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane Protein processing in endoplasmic reticulum

O43707;D6PXK4;F5GXS2;H7C144;K7EJH8;K7EP19;D6RH00;Q9H254-2;C9JRP8;M0QZQ3;Q9H254-4;Q9H254 Alpha-actinin-4 ACTN4 >sp|O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2;>tr|D6PXK4|D6PXK4_HUMAN Alpha actinin 4 short isoform OS=Homo sapiens GN=ACTN4 PE=2 SV=1 1.61 0.63 1.01 1 1.38 0.68 1.74 1.21 0 41 49.8 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament capping;actin filament organization;actin filament-based process;adult behavior;adult locomotory behavior;adult walking behavior;anatomical structure morphogenesis;axon guidance;axonogenesis;behavior;biological regulation;cardiac conduction;cell activation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;central nervous system neuron axonogenesis;central nervous system projection neuron axonogenesis;chemotaxis;circulatory system process;clustering of voltage-gated sodium channels;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;exocytosis;fertilization;heart process;locomotion;locomotory behavior;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane organization;multicellular organismal process;multicellular organismal signaling;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of heart contraction;negative regulation of heart rate;negative regulation of multicellular organismal process;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;neurological system process;neuron projection morphogenesis;neuronal ion channel clustering;organelle organization;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of growth;positive regulation of ion transmembrane transporter activity;positive regulation of molecular function;positive regulation of multicellular organism growth;positive regulation of multicellular organismal process;positive regulation of pinocytosis;positive regulation of sodium ion transmembrane transporter activity;positive regulation of sodium:hydrogen antiporter activity;positive regulation of transport;positive regulation of transporter activity;protein transport;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cardiac muscle contraction;regulation of cell death;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of endocytosis;regulation of growth;regulation of heart contraction;regulation of heart rate;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of organelle organization;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of pinocytosis;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of proton transport;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of sodium:hydrogen antiporter activity;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to external stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signaling;system process;taxis;transmission of nerve impulse;transport;vesicle-mediated transport actin binding;actin filament binding;ankyrin binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;identical protein binding;integrin binding;ion binding;lipid binding;metal ion binding;nucleoside binding;phospholipid binding;protein binding;protein complex binding;protein dimerization activity;protein homodimerization activity;receptor binding;spectrin binding;structural constituent of cytoskeleton;structural molecule activity adherens junction;anchoring junction;axon hillock;axon part;cell body fiber;cell cortex part;cell junction;cell part;cell projection;cell projection part;contractile fiber part;cortical cytoskeleton;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;initial segment;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;neuron projection;node of Ranvier;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear part;nucleoplasm part;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane;platelet alpha granule lumen;PML body;protein complex;pseudopodium;ribonucleoprotein complex;secretory granule lumen;spectrin;vesicle;vesicle lumen;Z disc Adherens junction;Amoebiasis;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Systemic lupus erythematosus;Tight junction

Q14517;D6RCE4 "Protocadherin Fat 1;Protocadherin Fat 1, nuclear form" FAT1 >sp|Q14517|FAT1_HUMAN Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2 0.94 1.07 1.18 0.99 0.37 0.51 0.64 1.07 3.54E-200 41 11.6 actin cytoskeleton organization;actin filament organization;actin filament-based process;anatomical structure morphogenesis;biological adhesion;cell adhesion;cell communication;cell migration;cell motility;cell-cell adhesion;cell-cell signaling;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;establishment or maintenance of cell polarity;homophilic cell adhesion;locomotion;organelle organization;signaling binding;calcium ion binding;cation binding;ion binding;metal ion binding cell junction;cell part;cell projection;cell-cell junction;cytoplasmic part;filopodium;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium;membrane part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane part

P98160;Q5SZJ2;Q5SZJ1;Q5SZI9 Basement membrane-specific heparan sulfate proteoglycan core protein;Endorepellin;LG3 peptide HSPG2 >sp|P98160|PGBM_HUMAN Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4 0.49 0.78 0.68 0.62 0.41 0.98 0.73 1.71 5.43E-193 42 12.2 "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological regulation;biosynthetic process;brain development;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;cardiac muscle tissue development;cartilage development;cartilage development involved in endochondral bone morphogenesis;catabolic process;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chondrocyte differentiation;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;embryonic morphogenesis;embryonic organ morphogenesis;embryonic skeletal system morphogenesis;endochondral ossification;extracellular matrix organization;extracellular structure organization;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;lipoprotein metabolic process;localization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;metabolic process;multicellular organismal process;muscle tissue development;nitrogen compound metabolic process;organ development;organ morphogenesis;ossification;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;protein localization;regulation of biological process;regulation of cellular process;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;skeletal system morphogenesis;striated muscle tissue development;sulfur compound metabolic process;terpenoid metabolic process;tissue development" binding;cation binding;ion binding;metal ion binding basal lamina;cell part;cytoplasmic part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;Golgi apparatus part;Golgi lumen;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;vacuolar lumen;vacuolar part;vesicle ECM-receptor interaction

P05787;CON__P05787;P05787-2;F8VUG2;F8W1U3;CON__H-INV:HIT000292931;Q9H552;CON__Q9H552;F8VP67;F8VRG4;CON__H-INV:HIT000016045;H0YIB2;F8VQY3;CON__REFSEQ:XP_092267 "Keratin, type II cytoskeletal 8" KRT8 ">sp|P05787|K2C8_HUMAN Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7;>P05787 SWISS-PROT:P05787 Tax_Id=9606 Gene_Symbol=KRT8 Keratin, type II cytoskeletal 8;>sp|P05787-2|K2C8_HUMAN Isoform 2 of Keratin, type II cytoskeletal 8 OS=Homo sapi" 1.12 1.03 1.42 1.91 0.18 0.32 0.68 1.05 0 42 62.5 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;interaction with host;interspecies interaction between organisms;multi-organism process;organelle organization;reproductive process;viral reproductive process;virus-host interaction structural molecule activity cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;nuclear matrix;nuclear part;nucleoplasm;organelle part;protein complex

Q03001-3;C9JB56;H7C4P1;P42331-5;P42331-3;P42331-6;P42331;P42331-4;O75626-3;O75626-2;O75626 >sp|Q03001-3|DYST_HUMAN Isoform 3 of Dystonin OS=Homo sapiens GN=DST 0.37 1.57 1.27 1.85 0.23 0.19 0.27 0.17 6.73E-205 42 19.7 "anatomical structure development;biological regulation;biosynthetic process;cell development;cell fate commitment;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;developmental process;developmental process involved in reproduction;embryonic organ development;embryonic placenta development;germ cell development;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;maternal placenta development;metabolic process;negative regulation of B cell activation;negative regulation of B cell proliferation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell activation;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lipopolysaccharide-mediated signaling pathway;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mononuclear cell proliferation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;positive regulation of B cell activation;positive regulation of B cell differentiation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;primary metabolic process;regulation of B cell activation;regulation of B cell differentiation;regulation of B cell proliferation;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of immune system process;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lipopolysaccharide-mediated signaling pathway;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;small GTPase mediated signal transduction;transcription, DNA-dependent" binding;cation binding;DNA binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;lipid binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleoside-triphosphatase regulator activity;phospholipid binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

P12814;P12814-3;P12814-2;B7TY16;H9KV75;H7C5W8;H0YJW3;G3V2W4;G3V2N5;H0YJ11;Q08043;G3V5M4;G3V2X9;G3V2E8;G3V380 Alpha-actinin-1 ACTN1 >sp|P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2;>sp|P12814-3|ACTN1_HUMAN Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1;>sp|P12814-2|ACTN1_HUMAN Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1;>tr|B7TY16|B7TY16_HUMAN 1.32 0.54 1.01 0.93 1.27 0.7 1.77 1.34 0 43 52.8 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;biological regulation;cell activation;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;focal adhesion assembly;muscle filament sliding;negative regulation of biological process;negative regulation of cellular component movement;negative regulation of cellular process;organelle organization;platelet activation;platelet degranulation;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of programmed cell death;secretion;secretion by cell;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;identical protein binding;integrin binding;ion binding;metal ion binding;protein binding;protein complex binding;protein dimerization activity;protein homodimerization activity;receptor binding;structural constituent of muscle;structural molecule activity actin filament;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;dendritic spine;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;fascia adherens;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;neuron projection;neuron spine;non-membrane-bounded organelle;nucleus;organelle;organelle lumen;organelle part;plasma membrane;platelet alpha granule lumen;protein complex;pseudopodium;ruffle;secretory granule lumen;vesicle;vesicle lumen;Z disc Adherens junction;Amoebiasis;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Systemic lupus erythematosus;Tight junction

Q07283;Q5VUA4-2;Q5VUA4;REV__Q6ZQQ6;REV__Q6ZQQ6-2;REV__E7ESW6 Trichohyalin TCHH >sp|Q07283|TRHY_HUMAN Trichohyalin OS=Homo sapiens GN=TCHH PE=1 SV=2 0.25 0.39 0.62 0.27 1.54 3.76 1.18 3.19 0 44 27.3 "biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;keratinization;macromolecule biosynthetic process;macromolecule metabolic process;meiosis;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;calcium ion binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane

P08729;CON__Q3KNV1 "Keratin, type II cytoskeletal 7" KRT7 ">sp|P08729|K2C7_HUMAN Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5;>Q3KNV1 TREMBL:Q3KNV1;Q96GE1 Tax_Id=9606 Gene_Symbol=KRT7 keratin 7" 0.94 0.89 0.92 1.53 0.43 0.36 0.97 1.03 0 45 69.7 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;interaction with host;interspecies interaction between organisms;multi-organism process;organelle organization;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;reproductive process;viral reproductive process;virus-host interaction structural molecule activity cell part;cytoplasmic part;cytoskeletal part;Golgi apparatus;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;membrane-bounded organelle;nucleus;organelle;organelle part;protein complex

Q5D862;CON__Q5D862 Filaggrin-2 FLG2 >sp|Q5D862|FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1;>Q5D862 SWISS-PROT:Q5D862 Tax_Id=9606 Gene_Symbol=FLG2 Filaggrin-2 0.38 0.49 0.44 0.19 2.75 2.8 1.78 1.09 9.96E-277 46 35.9 binding;calcium ion binding;cation binding;ion binding;metal ion binding;structural molecule activity

P07996;CON__Q28194;A8MZG1 Thrombospondin-1 THBS1 >sp|P07996|TSP1_HUMAN Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2;>Q28194 TREMBL:Q28194 (Bos taurus) Thrombospondin-1 1.21 1.01 1.46 0.93 0.34 0.16 0.46 0.61 0 46 42.8 "activation of MAPK activity;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological adhesion;biological regulation;blood vessel morphogenesis;cartilage development;cartilage development involved in endochondral bone morphogenesis;cell activation;cell adhesion;cell cycle arrest;cell cycle process;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to heat;cellular response to stimulus;cellular response to stress;chronic inflammatory response;defense response;developmental process;endocardial cushion development;engulfment of apoptotic cell;establishment of localization;establishment of localization in cell;exocytosis;growth plate cartilage development;immune response;immune system process;induction of apoptosis;induction of programmed cell death;inflammatory response;locomotion;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;mesenchyme development;metabolic process;negative regulation of angiogenesis;negative regulation of antigen processing and presentation;negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood vessel endothelial cell migration;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell adhesion;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cell-matrix adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cGMP-mediated signaling;negative regulation of cytokine production;negative regulation of dendritic cell antigen processing and presentation;negative regulation of developmental process;negative regulation of endothelial cell migration;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;negative regulation of fatty acid transport;negative regulation of fibrinolysis;negative regulation of fibroblast growth factor receptor signaling pathway;negative regulation of focal adhesion assembly;negative regulation of hydrolase activity;negative regulation of immune system process;negative regulation of interleukin-12 production;negative regulation of lipid transport;negative regulation of locomotion;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of nitric oxide mediated signal transduction;negative regulation of organic acid transport;negative regulation of peptidase activity;negative regulation of plasma membrane long-chain fatty acid transport;negative regulation of plasminogen activation;negative regulation of programmed cell death;negative regulation of protein processing;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transmembrane transport;negative regulation of transport;outflow tract morphogenesis;peptide cross-linking;phagocytosis, engulfment;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;platelet degranulation;positive regulation of angiogenesis;positive regulation of apoptosis;positive regulation of behavior;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of blood coagulation;positive regulation of blood vessel endothelial cell migration;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemotaxis;positive regulation of coagulation;positive regulation of cytokine biosynthetic process;positive regulation of cytokine production;positive regulation of developmental process;positive regulation of endothelial cell migration;positive regulation of eukaryotic cell surface binding;positive regulation of fibroblast migration;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of macrophage activation;positive regulation of macrophage chemotaxis;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein serine/threonine kinase activity;positive regulation of reactive oxygen species metabolic process;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transferase activity;positive regulation of transforming growth factor beta production;positive regulation of transforming growth factor beta receptor signaling pathway;positive regulation of transforming growth factor beta1 production;positive regulation of translation;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;positive regulation of tumor necrosis factor biosynthetic process;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of antigen processing and presentation;regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;regulation of apoptosis;regulation of behavior;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of blood coagulation;regulation of blood vessel endothelial cell migration;regulation of catalytic activity;regulation of cell activation;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cGMP-mediated signaling;regulation of chemotaxis;regulation of coagulation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of dendritic cell antigen processing and presentation;regulation of developmental process;regulation of endopeptidase activity;regulation of endothelial cell migration;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of eukaryotic cell surface binding;regulation of fatty acid transport;regulation of fibrinolysis;regulation of fibroblast growth factor receptor signaling pathway;regulation of fibroblast migration;regulation of focal adhesion assembly;regulation of gene expression;regulation of granulocyte chemotaxis;regulation of hydrolase activity;regulation of immune system process;regulation of interleukin-12 production;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of lipid transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of macrophage activation;regulation of macrophage chemotaxis;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell migration;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitric oxide mediated signal transduction;regulation of organic acid transport;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of plasma membrane long-chain fatty acid transport;regulation of plasminogen activation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein processing;regulation of protein serine/threonine kinase activity;regulation of reactive oxygen species metabolic process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of transforming growth factor beta production;regulation of transforming growth factor beta receptor signaling pathway;regulation of transforming growth factor beta1 production;regulation of translation;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmembrane transport;regulation of transport;regulation of tumor necrosis factor biosynthetic process;regulation of tumor necrosis factor production;regulation of wound healing;response to abiotic stimulus;response to calcium ion;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to glucose stimulus;response to heat;response to hexose stimulus;response to hormone stimulus;response to hypoxia;response to inorganic substance;response to magnesium ion;response to metal ion;response to monosaccharide stimulus;response to organic substance;response to oxygen levels;response to progesterone stimulus;response to steroid hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;response to wounding;secretion;secretion by cell;sprouting angiogenesis;tissue development;transport;vesicle-mediated transport" binding;calcium ion binding;carbohydrate binding;cation binding;cell surface binding;collagen binding;collagen V binding;cytokine binding;eukaryotic cell surface binding;extracellular matrix binding;fibrinogen binding;fibroblast growth factor binding;fibronectin binding;glycoprotein binding;glycosaminoglycan binding;growth factor binding;heparin binding;identical protein binding;integrin binding;ion binding;laminin binding;lipid binding;lipoprotein particle binding;low-density lipoprotein particle binding;metal ion binding;pattern binding;phosphatidylserine binding;phospholipid binding;polysaccharide binding;protein binding;protein complex binding;protein-lipid complex binding;proteoglycan binding;receptor binding;transforming growth factor beta binding cell part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;external side of plasma membrane;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;fibrinogen complex;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane part;platelet alpha granule lumen;protein complex;secretory granule lumen;vesicle;vesicle lumen ECM-receptor interaction;Focal adhesion;Malaria;Phagosome;TGF-beta signaling pathway

P04264 "Keratin, type II cytoskeletal 1" KRT1 ">sp|P04264|K2C1_HUMAN Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6" 0.03 10.59 0.05 11.02 0.52 2.78 0.28 0.99 0 49 67.7 "activation of immune response;anatomical structure development;biological regulation;complement activation;complement activation, lectin pathway;defense response;developmental process;epidermis development;fibrinolysis;humoral immune response;immune effector process;immune response;immune system process;innate immune response;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of blood coagulation;negative regulation of coagulation;negative regulation of multicellular organismal process;positive regulation of biological process;positive regulation of immune response;positive regulation of immune system process;positive regulation of response to stimulus;primary metabolic process;protein activation cascade;protein metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of blood coagulation;regulation of coagulation;regulation of developmental process;regulation of immune response;regulation of immune system process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of wound healing;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;tissue development" binding;carbohydrate binding;receptor activity;structural constituent of cytoskeleton;structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;membrane;organelle part;plasma membrane;protein complex

Q14204 Cytoplasmic dynein 1 heavy chain 1 DYNC1H1 >sp|Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 0.77 1.01 0.41 0.63 1.17 1.52 1.24 1.32 7.44E-174 51 14.1 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cell cycle process;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cytoplasmic mRNA processing body assembly;cytoskeleton organization;death;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;macromolecular complex assembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;mitotic spindle organization;organelle organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;spindle organization;stress granule assembly;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;centrosome;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle Phagosome;Vasopressin-regulated water reabsorption

P08670;B0YJC4;B0YJC5;Q5JVS8;P17661;H7C5W5;P41219;P41219-2;K7EKH6;F8W835;Q16352;P07197-2;P07196;E7EMV2;E7ESP9;P07197 Vimentin VIM >sp|P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4;>tr|B0YJC4|B0YJC4_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=2 SV=1 0.44 0.23 0.54 0.59 2.47 1.27 1.15 1.36 0 51 78.5 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;anatomical structure development;anterograde axon cargo transport;astrocyte development;astrocyte differentiation;axon cargo transport;axon transport of mitochondrion;Bergmann glial cell differentiation;biological regulation;cell communication;cell development;cell differentiation;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;establishment of localization;establishment of localization in cell;glial cell development;glial cell differentiation;interaction with host;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;interspecies interaction between organisms;intracellular transport;lens fiber cell development;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;multi-organism process;muscle filament sliding;negative regulation of biological process;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of neuron projection development;nervous system development;neurofilament bundle assembly;neurofilament cytoskeleton organization;organelle organization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of axon diameter;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cell projection size;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of developmental process;regulation of heart contraction;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of system process;reproductive process;retrograde axon cargo transport;signaling;synaptic transmission;system development;transport;viral reproductive process;virus-host interaction structural constituent of cytoskeleton;structural constituent of eye lens;structural molecule activity adherens junction;anchoring junction;axon;axon part;cell junction;cell leading edge;cell part;cell projection;cell projection part;cell-cell adherens junction;cell-cell junction;C-fiber;cilium part;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;fascia adherens;intermediate filament;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;microbody;neurofilament;neuromuscular junction;neuron projection;non-membrane-bounded organelle;organelle;organelle part;peroxisome;photoreceptor outer segment membrane;plasma membrane;protein complex;sarcolemma;synapse;vesicle;Z disc Amyotrophic lateral sclerosis (ALS);Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM)

F5GWP8;C9JTX4;C9J826;C9JK18;C9JKY1;C9JPI2;K7ERP3 JUP >tr|F5GWP8|F5GWP8_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=2 SV=1 0.82 1.07 0.5 0.53 1.95 1.63 1.23 0.92 0 52 64.8 anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;desmosome assembly;developmental process;epidermis development;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;skin development;tissue development structural molecule activity adherens junction;anchoring junction;apicolateral plasma membrane;cell junction;cell part;cell-cell adherens junction;cell-cell junction;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;desmosome;fascia adherens;intermediate filament;internal side of plasma membrane;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;organelle part;plasma membrane part;protein complex;Z disc

P08779;CON__P08779;K7ENW6;CON__Q9Z2K1;CON__Q3ZAW8;P35900;CON__P35900;CON__Q9D312;K7ENV3;E5RIJ0;REV__H7BZT2;H0YBJ0;Q8N1A0-2;Q8N1A0;CON__Q8N1A0;P06746;CON__A2A5Y0;O76013-2;REV__Q9NS87-3;Q14532;CON__Q14532;O76014;O76015;CON__O76015;O76013;CON__O76013;Q7Z3Y9;CON__Q7Z3Y9;CON__O76014;CON__REFSEQ:XP_986630;REV__Q5SZL2;REV__Q5SZL2-4 "Keratin, type I cytoskeletal 16" KRT16 ">sp|P08779|K1C16_HUMAN Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4;>P08779 SWISS-PROT:P08779 Tax_Id=9606 Gene_Symbol=KRT16 Keratin, type I cytoskeletal 16" 0.79 0.67 0.65 0.32 2.96 2.24 1.34 1.21 0 52 80.1 anatomical structure development;apoptosis;base-excision repair;biological regulation;biosynthetic process;cell death;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;cytoskeleton organization;death;developmental process;DNA metabolic process;DNA repair;DNA replication;DNA-dependent DNA replication;epidermis development;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;programmed cell death;pyrimidine dimer repair;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell differentiation;regulation of cellular localization;regulation of cellular process;regulation of developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of establishment of protein localization;regulation of keratinocyte differentiation;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of programmed cell death;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of secretion;regulation of transport;response to chemical stimulus;response to DNA damage stimulus;response to ethanol;response to organic substance;response to stimulus;response to stress;tissue development "binding;catalytic activity;cation binding;cytoskeletal protein binding;damaged DNA binding;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;ion binding;lyase activity;metal ion binding;microtubule binding;nucleic acid binding;nucleotidyltransferase activity;protein binding;structural constituent of cytoskeleton;structural constituent of epidermis;structural molecule activity;transferase activity;transferase activity, transferring phosphorus-containing groups;tubulin binding" cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;microtubule;nuclear part;nucleoplasm;organelle part;protein complex;spindle microtubule Base excision repair

P35908;CON__P35908 "Keratin, type II cytoskeletal 2 epidermal" KRT2 ">sp|P35908|K22E_HUMAN Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2;>P35908 SWISS-PROT:P35908 Tax_Id=9606 Gene_Symbol=KRT2 Keratin, type II cytoskeletal 2 epidermal" 0.06 20.88 0.05 22.74 0.29 2.1 0.12 0.63 0 52 76.5 cell activation;cell migration;cell motility;cell proliferation;cellular component movement;cellular process;developmental process;keratinization;keratinocyte activation;keratinocyte migration;keratinocyte proliferation;locomotion structural constituent of cytoskeleton;structural molecule activity cell part;cytoplasmic part;cytoskeletal part;Golgi apparatus;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;membrane-bounded organelle;organelle;organelle part;protein complex

CON__O95678;O95678 "Keratin, type II cytoskeletal 75" KRT75 ">O95678 SWISS-PROT:O95678 Tax_Id=9606 Gene_Symbol=KRT75 Keratin, type II cytoskeletal 75;>sp|O95678|K2C75_HUMAN Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2" 0.23 0.22 0.43 0.31 1.42 1.37 2.12 1.93 0 52 61.2 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P35580;P35580-2;F8W6L6;P35580-3;P35580-4;E7ERA5 Myosin-10 MYH10 >sp|P35580|MYH10_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3;>sp|P35580-2|MYH10_HUMAN Isoform 2 of Myosin-10 OS=Homo sapiens GN=MYH10;>tr|F8W6L6|F8W6L6_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=2 SV=1;>sp|P35580-3|MYH10_HUMAN Isoform 3 of Myosin-1 1.17 1.01 0.95 0.85 0.98 1.1 1 1.38 0 52 29.6 "actin cytoskeleton organization;actin filament-based movement;actin filament-based process;actomyosin structure organization;adult heart development;anatomical structure development;anatomical structure formation involved in morphogenesis;axon guidance;biological regulation;cardiac cell development;cardiac muscle cell development;cardiac myofibril assembly;cell cycle cytokinesis;cell cycle process;cell development;cell migration;cell motility;cell projection assembly;cell projection organization;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cerebellar Purkinje cell layer development;chemotaxis;chordate embryonic development;cytokinesis;cytokinesis after mitosis;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;establishment of localization;establishment of localization in cell;establishment of nucleus localization;establishment of organelle localization;exocytosis;fourth ventricle development;heart development;in utero embryonic development;lateral ventricle development;locomotion;membrane organization;multicellular organismal process;muscle cell development;myofibril assembly;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron migration;nuclear migration;organ development;organelle organization;plasma membrane organization;plasma membrane repair;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to chemical stimulus;response to external stimulus;response to stimulus;retina development in camera-type eye;secretion;secretion by cell;substrate-dependent cell migration, cell extension;system process;taxis;third ventricle development;transport;ventricular cardiac muscle cell development;vesicle-mediated transport"	"actin binding;actin filament binding;actin-dependent ATPase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	actin filament bundle;actomyosin;axon;cell body;cell cortex;cell division site part;cell part;cell projection;cell projection part;cleavage furrow;cytoplasmic part;cytoskeletal part;dendritic spine;growth cone;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;midbody;myosin complex;myosin II complex;neuromuscular junction;neuron projection;neuron spine;neuronal cell body;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;site of polarized growth;spindle;stress fiber;synapse	Tight junction;Viral myocarditis

Q13751;Q5THA1;REV__H0YLF6;REV__Q9BVR6;REV__H3BPU4;REV__Q9UGJ1-2;REV__Q9UGJ1;F5H149;Q9P1Z9;Q9P1Z9-2	Laminin subunit beta-3	LAMB3	>sp|Q13751|LAMB3_HUMAN Laminin subunit beta-3 OS=Homo sapiens GN=LAMB3 PE=1 SV=1	1.07 0.92 1.56 0.96 0.2	0.13 0.5	0.79 0	53	47.1 anatomical structure development;biological adhesion;brown fat cell differentiation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;fat cell differentiation;hemidesmosome assembly;tissue development	structural molecule activity	cell part;extracellular matrix part;extracellular region;extracellular region part;integral to membrane;intrinsic to membrane;laminin complex;laminin-5 complex;macromolecular complex;membrane part;protein complex
Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis

Q04695;CON__Q04695;K7EPJ9;K7ESE1;K7ELP7;CON__Q99PS0	"Keratin, type I cytoskeletal 17"	KRT17	">sp|Q04695|K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2;>Q04695 SWISS-PROT:Q04695 Tax_Id=9606 Gene_Symbol=KRT17 Keratin, type I cytoskeletal 17"	0.86 0.9	0.85 0.78 1.67 1.33 1.09 1.03 0	55	95.1 anatomical structure development;anatomical structure morphogenesis;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;epidermis development;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;keratinization;morphogenesis of an epithelium;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell growth;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of epidermis development;positive regulation of growth;positive regulation of hair follicle development;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of epidermis development;regulation of gene expression;regulation of growth;regulation of hair cycle;regulation of hair follicle development;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;tissue development;tissue morphogenesis	MHC class II receptor activity;molecular transducer activity;receptor activity;signal transducer activity;signaling receptor activity;structural constituent of cytoskeleton;structural molecule activity;transmembrane signaling receptor activity
cell part;cell periphery;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex

Q9P2E9;Q9P2E9-2;Q9P2E9-3;F8W7S5;A2A2S5;H0YBV2;B8ZZA5;G3V112;REV__Q9P2M7;A8K944;Q8NE09;Q8N4C6-6;F8W6D3;H0YDJ4;E9PN67;Q8N4C6-4;C9J066;P00451
Ribosome-binding protein 1	RRBP1	>sp|Q9P2E9|RRBP1_HUMAN Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4;>sp|Q9P2E9-2|RRBP1_HUMAN Isoform 1 of Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1;>sp|Q9P2E9-3|RRBP1_HUMAN Isoform 2 of Ribosome-binding protein 1 OS=Homo sapiens	1.19 1.12 1.11 0.75 0.7 0.48 1.14 1.24 0	55	54.9 "acute inflammatory response;acute-phase response;biological adhesion;biological regulation;biosynthetic process;blood coagulation, intrinsic pathway;cell activation;cell adhesion;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;inflammatory response;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;platelet activation;platelet degranulation;primary metabolic process;protein activation cascade;protein metabolic process;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of G-protein coupled receptor protein signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;response to stress;response to wounding;secretion;secretion by cell;signal transduction;termination of G-protein coupled receptor signaling pathway;termination of signal transduction;translation;transport;vesicle-mediated transport"	binding;calcium ion binding;catalytic activity;cation binding;copper ion binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;oxidoreductase activity;receptor activity;transition metal ion binding	cell part;cytoplasm;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;endoplasmic reticulum;endoplasmic reticulum part;extracellular region;extracellular region part;extracellular space;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded

organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;non-membrane-bounded organelle;organelle;organelle lumen;organelle part;plasma membrane;platelet alpha granule lumen;ribonucleoprotein complex;ribosome;secretory granule lumen;vesicle lumen
Complement and coagulation cascades;Protein processing in endoplasmic reticulum

P02533;CON__P02533;G3V186;Q9ULK0 "Keratin, type I cytoskeletal 14" KRT14 ">sp|P02533|K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4;>P02533 SWISS-PROT:P02533 Tax_Id=9606 Gene_Symbol=KRT14 Keratin, type I cytoskeletal 14" 0.96 1.06 0.91 1.11 1.3 1.12 0.88 0.99 0 56 79 anatomical structure development;biological regulation;cell differentiation;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;cytoskeleton organization;developmental process;epidermis development;epithelial cell differentiation;glutamate signaling pathway;hemidesmosome assembly;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;ionotropic glutamate receptor signaling pathway;organelle organization;regulation of biological process;regulation of cellular process;response to abiotic stimulus;response to chemical stimulus;response to inorganic substance;response to ionizing radiation;response to metal ion;response to radiation;response to stimulus;response to zinc ion;signal transduction;tissue development channel activity;excitatory extracellular ligand-gated ion channel activity;extracellular ligand-gated ion channel activity;extracellular-glutamate-gated ion channel activity;gated channel activity;glutamate receptor activity;ion channel activity;ion transmembrane transporter activity;ionotropic glutamate receptor activity;ligand-gated channel activity;ligand-gated ion channel activity;molecular transducer activity;passive transmembrane transporter activity;receptor activity;signal transducer activity;signaling receptor activity;structural constituent of cytoskeleton;structural molecule activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane signaling receptor activity;transmembrane transporter activity;transporter activity cell junction;cell part;cell periphery;cytoplasmic part;cytoskeletal part;cytosol;external encapsulating structure part;integral to membrane;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;keratin filament;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;outer membrane-bounded periplasmic space;periplasmic space;plasma membrane;postsynaptic membrane;protein complex;synapse part;synaptic membrane Neuroactive ligand-receptor interaction

P16144-4;P16144-2;P16144-3;P16144;P16144-5;J3QS11;J3QRK0;J3QQL2;J3KSH9 Integrin beta-4 ITGB4 >sp|P16144-4|ITB4_HUMAN Isoform Beta-4D of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp|P16144-2|ITB4_HUMAN Isoform Beta-4A of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp|P16144-3|ITB4_HUMAN Isoform Beta-4B of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp| 1.41 1.35 1.07 0.91 0.21 0.14 0.38 0.44 0 57 37.1 biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;developmental process;extracellular matrix organization;extracellular structure organization;filopodium assembly;hemidesmosome assembly;integrin-mediated signaling pathway;locomotion;microspike assembly;multicellular organismal development;multicellular organismal process;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;response to wounding;signal transduction receptor activity basal plasma membrane;basement membrane;cell junction;cell leading edge;cell part;cell surface;cell-substrate junction;extracellular matrix part;extracellular region part;hemidesmosome;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Regulation of actin cytoskeleton

Q13753;Q13753-2;REV__A6PVS8-3;REV__A6PVS8-2;REV__A6PVS8 Laminin subunit gamma-2 LAMC2 >sp|Q13753|LAMC2_HUMAN Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 PE=1 SV=2;>sp|Q13753-2|LAMC2_HUMAN Isoform Short of Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 1.08 0.95 1.44 0.96 0.21 0.13 0.49 0.78 0 57 42.1 anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;tissue development binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding extracellular matrix part;extracellular region;extracellular region part;laminin complex;laminin-5 complex;macromolecular complex;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis

Q8IVF2-3;Q8IVF2;Q8IVF2-2 Protein AHNAK2 AHNAK2 >sp|Q8IVF2-3|AHNK2_HUMAN Isoform 3 of Protein AHNAK2 OS=Homo sapiens GN=AHNAK2;>sp|Q8IVF2|AHNK2_HUMAN Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=21.02 0.87 0.68 0.2 1.72 1.93 1.49 1.04 9.07E-186 58 29.1 cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle

E9PPU0 EPPK1 >tr|E9PPU0|E9PPU0_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=4 SV=1 NaN NaN 1.12 0.3 3.84 3.16 NaN NaN 0 58 34.8 cell part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P02545;P02545-3;Q6UYC3;D6RAQ3;P02545-4;H0YAB0;REV__Q5VX52 Prelamin-A/C;Lamin-A/C LMNA >sp|P02545|LMNA_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1;>sp|P02545-3|LMNA_HUMAN Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA;>tr|Q6UYC3|Q6UYC3_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=2 SV=1;>tr|D6RAQ3|D6RAQ3_HUMAN Prelamin-A/ 0.97 1.11 1.4 1.66 0.96 0.67 0.72 0.65 0 59 68.4 activation of signaling protein activity involved in unfolded protein response;anaphase;anatomical structure development;biological regulation;cardiac cell development;cardiac muscle cell development;cell cycle phase;cell cycle process;cell development;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hypoxia;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment or maintenance of cell polarity;establishment or maintenance of cytoskeleton polarity;establishment or maintenance of microtubule cytoskeleton polarity;intracellular protein transport;intracellular transport;localization;M phase;M phase of mitotic cell cycle;macromolecule localization;macromolecule metabolic process;membrane disassembly;membrane organization;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic nuclear envelope disassembly;mitotic nuclear envelope reassembly;mitotic prophase;muscle cell development;muscle organ development;muscle structure development;nuclear envelope disassembly;nuclear envelope organization;nuclear envelope reassembly;nuclear import;nuclear transport;nucleocytoplasmic transport;organ development;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell aging;positive regulation of cellular process;positive regulation of developmental process;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;prophase;protein import;protein import into nucleus;protein localization;protein localization to nucleus;protein localization to organelle;protein metabolic process;protein targeting;protein transport;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell aging;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of hydrolase activity;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;sterol regulatory element binding protein import into nucleus;transport;ventricular cardiac muscle cell development structural molecule activity cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;envelope;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane-bounded organelle;nuclear envelope;nuclear part;nucleoplasm;nucleus;organelle;organelle envelope;organelle part;perinuclear region of cytoplasm;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM)

Q13813;Q13813-2;A6NG51;Q13813-3 "Spectrin alpha chain, non-erythrocytic 1" SPTAN1 ">sp|Q13813|SPTN1_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3;>sp|Q13813-2|SPTN1_HUMAN Isoform 2 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1;>tr|A6NG51|A6NG51_HUMAN Spectrin alpha chain, non-e" 1.17 0.82 1.11 0.98 1.05 1.04 1.32 1.05 0 61 29.9 actin filament capping;axon guidance;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;locomotion;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;taxis actin binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding;structural constituent of cytoskeleton;structural molecule activity adherens junction;anchoring junction;cell cortex part;cell junction;cell part;cell-cell adherens junction;cell-cell junction;contractile fiber part;cuticular plate;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;fascia adherens;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;membrane;membrane part;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;spectrin;Z disc

Q92817;K7EKI0;K7EQ87;A8MZ36 Envoplakin EVPL >sp|Q92817|EVPL_HUMAN Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3;>tr|K7EKI0|K7EKI0_HUMAN Envoplakin OS=Homo sapiens GN=EVPL PE=4 SV=1 0.99 1.16 0.59 0.18 2.26 2.41 1.13 0.53 0 62 37.1 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity" anchoring junction;cell junction;cell part;cell-cell junction;cornified envelope;cytoplasm;cytoskeleton;desmosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P12111-2;P12111;E9PCV6;E7ENL6;P12111-4;P12111-5;P12111-3;C9JNG9;I3L392 Collagen alpha-3(VI) chain COL6A3 >sp|P12111-2|CO6A3_HUMAN Isoform 2 of Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3;>sp|P12111|CO6A3_HUMAN Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5;>tr|E9PCV6|E9PCV6_HUMAN Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE 1.05 1.14 0.98 1.07 2.79 1.41 0.95 0.98 0 64 29.9 anatomical structure development;axon guidance;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;collagen catabolic process;collagen metabolic process;developmental process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;locomotion;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;muscle organ development;muscle structure development;organ development;response to chemical stimulus;response to external stimulus;response to stimulus;taxis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity anchoring collagen;cell part;collagen;collagen type VI;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;extracellular space;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;sarcolemma ECM-receptor interaction;Focal adhesion;Protein digestion and absorption

P13647;CON__P13647;F8W0C6;H0YI76;F8VV57;F8VU69 "Keratin, type II cytoskeletal 5" KRT5 ">sp|P13647|K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3;>P13647 SWISS-PROT:P13647 Tax_Id=9606 Gene_Symbol=KRT5 Keratin, type II cytoskeletal 5" 1.07 1.24 0.99 1.33 1.05 0.84 0.8 0.81 0 71 65.1 anatomical structure development;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;hemidesmosome assembly;tissue development structural constituent of cytoskeleton;structural molecule activity cell part;cytoplasmic part;cytoskeletal part;cytosol;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;organelle;organelle part;plasma membrane;protein complex

P04259 "Keratin, type II cytoskeletal 6B" KRT6B ">sp|P04259|K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5" 0.27 0.31 0.49 0.36 2.17 2.34 0.99 1.24 0 75 73 anatomical structure development;developmental process;ectoderm development;tissue development structural constituent of cytoskeleton;structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

P02751;P02751-3;P02751-8;P02751-15;P02751-5;P02751-14;P02751-17;P02751-7;P02751-6;F8W7G7;P02751-10;P02751-9;P02751-11;P02751-4;P02751-13;P02751-12;H0Y7Z1;P02751-16;P02751-2;H0Y4K8 Fibronectin;Anastellin;Ugl-Y1;Ugl-Y2;Ugl-Y3 FN1 >sp|P02751|FINC_HUMAN Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4;>sp|P02751-3|FINC_HUMAN Isoform 3 of Fibronectin OS=Homo sapiens GN=FN1;>sp|P02751-8|FINC_HUMAN Isoform 8 of Fibronectin OS=Homo sapiens GN=FN1;>sp|P02751-15|FINC_HUMAN Isoform 15 of Fibron 0.09 0.14 0.35 0.11 3.3 3.73 0.49 2.7 0 76 42 acute inflammatory response;acute-phase response;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological adhesion;biological regulation;calcium-independent cell-matrix adhesion;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;defense response;developmental process;establishment of localization;establishment of localization in cell;exocytosis;extracellular matrix organization;extracellular structure organization;immune system process;inflammatory response;leukocyte migration;locomotion;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;platelet activation;platelet degranulation;primary metabolic process;protein metabolic process;protein modification process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to stimulus;response to stress;response to wounding;secretion;secretion by cell;substrate adhesion-dependent cell spreading;transport;vesicle-mediated transport binding;carbohydrate binding;collagen binding;enzyme activator activity;enzyme regulator activity;extracellular matrix structural constituent;glycosaminoglycan binding;heparin binding;pattern binding;peptidase activator activity;peptidase regulator activity;polysaccharide binding;protein binding;structural molecule activity apical plasma membrane;basement membrane;cell part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;endoplasmic reticulum-Golgi intermediate compartment;extracellular matrix;extracellular matrix part;extracellular region;extracellular region part;fibrinogen complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane part;platelet alpha granule lumen;protein complex;proteinaceous extracellular matrix;secretory granule lumen;vesicle lumen Amoebiasis;Bacterial invasion of epithelial cells;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer

P02538;CON__P02538 "Keratin, type II cytoskeletal 6A" KRT6A ">sp|P02538|K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3;>P02538 SWISS-PROT:P02538 Tax_Id=9606 Gene_Symbol=KRT6A Keratin, type II cytoskeletal 6A"0.83 0.87 0.69 0.73 1.94 1.53 1.05 1.07 0 76 73 anatomical structure development;biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;ectoderm development;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;tissue development structural constituent of cytoskeleton;structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex

K7EKI8;O60437;K7EQ71;REV__Q9ULW3Periplakin PPL >tr|K7EKI8|K7EKI8_HUMAN Periplakin OS=Homo sapiens GN=PPL PE=4 SV=1;>sp|O60437|PEPL_HUMAN Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4;>tr|K7EQ71|K7EQ71_HUMAN Periplakin (Fragment) OS=Homo sapiens GN=PPL PE=4 SV=1 1.12 1.1 0.67 0.17 2.68 2.27 1.25 0.57 0 78 41.6 developmental process;keratinization structural constituent of cytoskeleton;structural molecule activity anchoring junction;cell junction;cell part;cell-cell junction;cytoplasmic part;cytoskeleton;desmosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nucleus;organelle;plasma membrane

P58107 Epiplakin EPPK1 >sp|P58107|EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 0.67 0.49 0.82 0.24 3.68 2.75 1.11 0.98 0 81 50.8 structural molecule activity cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle

P21333-2;P21333;Q5HY54;E9PHF0;F8WE98;H0Y5C6;H0Y5F3;H7C2E7 Filamin-A FLNA >sp|P21333-2|FLNA_HUMAN Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA;>sp|P21333|FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4;>tr|Q5HY54|Q5HY54_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1 1.06 0.59 0.86 0.75 0.92 0.66 1.55 1.09 0 92 44.6 "actin crosslink formation;actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament organization;actin filament-based process;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;cAMP-mediated signaling;cell activation;cell cycle process;cell junction assembly;cell junction organization;cell morphogenesis;cell morphogenesis involved in differentiation;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cellular response to stimulus;cilium assembly;cyclic-nucleotide-mediated signaling;cytoplasmic sequestering of protein;cytoskeleton organization;developmental process;dopamine receptor signaling pathway;early endosome to late endosome transport;endosome transport;epithelial to mesenchymal transition;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;inhibition of adenylate cyclase activity by dopamine receptor signaling pathway;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;intracellular transport;localization;macromolecule localization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane organization;microtubule cytoskeleton organization;microtubule-based process;mitotic spindle organization;negative regulation of adenylate cyclase activity;negative regulation of biological process;negative regulation of catabolic process;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of protein transport;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of transport;organelle assembly;organelle organization;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription factor import into nucleus;positive regulation of transmembrane transport;positive regulation of transport;posttranscriptional regulation of gene expression;protein localization;protein localization at cell surface;protein localization in membrane;protein stabilization;receptor clustering;regulation of adenylate cyclase activity;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of establishment of protein localization;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of lyase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein stability;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;response to stimulus;second-messenger-mediated signaling;secretion;secretion by cell;signal transduction;spindle assembly;spindle assembly involved in mitosis;spindle organization;transport;vesicle-mediated transport" actin binding;actin filament binding;binding;cytoskeletal protein binding;enzyme binding;Fc-gamma receptor I complex binding;glycoprotein binding;GTPase binding;identical protein binding;immunoglobulin receptor binding;molecular transducer activity;protein binding;protein dimerization activity;protein homodimerization activity;Rac GTPase binding;Ral GTPase binding;Ras GTPase binding;receptor binding;Rho GTPase binding;signal transducer activity;small GTPase binding actin cytoskeleton;cell cortex;cell part;chromosomal part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;Myb complex;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex;trans-Golgi network;vesicle Focal adhesion;MAPK signaling pathway

Q16787-1;B0YJ33;Q16787;Q16787-4;Q16787-3;K7EIP4;K7ERM0 Laminin subunit alpha-3 LAMA3 >sp|Q16787-1|LAMA3_HUMAN Isoform 1 of Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3;>tr|B0YJ33|B0YJ33_HUMAN Laminin alpha-3 chain variant 2 OS=Homo sapiens GN=LAMA3 PE=2 SV=1;>sp|Q16787|LAMA3_HUMAN Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3 PE=1 S 1.06 0.92 1.37 0.95 0.26 0.14 0.48 0.81 0 94 53.6 anatomical structure development;biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of developmental process;regulation of embryonic development;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;tissue development structural molecule activity basement membrane;extracellular matrix part;extracellular region part;laminin complex;laminin-1 complex;laminin-5 complex;macromolecular complex;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis

P20930;CON__P20930 Filaggrin FLG >sp|P20930|FILA_HUMAN Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3;>P20930 SWISS-PROT:P20930 Tax_Id=9606 Gene_Symbol=FLG Filaggrin 0.3 0.28 0.52 0.13 4.27 3.22 1.78 1.06 0 118 62.5 cell differentiation;cellular developmental process;cellular process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinocyte differentiation binding;calcium ion binding;cation binding;ion binding;metal ion binding;structural molecule activity cell part;cornified envelope;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle

O75369-2;O75369-9;O75369;O75369-8;O75369-6;O75369-3;E7EN95;O75369-7;O75369-5;O75369-4;H7C5L4;Q8WXT3 Filamin-B FLNB >sp|O75369-2|FLNB_HUMAN Isoform 2 of Filamin-B OS=Homo sapiens GN=FLNB;>sp|O75369-9|FLNB_HUMAN Isoform 9 of Filamin-B OS=Homo sapiens GN=FLNB;>sp|O75369|FLNB_HUMAN Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2;>sp|O75369-8|FLNB_HUMAN Isoform 8 of Filamin-B O 1.15 0.61 0.87 0.68 1.03 0.96 1.41 1.32 0 129 53.9 actin cytoskeleton organization;actin filament-based process;anatomical structure development;biological regulation;cell differentiation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;developmental process;maintenance of location;maintenance of

location in cell;maintenance of protein location;maintenance of protein location in cell;muscle tissue development;organelle organization;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction;skeletal muscle tissue development;striated muscle tissue development;tissue development actin binding;binding;cytoskeletal protein binding;protein binding actin cytoskeleton;actin filament bundle;actomyosin;adherens junction;anchoring junction;cell cortex;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;focal adhesion;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;stress fiber;Z disc Focal adhesion;MAPK signaling pathway
P15924;P15924-2 Desmoplakin DSP >sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3;>sp|P15924-2|DESP_HUMAN Isoform DPII of Desmoplakin OS=Homo sapiens GN=DSP 0.92 0.83 0.46 0.43 2.44 2.18 1.39 1.03 0 161 54.2 adherens junction organization;anatomical structure development;anatomical structure morphogenesis;biological adhesion;cardiac muscle tissue morphogenesis;cell adhesion;cell differentiation;cell junction organization;cell-cell adhesion;cell-cell junction organization;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cytoskeleton organization;developmental process;epidermal cell differentiation;epidermis development;epithelial cell differentiation;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;keratinocyte differentiation;localization;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;muscle tissue morphogenesis;organelle organization;peptide cross-linking;primary metabolic process;protein localization;protein localization to adherens junction;protein metabolic process;protein modification process;skin development;tissue development;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis;ventricular compact myocardium morphogenesis "binding;binding, bridging;protein binding;protein binding, bridging;structural constituent of cytoskeleton;structural molecule activity" anchoring junction;basolateral plasma membrane;cell junction;cell part;cell-cell contact zone;cell-cell junction;cornified envelope;cytoplasmic part;cytoskeletal part;cytoskeleton;desmosome;intercalated disc;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;plasma membrane part;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC)
P35579;P35579-2;Q5BKV1;B1AH99;Q7Z406;Q7Z406-6;F2Z2U8;Q7Z406-2;G8JLL9;Q7Z406-5;Q7Z406-4;M0QY43Myosin-9 MYH9 >sp|P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4;>sp|P35579-2|MYH9_HUMAN Isoform 2 of Myosin-9 OS=Homo sapiens GN=MYH9 0.92 0.74 0.72 0.61 1.13 1.25 1.2 1.74 0 180 66.6 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based movement;actin filament-based process;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;axon guidance;biological adhesion;biological regulation;blood vessel endothelial cell migration;cell adhesion;cell cycle phase;cell cycle process;cell differentiation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;chemotaxis;chordate embryonic development;cytokinesis;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;endothelial cell migration;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of lymphocyte polarity;establishment of meiotic spindle localization;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;establishment of T cell polarity;establishment or maintenance of cell polarity;immune system process;in utero embryonic development;integrin-mediated signaling pathway;leukocyte differentiation;leukocyte migration;locomotion;macromolecule metabolic process;meiotic metaphase I;meiotic spindle organization;membrane protein ectodomain proteolysis;membrane protein proteolysis;metabolic process;metaphase;microtubule cytoskeleton organization;microtubule-based process;monocyte differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;myoblast fusion;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle organization;platelet formation;primary metabolic process;protein metabolic process;protein transport;proteolysis;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of G-protein coupled receptor protein signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;spindle organization;syncytium formation;syncytium formation by plasma membrane fusion;taxis;termination of G-protein coupled receptor signaling pathway;termination of signal transduction;transport;uropod organization "actin binding;actin filament binding;actin-dependent ATPase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein anchor;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin filament bundle;actomyosin;actomyosin contractile ring;adherens junction;anchoring junction;cell cortex part;cell division site part;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cleavage furrow;contractile ring;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;immunological synapse;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;myosin complex;myosin II complex;neuromuscular junction;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ruffle;spindle;stress fiber;synapse;uropod;vesicle Tight junction;Viral myocarditis
Q09666;E9PJZ0;E9PKR9;E9PJC6;E9PLK4;Q09666-2;E9PQE3 Neuroblast differentiation-associated protein AHNAK AHNAK >sp|Q09666|AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 1.1 0.63 0.64 0.2 2 1.82 1.52 0.79 0 272 74 anatomical structure development;developmental process;nervous system development;system development cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded

organelle;nucleus;organelle
Q15149-3;H0YDN1;E9PKG0;E9PQ28;E9PIA2;REV__Q8IWV8-3;REV__Q8IWV8-4;REV__Q8IWV8 >sp|Q15149-3|PLEC_HUMAN Isoform 3 of Plectin OS=Homo sapiens GN=PLEC 1.08 0.75 3.01 0.91 0.76 0.89 1.13 1.11 0 317 63.2 cell part;contractile fiber;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle
Q15149-4;Q15149-7;Q15149-8;Q15149-9;Q15149-5;Q15149-6;Q15149-2;E9PMV1 >sp|Q15149-4|PLEC_HUMAN Isoform 4 of Plectin OS=Homo sapiens GN=PLEC;>sp|Q15149-7|PLEC_HUMAN Isoform 7 of Plectin OS=Homo sapiens GN=PLEC;>sp|Q15149-8|PLEC_HUMAN Isoform 8 of Plectin OS=Homo sapiens GN=PLEC;>sp|Q15149-9|PLEC_HUMAN Isoform 9 of Plectin OS=H 1.08 0.8 1.04 0.97 0.95 0.83 1.04 1.13 0 320 64.1

Supplemental Table S2 - Significantly changed transcripts
(TPM values determined by RNAseq)

Gene_ID	Ctrl 1	Ctrl 2	RDEB 1	RDEB 2	Gene Symbol
ENSG00000001630	219.375	171.292	67.0218	86.8908	CYP51A1
ENSG00000002587	10.4722	8.03751	1.14604	3.67416	HS3ST1
ENSG00000004399	3.54283	5.31761	6.74125	48.1254	PLXND1
ENSG00000008283	24.8398	26.4808	17.6657	10.8974	CYB561
ENSG00000008517	2.35807	4.55404	9.44722	10.1188	IL32
ENSG00000010278	815.039	695.718	190.08	152.374	CD9
ENSG00000016082	1.98961	7.58452	0.8644	0.980344	ISL1
ENSG00000020181	0.300783	0.243962	0.750587	14.8698	ADGRA2
ENSG00000020633	0.141246	0.848448	0.66834	4.7559	RUNX3
ENSG00000030419	31.2138	17.3299	8.11759	15.0769	IKZF2
ENSG00000040608	8.88308	11.8484	3.8589	3.41388	RTN4R
ENSG00000042062	5.9171	10.058	4.89906	19.4542	RIPOR3
ENSG00000049323	5.29477	8.126	50.6178	101.776	LTBP1
ENSG00000052802	596.484	407.137	65.8824	144.612	MSMO1
ENSG00000060982	7.45029	12.7211	33.3559	28.3559	BCAT1
ENSG00000063438	1.08288	1.39119	2.06679	26.3182	AHRR
ENSG00000071246	1.13492	1.59839	1.86829	3.91935	VASH1
ENSG00000074047	0.453459	0.254228	0.581978	13.6668	GLI2
ENSG00000074696	68.4659	84.8761	32.1509	34.3009	HACD3
ENSG00000079308	5.88204	8.31786	11.2202	45.0272	TNS1
ENSG00000079385	22.0141	10.3858	8.002	10.5848	CEACAM1
ENSG00000080166	2.05806	1.41815	0.905297	0.707374	DCT
ENSG00000080573	1.04917	2.16069	7.04528	97.6718	COL5A3
ENSG00000087303	2.38208	3.64374	3.93508	22.8678	NID2
ENSG00000088881	0.0982112	0.165714	0.281095	5.30251	EBF4
ENSG00000089327	200.947	127.542	53.6433	60.5689	FXYD5
ENSG00000090376	0.296709	0.803873	1.05064	7.96288	IRAK3
ENSG00000099864	1.58316	2.88225	3.68932	8.04844	PALM
ENSG00000099998	0.36686	0.898594	1.67627	13.5371	GGT5
ENSG00000100033	2.62618	2.65836	13.8305	14.6274	PRODH
ENSG00000100302	0.209861	0.2185	2.66357	0.409867	RASD2
ENSG00000101276	7.63643	7.606	5.55764	8.24042	SLC52A3
ENSG00000101670	82.4476	92.363	32.8489	35.3302	LIPG
ENSG00000101680	2.6273	8.82965	15.6429	20.2949	LAMA1
ENSG00000102393	10.6154	13.8046	6.23248	5.17589	GLA
ENSG00000102755	0.69509	1.72824	1.52737	5.1156	FLT1
ENSG00000102934	10.6705	17.7053	2.04174	1.88268	PLLP
ENSG00000103089	3.46698	0.37535	0.165209	0.275393	FA2H
ENSG00000103569	34.0485	2.26304	0.719941	1.56718	AQP9
ENSG00000103811	55.1508	45.0049	10.6438	4.83595	CTSH
ENSG00000104332	24.9312	16.5153	4.4086	8.00997	SFRP1
ENSG00000105088	1.34826	1.15854	9.06138	15.4019	OLFM2
ENSG00000105270	1.01476	2.47279	1.62983	6.81732	CLIP3
ENSG00000105755	137.501	81.2927	41.2383	34.0098	ETHE1
ENSG00000106624	2.43072	2.47617	17.9042	96.0105	AEBP1
ENSG00000106976	0.457918	2.1311	2.34171	29.4054	DNM1
ENSG00000107165	21.9904	6.53733	3.6464	2.896	TYRP1
ENSG00000107249	0.920932	0.603315	1.89005	15.5474	GLIS3
ENSG00000107738	38.5452	13.1708	8.75476	4.25003	VSIR
ENSG00000108511	1.05797	1.90149	3.88478	8.79869	HOXB6

ENSG00000109255	2.24607	5.98258	0.453032	0.234523	NMU
ENSG00000109906	2.70213	3.37731	10.8443	11.1626	ZBTB16
ENSG00000110944	2.77404	5.15469	1.4491	1.6679	IL23A
ENSG00000111057	88.2275	180.242	37.8838	33.9938	KRT18
ENSG00000111319	72.1453	78.5888	19.4843	34.812	SCNN1A
ENSG00000112379	0.8455	0.864115	0.436474	0.510529	ARFGEF3
ENSG00000112414	23.197	43.6702	11.3232	13.7789	ADGRG6
ENSG00000112796	2.628	3.07735	0.553972	2.4614	ENPP5
ENSG00000114378	11.6361	4.01475	1.56871	2.61249	HYAL1
ENSG00000115159	37.644	43.5881	16.4684	23.9881	GPD2
ENSG00000115318	1.22824	0.918055	0.971154	12.0469	LOXL3
ENSG00000115616	0.610358	0.390618	0.146467	0.141536	SLC9A2
ENSG00000115884	1443.68	1175.83	411.645	526.228	SDC1
ENSG00000116183	0.206069	0.568826	12.3836	1.4707	PAPPA2
ENSG00000116741	59.2882	6.50074	5.7939	2.15321	RGS2
ENSG00000116962	1.0115	1.3417	5.168	44.565	NID1
ENSG00000117472	241.697	95.7069	5.65565	32.5357	TSPAN1
ENSG00000117600	0.0358009	0.149637	0.25501	0.749738	PLPPR4
ENSG00000118596	12.5114	26.2433	33.0681	44.0146	SLC16A7
ENSG00000119655	152.508	144.114	33.8468	40.1305	NPC2
ENSG00000119888	6.84329	22.0306	3.38125	1.82568	EPCAM
ENSG00000120093	1.57918	1.71022	4.62608	36.9063	HOXB3
ENSG00000120756	11.9076	15.3993	5.41303	9.6225	PLS1
ENSG00000120820	1.65193	3.27029	7.7004	13.2225	GLT8D2
ENSG00000120885	12.604	12.1561	3.89262	6.4951	CLU
ENSG00000121898	0.482154	0.80707	0.953694	7.77992	CPXM2
ENSG00000122870	2.00377	2.47003	5.62293	14.5167	BICC1
ENSG00000124171	16.9184	9.07081	4.28891	5.87818	PARD6B
ENSG00000125675	0.15706	0.515379	1.93772	10.3975	GRIA3
ENSG00000125775	64.4713	14.3578	8.33298	9.45596	SDCBP2
ENSG00000126016	0.203209	0.321128	1.0376	2.09101	AMOT
ENSG00000127124	0.398425	1.907	1.61966	7.27292	HIVEP3
ENSG00000128274	24.4234	17.5081	4.41528	7.30987	A4GALT
ENSG00000129353	129.855	92.3879	46.4153	53.476	SLC44A2
ENSG00000129451	586.294	154.487	35.8703	77.8064	KLK10
ENSG00000131196	0.528076	1.95905	5.28463	5.15784	NFATC1
ENSG00000131711	2.23797	10.0037	13.5056	51.5451	MAP1B
ENSG00000132205	0.591193	1.20406	1.87488	6.28883	EMILIN2
ENSG00000132530	28.1488	60.4711	83.3049	178.219	XAF1
ENSG00000133110	1.21638	0.718975	15.6221	99.6885	POSTN
ENSG00000133935	13.8154	13.2075	4.75157	6.2269	ERG28
ENSG00000134013	6.19608	32.2846	43.0004	277.804	LOXL2
ENSG00000134874	1.40906	1.81315	12.7167	20.8122	DZIP1
ENSG00000134986	5.27786	12.0967	17.1497	59.4747	NREP
ENSG00000135046	1410.62	466.248	220.12	211.007	ANXA1
ENSG00000135218	0.513389	1.38059	7.98843	2.07997	CD36
ENSG00000135480	698.179	490.604	247.481	167.182	KRT7
ENSG00000135549	14.1679	13.6051	6.22006	11.1339	PKIB
ENSG00000135926	1044.93	410.812	166.33	152.13	TMBIM1
ENSG00000136010	2.53964	14.7966	45.6532	22.9608	ALDH1L2
ENSG00000136155	246.28	14.9206	12.1929	14.6545	SCEL
ENSG00000136205	2.59161	5.0156	11.2823	66.5406	TNS3
ENSG00000136378	0.972779	1.59821	2.85943	9.06895	ADAMTS7
ENSG00000136542	70.1116	43.3701	17.9074	10.339	GALNT5

ENSG00000136802	134.109	144.942	58.4788	49.4819	LRRC8A
ENSG00000136859	0.32207	0.248403	0.374296	6.96662	ANGPTL2
ENSG00000137440	956.565	1631.51	109.708	302.235	FGFBP1
ENSG00000137767	77.6403	70.3473	27.8486	27.0843	SQOR
ENSG00000138678	38.812	7.70162	1.65181	3.10702	GPAT3
ENSG00000138685	1.32602	1.53449	2.33852	15.9821	FGF2
ENSG00000139364	1.19249	3.30267	3.04499	30.3693	TMEM132B
ENSG00000139946	0.30109	0.221161	0.452755	6.84274	PELI2
ENSG00000140092	2.32959	3.07562	3.94026	27.9523	FBLN5
ENSG00000140557	0.168267	0.393757	0.389256	2.69028	ST8SIA2
ENSG00000141738	40.7226	29.8978	8.95032	11.7932	GRB7
ENSG00000141756	3.65833	17.0302	21.1554	76.1413	FKBP10
ENSG00000141837	1.43085	1.35823	1.96574	4.98661	CACNA1A
ENSG00000142910	356.742	234.71	85.6822	71.2545	TINAGL1
ENSG00000143369	365.309	71.0581	20.2207	52.5812	ECM1
ENSG00000143520	0.207703	0.165498	1.12818	0.383557	FLG2
ENSG00000143816	5.84888	5.51028	0.70915	1.89317	WNT9A
ENSG00000143867	0.354876	0.802164	1.21311	2.71117	OSR1
ENSG00000144063	185.055	77.2531	22.5957	36.1328	MALL
ENSG00000144152	0.848154	1.67045	2.32897	17.5649	FBLN7
ENSG00000144218	3.03781	5.84328	7.16352	19.497	AFF3
ENSG00000144339	0.118318	1.12759	0.703202	4.64919	TMEFF2
ENSG00000144355	1.344	4.66327	0.744342	0.95188	DLX1
ENSG00000144642	6.62784	11.7724	21.2418	30.5628	RBMS3
ENSG00000145050	42.7462	61.0704	21.1734	20.422	MANF
ENSG00000145569	2.8872	5.63512	3.01339	5.5679	FAM105A
ENSG00000145824	0.400589	0.420441	21.301	0.53378	CXCL14
ENSG00000146070	9.62335	4.27868	1.20571	3.20838	PLA2G7
ENSG00000146555	0.216751	0.714714	1.76704	3.3477	SDK1
ENSG00000147100	18.0215	18.6096	5.70569	7.41002	SLC16A2
ENSG00000147155	86.7328	97.7141	13.3466	24.2009	EBP
ENSG00000148248	80.5575	94.1371	36.7113	35.287	SURF4
ENSG00000148344	47.7657	10.4623	3.67168	7.51665	PTGES
ENSG00000148516	1.90349	5.3837	4.14242	53.2112	ZEB1
ENSG00000148671	238.552	93.0525	16.4234	35.9222	ADIRF
ENSG00000148848	0.364234	0.420662	0.867308	9.58767	ADAM12
ENSG00000149294	0.195373	0.651946	0.927461	1.9239	NCAM1
ENSG00000149591	20.0431	26.7237	74.4712	57.6433	TAGLN
ENSG00000150394	5.10077	10.4134	16.0612	28.2168	CDH8
ENSG00000151640	0.343527	1.53015	9.67584	1.93256	DPYSL4
ENSG00000151892	0.225971	0.523946	0.437571	2.81707	GFRA1
ENSG00000152377	2.21724	1.85824	5.85178	7.19768	SPOCK1
ENSG00000152402	0.109222	0.268179	0.457752	4.73192	GUCY1A2
ENSG00000152910	0.757198	0.803454	8.04988	1.3526	CNTNAP4
ENSG00000152952	17.2383	19.585	36.2474	116.779	PLOD2
ENSG00000153292	58.9338	45.8823	8.2354	18.331	ADGRF1
ENSG00000153551	56.2233	38.8108	10.0959	14.1444	CMTM7
ENSG00000153802	29.0981	20.316	1.01665	7.92741	TMPRSS11D
ENSG00000153823	1.12115	3.67307	5.74572	7.9348	PID1
ENSG00000154027	2.9741	8.92003	6.60234	41.4562	AK5
ENSG00000154096	1.29567	2.39611	6.33186	50.5851	THY1
ENSG00000154277	1.11958	2.29102	4.90647	9.94989	UCHL1
ENSG00000154736	0.0705375	0.119034	0.457734	2.67235	ADAMTS5
ENSG00000154764	35.6233	41.6706	9.88939	17.4356	WNT7A

ENSG00000155629	2.69919	3.10572	2.43283	3.8941	PIK3AP1
ENSG00000155816	0.351018	1.07335	0.989909	3.66502	FMN2
ENSG00000155886	0.231874	0.370312	0.886399	0.788713	SLC24A2
ENSG00000155966	0.0727876	0.156562	0.352237	0.269915	AFF2
ENSG00000156103	0.115066	0.262302	0.611534	2.75065	MMP16
ENSG00000156453	124.837	25.5	14.7038	12.7631	PCDH1
ENSG00000157613	3.10893	6.74448	6.9026	28.9412	CREB3L1
ENSG00000158106	3.86975	5.81928	1.22455	0.845489	RHPN1
ENSG00000158201	28.0463	29.3316	6.4453	14.1795	ABHD3
ENSG00000158373	79.0691	90.5071	37.2782	25.1981	HIST1H2BD
ENSG00000158457	2.4421	3.59249	0.52469	0.63454	TSPAN33
ENSG00000159167	0.244563	0.423537	0.892702	6.03172	STC1
ENSG00000159403	2.03771	7.75959	23.1813	92.9282	C1R
ENSG00000159674	3.26582	4.80381	7.74301	67.9641	SPON2
ENSG00000160446	35.1356	32.1292	11.0131	7.86305	ZDHHC12
ENSG00000160886	8.93193	24.0857	1.71051	3.48756	LY6K
ENSG00000162496	39.5295	17.2832	6.93758	5.32069	DHRS3
ENSG00000162576	29.2481	18.5194	12.7814	89.0623	MXRA8
ENSG00000162687	0.116285	0.298163	1.3084	1.154	KCNT2
ENSG00000162733	2.00805	1.06448	8.22865	57.2339	DDR2
ENSG00000162745	0.615006	2.21645	1.93881	8.30265	OLFML2B
ENSG00000162892	0.335479	1.80331	2.51217	21.1127	IL24
ENSG00000163064	0.303359	0.191426	2.05688	6.87516	EN1
ENSG00000163520	0.76289	2.21045	4.62973	24.006	FBLN2
ENSG00000163661	0.203923	0.336899	7.68987	16.8711	PTX3
ENSG00000164120	21.2917	3.67096	0.744717	2.53977	HPGD
ENSG00000164125	1.66084	2.80772	3.11428	20.2383	FAM198B
ENSG00000164176	0.0569659	0.286742	0.401389	3.29375	EDIL3
ENSG00000164379	24.1792	7.29607	2.66752	4.5392	FOXQ1
ENSG00000164619	1.06446	2.34208	1.81387	21.4816	BMPER
ENSG00000164932	1.89746	3.54208	3.84777	42.0619	CTHRC1
ENSG00000165124	0.131326	0.444898	1.64967	2.00859	SVEP1
ENSG00000165194	0.0333574	2.2642	0.316396	1.74541	PCDH19
ENSG00000165959	11.322	23.7044	7.24072	9.00023	CLMN
ENSG00000166086	2.58419	3.8605	7.64523	12.7595	JAM3
ENSG00000166265	0.43459	1.70546	5.32083	3.1075	CYYR1
ENSG00000166341	0.376691	0.335112	0.581571	7.23727	DCHS1
ENSG00000166741	0.483249	0.912162	10.949	67.509	NNMT
ENSG00000166920	22.973	1.32809	0.828345	2.2817	C15orf48
ENSG00000166963	0.508341	1.00541	1.61814	5.93574	MAP1A
ENSG00000167244	0.371428	0.882057	0.865265	1.79102	IGF2
ENSG00000167306	51.8354	9.07423	4.77767	6.26036	MYO5B
ENSG00000167653	12.0845	0.397334	0.329241	0.71898	PSCA
ENSG00000167656	57.7003	20.9695	2.04635	4.41967	LY6D
ENSG00000167754	1334.14	261.544	94.8909	124.437	KLK5
ENSG00000167757	248.314	40.7697	23.6025	34.4442	KLK11
ENSG00000167779	18.0572	151.918	13.9572	13.8751	IGFBP6
ENSG00000168497	1.62197	2.02768	0.457827	0.691429	CAVIN2
ENSG00000168646	0.121177	0.174436	0.661482	4.05657	AXIN2
ENSG00000168916	1.61655	5.52515	8.85342	10.347	ZNF608
ENSG00000169071	0.280986	0.161171	1.26338	3.08887	ROR2
ENSG00000169083	0.687044	1.22295	1.37526	4.82784	AR
ENSG00000169122	0.825665	1.6473	3.54563	8.02976	FAM110B
ENSG00000169403	11.0224	16.1107	6.0722	4.93229	PTAFR

ENSG00000169439	3.54306	1.40423	6.17268	27.1414	SDC2
ENSG00000169908	271.625	96.1002	36.6805	44.4473	TM4SF1
ENSG00000170175	22.2887	27.892	13.1533	12.5504	CHRNB1
ENSG00000170345	50.6665	192.161	22.1352	28.0389	FOS
ENSG00000170390	0.0310091	0.123073	0.178171	1.47378	DCLK2
ENSG00000170540	78.7015	136.62	38.2115	41.2055	ARL6IP1
ENSG00000170558	0.413624	0.537703	0.862366	9.91639	CDH2
ENSG00000171124	34.886	26.1687	17.6016	21.1623	FUT3
ENSG00000171236	3.1569	5.33676	2.12105	3.27436	LRG1
ENSG00000171345	964.348	407.098	13.8409	74.5109	KRT19
ENSG00000171346	737.9	477.178	58.9179	166.825	KRT15
ENSG00000171408	0.317315	0.680346	0.619439	4.36994	PDE7B
ENSG00000172817	0.606138	0.443461	2.58761	23.2355	CYP7B1
ENSG00000172893	107.19	105.976	27.259	44.5445	DHCR7
ENSG00000172915	0.226883	0.7114	1.10127	2.07146	NBEA
ENSG00000172985	0.276996	0.237216	3.14461	14.6592	SH3RF3
ENSG00000173917	0.40139	0.427624	3.44568	15.443	HOXB2
ENSG00000175591	13.452	7.98813	3.17891	2.85364	P2RY2
ENSG00000176887	0.201866	0.952608	2.1393	3.84447	SOX11
ENSG00000176971	0.3795	0.712501	2.16674	3.84563	FIBIN
ENSG00000176998	1.86909	1.3845	0.332359	0.329597	HCG4
ENSG00000178860	0.25193	0.0268257	3.7537	4.22039	MSC
ENSG00000179059	1.94043	3.25605	16.957	10.2464	ZFP42
ENSG00000179163	13.3236	9.13731	3.71121	3.13641	FUCA1
ENSG00000179218	847.706	1153.84	206.128	355.535	CALR
ENSG00000179242	8.07087	12.5852	1.80234	4.40732	CDH4
ENSG00000179403	44.0189	46.703	6.58051	14.6368	VWA1
ENSG00000179593	32.2894	33.0392	14.4355	11.7137	ALOX15B
ENSG00000179913	23.5413	26.0207	3.81225	4.7978	B3GNT3
ENSG00000180447	0.428893	0.357194	0.85096	10.3353	GAS1
ENSG00000181126	2.20364	1.74113	0.484491	1.24003	HLA-V
ENSG00000181885	255.622	98.0548	21.2548	13.3463	CLDN7
ENSG00000182107	20.4854	19.0619	6.80586	4.13407	TMEM30B
ENSG00000182326	4.04478	8.26972	11.8516	32.3488	C1S
ENSG00000182463	0.427361	1.54507	4.16331	2.77308	TSHZ2
ENSG00000182492	0.0263198	0.0946319	1.63545	13.297	BGN
ENSG00000182742	0.207499	0.307557	0.750295	4.17807	HOXB4
ENSG00000182752	2.49614	2.35294	6.0732	91.9582	PAPPA
ENSG00000183160	4.05148	10.8325	9.92639	50.0705	TMEM119
ENSG00000183742	87.2785	35.6003	10.097	8.64103	MACC1
ENSG00000183780	18.3103	11.8904	11.9474	27.1277	SLC35F3
ENSG00000184226	0.379054	0.500837	0.977579	2.84511	PCDH9
ENSG00000184254	1044.22	336.285	146.708	181.219	ALDH1A3
ENSG00000184838	0.186634	0.455408	0.681901	5.28891	PRR16
ENSG00000185532	0.363401	0.576974	0.76705	11.8202	PRKG1
ENSG00000185664	24.8131	13.7091	10.7166	6.01055	PMEL
ENSG00000186204	12.319	4.05248	1.93913	3.51144	CYP4F12
ENSG00000186529	21.9016	6.77727	3.54979	7.43339	CYP4F3
ENSG00000186847	6135.15	6465.98	2440.37	3079.68	KRT14
ENSG00000187990	90.5466	79.5143	32.8181	26.1582	HIST1H2BG
ENSG00000188910	143.971	126.998	52.6828	36.3146	GJB3
ENSG00000189143	116.578	14.7248	6.20021	13.0608	CLDN4
ENSG00000189184	0.101594	0.14699	0.343014	9.46405	PCDH18
ENSG00000189280	113.865	86.8812	32.0476	18.9819	GJB5

ENSG00000189433	31.6815	17.9096	2.39575	6.77131	GJB4
ENSG00000196628	11.0376	20.1074	34.818	51.6465	TCF4
ENSG00000196872	5.88278	4.58827	0.50298	0.892691	KIAA1211L
ENSG00000196876	0.726886	1.55383	4.71666	12.3426	SCN8A
ENSG00000196890	18.2878	18.6643	3.28721	1.34557	HIST3H2BB
ENSG00000196950	38.3365	45.1484	24.8985	18.7117	SLC39A10
ENSG00000197635	1.34914	1.64791	3.28507	21.0453	DPP4
ENSG00000197956	2085.32	1963.36	529.039	595.736	S100A6
ENSG00000198795	0.90249	0.619835	1.20081	11.7544	ZNF521
ENSG00000198796	0.495346	2.61933	2.74273	12.0205	ALPK2
ENSG00000204131	0.0655167	0.0471888	0.154785	2.44569	NHSL2
ENSG00000204262	10.7842	24.8188	81.3011	225.056	COL5A2
ENSG00000204539	1.79343	0	1.91044	0.0369284	CDSN
ENSG00000204632	15.7666	1.56069	0.229717	0	HLA-G
ENSG00000204644	0.597048	0.883221	0.053838	0.24367	ZFP57
ENSG00000204839	18.4233	26.1552	6.74312	9.35031	MROH6
ENSG00000214711	12.8469	1.11867	1.18938	1.78841	CAPN14
ENSG00000218537	2.31033	2.36564	5.28651	3.63738	MIF-AS1
ENSG00000224689	7.66015	8.40891	4.38752	8.48278	ZNF812P
ENSG00000224769	3.17376	0.349285	0.152021	0.173579	MUC20P1
ENSG00000225614	0.0514285	0.142907	0.279134	5.47424	ZNF469
ENSG00000226958	32562.3	3445.44	2109.61	2262.65	CTD-2328D6.1
ENSG00000230662	0.189974	1.02024	0.592297	6.89949	TNPO1P2
ENSG00000231991	3.22876	2.68647	1.21843	4.71481	ANXA2P2
ENSG00000235531	3.78961	6.42493	15.7961	31.3477	MSC-AS1
ENSG00000235750	30.8583	31.7834	11.3876	10.2779	KIAA0040
ENSG00000235863	3.00312	4.21892	3.25136	3.68408	B3GALT4
ENSG00000237973	1.95602	1.62142	3.47415	3.17072	MTCO1P12
ENSG00000240563	1.43807	2.03121	4.74626	5.0038	L1TD1
ENSG00000243444	1.13905	1.74095	2.10885	6.13818	PALM2
ENSG00000256618	20773.7	20228.2	27988	23798.5	MTRNR2L1
ENSG00000259207	0.229852	0.143444	0.475856	7.34084	ITGB3
ENSG00000271043	37388.5	38681.4	47961.9	48105.9	MTRNR2L2
ENSG00000271225	3.47643	16.5983	0.332109	1.23496	BNIP3P4

Supplemental Table S4 - Filtered list of extracellular proteome

Normalized SILAC protein ratios of ECM isolated from primary human keratinocytes derived from two RDEB and two healthy donors. Annotated spectra of single peptide identifications are available as supplemental information.

Protein IDs Protein names Gene names Fasta headers norm Ctrl1_1 norm Ctrl1_2 norm Ctrl2_1 norm Ctrl2_2 norm RDEB1_1 norm RDEB1_2 norm RDEB2_1 norm RDEB2_2 matrisome ECM Glycoproteins Collagens Proteoglycans ECM-affiliated Proteins ECM Regulators Secreted Factors GOBP(cell adhesion) GOBP name GOMF name GOCC (extracellular) GOCC name KEGG name PEP Intensity Peptides

P25054-2;P25054 Adenomatous polyposis coli protein APC >sp|P25054-2|APC_HUMAN Isoform Short of Adenomatous polyposis coli protein OS=Homo sapiens GN=APC;>sp|P25054|APC_HUMAN Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2 1.09 NaN 0.66 0.92 1.20 1.61 1.08 NaN + anatomical structure development;anatomical structure homeostasis;anatomical structure morphogenesis;anterior/posterior pattern specification;axis specification;axonogenesis;biological adhesion;biological regulation;canonical Wnt receptor signaling pathway;cell activation;cell adhesion;cell cycle arrest;cell cycle checkpoint;cell cycle cytokinesis;cell cycle process;cell differentiation;cell junction assembly;cell junction organization;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;cytokinesis;cytokinesis after mitosis;cytoplasmic microtubule organization;cytoskeleton organization;developmental process;dorsal/ventral pattern formation;epidermis development;hair cycle process;hair follicle development;hemopoietic or lymphoid organ development;homeostatic process;immune system process;kidney development;leukocyte activation;leukocyte differentiation;locomotion;lymphocyte activation;lymphocyte differentiation;macromolecular complex assembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule-based process;mitotic cell cycle checkpoint;mitotic cell cycle spindle assembly checkpoint;mitotic cell cycle spindle checkpoint;mitotic metaphase/anaphase transition;molting cycle;molting cycle process;multicellular organismal process;muscle cell homeostasis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cyclin-dependent protein kinase activity;negative regulation of cytoskeleton organization;negative regulation of developmental process;negative regulation of epithelial cell proliferation;negative regulation of epithelial cell proliferation involved in prostate gland development;negative regulation of intracellular protein kinase cascade;negative regulation of kinase activity;negative regulation of MAPKKK cascade;negative regulation of microtubule depolymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of mitosis;negative regulation of mitotic metaphase/anaphase transition;negative regulation of molecular function;negative regulation of nuclear division;negative regulation of odontogenesis;negative regulation of organelle organization;negative regulation of programmed cell death;negative regulation of protein complex disassembly;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of reproductive process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transferase activity;negative regulation of Wnt receptor signaling pathway;neuron projection morphogenesis;organ development;organelle organization;pattern specification process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell adhesion;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of epithelial cell differentiation;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of microtubule polymerization;positive regulation of microtubule polymerization or depolymerization;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of protein catabolic process;positive regulation of protein complex assembly;positive regulation of protein metabolic process;positive regulation of protein polymerization;positive regulation of pseudopodium assembly;protein complex assembly;protein complex subunit organization;proximal/distal pattern formation;regionalization;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of attachment of spindle microtubules to kinetochore;regulation of biological process;regulation of biological quality;regulation of canonical Wnt receptor signaling pathway;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell differentiation;regulation of cell division;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome segregation;regulation of cyclin-dependent protein kinase activity;regulation of cytoskeleton organization;regulation of developmental process;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of epithelial cell proliferation involved in prostate gland development;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule depolymerization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic metaphase/anaphase transition;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of odontogenesis;regulation of organ morphogenesis;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoclast differentiation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of protein serine/threonine kinase activity;regulation of pseudopodium assembly;regulation of reproductive process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of Wnt receptor signaling pathway;response to DNA damage stimulus;response to stimulus;response to stress;retina development in camera-type eye;signal transduction;skin development;somatic stem cell maintenance;spindle assembly checkpoint;spindle checkpoint;stem cell maintenance;T cell activation;T cell differentiation;T cell differentiation in thymus;thymus development;tight junction assembly;tissue development;Wnt receptor signaling pathway binding;cytoskeletal protein binding;enzyme regulator activity;kinase regulator activity;microtubule binding;microtubule plus-end binding;protein binding;protein kinase regulator activity;tubulin binding adherens junction;anchoring junction;axon part;axonal growth cone;beta-catenin destruction complex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;centrosome;chromosomal part;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytosol;growth cone;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;lamellipodium;lateral plasma membrane;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;microtubule;microtubule organizing center;microtubule plus end;non-membrane-bounded organelle;nucleus;occluding junction;organelle;organelle part;plasma membrane part;protein complex;ruffle membrane;site of polarized growth;tight junction Basal cell carcinoma;Colorectal cancer;Endometrial cancer;Pathways in cancer;Regulation of actin cytoskeleton;Wnt signaling pathway 0.0010609 26256000 1

G3V1B6;H7C1U8;C9J574;Q9BUR5-2;Q9BUR5 Apolipoprotein O APOO >tr|G3V1B6|G3V1B6_HUMAN Apolipoprotein O OS=Homo sapiens GN=APOO PE=2 SV=1;>tr|H7C1U8|H7C1U8_HUMAN Apolipoprotein O (Fragment) OS=Homo sapiens GN=APOO PE=2 SV=1;>tr|C9J574|C9J574_HUMAN Apolipoprotein O OS=Homo sapiens GN=APOO PE=2 SV=1;>sp|Q9BUR5-2|APOO_HU NaN NaN 1.77 NaN 24.89 NaN NaN NaN establishment of localization;lipid transport;organic substance transport;transport + cell part;extracellular region part;extracellular space;high-density lipoprotein particle;integral to membrane;intrinsic to membrane;low-density lipoprotein particle;macromolecular complex;membrane part;plasma lipoprotein particle;protein-lipid complex;triglyceride-rich lipoprotein particle;very-low-density lipoprotein particle 0.00079091 5418100 1

H0YDI1;P19256-2;B1AMW1;P19256-3;P19256 Lymphocyte function-associated antigen 3 CD58 ">tr|H0YDI1|H0YDI1_HUMAN Lymphocyte function-associated antigen 3 (Fragment) OS=Homo sapiens GN=CD58 PE=2 SV=1;>sp|P19256-2|LFA3_HUMAN Isoform 2 of Lymphocyte function-associated antigen 3 OS=Homo sapiens GN=CD58;>tr|B1AMW1|B1AMW1_HUMAN CD58 antigen, (Lymph" NaN NaN 1.40 NaN 9.71 NaN NaN NaN + biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell-cell adhesion;cellular component movement;cellular process;coagulation;hemostasis;immune system process;leukocyte migration;locomotion;multicellular organismal process;regulation of biological quality;regulation of body fluid levels anchored to membrane;cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Cell adhesion molecules (CAMs) 0.0010377 1891300 1

Q15517;G8JLG2 Corneodesmosin CDSN >sp|Q15517|CDSN_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=1 SV=3;>tr|G8JLG2|G8JLG2_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=2 SV=1 0.40 NaN 0.12 NaN 3.84 NaN 2.00 NaN + anatomical structure morphogenesis;biological adhesion;cell adhesion;cell differentiation;cell-cell adhesion;cellular developmental process;cellular process;developmental process;epidermal cell differentiation;epidermis morphogenesis;epithelial cell differentiation;keratinocyte differentiation;skin morphogenesis;tissue morphogenesis binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity + anchoring junction;cell junction;cell part;cell-cell junction;cornified envelope;cytoskeleton;desmosome;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 8.8038E-07 4971900 1

H0YAS8;P10909-3;P10909-4;P10909;P10909-5;P10909-2 Clusterin;Clusterin beta chain;Clusterin alpha chain CLU >tr|H0YAS8|H0YAS8_HUMAN Clusterin beta chain (Fragment) OS=Homo sapiens GN=CLU PE=4 SV=1;>sp|P10909-3|CLUS_HUMAN Isoform 3 of Clusterin OS=Homo sapiens GN=CLU;>sp|P10909-4|CLUS_HUMAN Isoform 4 of Clusterin OS=Homo sapiens GN=CLU;>sp|P10909|CLUS_HUMAN Clust NaN NaN NaN NaN NaN NaN NaN NaN "activation of immune response;apoptotic mitochondrial changes;biological regulation;cell activation;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone-mediated protein folding;cholesterol transport;complement activation;complement activation, classical pathway;death;defense response;establishment of localization;establishment of localization in cell;exocytosis;humoral immune response;immune effector process;immune response;immune system process;innate immune response;lipid metabolic process;lipid transport;macromolecule metabolic process;metabolic process;mitochondrion organization;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of programmed cell death;negative regulation of protein complex assembly;negative regulation of protein homooligomerization;negative regulation of protein oligomerization;organelle organization;organic substance transport;platelet activation;platelet degranulation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell death;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of immune response;positive regulation of immune system process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of programmed cell death;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;positive regulation of proteolysis;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;posttranscriptional regulation of gene expression;primary metabolic process;protein activation cascade;protein folding;protein metabolic process;protein stabilization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catabolic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of immune response;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein homooligomerization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein oligomerization;regulation of protein stability;regulation of protein ubiquitination;regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of proteolysis;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;release of cytochrome c from mitochondria;response to biotic stimulus;response to chemical stimulus;response to misfolded protein;response to organic substance;response to other organism;response to stimulus;response to stress;response to topologically incorrect protein;response to virus;reverse cholesterol transport;secretion;secretion by cell;sterol transport;transport;vesicle-mediated transport" binding;enzyme binding;misfolded protein binding;protein binding;ubiquitin protein ligase binding + cell part;chromaffin granule;cytoplasmic membrane-bounded vesicle;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle part;cytosol;endoplasmic reticulum;extracellular region part;high-density lipoprotein particle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma lipoprotein particle;platelet alpha granule lumen;protein-lipid complex;secretory granule lumen;spherical high-density lipoprotein particle;stored secretory granule;vesicle;vesicle lumen 5.9969E-06 787770 1

A6NCT7;Q07092-2;Q07092;A6NDR9 Collagen alpha-1(XVI) chain COL16A1 >tr|A6NCT7|A6NCT7_HUMAN Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL16A1 PE=2 SV=1;>sp|Q07092-2|COGA1_HUMAN Isoform 2 of Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL16A1;>sp|Q07092|COGA1_HUMAN Collagen alpha-1(XVI) chain OS=Homo sapiens GN=COL1 NaN NaN NaN NaN NaN NaN NaN NaN + + + biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;collagen catabolic process;collagen metabolic process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;female pregnancy;integrin-mediated signaling pathway;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;multi-organism process;regulation of biological process;regulation of cellular process;reproductive process;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to organic nitrogen;response to organic substance;response to stimulus;signal transduction binding;integrin binding;protein binding;protein complex binding;receptor binding + anchoring collagen;cell part;collagen;collagen type XVI;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;FACIT collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part 8.9992E-06 950150 1

Q02388-2;Q02388 Collagen alpha-1(VII) chain COL7A1 >sp|Q02388-2|CO7A1_HUMAN Isoform 2 of Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1;>sp|Q02388|CO7A1_HUMAN Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2 NaN NaN 0.02 NaN 0.01 NaN NaN NaN + + + anatomical structure development;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;developmental process;epidermis development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;tissue development endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity + anchoring collagen;basement membrane;cell part;collagen;collagen type VII;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part 2.7001E-09 17629000 1

O94919 Endonuclease domain-containing 1 protein ENDOD1>sp|O94919|ENDD1_HUMAN Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2 0.80 NaN 1.16 1.09 1.41 1.97 1.31 NaN cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process "binding;catalytic activity;cation binding;endonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nuclease activity;nucleic acid binding" + extracellular region Apoptosis 2.3848E-09 7155500 1

P01834 Ig kappa chain C region IGKC >sp|P01834|IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1 NaN NaN NaN NaN NaN NaN NaN NaN "activation of immune response;biological regulation;complement activation;complement activation, classical pathway;defense response;humoral immune response;immune effector process;immune response;immune system process;innate immune response;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of immune response;positive regulation of immune system process;positive regulation of response to stimulus;primary metabolic process;protein activation cascade;protein metabolic process;regulation of biological process;regulation of immune response;regulation of immune system process;regulation of response to stimulus;response to stimulus;response to stress" antigen binding;binding + cell part;extracellular region;membrane;plasma membrane 0.00074596 558550 1

P06756-3;P06756-2;P06756 Integrin alpha-V;Integrin alpha-V heavy chain;Integrin alpha-V light chain ITGAV >sp|P06756-3|ITAV_HUMAN Isoform 3 of Integrin alpha-V OS=Homo sapiens GN=ITGAV;>sp|P06756-2|ITAV_HUMAN Isoform 2 of Integrin alpha-V OS=Homo sapiens GN=ITGAV;>sp|P06756|ITAV_HUMAN Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2 NaN 1.06 NaN NaN NaN NaN NaN 0.79 + "anatomical structure formation involved in morphogenesis;angiogenesis;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptotic cell clearance;axon guidance;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;coagulation;developmental process;endocytosis;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of organism into cell of other organism by promotion of phagocytosis in other organism involved in symbiotic interaction;entry of symbiont into host cell by promotion of host phagocytosis;entry of virus into host cell;ERK1 and ERK2 cascade;establishment of localization;extracellular matrix organization;extracellular structure organization;hemostasis;immune system process;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;leukocyte migration;locomotion;MAPKKK cascade;membrane invagination;membrane organization;modification by symbiont of host morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by symbiont of host cellular process;modulation by symbiont of host phagocytosis;modulation of phagocytosis in other organism involved in symbiotic interaction;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multicellular organismal process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of entry of bacterium into host cell;negative regulation of lipid storage;negative regulation of lipid transport;negative regulation of lipoprotein metabolic process;negative regulation of locomotion;negative regulation of low-density lipoprotein particle receptor biosynthetic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of macrophage derived foam cell differentiation;negative regulation of metabolic process;negative regulation of multi-organism process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of receptor biosynthetic process;negative regulation of transport;phagocytosis;positive regulation by organism of phagocytosis in other organism involved in symbiotic interaction;positive regulation by symbiont of host phagocytosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of locomotion;positive regulation of osteoblast proliferation;positive regulation of phagocytosis;positive regulation of transport;regulation of apoptosis;regulation of apoptotic cell clearance;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell adhesion;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of endocytosis;regulation of entry of bacterium into host cell;regulation of lipid storage;regulation of lipid transport;regulation of lipoprotein metabolic process;regulation of localization;regulation of locomotion;regulation of low-density lipoprotein particle receptor biosynthetic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of macrophage derived foam cell differentiation;regulation of metabolic process;regulation of multi-organism process;regulation of osteoblast proliferation;regulation of phagocytosis;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of receptor biosynthetic process;regulation of symbiosis, encompassing mutualism through parasitism;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis;transport;vesicle-mediated transport" binding;calcium channel activity;cation binding;cation channel activity;cation transmembrane transporter activity;channel activity;cytokine binding;gated channel activity;growth factor binding;ion binding;ion channel activity;ion transmembrane transporter activity;metal ion binding;passive transmembrane transporter activity;protein binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transforming growth factor beta binding;transmembrane transporter activity;transporter activity;voltage-gated calcium channel activity;voltage-gated cation channel activity;voltage-gated channel activity;voltage-gated ion channel activity alphav-beta3 integrin-IGF-1-IGF1R complex;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;external side of plasma membrane;integrin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;phagocytic vesicle;plasma membrane part;protein complex;receptor complex;vesicle Arrhythmogenic right ventricular cardiomyopathy (ARVC);Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Small cell lung cancer 0.00068122 1223900 1

H7C0L5;Q14624-4;Q14624-3;Q14624-2;Q14624;B7ZKJ8 Inter-alpha-trypsin inhibitor heavy chain H4;70 kDa inter-alpha-trypsin inhibitor heavy chain H4;35 kDa inter-alpha-trypsin inhibitor heavy chain H4ITIH4 >tr|H7C0L5|H7C0L5_HUMAN 35 kDa inter-alpha-trypsin inhibitor heavy chain H4 (Fragment) OS=Homo sapiens GN=ITIH4 PE=4 SV=1;>sp|Q14624-4|ITIH4_HUMAN Isoform 4 of Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4;>sp|Q14624-3|ITIH4_HUMAN I 0.05 90.12 0.00 NaN 0.03 NaN 0.05 0.84 + + acute inflammatory response;acute-phase response;amine metabolic process;aminoglycan metabolic process;carbohydrate metabolic process;defense response;glycosaminoglycan metabolic process;hyaluronan metabolic process;inflammatory response;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;polysaccharide metabolic process;primary metabolic process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;response to stress;response to wounding endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity + cell part;cytoplasm;extracellular region;intracellular part;membrane;plasma membrane 0.001212 13505000 1

C9JD84;Q14766-3;E7EV71;Q14766-2;Q14766-5;Q14766;Q14766-4 Latent-transforming growth factor beta-binding protein 1 LTBP1 >tr|C9JD84|C9JD84_HUMAN Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1 PE=2 SV=1;>sp|Q14766-3|LTBP1_HUMAN Isoform 3 of Latent-transforming growth factor beta-binding protein 1 OS=Homo sapiens GN=LTBP1;>tr|E7EV71|E7EV71_HU 0.94 1.14 0.90 1.07 0.77 0.82 1.03 1.19 + + biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular sequestering of receptor ligand;extracellular structure organization;maintenance of location;maintenance of location in cell;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;maintenance of protein location in extracellular region;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transforming growth factor beta receptor signaling pathway by extracellular sequestering of TGFbeta;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway "binding;calcium ion binding;catalytic activity;cation binding;ion binding;kinase activity;metal ion binding;molecular transducer activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;receptor activity;signal transducer activity;signaling receptor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transforming growth factor beta-activated receptor activity;transmembrane receptor protein kinase activity;transmembrane receptor protein serine/threonine kinase activity;transmembrane signaling receptor activity" + extracellular matrix;extracellular region part;proteinaceous extracellular matrix 0.00062768 3136000 1

Q14210 Lymphocyte antigen 6D LY6D >sp|Q14210|LY6D_HUMAN Lymphocyte antigen 6D OS=Homo sapiens GN=LY6D PE=1 SV=1 1.02 1.67 2.63 2.92 0.69 0.67 0.29 0.17 + biological adhesion;cell activation;cell adhesion;cell differentiation;cellular developmental process;cellular process;developmental process;immune system process;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;response to chemical stimulus;response to organic substance;response to stilbenoid;response to stimulus anchored to membrane;cell part;cell surface;intrinsic to membrane;membrane;membrane part;plasma membrane 0.00017169 25208000 1

H0YAH0;O60245;O60245-2;O60245-3;F5GWJ1 Protocadherin-7 PCDH7 >tr|H0YAH0|H0YAH0_HUMAN Protocadherin-7 (Fragment) OS=Homo sapiens GN=PCDH7 PE=4 SV=1;>sp|O60245|PCDH7_HUMAN Protocadherin-7 OS=Homo sapiens GN=PCDH7 PE=1 SV=2;>sp|O60245-2|PCDH7_HUMAN Isoform B of Protocadherin-7 OS=Homo sapiens GN=PCDH7;>sp|O60245-3|PCDH NaN NaN NaN NaN NaN NaN NaN NaN + biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane;plasma membrane part 0.000021913 162260 1

H0Y8D1;Q8NHM4;P07478;P07477;CON__P07477;E7EQ64 Putative trypsin-6;Trypsin-2;Trypsin-1;Alpha-trypsin chain 1;Alpha-trypsin chain 2 PRSS1;TRY6;PRSS2 >tr|H0Y8D1|H0Y8D1_HUMAN Trypsin-1 (Fragment) OS=Homo sapiens GN=PRSS1 PE=2 SV=1;>sp|Q8NHM4|TRY6_HUMAN Putative trypsin-6 OS=Homo sapiens GN=TRY6 PE=5 SV=1;>sp|P07478|TRY2_HUMAN Trypsin-2 OS=Homo sapiens GN=PRSS2 PE=1 SV=1;>sp|P07477|TRY1_HUMAN Trypsin-1 OS NaN NaN 0.15 NaN 0.00 NaN NaN NaN + + biological regulation;cell migration;cell motility;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;defense response;digestion;endothelial cell migration;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune response;immune system process;innate immune response;locomotion;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of cell adhesion;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;response to stimulus;response to stress "binding;calcium ion binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity" + extracellular matrix;extracellular region;extracellular region part;extracellular space Neuroactive ligand-receptor interaction;Pancreatic secretion;Protein digestion and absorption 1.4468E-10 558250000 1

B1AN99;F8W7P3;P35030-3;P35030-2;P35030-4;P35030 Trypsin-3PRSS3 >tr|B1AN99|B1AN99_HUMAN Trypsin-3 (Fragment) OS=Homo sapiens GN=PRSS3 PE=2 SV=1;>tr|F8W7P3|F8W7P3_HUMAN Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=2 SV=1;>sp|P35030-3|TRY3_HUMAN Isoform C of Trypsin-3 OS=Homo sapiens GN=PRSS3;>sp|P35030-2|TRY3_HUMAN Isoform B o NaN 22.46 0.10 18.00 0.08 0.70 NaN 4.62 + + cell migration;cell motility;cellular component movement;cellular process;defense response;digestion;endothelial cell migration;immune response;immune system process;innate immune response;locomotion;macromolecule metabolic process;metabolic process;multicellular organismal process;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;response to stimulus;response to stress;zymogen activation "binding;calcium ion binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity" + extracellular region part;extracellular space Neuroactive ligand-receptor interaction;Pancreatic secretion;Protein digestion and absorption 1.4842E-26 15605000 1

H0Y4H1;H0Y7Z9;H0Y6Z7;P10586-2;P10586 Receptor-type tyrosine-protein phosphatase F PTPRF >tr|H0Y4H1|H0Y4H1_HUMAN Receptor-type tyrosine-protein phosphatase F (Fragment) OS=Homo sapiens GN=PTPRF PE=4 SV=1;>tr|H0Y7Z9|H0Y7Z9_HUMAN Receptor-type tyrosine-protein phosphatase F (Fragment) OS=Homo sapiens GN=PTPRF PE=4 SV=1;>tr|H0Y6Z7|H0Y6Z7_HUMAN Re NaN NaN NaN NaN NaN NaN NaN NaN + biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;dephosphorylation;enzyme linked receptor protein signaling pathway;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;transmembrane receptor protein tyrosine phosphatase signaling pathway "binding;carbohydrate binding;catalytic activity;glycosaminoglycan binding;heparin binding;hydrolase activity;hydrolase activity, acting on ester bonds;molecular transducer activity;pattern binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;polysaccharide binding;protein tyrosine phosphatase activity;receptor activity;signal transducer activity;signaling receptor activity;transmembrane receptor protein phosphatase activity;transmembrane receptor protein tyrosine phosphatase activity;transmembrane signaling receptor activity" cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Adherens junction;Cell adhesion molecules (CAMs);Insulin signaling pathway 0.00073052 517080 1

O95197-3;O95197-4;O95197-7;O95197-2;O95197 Reticulon-3 RTN3 >sp|O95197-3|RTN3_HUMAN Isoform 3 of Reticulon-3 OS=Homo sapiens GN=RTN3;>sp|O95197-4|RTN3_HUMAN Isoform 4 of Reticulon-3 OS=Homo sapiens GN=RTN3;>sp|O95197-7|RTN3_HUMAN Isoform 7 of Reticulon-3 OS=Homo sapiens GN=RTN3;>sp|O95197-2|RTN3_HUMAN Isoform 2 of NaN NaN NaN 0.42 NaN 2.69 NaN NaN apoptosis;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;death;endoplasmic reticulum organization;endoplasmic reticulum tubular network organization;establishment of localization;interaction with host;interspecies interaction between organisms;multi-organism process;organelle organization;programmed cell death;reproductive process;response to stimulus;response to stress;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction + cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular region part;extracellular space;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 0.0010692 1174000 1

P31151 Protein S100-A7 S100A7 >sp|P31151|S10A7_HUMAN Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4 NaN 14.95 NaN NaN NaN NaN NaN 1.33 + + anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;cell differentiation;cellular developmental process;cellular process;defense response;defense response to bacterium;defense response to Gram-negative bacterium;developmental process;epidermal cell differentiation;epithelial cell differentiation;immune response;immune system process;innate immune response;keratinocyte differentiation;maintenance of location;multi-organism process;positive regulation of behavior;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of ERK1 and ERK2 cascade;positive regulation of granulocyte chemotaxis;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of lymphocyte migration;positive regulation of MAPKKK cascade;positive regulation of monocyte chemotaxis;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of T cell chemotaxis;positive regulation of T cell migration;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of chemotaxis;regulation of ERK1 and ERK2 cascade;regulation of granulocyte chemotaxis;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of lymphocyte migration;regulation of MAPKKK cascade;regulation of monocyte chemotaxis;regulation of response to external stimulus;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell chemotaxis;regulation of T cell migration;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to inorganic substance;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to other organism;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;sequestering of metal ion binding;calcium ion binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding + adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytosol;endoplasmic reticulum;extracellular region;focal adhesion;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 0.0011997 4153800 1

P10599-2;P10599 Thioredoxin TXN >sp|P10599-2|THIO_HUMAN Isoform 2 of Thioredoxin OS=Homo sapiens GN=TXN;>sp|P10599|THIO_HUMAN Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 NaN NaN NaN NaN NaN NaN NaN NaN "antibiotic metabolic process;biological regulation;biosynthetic process;carbohydrate homeostasis;cell communication;cell proliferation;cell redox homeostasis;cell-cell signaling;cellular biosynthetic process;cellular chemical homeostasis;cellular component movement;cellular glucose homeostasis;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to drug;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to hyperoxia;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;chemical homeostasis;defense response;drug metabolic process;electron transport chain;generation of precursor metabolites and energy;glucose homeostasis;glycerol ether metabolic process;homeostatic process;immune response;immune system process;innate immune response;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of protein export from nucleus;negative regulation of protein transport;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;organic ether metabolic process;oxidation-reduction process;positive regulation of binding;positive regulation of DNA binding;positive regulation of molecular function;primary metabolic process;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA binding;regulation of establishment of protein localization;regulation of gene expression;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein localization;regulation of protein transport;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;response to abiotic stimulus;response to activity;response to axon injury;response to carbohydrate stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to dexamethasone stimulus;response to drug;response to endogenous stimulus;response to glucocorticoid stimulus;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to hyperoxia;response to inorganic substance;response to metal ion;response to monosaccharide stimulus;response to organic substance;response to oxygen levels;response to radiation;response to selenium ion;response to steroid hormone stimulus;response to stimulus;response to stress;response to thyroid hormone stimulus;response to thyroxine stimulus;response to wounding;RNA biosynthetic process;RNA metabolic process;signal transduction;signaling;small molecule metabolic process;transcription, DNA-dependent" "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;peptide disulfide oxidoreductase activity;protein disulfide oxidoreductase activity" + axon;cell body;cell part;cell projection;cytoplasmic part;cytosol;dendrite;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;neuronal cell body;nuclear part;nucleoplasm;organelle;organelle part 4.5929E-09 2936600 1

Q5JQ13;P18206-2;P18206 Vinculin VCL >tr|Q5JQ13|Q5JQ13_HUMAN Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=2 SV=1;>sp|P18206-2|VINC_HUMAN Isoform 1 of Vinculin OS=Homo sapiens GN=VCL;>sp|P18206|VINC_HUMAN Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4 NaN 1.27 NaN NaN NaN NaN NaN 0.98 + adherens junction assembly;adherens junction organization;anatomical structure morphogenesis;apical junction assembly;biological adhesion;biological regulation;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell projection assembly;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;developmental process;epithelial cell-cell adhesion;establishment of localization;establishment of localization in cell;exocytosis;lamellipodium assembly;localization;macromolecule localization;morphogenesis of an epithelium;multicellular organismal process;muscle contraction;muscle system process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;platelet activation;platelet degranulation;protein localization;protein localization at cell surface;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of locomotion;secretion;secretion by cell;system process;tissue morphogenesis;transport;vesicle-mediated transport actin binding;beta-catenin binding;binding;cadherin binding;cell adhesion molecule binding;cytoskeletal protein binding;protein binding;structural molecule activity + actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;costamere;cytoplasmic part;cytoskeleton;cytosol;extracellular region;fascia adherens;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;sarcolemma;Z disc Adherens junction;Amoebiasis;Bacterial invasion of epithelial cells;Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Shigellosis 1.0217E-07 1681900 1

Q12904;Q12904-2;D6R937 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;Endothelial monocyte-activating polypeptide 2 AIMP1 >sp|Q12904|AIMP1_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2;>sp|Q12904-2|AIMP1_HUMAN Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=A 1.08 0.82 0.58 0.93 1.37 1.10 1.63 1.00 + alcohol metabolic process;amine metabolic process;amino acid activation;anatomical structure formation involved in morphogenesis;angiogenesis;apoptosis;biological adhesion;biological regulation;carbohydrate metabolic process;carboxylic acid metabolic process;cell adhesion;cell communication;cell death;cell migration;cell motility;cell-cell signaling;cellular amine metabolic process;cellular amino acid metabolic process;cellular carbohydrate metabolic process;cellular component movement;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chemotaxis;death;defense response;developmental process;glucose metabolic process;hexose metabolic process;immune system process;inflammatory response;leukocyte migration;locomotion;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;response to wounding;RNA metabolic process;signal transduction;signaling;small molecule metabolic process;taxis;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process binding;cell surface binding;cytokine activity;identical protein binding;nucleic acid binding;protein binding;protein dimerization activity;protein homodimerization activity;receptor binding;RNA binding;tRNA binding + aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;extracellular region part;extracellular space;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;protein complex;transport vesicle;vesicle 3.3244E-17 12019000 2

B4DT77;P20073-2;P20073 Annexin;Annexin A7 ANXA7 >tr|B4DT77|B4DT77_HUMAN Annexin OS=Homo sapiens GN=ANXA7 PE=2 SV=1;>sp|P20073-2|ANXA7_HUMAN Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7;>sp|P20073|ANXA7_HUMAN Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 NaN 0.73 NaN 0.31 NaN 2.40 NaN 0.57 + + behavior;behavioral interaction between organisms;biological regulation;calcium ion homeostasis;cation homeostasis;cell proliferation;cell volume homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular water homeostasis;chemical homeostasis;divalent inorganic cation homeostasis;hemostasis;homeostatic process;ion homeostasis;metal ion homeostasis;multicellular organismal process;multi-organism process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to abiotic stimulus;response to osmotic stress;response to salt stress;response to stimulus;response to stress;social behavior;water homeostasis binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;ion binding;lipid binding;metal ion binding;phospholipid binding cell part;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;nuclear envelope;nuclear part;nucleus;organelle;organelle envelope;organelle membrane;organelle part;plasma membrane;vesicle 2.0864E-29 2463100 2

O76027 Annexin A9 ANXA9 >sp|O76027|ANXA9_HUMAN Annexin A9 OS=Homo sapiens GN=ANXA9 PE=1 SV=3 NaN NaN NaN 0.21 NaN 2.90 NaN NaN + + + biological adhesion;cell adhesion;cell-cell adhesion;cellular process acetylcholine binding;acetylcholine receptor activity;amine binding;binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;identical protein binding;ion binding;lipid binding;metal ion binding;molecular transducer activity;neurotransmitter binding;neurotransmitter receptor activity;phosphatidylserine binding;phospholipid binding;protein binding;protein dimerization activity;protein homodimerization activity;receptor activity;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity cell part;cell surface;cytoplasmic part;cytosol;intracellular part 0.000021236 1799400 2

P62330 ADP-ribosylation factor 6 ARF6 >sp|P62330|ARF6_HUMAN ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2 1.19 NaN 1.02 0.89 1.49 1.88 0.97 NaN + actin cytoskeleton organization;actin filament-based process;anatomical structure development;apoptosis;biological adhesion;biological regulation;cell adhesion;cell death;cell projection organization;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to stimulus;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;death;developmental process;establishment of cell polarity;establishment of epithelial cell polarity;establishment of localization;establishment of protein localization;establishment or maintenance of cell polarity;intracellular signal transduction;liver development;localization;macromolecule localization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of endocytosis;negative regulation of receptor-mediated endocytosis;negative regulation of transport;organ development;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of establishment of protein localization in plasma membrane;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;programmed cell death;protein localization;protein localization at cell surface;protein transport;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular localization;regulation of cellular process;regulation of cytoskeleton organization;regulation of dendrite development;regulation of dendritic spine development;regulation of developmental process;regulation of endocytosis;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of filopodium assembly;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organelle organization;regulation of protein complex assembly;regulation of protein localization;regulation of protein polymerization;regulation of Rac protein signal transduction;regulation of Ras protein signal transduction;regulation of receptor-mediated endocytosis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;ruffle organization;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell cortex;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome;endocytic vesicle;endosomal part;endosome;endosome membrane;filopodium membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane part;recycling endosome;ruffle;vesicle Endocytosis;Fc gamma R-mediated phagocytosis 3.5955E-06 4728600 2

A6NLG9;P21810;C9JKG1 Biglycan BGN >tr|A6NLG9|A6NLG9_HUMAN Biglycan OS=Homo sapiens GN=BGN PE=2 SV=1;>sp|P21810|PGS1_HUMAN Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2;>tr|C9JKG1|C9JKG1_HUMAN Biglycan (Fragment) OS=Homo sapiens GN=BGN PE=2 SV=1 NaN NaN NaN NaN NaN NaN NaN NaN + + amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;biosynthetic process;blood vessel remodeling;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chondroitin sulfate biosynthetic process;chondroitin sulfate catabolic process;chondroitin sulfate metabolic process;dermatan sulfate biosynthetic process;dermatan sulfate metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;nitrogen compound metabolic process;peptide cross-linking;peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan;peptidyl-amino acid modification;peptidyl-serine modification;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;protein metabolic process;protein modification process;sulfur compound biosynthetic process;sulfur compound catabolic process;sulfur compound metabolic process;tissue remodeling binding;carbohydrate binding;extracellular matrix binding;extracellular matrix structural constituent;glycosaminoglycan binding;pattern binding;polysaccharide binding;structural molecule activity + cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular matrix;extracellular region part;Golgi apparatus part;Golgi lumen;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;proteinaceous extracellular matrix;sarcolemma;transport vesicle;vacuolar lumen;vacuolar part;vesicle 0.00019258 448840 2

C9JUG7;B4DG50;F8W9N7;P47755;F8WED3 F-actin-capping protein subunit alpha-2 CAPZA2 >tr|C9JUG7|C9JUG7_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=2 SV=1;>tr|B4DG50|B4DG50_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=2 SV=1;>tr|F8W9N7|F8W9N7_HUMAN F-actin-capping protein subunit NaN 1.38 0.85 2.87 0.50 0.81 NaN 0.83 actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;defense response;hemostasis;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;protein complex assembly;protein complex subunit organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to stimulus;response to stress + cell cortex part;cell part;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular region;F-actin capping protein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;protein complex 8.1912E-34 10972000 2

A6NNI4;P21926;G8JLH6;F5GXT1 CD9 antigen CD9 >tr|A6NNI4|A6NNI4_HUMAN CD9 antigen OS=Homo sapiens GN=CD9 PE=2 SV=1;>sp|P21926|CD9_HUMAN CD9 antigen OS=Homo sapiens GN=CD9 PE=1 SV=4;>tr|G8JLH6|G8JLH6_HUMAN CD9 antigen (Fragment) OS=Homo sapiens GN=CD9 PE=2 SV=1;>tr|F5GXT1|F5GXT1_HUMAN CD9 antigen (Frag 0.84 1.14 1.84 NaN 0.89 NaN 0.87 0.74 + anatomical structure development;anatomical structure formation involved in morphogenesis;biological adhesion;biological regulation;brain development;cell activation;cell adhesion;cell development;cell junction assembly;cell junction organization;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane fusion;cellular membrane organization;cellular process;cellular process involved in reproduction;cellular process involved in reproduction in multicellular organism;developmental process;establishment of localization;establishment of localization in cell;exocytosis;fusion of sperm to egg plasma membrane;glial cell development;membrane fusion;membrane organization;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;oligodendrocyte development;organ development;paranodal junction assembly;plasma membrane fusion;platelet activation;platelet degranulation;regulation of biological process;regulation of cell proliferation;regulation of cellular process;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to stimulus;response to stress;response to water;response to water deprivation;secretion;secretion by cell;transport;vesicle-mediated transport apical plasma membrane;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;external side of plasma membrane;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;organelle membrane;organelle part;plasma membrane part;platelet alpha granule membrane;secretory granule membrane;vesicle membrane Hematopoietic cell lineage 0.00020285 13497000 2

P60953;E7ETU3;P60953-1 Cell division control protein 42 homolog CDC42 >sp|P60953|CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2;>tr|E7ETU3|E7ETU3_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=2 SV=1;>sp|P60953-1|CDC42_HUMAN Isoform 1 of Cell division contr 0.73 1.67 0.69 1.68 0.82 1.41 0.72 1.01 + actin cytoskeleton organization;actin filament branching;actin filament bundle assembly;actin filament organization;actin filament-based process;adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;axon guidance;biological adhesion;biological regulation;blood coagulation;canonical Wnt receptor signaling pathway;cardiac conduction system development;cell adhesion;cell communication;cell development;cell differentiation;cell fate determination;cell junction organization;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell junction organization;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to stimulus;chemotaxis;circulatory system process;coagulation;cytoskeleton organization;cytoskeleton-dependent intracellular transport;defense response;developmental process;ectodermal placode formation;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epithelial cell development;epithelial cell-cell adhesion;epithelial-mesenchymal cell signaling;establishment of Golgi localization;establishment of localization;establishment of localization in cell;establishment of nucleus localization;establishment of organelle localization;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;filopodium assembly;Golgi organization;growth;hair cycle process;hair follicle morphogenesis;hair follicle placode formation;heart contraction;heart process;hemostasis;immune response;immune system process;innate immune response;intracellular signal transduction;intracellular transport;keratinization;keratinocyte development;leukocyte differentiation;localization;locomotion;lymphocyte costimulation;macromolecule localization;macrophage differentiation;microspike assembly;microtubule-based movement;microtubule-based process;microtubule-based transport;molting cycle;molting cycle process;multicellular organism growth;multicellular organismal process;muscle cell differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein complex assembly;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;neuron fate determination;nuclear migration;organelle organization;organelle transport along microtubule;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell cycle cytokinesis;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokinesis;positive regulation of developmental process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of gene expression;positive regulation of hair follicle cell proliferation;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JNK cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of metalloenzyme activity;positive regulation of molecular function;positive regulation of muscle cell differentiation;positive regulation of neuron apoptosis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidyl-serine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein transport;positive regulation of pseudopodium assembly;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of synapse structural plasticity;positive regulation of T cell activation;positive regulation of transferase activity;positive regulation of transport;posttranscriptional regulation of gene expression;protein localization;regulation of apoptosis;regulation of attachment of spindle microtubules to kinetochore;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell cycle cytokinesis;regulation of cell cycle process;regulation of cell death;regulation of cell differentiation;regulation of cell division;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome segregation;regulation of cytokinesis;regulation of cytoskeleton organization;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of epidermal growth factor receptor signaling pathway;regulation of establishment of protein localization;regulation of filopodium assembly;regulation of gene expression;regulation of hair follicle cell proliferation;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JNK cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of metalloenzyme activity;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of mitosis;regulation of mitotic cell cycle;regulation of molecular function;regulation of muscle cell differentiation;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein binding;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein heterodimerization activity;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein transport;regulation of pseudopodium assembly;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of stress-activated protein kinase signaling cascade;regulation of synapse organization;regulation of synapse structural plasticity;regulation of T cell activation;regulation of transferase activity;regulation of transport;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;signal transduction;signaling;small GTPase mediated signal transduction;sprouting angiogenesis;submandibular salivary gland formation;system process;T cell costimulation;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;Wnt receptor signaling pathway "binding;catalytic activity;enzyme binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;kinase binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein kinase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" apical part of cell;cell body;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;filopodium;Golgi apparatus part;Golgi membrane;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;midbody;mitotic spindle;neuron projection;neuronal cell body;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;spindle;spindle midzone;stored secretory granule;vesicle Adherens junction;Axon guidance;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Endocytosis;Epithelial cell signaling in Helicobacter pylori infection;Fc gamma R-mediated phagocytosis;Focal adhesion;GnRH signaling pathway;Leukocyte transendothelial migration;MAPK signaling pathway;MAPK signaling pathway - yeast;Neurotrophin signaling pathway;Pancreatic cancer;Pathogenic Escherichia coli infection;Pathways in cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;T cell receptor signaling pathway;Tight junction;VEGF signaling pathway 6.8121E-14 35635000 2

Q12860-2;Q12860;H0YIJ1;Q12860-3 Contactin-1 CNTN1 >sp|Q12860-2|CNTN1_HUMAN Isoform 2 of Contactin-1 OS=Homo sapiens GN=CNTN1;>sp|Q12860|CNTN1_HUMAN Contactin-1 OS=Homo sapiens GN=CNTN1

```
PE=1 SV=1;>tr|H0YIJ1|H0YIJ1_HUMAN Contactin-1 (Fragment) OS=Homo sapiens GN=CNTN1 PE=2 SV=1;>sp|Q12860-3|CNTN1_HUMAN Isof     NaN NaN 1.17 NaN 2.57 NaN NaN NaN                                                  +
anatomical structure development;axon guidance;biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cerebellum
development;chemotaxis;developmental process;locomotion;Notch signaling pathway;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component
organization;positive regulation of cellular process;positive regulation of gene expression;positive regulation of ion transport;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive
regulation of neuron projection development;positive regulation of sodium ion transport;positive regulation of transport;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell
projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of ion transport;regulation of localization;regulation of
macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system
development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of sodium ion transport;regulation of transport;response to chemical stimulus;response to external
stimulus;response to stimulus;signal transduction;taxis binding;carbohydrate binding         anchored to membrane;cell part;intrinsic to membrane;membrane;membrane part;plasma membrane       Cell adhesion molecules (CAMs)
0.00084369     1470100  2
H7C469;P07339;H7C1V0;F8WD96;C9JH19       Cathepsin D;Cathepsin D light chain;Cathepsin D heavy chain    CTSD      >tr|H7C469|H7C469_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=3
SV=1;>sp|P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1;>tr|H7C1V0|H7C1V0_HUMAN Cathepsin D light chain (Fragment) OS=Homo sapiens GN=CTSD PE=2 SV=1;>tr|F8WD96       0.87 0.48 0.54
0.37 3.93 1.65 2.64 1.04 +                                  +                    antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen
processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation
of peptide or polysaccharide antigen via MHC class II;autophagic vacuole assembly;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at
cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic
process;collagen metabolic process;death;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune system process;macromolecule metabolic process;metabolic process;multicellular
organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;organelle assembly;organelle organization;primary metabolic
process;protein metabolic process;proteolysis;response to biotic stimulus;response to stimulus;vacuole organization       "aspartic-type endopeptidase activity;aspartic-type peptidase activity;catalytic activity;endopeptidase activity;hydrolase
activity;peptidase activity;peptidase activity, acting on L-amino acid peptides"  +      cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular region part;extracellular space;integral to
membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal lumen;lysosome;lytic vacuole;melanosome;membrane
part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrion;organelle;organelle lumen;organelle part;pigment granule;vacuolar lumen;vacuolar part;vacuole;vesicle       ko05152;Lysosome
0.000068348   7765400  2
P81605;P81605-2   Dermcidin;Survival-promoting peptide;DCD-1     DCD       >sp|P81605|DCD_HUMAN Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2;>sp|P81605-2|DCD_HUMAN Isoform 2 of Dermcidin OS=Homo sapiens
GN=DCD       0.46 6.88 0.05 18.34       0.45 0.92 0.12 1.47                                                          cell killing;defense response;defense response to bacterium;defense response to fungus;killing of cells of other organism;macromolecule
metabolic process;metabolic process;multi-organism process;primary metabolic process;protein metabolic process;proteolysis;response to bacterium;response to biotic stimulus;response to fungus;response to other organism;response to
stimulus;response to stress     catalytic activity;hydrolase activity;peptidase activity  +      extracellular region         7.5494E-11      17547000         2
P13726;P13726-2   Tissue factor   F3    >sp|P13726|TF_HUMAN Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=1;>sp|P13726-2|TF_HUMAN Isoform 2 of Tissue factor OS=Homo sapiens GN=F3   1.46 1.27 1.01 0.66 0.72 0.49 1.04
1.38                                                     "activation of blood coagulation via clotting cascade;activation of caspase activity;activation of plasma proteins involved in acute inflammatory response;biological regulation;blood coagulation,
extrinsic pathway;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of
programmed cell death;positive regulation of angiogenesis;positive regulation of behavior;positive regulation of biological process;positive regulation of blood coagulation;positive regulation of caspase activity;positive regulation of
catalytic activity;positive regulation of cell communication;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive
regulation of cellular process;positive regulation of chemotaxis;positive regulation of coagulation;positive regulation of developmental process;positive regulation of endothelial cell proliferation;positive regulation of epithelial cell
proliferation;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of locomotion;positive regulation of molecular function;positive regulation of multicellular organismal
process;positive regulation of peptidase activity;positive regulation of platelet-derived growth factor receptor signaling pathway;positive regulation of positive chemotaxis;positive regulation of protein kinase B signaling cascade;positive
regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein activation cascade;protein maturation;protein
metabolic process;protein processing;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of blood coagulation;regulation of
catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular
process;regulation of chemotaxis;regulation of coagulation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of
endopeptidase activity;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of localization;regulation of
locomotion;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of peptidase activity;regulation of platelet-derived
growth factor receptor signaling pathway;regulation of positive chemotaxis;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of response to external stimulus;regulation of response to
stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of wound healing;response to stimulus"    binding;cell surface binding;lipid binding;phospholipid binding   +      cell
part;extracellular matrix;extracellular region part;extracellular space;integral to membrane;intrinsic to external side of plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part
Complement and coagulation cascades  1.1479E-16      14595000         2
H7C024;P35052;H7C410;C9J4Y6;H7BZE9 Glypican-1;Secreted glypican-1     GPC1       >tr|H7C024|H7C024_HUMAN Glypican-1 (Fragment) OS=Homo sapiens GN=GPC1 PE=3 SV=1;>sp|P35052|GPC1_HUMAN Glypican-1
OS=Homo sapiens GN=GPC1 PE=1 SV=2;>tr|H7C410|H7C410_HUMAN Glypican-1 (Fragment) OS=Homo sapiens GN=GPC1 PE=3 SV=1;>tr|C9J4Y6|C9J4Y6_HUMAN Glypi       NaN NaN 1.73 NaN 1.21 NaN NaN NaN +
+                              "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure formation involved in morphogenesis;axon guidance;biological
regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell differentiation;cellular catabolic process;cellular component assembly;cellular
component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular
component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to
stimulus;chemotaxis;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic
process;glial cell differentiation;glycoprotein metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;heparan sulfate proteoglycan catabolic process;heparan
sulfate proteoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;locomotion;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;myelin
assembly;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of fibroblast growth factor receptor signaling pathway;negative regulation of response
to stimulus;negative regulation of signal transduction;negative regulation of signaling;nitrogen compound metabolic process;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic
process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle
cell differentiation;positive regulation of skeletal muscle cell differentiation;positive regulation of striated muscle cell differentiation;primary metabolic process;proteoglycan catabolic process;proteoglycan metabolic process;regulation of
biological process;regulation of cell communication;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of fibroblast growth factor receptor signaling pathway;regulation of muscle
cell differentiation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of striated muscle cell differentiation;response to abiotic
stimulus;response to chemical stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;Schwann cell differentiation;signal transduction;sulfur compound
catabolic process;sulfur compound metabolic process;taxis;terpenoid metabolic process"   binding;cation binding;copper ion binding;extracellular matrix binding;fibroblast growth factor binding;growth factor binding;ion binding;laminin
binding;metal ion binding;protein binding;transition metal ion binding        +      anchored to membrane;cell part;cytoplasmic part;endosome;extracellular matrix;extracellular region part;extracellular space;Golgi apparatus part;Golgi
lumen;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma
membrane;lysosomal lumen;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;plasma membrane part;proteinaceous extracellular
matrix;vacuolar lumen;vacuolar part              9.0362E-12      4194900  2
P17931;G3V3R6    Galectin-3       LGALS3 >sp|P17931|LEG3_HUMAN Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5;>tr|G3V3R6|G3V3R6_HUMAN Galectin-3 OS=Homo sapiens GN=LGALS3 PE=2 SV=1  1.36 1.31 2.09
2.27 0.48 0.39 0.55 0.82 +                                 +                         anatomical structure development;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or
biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular
process;defense response;developmental process;extracellular matrix organization;extracellular structure organization;immune response;immune system process;innate immune response;macromolecule metabolic process;metabolic
process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;response to stimulus;response to
stress;RNA metabolic process;RNA processing;RNA splicing;skeletal system development;system development    binding;carbohydrate binding +      cell part;cytoplasmic part;extracellular matrix;extracellular region part;intracellular
membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial
part;nuclear part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane;proteinaceous extracellular matrix;ribonucleoprotein complex;spliceosomal complex             1.1926E-07     16074000
2
Q9Y5X9-2;J3QQQ0;Q9Y5X9;B4DTR8       Endothelial lipase   LIPG       >sp|Q9Y5X9-2|LIPE_HUMAN Isoform 2 of Endothelial lipase OS=Homo sapiens GN=LIPG;>tr|J3QQQ0|J3QQQ0_HUMAN Endothelial lipase OS=Homo sapiens
GN=LIPG PE=3 SV=1;>sp|Q9Y5X9|LIPE_HUMAN Endothelial lipase OS=Homo sapiens GN=LIPG PE=1 SV=1;>tr|B4DTR8|B4DTR8_HUMAN 1.13 0.83 1.93 1.39 0.46 0.19 0.44 0.56                                                         biological
regulation;catabolic process;cell proliferation;cellular catabolic process;cellular component organization;cellular component organization or biogenesis;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic
process;cellular process;chemical homeostasis;cholesterol homeostasis;cholesterol transport;establishment of localization;high-density lipoprotein particle remodeling;homeostatic process;lipid catabolic process;lipid homeostasis;lipid
metabolic process;lipid transport;macromolecular complex remodeling;macromolecular complex subunit organization;metabolic process;multicellular organismal process;organic substance transport;organophosphate metabolic
process;phospholipid catabolic process;phospholipid homeostasis;phospholipid metabolic process;plasma lipoprotein particle organization;plasma lipoprotein particle remodeling;positive regulation of biological process;positive regulation
of cholesterol transport;positive regulation of high-density lipoprotein particle clearance;positive regulation of lipid transport;positive regulation of lipoprotein particle clearance;positive regulation of multicellular organismal process;positive
regulation of sterol transport;positive regulation of transport;primary metabolic process;protein-lipid complex remodeling;protein-lipid complex subunit organization;regulation of biological process;regulation of biological quality;regulation
of cellular metabolic process;regulation of cellular process;regulation of cholesterol transport;regulation of high-density lipoprotein particle clearance;regulation of lipid transport;regulation of lipoprotein metabolic process;regulation of
lipoprotein particle clearance;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of sterol transport;regulation of
transport;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to stimulus;reverse cholesterol transport;sterol homeostasis;sterol
transport;transport   "binding;carbohydrate binding;carboxylic ester hydrolase activity;catalytic activity;glycosaminoglycan binding;heparin binding;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;lipoprotein lipase
activity;pattern binding;phosphatidylcholine 1-acylhydrolase activity;phospholipase activity;polysaccharide binding;retinyl-palmitate esterase activity;triglyceride lipase activity"   +      extracellular region;extracellular region
part;extracellular space   Glycerolipid metabolism6.197E-10        13756000         2
Q08431-2;Q08431-3;F5GZN3;F5H7N9;Q08431;H0YKS8  Lactadherin;Lactadherin short form;Medin    MFGE8   >sp|Q08431-2|MFGM_HUMAN Isoform 2 of Lactadherin OS=Homo sapiens GN=MFGE8;>sp|Q08431-
3|MFGM_HUMAN Isoform 3 of Lactadherin OS=Homo sapiens GN=MFGE8;>tr|F5GZN3|F5GZN3_HUMAN Lactadherin short form OS=Homo sapiens GN=MFGE8 PE=2 SV=1;>tr|F5H7N9|F5H7N9_HUMAN La   0.86 1.09 NaN 0.52
NaN 1.51 0.75 1.09 +      +                                      +      "anatomical structure formation involved in morphogenesis;angiogenesis;biological adhesion;biological regulation;cell adhesion;cell recognition;cellular component
organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;developmental process;fertilization;interaction with host;interspecies interaction between organisms;membrane
invagination;membrane organization;multi-organism process;phagocytosis, engulfment;phagocytosis, recognition;positive regulation of apoptotic cell clearance;positive regulation of biological process;positive regulation of cellular
component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of phagocytosis;positive regulation of transport;regulation of apoptotic cell clearance;regulation of biological
process;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of phagocytosis;regulation of transport;regulation of vesicle-mediated transport;reproductive
process;single fertilization;viral reproductive process;virus-host interaction"      binding;lipid binding;phosphatidylethanolamine binding;phosphatidylserine binding;phospholipid binding      +      cell part;external side of plasma
membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;extrinsic to membrane;extrinsic to plasma membrane;membrane part;membrane-
bounded organelle;membrane-bounded vesicle;organelle;plasma membrane part;vesicle           9.7368E-12      5895400  2
O60487   Myelin protein zero-like protein 2  MPZL2    >sp|O60487|MPZL2_HUMAN Myelin protein zero-like protein 2 OS=Homo sapiens GN=MPZL2 PE=1 SV=1      NaN NaN 1.50 NaN 1.63 NaN NaN NaN
+      anatomical structure morphogenesis;biological adhesion;cell activation;cell adhesion;cell differentiation;cell-cell adhesion;cellular developmental process;cellular process;developmental process;homophilic cell adhesion;immune
system process;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;T cell activation;T cell differentiation;T cell differentiation in thymus                    cell part;cytoskeleton;integral to
membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;non-membrane-bounded organelle;organelle;plasma membrane            0.00023955
2620900  2
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C9K028;E5RHP0;E7ERL0;P22392;P15531;P15531-2;J3KPD9;P22392-2;Q32Q12 Nucleoside diphosphate kinase B;Nucleoside diphosphate kinase A;Nucleoside diphosphate kinase NME1;NME2;NME1-NME2 >tr|C9K028|C9K028_HUMAN Nucleoside diphosphate kinase A (Fragment) OS=Homo sapiens GN=NME1 PE=2 SV=1;>tr|E5RHP0|E5RHP0_HUMAN Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=2 SV=1;>tr|E7ERL0|E7ERL0_HUMAN Nucleoside diphosphate kinase A OS=Homo s 0.68 NaN NaN 1.22 NaN 0.89 1.22 NaN + "anatomical structure development;biological adhesion;biological regulation;biosynthetic process;carbohydrate homeostasis;cell adhesion;cellular biosynthetic process;cellular chemical homeostasis;cellular component organization;cellular component organization or biogenesis;cellular glucose homeostasis;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to drug;cellular response to fatty acid;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to lipid;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;CTP biosynthetic process;CTP metabolic process;developmental process;endocytosis;establishment of localization;glucose homeostasis;GTP biosynthetic process;GTP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;hippocampus development;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte differentiation;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;positive regulation of binding;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of DNA binding;positive regulation of epidermal cell differentiation;positive regulation of epidermis development;positive regulation of epithelial cell differentiation;positive regulation of epithelial cell proliferation;positive regulation of keratinocyte differentiation;positive regulation of molecular function;positive regulation of neuron projection development;primary metabolic process;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of DNA binding;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of gene expression;regulation of immune system process;regulation of keratinocyte differentiation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;response to amine stimulus;response to cAMP;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to fatty acid;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to lipid;response to monosaccharide stimulus;response to organic nitrogen;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to testosterone stimulus;ribonucleoside metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;transcription, DNA-dependent;transport;UTP biosynthetic process;UTP metabolic process;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;deoxyribonuclease activity;DNA binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;kinase activity;magnesium ion binding;metal ion binding;nuclease activity;nucleic acid binding;nucleic acid binding transcription factor activity;nucleobase-containing compound kinase activity;nucleoside diphosphate kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;phosphotransferase activity, nitrogenous group as acceptor;phosphotransferase activity, phosphate group as acceptor;protein histidine kinase activity;protein kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleoprotein binding;ribonucleotide binding;ribosomal small subunit binding;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cell projection;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;ruffle Purine metabolism;Pyrimidine metabolism 0.00023936 6608100 2

J3KSC4;J3QLK0;B1AH77;B1AH80;P63000;P60763;P15153;P63000-2;B1AH78 Ras-related C3 botulinum toxin substrate 1;Ras-related C3 botulinum toxin substrate 3;Ras-related C3 botulinum toxin substrate 2 RAC3;RAC2;RAC1 >tr|J3KSC4|J3KSC4_HUMAN Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens GN=RAC3 PE=3 SV=1;>tr|J3QLK0|J3QLK0_HUMAN Ras-related C3 botulinum toxin substrate 3 (Fragment) OS=Homo sapiens GN=RAC3 PE=3 SV=1;>tr|B1AH77|B1AH77_HUMAN Ras-rela 0.88 1.99 1.02 1.62 0.93 0.97 0.65 1.01 + "actin cytoskeleton organization;actin filament organization;actin filament polymerization;actin filament-based process;actin polymerization or depolymerization;anatomical structure arrangement;anatomical structure homeostasis;anatomical structure morphogenesis;auditory receptor cell morphogenesis;axon guidance;biological adhesion;biological regulation;bone resorption;cell activation;cell adhesion;cell chemotaxis;cell differentiation;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell morphogenesis involved in neuron differentiation;cell motility;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to stimulus;cerebral cortex cell migration;cerebral cortex radially oriented cell migration;chemotaxis;cochlea morphogenesis;cytoskeleton organization;defense response;dendrite morphogenesis;developmental process;dopaminergic neuron differentiation;embryonic morphogenesis;embryonic olfactory bulb interneuron precursor migration;engulfment of apoptotic cell;enzyme linked receptor protein signaling pathway;epithelial cell morphogenesis;forebrain cell migration;homeostatic process;hyperosmotic response;immune response;immune system process;inflammatory response;innate immune response;intracellular signal transduction;lamellipodium assembly;leukocyte chemotaxis;leukocyte migration;localization;localization within membrane;locomotion;lymphocyte costimulation;macromolecular complex assembly;macromolecular complex subunit organization;mast cell chemotaxis;membrane invagination;membrane organization;multicellular organismal process;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of endocytosis;negative regulation of interleukin-23 production;negative regulation of multicellular organismal process;negative regulation of receptor-mediated endocytosis;negative regulation of transport;nerve growth factor receptor signaling pathway;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;neuron projection development;neuron projection morphogenesis;non-canonical Wnt receptor signaling pathway;organelle organization;phagocytosis, engulfment;platelet activation;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of lamellipodium assembly;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of protein complex assembly;positive regulation of protein polymerization;positive regulation of Ras protein signal transduction;positive regulation of response to stimulus;positive regulation of Rho protein signal transduction;positive regulation of signal transduction;positive regulation of signaling;positive regulation of small GTPase mediated signal transduction;positive regulation of T cell activation;positive regulation of transferase activity;protein complex assembly;protein complex subunit organization;protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of cytoskeleton organization;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of endocytosis;regulation of establishment of planar polarity;regulation of hydrogen peroxide metabolic process;regulation of immune effector process;regulation of immune system process;regulation of interleukin-23 production;regulation of kinase activity;regulation of lamellipodium assembly;regulation of leukocyte activation;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein polymerization;regulation of Ras protein signal transduction;regulation of reactive oxygen species metabolic process;regulation of receptor-mediated endocytosis;regulation of respiratory burst;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of T cell activation;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to osmotic stress;response to stimulus;response to stress;response to wounding;ruffle organization;signal transduction;small GTPase mediated signal transduction;substrate adhesion-dependent cell spreading;substrate-independent telencephalic tangential interneuron migration;substrate-independent telencephalic tangential migration;system process;T cell costimulation;tangential migration from the subventricular zone to the olfactory bulb;taxis;telencephalon cell migration;tissue homeostasis;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproduction;Wnt receptor signaling pathway;Wnt receptor signaling pathway, planar cell polarity pathway" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell body;cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;endomembrane system;envelope;extrinsic to membrane;extrinsic to plasma membrane;filamentous actin;Golgi apparatus part;Golgi membrane;growth cone;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;leading edge membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuronal cell body;nuclear envelope;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;phagocytic cup;pigment granule;plasma membrane;plasma membrane part;protein complex;ruffle membrane;site of polarized growth;trans-Golgi network;vesicle Adherens junction;Amyotrophic lateral sclerosis (ALS);Axon guidance;B cell receptor signaling pathway;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Colorectal cancer;Epithelial cell signaling in Helicobacter pylori infection;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Leukocyte transendothelial migration;MAPK signaling pathway;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Osteoclast differentiation;Pancreatic cancer;Pancreatic secretion;Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;Toll-like receptor signaling pathway;VEGF signaling pathway;Viral myocarditis;Wnt signaling pathway 8.7302E-128 31939000 2

R4GN49;P29034 Protein S100-A2 S100A2 >tr|R4GN49|R4GN49_HUMAN Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=4 SV=1;>sp|P29034|S10A2_HUMAN Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=1 SV=3 0.66 0.38 0.43 0.46 3.18 1.78 1.66 1.14 + + cell migration;cell motility;cellular component movement;cellular process;endothelial cell migration;locomotion binding;calcium ion binding;cation binding;ion binding;metal ion binding 0.00013229 65544000 2

P31431;B4E1S6;P31431-2 Syndecan-4;Syndecan SDC4 >sp|P31431|SDC4_HUMAN Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2;>tr|B4E1S6|B4E1S6_HUMAN Syndecan OS=Homo sapiens GN=SDC4 PE=2 SV=1;>sp|P31431-2|SDC4_HUMAN Isoform 2 of Syndecan-4 OS=Homo sapiens GN=SDC4 1.34 NaN 1.05 0.91 1.05 1.15 1.05 NaN + + "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of actin filament bundle assembly;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of focal adhesion assembly;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of protein kinase activity;positive regulation of stress fiber assembly;positive regulation of transferase activity;primary metabolic process;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of biological process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell-matrix adhesion;regulation of

cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular
process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of focal adhesion assembly;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic
process;regulation of molecular function;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic
process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of stress fiber assembly;regulation of transferase
activity;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;sulfur compound metabolic process;terpenoid metabolic
process;tube development;ureteric bud development" molecular transducer activity;receptor activity;signal transducer activity;signaling receptor activity;thrombospondin receptor activity + adherens junction;anchoring junction;cell
junction;cell part;cell surface;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;costamere;cytoplasmic part;extracellular region;focal adhesion;Golgi apparatus part;Golgi lumen;integral to membrane;integral to
plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;membrane part;membrane raft;membrane-enclosed lumen;organelle
lumen;organelle part;plasma membrane part;vacuolar lumen;vacuolar part Cell adhesion molecules (CAMs);ECM-receptor interaction;Malaria 0.00028389 9227500 2
B4DIT7;F5H6P0;P21980 Protein-glutamine gamma-glutamyltransferase 2 TGM2 >tr|B4DIT7|B4DIT7_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=2
SV=1;>tr|F5H6P0|F5H6P0_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=2 SV=1;>sp|P21980|TGM2_HUMAN Protein-glutamine gamma-gl NaN NaN 2.56 NaN 3.13 NaN NaN NaN +
\+ anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptotic cell clearance;biological regulation;blood vessel remodeling;branching involved in salivary gland
morphogenesis;calcium ion homeostasis;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component
organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion
homeostasis;cellular process;cellular protein metabolic process;chemical homeostasis;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion
concentration;elevation of cytosolic calcium ion concentration involved in G-protein signaling coupled to IP3 second messenger;endocytosis;establishment of localization;homeostatic process;induction of apoptosis;induction of programmed
cell death;ion homeostasis;isopeptide cross-linking;isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic
process;macromolecule modification;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an
epithelium;multicellular organismal process;peptide cross-linking;peptidyl-amino acid modification;peptidyl-glutamine modification;peptidyl-lysine modification;phagocytosis;positive regulation of apoptosis;positive regulation of biological
process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of defense
response;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of inflammatory response;positive regulation of intracellular protein kinase cascade;positive regulation of programmed cell death;positive regulation of
response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smooth muscle cell proliferation;primary metabolic process;protein
complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein modification process;protein oligomerization;regulation of apoptosis;regulation of biological process;regulation of
biological quality;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of defense response;regulation of I-kappaB kinase/NF-kappaB
cascade;regulation of inflammatory response;regulation of intracellular protein kinase cascade;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to
stress;regulation of signal transduction;regulation of signaling;regulation of smooth muscle cell proliferation;salivary gland cavitation;tissue morphogenesis;tissue remodeling;transport;tube formation;tube lumen cavitation;vesicle-mediated
transport "binding;catalytic activity;cation binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ion binding;metal ion binding;nucleotide binding;protein-glutamine gamma-glutamyltransferase activity;purine
nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring amino-acyl groups"
cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle;plasma membraneHuntington's disease 0.00026627
361980 2
Q6ZMP0;Q6ZMP0-2;B4DR13 Thrombospondin type-1 domain-containing protein 4 THSD4 >sp|Q6ZMP0|THSD4_HUMAN Thrombospondin type-1 domain-containing protein 4 OS=Homo sapiens GN=THSD4 PE=2
SV=2;>sp|Q6ZMP0-2|THSD4_HUMAN Isoform 2 of Thrombospondin type-1 domain-containing protein 4 OS=Homo sapiens GN=THSD4;>tr|B4DR13|B4DR13_HUMAN Thrombospon NaN NaN NaN NaN NaN NaN NaN NaN + +
cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or
biogenesis at cellular level;cellular process;elastic fiber assembly;extracellular matrix assembly;extracellular matrix organization;extracellular structure organization "catalytic activity;endopeptidase activity;hydrolase
activity;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides"+ extracellular matrix;extracellular matrix part;extracellular region part;fibril;microfibril
0.00056304 1555100 2
Q9GZM7-3;Q9GZM7;B4DNS5;E7EUP2 Tubulointerstitial nephritis antigen-like TINAGL1 >sp|Q9GZM7-3|TINAL_HUMAN Isoform 3 of Tubulointerstitial nephritis antigen-like OS=Homo sapiens
GN=TINAGL1;>sp|Q9GZM7|TINAL_HUMAN Tubulointerstitial nephritis antigen-like OS=Homo sapiens GN=TINAGL1 PE=1 SV=1;>tr|B4DNS5|B4DNS5_HUMAN Tubulointerstitial neph NaN 0.95 NaN NaN NaN NaN NaN 1.14 +
\+ cellular process;endosome transport;establishment of localization;establishment of localization in cell;immune response;immune system process;intracellular transport;macromolecule metabolic
process;metabolic process;primary metabolic process;protein metabolic process;proteolysis;response to stimulus;transport;vesicle-mediated transport "binding;carbohydrate binding;cargo receptor activity;catalytic activity;cysteine-type
peptidase activity;extracellular matrix structural constituent;hydrolase activity;pattern binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;polysaccharide binding;receptor activity;scavenger receptor
activity;structural molecule activity" + cell part;cytoplasm;extracellular region part;extracellular space;intracellular part 0.000020318 4488000 2
K7ENK9;K7EKX0;Q15836;J3QRU4;P63027;F8WCA0;L7N2F9;P23763-2;F5GZV7;P23763-3;P23763 Vesicle-associated membrane protein 3;Vesicle-associated membrane protein 2;Vesicle-associated membrane protein 1
VAMP2;VAMP3;VAMP1 >tr|K7ENK9|K7ENK9_HUMAN Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=4 SV=1;>tr|K7EKX0|K7EKX0_HUMAN Vesicle-associated membrane protein 3 OS=Homo
sapiens GN=VAMP3 PE=4 SV=1;>sp|Q15836|VAMP3_HUMAN Vesicle-associated membrane protein 3 O 1.21 1.37 0.95 1.00 1.66 1.39 1.09 0.95 + "anatomical structure morphogenesis;biological
adhesion;biological regulation;calcium ion-dependent exocytosis;cell adhesion;cell morphogenesis;cell morphogenesis involved in differentiation;cell-substrate adhesion;cellular component assembly;cellular component
morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular
metabolic process;cellular process;cellular protein metabolic process;developmental process;endosome transport;energy derivation by oxidation of organic compounds;energy reserve metabolic process;establishment of
localization;establishment of localization in cell;establishment of protein localization;exocytosis;generation of precursor metabolites and energy;glutamate secretion;Golgi to plasma membrane protein transport;Golgi to plasma membrane
transport;Golgi vesicle transport;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;membrane docking;membrane
fusion;membrane organization;metabolic process;neurotransmitter secretion;neurotransmitter transport;oxidation-reduction process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation
of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of receptor recycling;positive regulation of signaling;post-Golgi vesicle-mediated transport;primary
metabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of
cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of macromolecule metabolic process;regulation of
metabolic process;regulation of neurotransmitter levels;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of receptor recycling;regulation of secretion;regulation of
signaling;regulation of transport;retrograde transport, endosome to Golgi;secretion;secretion by cell;signal release;small molecule metabolic process;substrate adhesion-dependent cell spreading;transport;vesicle docking;vesicle docking
involved in exocytosis;vesicle-mediated transport" apical plasma membrane;cell junction;cell part;cell projection;clathrin coated vesicle membrane;clathrin sculpted gamma-aminobutyric acid transport vesicle
membrane;clathrin sculpted glutamate transport vesicle membrane;clathrin sculpted monoamine transport vesicle membrane;clathrin-coated vesicle;coated vesicle;coated vesicle membrane;cytoplasmic membrane-bounded
vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded
organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded
vesicle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;neuron projection;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;plasma membrane;plasma membrane
part;protein complex;recycling endosome;secretory granule membrane;SNARE complex;stored secretory granule;synapse;synapse part;synaptic vesicle membrane;transport vesicle membrane;vesicle;vesicle membrane Phagosome;Salivary
secretion;SNARE interactions in vesicular transport;Vasopressin-regulated water reabsorption 0.000025105 23488000 2
D6RGZ6;P13611-2;P13611-5;P13611;Q86W61;P13611-4;E9PF17;P13611-3 Versican core protein VCAN >tr|D6RGZ6|D6RGZ6_HUMAN Versican core protein (Fragment) OS=Homo sapiens GN=VCAN PE=2 SV=1;>sp|P13611-2|CSPG2_HUMAN Isoform V1 of Versican core protein OS=Homo sapiens GN=VCAN;>sp|P13611-5|CSPG2_HUMAN Isoform Vint of Versican core protein OS=Homo sapiens G NaN NaN 1.30 NaN 0.24 NaN NaN NaN +
\+ + amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;biological adhesion;biosynthetic process;carbohydrate
biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell adhesion;cell migration;cell motility;cell recognition;cellular biosynthetic process;cellular catabolic process;cellular component
movement;cellular metabolic process;cellular process;chondroitin sulfate biosynthetic process;chondroitin sulfate catabolic process;chondroitin sulfate metabolic process;dermatan sulfate biosynthetic process;dermatan sulfate metabolic
process;developmental process;glial cell migration;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;heart development;locomotion;macromolecule biosynthetic
process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;nitrogen compound metabolic process;organ
development;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;sulfur compound biosynthetic process;sulfur compound catabolic process;sulfur compound
metabolic process binding;calcium ion binding;carbohydrate binding;cation binding;glycosaminoglycan binding;hyaluronic acid binding;ion binding;metal ion binding;pattern binding;polysaccharide binding + cell part;cytoplasmic
part;extracellular matrix;extracellular region part;extracellular space;Golgi apparatus part;Golgi lumen;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-enclosed lumen;organelle
lumen;organelle part;proteinaceous extracellular matrix;vacuolar lumen;vacuolar part Cell adhesion molecules (CAMs) 0.00022535 2406200 2
O75083;D6RD66;O75083-3 WD repeat-containing protein 1 WDR1 >sp|O75083|WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4;>tr|D6RD66|D6RD66_HUMAN WD repeat-containing
protein 1 (Fragment) OS=Homo sapiens GN=WDR1 PE=2 SV=1;>sp|O75083-3|WDR1_HUMAN Isoform 2 of WD repeat-containing protein 1 O 0.20 NaN NaN NaN NaN NaN 0.47 NaN cell
activation;cellular process;establishment of localization;establishment of localization in cell;exocytosis;multicellular organismal process;neurological system process;platelet activation;platelet degranulation;secretion;secretion by
cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;system process;transport;vesicle-mediated transport + cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;intracellular
non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 0.000099329 2841000 2
H7C3D3;B4DQX7;B4DQR8;H0Y2Y8;Q15942 Zyxin ZYX >tr|H7C3D3|H7C3D3_HUMAN Zyxin (Fragment) OS=Homo sapiens GN=ZYX PE=4 SV=1;>tr|B4DQX7|B4DQX7_HUMAN Zyxin OS=Homo sapiens GN=ZYX
PE=2 SV=1;>tr|B4DQR8|B4DQR8_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=2 SV=1;>tr|H0Y2Y8|H0Y2Y8_HUMAN Zyxin (Fragment) OS=Homo sapiens NaN NaN 0.95 NaN 1.85 NaN NaN NaN
\+ biological adhesion;biological regulation;cell adhesion;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;interaction with host;interspecies interaction between organisms;multi-organism
process;regulation of biological process;regulation of cellular process;reproductive process;response to stimulus;signal transduction;signaling;viral reproductive process;virus-host interaction binding;cation binding;ion binding;metal ion
binding;transition metal ion binding;zinc ion binding actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeletal part;focal adhesion;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to
membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part;stress fiber Focal adhesion 0.00051953 1281700 2
H3BUH7;H3BPS8;H3BQN4;P04075;J3KPS3;P04075-2;H3BMQ8;H3BR04;H3BU78 Fructose-bisphosphate aldolase;Fructose-bisphosphate aldolase A ALDOA >tr|H3BUH7|H3BUH7_HUMAN Fructose-bisphosphate aldolase A
(Fragment) OS=Homo sapiens GN=ALDOA PE=2 SV=1;>tr|H3BPS8|H3BPS8_HUMAN Fructose-bisphosphate aldolase A (Fragment) OS=Homo sapiens GN=ALDOA PE=2 SV=1;>tr|H3BQN4|H3BQN4_HUMAN Fructose-bisphosphate aldo 0.47 2.51 0.21 2.45 0.42 0.93 0.84 1.07 "actin cytoskeleton organization;actin filament organization;actin filament-based process;alcohol biosynthetic process;alcohol catabolic
process;alcohol metabolic process;anatomical structure homeostasis;ATP biosynthetic process;ATP metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic
process;carbohydrate metabolic process;catabolic process;cell activation;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular
component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular
homeostasis;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in
cell;exocytosis;fructose 1,6-bisphosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle
biosynthetic process;heterocycle metabolic process;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;homeostatic process;macromolecular complex assembly;macromolecular complex subunit
organization;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multicellular organismal process;muscle cell homeostasis;muscle contraction;muscle system
process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate
metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organelle organization;platelet activation;platelet degranulation;primary
metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;purine nucleoside triphosphate biosynthetic
process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic
process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of anatomical structure
morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of
developmental process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;secretion by cell;small molecule
biosynthetic process;small molecule catabolic process;small molecule metabolic process;striated muscle contraction;system process;transport;vesicle-mediated transport" actin binding;aldehyde-lyase activity;binding;carbohydrate

binding;carbon-carbon lyase activity;catalytic activity;cytoskeletal protein binding;fructose binding;fructose-bisphosphate aldolase activity;identical protein binding;lyase activity;monosaccharide binding;protein binding;sugar binding;tubulin binding + actin cytoskeleton;cell part;contractile fiber part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;I band;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;non-membrane-bounded organelle;organelle;organelle lumen;organelle part;platelet alpha granule lumen;secretory granule lumen;vesicle;vesicle lumen Carbon fixation in photosynthetic organisms;Fructose and mannose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway 1.4517E-25 26756000 3

Q07021;I3L3Q7;I3L3B0 "Complement component 1 Q subcomponent-binding protein, mitochondrial" C1QBP ">sp|Q07021|C1QBP_HUMAN Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP PE=1 SV=1;>tr|I3L3Q7|I3L3Q7_HUMAN Complement component 1 Q subcomponent-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=C1QBP" 1.29 0.70 1.11 0.53 2.19 1.72 1.58 1.26 "activation of immune response;apoptosis;biological regulation;biosynthetic process;blood coagulation, intrinsic pathway;cell death;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;complement activation;complement activation, classical pathway;death;defense response;humoral immune response;immune effector process;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;interaction with host;interspecies interaction between organisms;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;mature ribosome assembly;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of defense response;negative regulation of defense response to virus;negative regulation of gene expression;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of interferon-gamma production;negative regulation of interleukin-12 production;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of multicellular organismal process;negative regulation of multi-organism process;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of RNA splicing;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle assembly;phosphatidylinositol 3-kinase cascade;phosphatidylinositol-mediated signaling;positive regulation of apoptosis;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemotaxis;positive regulation of dendritic cell chemotaxis;positive regulation of immune response;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitochondrial translation;positive regulation of mitochondrion organization;positive regulation of neutrophil chemotaxis;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein activation cascade;protein metabolic process;regulation of acute inflammatory response;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of complement activation;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of dendritic cell chemotaxis;regulation of gene expression;regulation of humoral immune response;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of interferon-gamma production;regulation of interleukin-12 production;regulation of intracellular protein kinase cascade;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitochondrial translation;regulation of mitochondrion organization;regulation of mRNA processing;regulation of multicellular organismal process;regulation of multi-organism process;regulation of neutrophil chemotaxis;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein activation cascade;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein processing;regulation of response to biotic stimulus;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA splicing;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;signal transduction;transcription, DNA-dependent;viral reproductive process;virus-host interaction" adrenergic receptor binding;binding;carbohydrate binding;complement binding;complement component C1q binding;glycosaminoglycan binding;G-protein-coupled receptor binding;hyaluronic acid binding;kininogen binding;mRNA binding;nucleic acid binding;opsonin binding;pattern binding;polysaccharide binding;protein binding;protein binding transcription factor activity;receptor binding;RNA binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding;transcription factor binding transcription factor activity + cell part;cell surface;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle lumen;organelle part;plasma membrane 5.1388E-64 95327000 3

E9PMR4;P48509;E9PRJ3;E9PLZ6;K4DIB7CD151 antigen CD151 >tr|E9PMR4|E9PMR4_HUMAN CD151 antigen OS=Homo sapiens GN=CD151 PE=2 SV=1;>sp|P48509|CD151_HUMAN CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3;>tr|E9PRJ3|E9PRJ3_HUMAN CD151 antigen (Fragment) OS=Homo sapiens GN=CD151 PE=2 SV=1 1.25 1.01 1.35 NaN 0.49 NaN 0.60 0.64 + biological adhesion;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell motility;cell proliferation;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;immune system process;leukocyte activation;leukocyte proliferation;locomotion;lymphocyte activation;lymphocyte proliferation;mononuclear cell proliferation;T cell activation;T cell proliferation cell part;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part 1.101E-09 18004000 3

Q99715-4;D6RGG3;Q99715;Q99715-2;H0Y4P7;H0Y5N9 Collagen alpha-1(XII) chain COL12A1 >sp|Q99715-4|COCA1_HUMAN Isoform 4 of Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1;>tr|D6RGG3|D6RGG3_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=2 SV=1;>sp|Q99715|COCA1_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL1NaN 0.96 NaN NaN NaN NaN NaN 1.75 + + + anatomical structure development;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen fibril organization;collagen metabolic process;developmental process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;skeletal system development;system development extracellular matrix structural constituent;extracellular matrix structural constituent conferring tensile strength;structural molecule activity + anchoring collagen;cell part;collagen;collagen type XII;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;FACIT collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vesicle Protein digestion and absorption 2.3983E-08 1337000 3

P08123 Collagen alpha-2(I) chain COL1A2 >sp|P08123|CO1A2_HUMAN Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=7 NaN NaN 0.77 NaN 33.07 NaN NaN NaN + + anatomical structure development;anatomical structure morphogenesis;biological regulation;blood vessel development;cell activation;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;collagen catabolic process;collagen fibril organization;collagen metabolic process;developmental process;enzyme linked receptor protein signaling pathway;epidermis morphogenesis;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune system process;intracellular signal transduction;leukocyte migration;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;odontogenesis;organ morphogenesis;platelet activation;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein oligomerization;protein trimerization;Ras protein signal transduction;regulation of biological process;regulation of biological quality;regulation of blood pressure;regulation of cellular process;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to organic nitrogen;response to organic substance;response to stimulus;Rho protein signal transduction;signal transduction;skeletal system development;skin morphogenesis;small GTPase mediated signal transduction;system development;tissue morphogenesis;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway "binding;binding, bridging;cation binding;extracellular matrix structural constituent;growth factor binding;identical protein binding;ion binding;metal ion binding;platelet-derived growth factor binding;protein binding;protein binding, bridging;structural molecule activity" + cell part;collagen;collagen type I;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;fibrillar collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Protein digestion and absorption 2.2592E-08 2590600 3

P01040;C9J0E4 Cystatin-A CSTA >sp|P01040|CYTA_HUMAN Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1;>tr|C9J0E4|C9J0E4_HUMAN Cystatin-A OS=Homo sapiens GN=CSTA PE=2 SV=1 0.27 0.97 0.05 11.04 0.31 1.13 1.89 0.47 + + + biological adhesion;biological regulation;cell adhesion;cell differentiation;cell-cell adhesion;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity "binding;binding, bridging;cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;protein binding;protein binding, bridging;structural molecule activity" cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 6.1704E-14 22932000 3

Q7L576-2;Q7L576;Q7L576-3;H7C229;E7EW33;F5H583;E7EVJ5;Q96F07-2;E7EVF4;Q96F07;E7EWA4;H0YL50 Cytoplasmic FMR1-interacting protein 1;Cytoplasmic FMR1-interacting protein 2 CYFIP1;CYFIP2 >sp|Q7L576-2|CYFP1_HUMAN Isoform 2 of Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1;>sp|Q7L576|CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1;>sp|Q7L576-3|CYFP1_HUMAN Isoform 3 of Cytoplasmic FMR1- NaN NaN 0.42 NaN 6.81 NaN NaN NaN + apoptosis;axon extension;biological adhesion;biological regulation;cell adhesion;cell death;cell growth;cell projection assembly;cell projection organization;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;death;defense response;developmental cell growth;developmental growth;developmental growth involved in morphogenesis;developmental process;growth;immune response;immune system process;innate immune response;lamellipodium assembly;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of proteolysis;programmed cell death;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;response to stimulus;response to stress;ruffle organization actin binding;actin filament binding;binding;cytoskeletal protein binding;enzyme binding;GTPase binding;protein binding;Rac GTPase binding;Ras GTPase binding;Rho GTPase binding;small GTPase binding cell junction;cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;intracellular part;lamellipodium;macromolecular complex;mRNA cap binding complex;neuron projection;perinuclear region of cytoplasm;protein complex;RNA cap binding complex;ruffle;synapse Regulation of actin cytoskeleton 2.3754E-06 13219000 3

P07585;P07585-2;H0YIH3;F8VXZ8;F8VNV6;F8VUF6;F8VWU0;P07585-3 Decorin DCN >sp|P07585|PGS2_HUMAN Decorin OS=Homo sapiens GN=DCN PE=1 SV=1;>sp|P07585-2|PGS2_HUMAN Isoform B of Decorin OS=Homo sapiens GN=DCN NaN NaN 1.76 NaN 5.75 NaN NaN NaN + + aging;amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chondroitin sulfate biosynthetic process;chondroitin sulfate catabolic process;chondroitin sulfate metabolic process;dermatan sulfate biosynthetic process;dermatan sulfate metabolic process;developmental process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic

process;glycosaminoglycan metabolic process;kidney development;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;muscle tissue
development;nitrogen compound metabolic process;organ development;organ morphogenesis;peptide cross-linking;peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan;peptidyl-amino acid modification;peptidyl-serine
modification;placenta development;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;protein metabolic process;protein modification process;response to
abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to external stimulus;response to lipopolysaccharide;response to mechanical stimulus;response to molecule of bacterial origin;response to organic
substance;response to stimulus;response to stress;response to wounding;skeletal muscle tissue development;striated muscle tissue development;sulfur compound biosynthetic process;sulfur compound catabolic process;sulfur compound
metabolic process;tissue development;wound healing binding;carbohydrate binding;extracellular matrix binding;glycosaminoglycan binding;pattern binding;polysaccharide binding + anchoring collagen;cell part;collagen;collagen
type VI;cytoplasmic part;extracellular matrix part;extracellular region part;extracellular space;Golgi apparatus part;Golgi lumen;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-enclosed
lumen;organelle lumen;organelle part;vacuolar lumen;vacuolar part TGF-beta signaling pathway 3.1478E-07 5024900 3
Q6E0U4-4;Q6E0U4-16;Q6E0U4-2;Q6E0U4;CON__A3EZ82;Q6E0U4-7;Q6E0U4-3;Q6E0U4-5;E7EUS0;Q6E0U4-6;Q6E0U4-13;Q6E0U4-11;Q6E0U4-14;Q6E0U4-12;Q6E0U4-10;Q6E0U4-9;C9J186;M0QZV2;M0R265;Q6E0U4-
8;H7C145;M0R0A5;H7BZ95;C9JCN1;C9IYI1 Dermokine DMKN >sp|Q6E0U4-4|DMKN_HUMAN Isoform 4 of Dermokine OS=Homo sapiens GN=DMKN;>sp|Q6E0U4-16|DMKN_HUMAN Isoform 16 of Dermokine OS=Homo
sapiens GN=DMKN;>sp|Q6E0U4-2|DMKN_HUMAN Isoform 2 of Dermokine OS=Homo sapiens GN=DMKN;>sp|Q6E0U4|DMKN_HUMAN Dermokine OS=Homo s NaN NaN NaN NaN NaN NaN NaN NaN
+ extracellular region part;extracellular space 1.0811E-09 3564900 3
Q92520;C9JP35;C9JMN4 Protein FAM3C FAM3C >sp|Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1;>tr|C9JP35|C9JP35_HUMAN Protein FAM3C (Fragment) OS=Homo sapiens
GN=FAM3C PE=2 SV=1;>tr|C9JMN4|C9JMN4_HUMAN Protein FAM3C (Fragment) OS=Homo sapiens GN=FAM3C PE=2 SV=1 NaN NaN 1.52 NaN 0.41 NaN NaN NaN developmental
process;multicellular organismal development;multicellular organismal process binding;cytokine activity;protein binding;receptor binding + cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic
vesicle;extracellular region;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;organelle;vesicle 1.3818E-13 3971600 3
Q14512 Fibroblast growth factor-binding protein 1 FGFBP1 >sp|Q14512|FGFP1_HUMAN Fibroblast growth factor-binding protein 1 OS=Homo sapiens GN=FGFBP1 PE=1 SV=1 1.39 0.93 1.55 1.23 0.26 0.08 0.39 0.21 +
+ biological regulation;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular
process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of fibroblast growth factor receptor signaling
pathway;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cell proliferation;regulation of
cellular process;regulation of fibroblast growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;signaling
binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding + cell part;cell surface;extracellular region part;extracellular space;membrane;plasma membrane 2.0803E-136
256910000 3
P06241-3;Q5R3A8;P06241-2;P06241;P07947;J3QRU1;P07948-2;P08631-3;P08631-2;A8K4G3;P06239;P07948;Q573B4;P08631-4;H0Y3C5;P08631;J3KPD6;P12931;P06239-3;P12931-
2;F8VXD2;H0YE20;K7ELV5;F8VYH9;B4DNF9;F8VZZ0;E5RIU6;F8VTV8;F8VWX7;F8VZ51;K7EJ83;E7ESI2;Q8IZL9-2;Q00535-2;H0YAZ9;P24941-2;Q8IZL9-3;H0Y9P2;B3KUS6;Q9UPZ9-
2;Q00535;P06493;P24941;P11802;Q00526;Q8IZL9-5;Q00534;Q8IZL9-4;E7EUK8;Q8IZL9;G3V5T9;Q96Q40-2;H7C265;P50750;Q96Q40-4;E5RGN0;Q96Q40-3;O94921-3;Q96Q40-5;E9PJX5;Q96Q40;O94921-
2;Q8IXN4;F5H3M4;O94921;F5H6Z0;Q07002;Q07002-2;P50750-2;Q00536;Q00536-3;Q07002-3;P51451;Q00537-2;Q00537;P09769;Q00536-2;P20794-3;P20794;Q9UPZ9;P20794-2;P11362-6;P11362-5;H7BXU9;P21802-22;P21802-
4;P22607-3;P21802-20;P21802-15;P21802-21;E7EVR7;P21802-23;P11362-4;P11362-14;P11362-3;E7EU09;J3KPQ0;P22455-2;P21802-8;P21802-2;P21802-13;P21802-17;P21802-12;P21802-6;P22455;P22607-2;P11362-20;P21802-
7;P21802-5;P21802-10;P21802-18;P11362-7;P11362-2;P21802;P21802-3;P21802-16;P11362-19;P11362;J3KNT4;P21802-11;P11362-21;J3QSD7;Q9NYV4-3;Q14004-2;Q9NYV4-2;Q9NYV4;Q14004 Tyrosine-protein kinase
Fyn;Tyrosine-protein kinase Yes;Tyrosine-protein kinase Lck;Tyrosine-protein kinase Lyn;Tyrosine-protein kinase HCK;Proto-oncogene tyrosine-protein kinase Src FYN;YES1;HCK;LCK;LYN;SRC >sp|P06241-3|FYN_HUMAN
Isoform 3 of Tyrosine-protein kinase Fyn OS=Homo sapiens GN=FYN;>tr|Q5R3A8|Q5R3A8_HUMAN Tyrosine-protein kinase Fyn OS=Homo sapiens GN=FYN PE=2 SV=1;>sp|P06241-2|FYN_HUMAN Isoform 2 of Tyrosine-protein
kinase Fyn OS=Homo sapiens GN=F 1.44 1.29 1.03 1.73 0.98 0.59 0.69 0.73 + "actin cytoskeleton organization;actin filament-based process;activated T cell proliferation;activation of caspase
activity;activation of immune response;activation of innate immune response;activation of MAPK activity;activation of MAPKK activity;activation of protein kinase activity;adult behavior;aging;alternative nuclear mRNA splicing, via
spliceosome;alveolar secondary septum development;amine transport;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;anatomical structure development;anatomical structure formation
involved in morphogenesis;anatomical structure homeostasis;anatomical structure morphogenesis;angiogenesis;anion homeostasis;antigen receptor-mediated signaling pathway;apoptosis;appendage morphogenesis;associative
learning;astrocyte development;auditory receptor cell development;axis elongation;axon extension;axon guidance;axonogenesis;B cell homeostasis;B cell receptor signaling pathway;behavior;behavioral response to cocaine;biological
adhesion;biological regulation;biomineral tissue development;biosynthetic process;blood coagulation;bone mineralization;bone morphogenesis;bone resorption;branch elongation involved in salivary gland morphogenesis;branch elongation
of an epithelium;branching involved in embryonic placenta morphogenesis;branching involved in mammary gland duct morphogenesis;branching involved in prostate gland morphogenesis;branching involved in salivary gland
morphogenesis;branching morphogenesis of a nerve;branching morphogenesis of a tube;bud elongation involved in lung branching;calcium ion homeostasis;calcium ion import;calcium ion transmembrane transport;calcium ion
transport;calcium ion transport into cytosol;carbohydrate homeostasis;carbohydrate transport;cardiac cell development;cardiac muscle cell development;cardiac muscle tissue morphogenesis;cardiac septum morphogenesis;catabolic
process;cation homeostasis;cation transport;cell activation;cell adhesion;cell aging;cell communication;cell cycle;cell cycle arrest;cell cycle checkpoint;cell cycle phase;cell cycle process;cell death;cell dedifferentiation;cell development;cell
differentiation;cell division;cell fate commitment;cell growth;cell maturation;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell surface receptor linked
signaling pathway;cell-cell signaling;cell-cell signaling involved in cell fate commitment;cell-matrix adhesion;cell-substrate adhesion;cellular biosynthetic process;cellular calcium ion homeostasis;cellular catabolic process;cellular cation
homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component
maintenance;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component
organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecular complex assembly;cellular
macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane
organization;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex assembly;cellular protein
localization;cellular protein metabolic process;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to external
stimulus;cellular response to extracellular stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to heat;cellular response to hormone stimulus;cellular response to
hydrogen peroxide;cellular response to inorganic substance;cellular response to insulin stimulus;cellular response to interferon-gamma;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response
to nitric oxide;cellular response to nutrient;cellular response to nutrient levels;cellular response to organic substance;cellular response to oxidative stress;cellular response to peptide hormone stimulus;cellular response to progesterone
stimulus;cellular response to reactive oxygen species;cellular response to retinoic acid;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to stress;cellular response to vitamin;cellular response to
vitamin A;cellular zinc ion homeostasis;central nervous system neuron development;centrosome cycle;centrosome duplication;centrosome organization;cerebellar cortex formation;chemical homeostasis;chemotaxis;chondrocyte
differentiation;chordate embryonic development;chromatin modification;chromatin organization;chromosome condensation;chromosome organization;circadian rhythm;circulatory system process;coagulation;cognition;columnar/cuboidal
epithelial cell differentiation;coronal suture morphogenesis;corpus callosum development;cortical actin cytoskeleton organization;cortical cytoskeleton organization;covalent chromatin modification;cranial suture morphogenesis;craniofacial
suture morphogenesis;cytokine secretion;cytokine-mediated signaling pathway;cytoskeleton organization;cytosolic calcium ion homeostasis;cytosolic calcium ion transport;death;dedifferentiation;defense response;defense response to
bacterium;defense response to Gram-positive bacterium;dendrite morphogenesis;dendritic cell differentiation;dentate gyrus development;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection
of mechanical stimulus involved in sensory perception;detection of mechanical stimulus involved in sensory perception of pain;detection of stimulus;detection of stimulus involved in sensory perception;developmental cell
growth;developmental growth;developmental growth involved in morphogenesis;developmental induction;developmental maturation;developmental process;developmental process involved in reproduction;digestive tract
morphogenesis;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;DNA conformation change;DNA damage checkpoint;DNA damage response, signal transduction by p53 class
mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA integrity checkpoint;DNA metabolic process;DNA packaging;DNA repair;DNA replication;elevation of cytosolic calcium ion
concentration;embryo development;embryo development ending in birth or egg hatching;embryonic appendage morphogenesis;embryonic cranial skeleton morphogenesis;embryonic digestive tract morphogenesis;embryonic limb
morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;embryonic pattern specification;embryonic skeletal system morphogenesis;endocytosis;endodermal digestive tract morphogenesis;enzyme linked receptor protein
signaling pathway;epidermal growth factor receptor signaling pathway;epithelial cell differentiation;epithelial cell differentiation involved in prostate gland development;epithelial cell proliferation;epithelial cell proliferation involved in
salivary gland morphogenesis;epithelium development;erythrocyte differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;Fc receptor mediated inhibitory signaling
pathway;feeding behavior;female gamete generation;fibroblast growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway involved in hemopoiesis;fibroblast growth factor receptor signaling pathway
involved in mammary gland specification;fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptosis in bone marrow;fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex
development;fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow;forebrain development;forebrain neuroblast division;forebrain neuron development;forebrain ventricular
zone progenitor cell division;G0 to G1 transition;G1 phase;G1 phase of mitotic cell cycle;G1/S transition of mitotic cell cycle;G2 phase;G2 phase of mitotic cell cycle;G2/M transition checkpoint;G2/M transition DNA damage
checkpoint;G2/M transition of mitotic cell cycle;gamete generation;generation of neurons;gland development;glandular epithelial cell differentiation;glial cell development;glial cell differentiation;glucose homeostasis;glucose
transport;growth;growth hormone secretion;hair cycle process;hair follicle morphogenesis;hemopoiesis;hemopoietic or lymphoid organ development;hemopoietic progenitor cell differentiation;hemopoietic stem cell
differentiation;hemostasis;hexose transport;hippocampus development;histamine secretion;histamine secretion by mast cell;histamine secretion involved in inflammatory response;histamine transport;histone modification;histone
phosphorylation;homeostasis of number of cells;homeostatic process;hormone secretion;hormone transport;immune effector process;immune response;immune response-activating cell surface receptor signaling pathway;immune response-
activating signal transduction;immune response-inhibiting cell surface receptor signaling pathway;immune response-inhibiting signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-
regulating signaling pathway;immune system process;in utero embryonic development;induction of apoptosis;induction of programmed cell death;inflammatory response;innate immune response;innate immune response-activating signal
transduction;inner ear morphogenesis;inner ear receptor cell development;inositol lipid-mediated signaling;insulin receptor signaling pathway;integrin-mediated signaling pathway;interaction with host;interferon-gamma-mediated signaling
pathway;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;ion
homeostasis;ion transmembrane transport;ion transport;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;karyogamy;lacrimal gland development;lateral sprouting from an epithelium;lateral ventricle
development;layer formation in cerebral cortex;learning;learning or memory;lens fiber cell development;leukocyte activation;leukocyte degranulation;leukocyte differentiation;leukocyte homeostasis;leukocyte migration;leukocyte migration
involved in immune response;leukocyte proliferation;limb bud formation;limb morphogenesis;lipopolysaccharide-mediated signaling pathway;localization;locomotion;lung alveolus development;lung epithelium development;lung lobe
morphogenesis;lung-associated mesenchyme development;lymphocyte activation;lymphocyte costimulation;lymphocyte differentiation;lymphocyte homeostasis;lymphocyte proliferation;M phase;M phase of mitotic cell
cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;macromolecule
modification;maintenance of fidelity involved in DNA-dependent DNA replication;male gamete generation;mammary gland bud formation;MAPKKK cascade;meiosis;membrane depolarization;membrane disassembly;membrane
invagination;membrane organization;membranous septum morphogenesis;mesenchymal cell differentiation;mesenchymal cell differentiation involved in lung development;mesenchymal cell proliferation;mesenchymal cell proliferation
involved in lung development;mesenchymal-epithelial cell signaling;mesenchyme development;mesoderm development;metabolic process;metal ion homeostasis;metal ion transport;microtubule organizing center organization;midbrain
development;middle ear morphogenesis;mitosis;mitotic cell cycle checkpoint;mitotic cell cycle G2/M transition checkpoint;mitotic cell cycle G2/M transition DNA damage checkpoint;mitotic nuclear envelope disassembly;mitotic
prometaphase;mitotic prophase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;molting cycle;molting cycle process;mononuclear cell proliferation;monosaccharide
transport;monovalent inorganic cation transport;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;motor axon guidance;mRNA
metabolic process;mRNA processing;multicellular organism growth;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell
development;muscle tissue development;muscle tissue morphogenesis;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;myeloid cell differentiation;negative regulation of
anoikis;negative regulation of apoptosis;negative regulation of B cell activation;negative regulation of B cell proliferation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase
activity;negative regulation of catabolic process;negative regulation of catalytic activity;negative regulation of cell activation;negative regulation of cell adhesion;negative regulation of cell aging;negative regulation of cell
communication;negative regulation of cell cycle;negative regulation of cell cycle arrest;negative regulation of cell cycle process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell
proliferation;negative regulation of cell-matrix adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular
macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cellular senescence;negative
regulation of developmental process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of epithelial cell proliferation;negative
regulation of ERK1 and ERK2 cascade;negative regulation of focal adhesion assembly;negative regulation of gene expression;negative regulation of hydrolase activity;negative regulation of immune response;negative regulation of immune
system process;negative regulation of intracellular protein kinase cascade;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of kinase activity;negative regulation of
leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation
of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of MAPKKK cascade;negative regulation of mast cell proliferation;negative regulation of metabolic process;negative regulation of
mitosis;negative regulation of molecular function;negative regulation of mononuclear cell proliferation;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte differentiation;negative regulation of
nitrogen compound metabolic process;negative regulation of nuclear division;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of organelle
organization;negative regulation of osteoblast differentiation;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of protein catabolic process;negative regulation of protein complex

assembly;negative regulation of protein export from nucleus;negative regulation of protein homooligomerization;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein
modification process;negative regulation of protein oligomerization;negative regulation of protein serine/threonine kinase activity;negative regulation of protein transport;negative regulation of protein ubiquitination;negative regulation of
response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequestering of calcium ion;negative regulation of signal transduction;negative regulation of signaling;negative regulation of synaptic
plasticity;negative regulation of toll-like receptor 2 signaling pathway;negative regulation of toll-like receptor 4 signaling pathway;negative regulation of toll-like receptor signaling pathway;negative regulation of transcription from RNA
polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of transport;nerve growth factor receptor signaling pathway;neuroblast
division;neurogenesis;neurological system process;neuromuscular junction development;neuron apoptosis;neuron death;neuron development;neuron migration;neuron projection development;neuron projection morphogenesis;neuron-neuron
synaptic transmission;nitrogen compound metabolic process;nitrogen compound transport;Notch signaling pathway;nuclear division;nuclear envelope disassembly;nuclear envelope organization;nuclear mRNA splicing, via
spliceosome;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;odontogenesis;oligodendrocyte development;oligodendrocyte differentiation;oogenesis;organ
development;organ growth;organ induction;organ morphogenesis;organ regeneration;organelle fission;organelle fusion;organelle organization;organic substance transport;otic vesicle formation;outer ear morphogenesis;outflow tract septum
morphogenesis;paraxial mesoderm development;pattern recognition receptor signaling pathway;pattern specification process;peptide hormone secretion;peptide secretion;peptide transport;peptidyl-amino acid modification;peptidyl-serine
modification;peptidyl-serine phosphorylation;peptidyl-threonine modification;peptidyl-threonine phosphorylation;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phagocytosis;phosphate ion homeostasis;phosphate-
containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;phosphorylation of RNA polymerase II C-terminal domain;photoreceptor cell maintenance;platelet
activation;platelet degranulation;positive regulation of actin cytoskeleton reorganization;positive regulation of actin filament polymerization;positive regulation of antigen receptor-mediated signaling pathway;positive regulation of
apoptosis;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of calcium ion-dependent exocytosis;positive regulation of canonical Wnt receptor signaling
pathway;positive regulation of cardiac muscle cell proliferation;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell
communication;positive regulation of cell cycle;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell development;positive regulation of cell
differentiation;positive regulation of cell division;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cell
size;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component
organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokine secretion;positive regulation of cytoskeleton
organization;positive regulation of defense response;positive regulation of dendritic cell apoptosis;positive regulation of developmental process;positive regulation of DNA biosynthetic process;positive regulation of DNA metabolic
process;positive regulation of DNA replication;positive regulation of DNA-dependent DNA replication initiation;positive regulation of epithelial cell proliferation;positive regulation of epithelial cell proliferation involved in lung
morphogenesis;positive regulation of ERK1 and ERK2 cascade;positive regulation of exocytosis;positive regulation of Fc receptor mediated stimulatory signaling pathway;positive regulation of fibroblast proliferation;positive regulation of
gamma-delta T cell activation;positive regulation of gamma-delta T cell differentiation;positive regulation of gene expression;positive regulation of glial cell proliferation;positive regulation of gliogenesis;positive regulation of hormone
secretion;positive regulation of hydrolase activity;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive
regulation of insulin secretion;positive regulation of integrin activation;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive
regulation of JAK-STAT cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of leukocyte apoptosis;positive regulation of leukocyte degranulation;positive regulation of leukocyte
proliferation;positive regulation of ligase activity;positive regulation of lipase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of
lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive
regulation of MAPKKK cascade;positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway;positive regulation of mast cell activation;positive regulation of mast cell activation involved in immune
response;positive regulation of mast cell degranulation;positive regulation of mast cell proliferation;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of metalloenzyme
activity;positive regulation of mitotic cell cycle;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of neural precursor cell
proliferation;positive regulation of neurogenesis;positive regulation of neuron apoptosis;positive regulation of neuron differentiation;positive regulation of neuron projection development;positive regulation of nitrogen compound metabolic
process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of oligodendrocyte progenitor proliferation;positive regulation of organelle organization;positive regulation of peptidase activity;positive
regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase
activity;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphorus metabolic process;positive regulation of
phosphorylation;positive regulation of podosome assembly;positive regulation of programmed cell death;positive regulation of protein binding;positive regulation of protein complex assembly;positive regulation of protein import into
nucleus, translocation;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein modification process;positive
regulation of protein phosphorylation;positive regulation of protein polymerization;positive regulation of protein secretion;positive regulation of protein serine/threonine kinase activity;positive regulation of protein targeting to
membrane;positive regulation of protein transport;positive regulation of protein ubiquitination;positive regulation of proteolysis;positive regulation of reproductive process;positive regulation of response to stimulus;positive regulation of
RNA metabolic process;positive regulation of secretion;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smooth muscle contraction;positive regulation of stress-activated protein kinase
signaling cascade;positive regulation of T cell activation;positive regulation of T cell differentiation;positive regulation of T cell receptor signaling pathway;positive regulation of transcription from RNA polymerase II promoter;positive
regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of translation;positive regulation of transport;positive regulation of tyrosine phosphorylation of STAT protein;positive regulation of
tyrosine phosphorylation of Stat5 protein;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;positive regulation of uterine smooth muscle
contraction;positive regulation of viral reproduction;positive regulation of viral transcription;positive regulation of Wnt receptor signaling pathway;post-embryonic development;posttranscriptional regulation of gene expression;potassium
ion transport;primary metabolic process;progesterone receptor signaling pathway;programmed cell death;pronuclear fusion;prophase;prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis;prostate
epithelial cord elongation;prostate gland epithelium morphogenesis;prostate gland growth;prostate gland morphogenetic growth;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein
autophosphorylation;protein complex assembly;protein complex subunit organization;protein localization;protein localization in membrane;protein localization to chromosome;protein localization to kinetochore;protein localization to
organelle;protein localization to synapse;protein metabolic process;protein modification process;protein phosphorylation;protein secretion;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;pyramidal
neuron development;Ras protein signal transduction;receptor catabolic process;receptor clustering;receptor metabolic process;re-entry into mitotic cell cycle;regeneration;regulated secretory pathway;regulation of actin cytoskeleton
organization;regulation of actin cytoskeleton reorganization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or
depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of anoikis;regulation of antigen receptor-mediated signaling pathway;regulation of apoptosis;regulation of B cell
activation;regulation of B cell apoptosis;regulation of B cell proliferation;regulation of B cell receptor signaling pathway;regulation of behavior;regulation of bile acid biosynthetic process;regulation of binding;regulation of biological
process;regulation of biological quality;regulation of biosynthetic process;regulation of blood coagulation;regulation of body fluid levels;regulation of bone remodeling;regulation of bone resorption;regulation of branching involved in
prostate gland morphogenesis;regulation of branching involved in salivary gland morphogenesis;regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling;regulation of calcium ion
transport;regulation of calcium ion transport into cytosol;regulation of calcium ion-dependent exocytosis;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac muscle cell proliferation;regulation of cardiac muscle
tissue development;regulation of cardiac muscle tissue growth;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation
of cell aging;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell
division;regulation of cell fate commi" "acetylcholine receptor activator activity;acetylcholine receptor regulator activity;adenyl nucleotide binding;adenyl ribonucleotide binding;antigen binding;ATP binding;binding;binding,
bridging;carbohydrate binding;catalytic activity;cation binding;cyclin binding;cyclin-dependent protein kinase activity;DNA binding;enzyme binding;ErbB-2 class receptor binding;ErbB-3 class receptor binding;Fc-gamma receptor I
complex binding;fibroblast growth factor binding;fibroblast growth factor-activated receptor activity;glycolipid binding;glycosaminoglycan binding;glycosphingolipid binding;growth factor binding;heme binding;heparin binding;histone
kinase activity;hydrolase activity;hydrolase activity, acting on ester bonds;immunoglobulin receptor binding;integrin binding;ion binding;iron ion binding;kinase activity;kinase binding;lipid binding;magnesium ion binding;metal ion
binding;molecular transducer activity;non-membrane spanning protein tyrosine kinase activity;nucleic acid binding;nucleotide binding;pattern binding;phosphatase activity;phosphoprotein binding;phosphoprotein phosphatase
activity;phosphoric ester hydrolase activity;phosphotransferase activity, alcohol group as acceptor;phosphotyrosine binding;polysaccharide binding;protein binding;protein binding transcription factor activity;protein binding,
bridging;protein complex binding;protein domain specific binding;protein kinase activity;protein kinase binding;protein phosphorylated amino acid binding;protein serine/threonine kinase activity;protein serine/threonine phosphatase
activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activator activity;receptor activity;receptor binding;receptor regulator activity;receptor
signaling protein activity;receptor signaling protein tyrosine kinase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA binding;RNA polymerase II carboxy-terminal domain kinase
activity;SH2 domain binding;SH3/SH2 adaptor activity;signal transducer activity;signaling adaptor activity;signaling receptor activity;snRNA binding;sphingolipid binding;tau-protein kinase activity;tetrapyrrole binding;transcription
coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing
groups;transition metal ion binding;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity"   +   "actin cytoskeleton;adherens junction;alpha2-
beta1 integrin complex;anchoring junction;axon;Cajal body;carboxy-terminal domain protein kinase complex;caveola;cell body;cell cortex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell surface;cell-
cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;chromatin;chromosomal part;chromosome;chromosome, telomeric region;cilium;condensed chromosome;cyclin-dependent protein kinase 5 holoenzyme
complex;cyclin-dependent protein kinase holoenzyme complex;cytoplasm;cytoplasmic cyclin-dependent protein kinase holoenzyme complex;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal
part;cytoskeleton;cytosol;endocytic vesicle;endoplasmic reticulum;endosome;excitatory synapse;extracellular region;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;filopodium;focal
adhesion;Golgi apparatus;growth cone;immunological synapse;integral to membrane;integral to plasma membrane;integrin complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular
organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium;late endosome;leading edge membrane;lysosome;lytic vacuole;macromolecular complex;membrane;membrane
part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microtubule;microtubule organizing center;microtubule organizing center part;midbody;mitochondrial crista;mitochondrial inner
membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrion;mitotic spindle;neuromuscular junction;neuron projection;neuronal cell body;non-membrane-
bounded organelle;nonmotile primary cilium;nuclear body;nuclear cyclin-dependent protein kinase holoenzyme complex;nuclear membrane;nuclear part;nuclear speck;nucleolus;nucleoplasm;nucleoplasm part;nucleus;occluding
junction;organelle;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part;pericentriolar material;perikaryon;perinuclear region of cytoplasm;photoreceptor inner segment;photoreceptor outer segment;plasma
membrane;plasma membrane part;PML body;positive transcription elongation factor complex b;postsynaptic density;postsynaptic membrane;primary cilium;protein complex;receptor complex;ruffle;ruffle membrane;sex chromosome;site of
polarized growth;spindle;spindle microtubule;synapse;synapse part;synaptic membrane;tight junction;transcription elongation factor complex;transcription factor complex;transport vesicle;vacuole;vesicle;X chromosome;Y chromosome"
Adherens junction;Alzheimer's disease;Axon guidance;B cell receptor signaling pathway;Bacterial invasion of epithelial cells;Bladder cancer;Cell cycle;Chemokine signaling pathway;Chronic myeloid leukemia;Endocytosis;Epithelial cell
signaling in Helicobacter pylori infection;ErbB signaling pathway;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;ko05152;Long-term depression;MAPK
signaling pathway;Measles;Melanoma;Natural killer cell mediated cytotoxicity;Non-small cell lung cancer;Oocyte meiosis;Osteoclast differentiation;p53 signaling pathway;Pancreatic cancer;Pathogenic Escherichia coli infection;Pathways
in cancer;Primary immunodeficiency;Prion diseases;Progesterone-mediated oocyte maturation;Prostate cancer;Regulation of actin cytoskeleton;Small cell lung cancer;T cell receptor signaling pathway;Tight junction;VEGF signaling
pathway;Viral myocarditis   2.2609E-07   16234000   3
G3V1S6;Q10471;B7Z8V8;Q8N4A0-2;F8VUJ3;Q8N4A0   Polypeptide N-acetylgalactosaminyltransferase 2;Polypeptide N-acetylgalactosaminyltransferase 2 soluble form   GALNT2 >tr|G3V1S6|G3V1S6_HUMAN Polypeptide N-
acetylgalactosaminyltransferase 2 soluble form OS=Homo sapiens GN=GALNT2 PE=2 SV=1;>sp|Q10471|GALT2_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1 1.01 0.94 1.50
1.36 0.60 0.70 1.01 1.43   biosynthetic process;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular
process;cellular protein metabolic process;glycosylation;immunoglobulin biosynthetic process;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic
process;O-glycan processing;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-threonine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic
process;protein modification process;protein O-linked glycosylation;protein O-linked glycosylation via serine;protein O-linked glycosylation via threonine"acetylgalactosaminyltransferase activity;binding;catalytic activity;cation binding;ion
binding;manganese ion binding;metal ion binding;polypeptide N-acetylgalactosaminyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;transition metal
ion binding;UDP-glycosyltransferase activity"   +   cell part;cytoplasmic part;extracellular region;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi stack;integral to Golgi membrane;integral to
membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to Golgi membrane;intrinsic to membrane;intrinsic to organelle
membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm   Mucin type O-Glycan biosynthesis2.8337E-59   15596000   3
Q92896;Q92896-3;Q92896-2;H3BM42Golgi apparatus protein 1   GLG1   >sp|Q92896|GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2;>sp|Q92896-3|GSLG1_HUMAN Isoform 3 of Golgi
apparatus protein 1 OS=Homo sapiens GN=GLG1;>sp|Q92896-2|GSLG1_HUMAN Isoform 2 of Golgi apparatus protein 1 OS=Homo sapiens GN=GL   1.27 1.24 1.72 0.95 1.41 0.61 1.03 0.86
anatomical structure morphogenesis;biological regulation;bone morphogenesis;developmental process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative
regulation of protein processing;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling
pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of biological process;regulation of cartilage development;regulation of cell communication;regulation of cell
differentiation;regulation of cellular process;regulation of chondrocyte differentiation;regulation of developmental process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic
process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein processing;regulation of
response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway
binding;protein binding;receptor binding   +   cell part;cytoplasmic part;extracellular matrix;extracellular region part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to

membrane;membrane;membrane part;organelle membrane;organelle part Cell adhesion molecules (CAMs) 3.0759E-08 7705800 3

K7EMV3;K7EP01;B4DEB1;K7EK07;Q6NXT2;Q71DI3;Q16695;P84243;P68431;K7ES00 Histone H3;Histone H3.3C;Histone H3.2;Histone H3.1t;Histone H3.3;Histone H3.1 H3F3B;H3F3A;H3F3C;HIST2H3A;HIST3H3;HIST1H3A >tr|K7EMV3|K7EMV3_HUMAN Histone H3 OS=Homo sapiens GN=H3F3B PE=3 SV=1;>tr|K7EP01|K7EP01_HUMAN Histone H3.3 OS=Homo sapiens GN=H3F3B PE=4 SV=1;>tr|B4DEB1|B4DEB1_HUMAN Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1;>tr|K7EK07|K7EK07_HUMAN Histone H3 (Fragment 1.20 1.30 1.08 3.96 0.45 0.45 0.38 0.32 anatomical structure homeostasis;biological regulation;blood coagulation;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;coagulation;DNA metabolic process;hemostasis;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;regulation of gene silencing;S phase;telomere maintenance;telomere organization binding;DNA binding;nucleic acid binding + cell part;chromosomal part;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleosome;nucleus;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus 2.8308E-07 704790000 3

Q53GQ0;E9PI21 Estradiol 17-beta-dehydrogenase 12 HSD17B12 >sp|Q53GQ0|DHB12_HUMAN Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 0.63 0.48 0.97 0.24 3.31 1.98 1.54 0.93 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;estrogen biosynthetic process;estrogen metabolic process;extracellular matrix organization;extracellular structure organization;fatty acid biosynthetic process;fatty acid metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;hormone biosynthetic process;hormone metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular process;regulation of hormone levels;small molecule biosynthetic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;thioester biosynthetic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process "binding;carbohydrate binding;catalytic activity;estradiol 17-beta-dehydrogenase activity;glycosaminoglycan binding;heparin binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;pattern binding;polysaccharide binding;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" + cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular matrix;extracellular region part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Biosynthesis of unsaturated fatty acids;Steroid hormone biosynthesis 2.4745E-17 32517000 3

P05161 Ubiquitin-like protein ISG15 ISG15 >sp|P05161|ISG15_HUMAN Ubiquitin-like protein ISG15 OS=Homo sapiens GN=ISG15 PE=1 SV=5 NaN NaN 1.72 2.06 0.65 0.82 NaN NaN biological regulation;catabolic process;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;immune effector process;immune system process;interaction with host;interspecies interaction between organisms;ISG15-protein conjugation;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of type I interferon production;primary metabolic process;protein metabolic process;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cellular process;regulation of cytokine production;regulation of multicellular organismal process;regulation of type I interferon production;reproductive process;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;signal transduction;signaling;type I interferon-mediated signaling pathway;viral reproductive process;virus-host interaction protein tag + cell part;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular part RIG-I-like receptor signaling pathway 1.0632E-14 9605200 3

E7EMF1;E7ESP4;P17301;E9PB77 Integrin alpha-2 ITGA2 >tr|E7EMF1|E7EMF1_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=2 SV=1;>tr|E7ESP4|E7ESP4_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=2 SV=1;>sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1;>tr|E9PB77|E9PB77_HUMAN Integr NaN NaN 1.37 NaN 1.29 NaN NaN NaN + anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular process;cellular response to stimulus;chemotaxis;coagulation;developmental process;hemostasis;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;locomotion;multicellular organismal process;multi-organism process;organ morphogenesis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis;viral reproductive process;virus-host interaction binding;cation binding;collagen binding;ion binding;metal ion binding;protein binding basal part of cell;cell part;cell surface;external side of plasma membrane;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Small cell lung cancer 1.2713E-07 1221800 3

P26006;P26006-1;H0YA49;D6R9X8 Integrin alpha-3;Integrin alpha-3 heavy chain;Integrin alpha-3 light chain ITGA3 >sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5;>sp|P26006-1|ITA3_HUMAN Isoform 2 of Integrin alpha-3 OS=Homo sapiens GN=ITGA3;>tr|H0YA49|H0YA49_HUMAN Integrin alpha-3 (Fragment) OS=Homo sapiens GN=ITGA3 PE=4 SV=1 0.99 0.91 1.27 NaN 0.86 NaN 0.95 0.95 + behavior;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular process;cellular response to stimulus;coagulation;cognition;hemostasis;immune system process;integrin-mediated signaling pathway;learning or memory;leukocyte migration;locomotion;memory;multicellular organismal process;neurological system process;neuron migration;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;response to stimulus;signal transduction;system process binding;cation binding;ion binding;metal ion binding basolateral plasma membrane;cell part;cell surface;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex;synapse Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer 1.3885E-07 7400000 3

P11047 Laminin subunit gamma-1 LAMC1 >sp|P11047|LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=31.89 1.04 1.20 1.22 0.60 0.28 0.69 0.61 + + + anatomical structure development;anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;chemotaxis;developmental process;endoderm development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of epithelial cell proliferation;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of epithelial cell proliferation;response to chemical stimulus;response to external stimulus;response to stimulus;substrate adhesion-dependent cell spreading;taxis;tissue development binding;extracellular matrix structural constituent;glycolipid binding;glycosphingolipid binding;lipid binding;sphingolipid binding;structural molecule activity + extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;laminin complex;laminin-1 complex;laminin-10 complex;laminin-11 complex;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;organelle;protein complex;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Prion diseases;Small cell lung cancer;Toxoplasmosis 1.4275E-08 12986000 3

P49257 Protein ERGIC-53 LMAN1 >sp|P49257|LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2 1.10 0.77 1.45 0.73 1.33 0.98 0.97 0.94 + + biological regulation;blood coagulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;coagulation;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi organization;Golgi vesicle transport;hemostasis;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of organelle organization;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular process;regulation of organelle organization;transport;vesicle-mediated transport binding;carbohydrate binding;cation binding;ion binding;mannose binding;metal ion binding;monosaccharide binding;protein binding;sugar binding;unfolded protein binding cell part;coated vesicle membrane;contractile fiber part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;ER to Golgi transport vesicle membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;sarcomere;transport vesicle membrane;vesicle membrane Protein processing in endoplasmic reticulum 9.5675E-08 18897000 3

O95274 Ly6/PLAUR domain-containing protein 3 LYPD3 >sp|O95274|LYPD3_HUMAN Ly6/PLAUR domain-containing protein 3 OS=Homo sapiens GN=LYPD3 PE=1 SV=2 1.53 0.62 1.33 0.68 2.26 1.51 1.52 0.64 + biological adhesion;cell adhesion;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular process anchored to membrane;anchored to plasma membrane;cell part;integral to membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part 4.1047E-10 20339000 3

F8WE65;C9J5S7;P62937;Q567Q0 Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase A PPIA >tr|F8WE65|F8WE65_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=2 SV=1;>tr|C9J5S7|C9J5S7_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=2 SV=1;>sp|P62937|PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo 0.50 0.73 0.62 1.53 1.32 2.18 0.78 0.83 biological regulation;biosynthetic process;cell activation;cell migration;cell motility;cellular biosynthetic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;DNA metabolic process;DNA replication;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;establishment of localization;establishment of localization in cell;exocytosis;immune system process;interaction with host;interspecies interaction between organisms;leukocyte migration;lipid particle organization;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-proline modification;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cellular process;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of reproductive process;positive regulation of secretion;positive regulation of transport;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;protein folding;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of localization;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of reproductive process;regulation of secretion;regulation of transport;regulation of viral genome replication;regulation of viral reproduction;release of virus from host;reproductive process;RNA-dependent DNA replication;secretion;secretion by cell;transport;uncoating of virus;vesicle-mediated transport;viral reproductive process binding;catalytic activity;cis-trans isomerase activity;isomerase activity;peptide binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;unfolded protein binding;virion binding + cell part;cytoplasmic part;cytosol;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.0083E-16 43401000 3

P13489;E9PMJ3;E9PLZ3;E9PIM9;E9PMA9;E9PMN0;E9PIK5;H0YCR7 Ribonuclease inhibitor RNH1 >sp|P13489|RINI_HUMAN Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2;>tr|E9PMJ3|E9PMJ3_HUMAN Ribonuclease H1 (Fragment) OS=Homo sapiens GN=RNH1 PE=2 SV=1;>tr|E9PLZ3|E9PLZ3_HUMAN Ribonuclease H1 (Fragment) OS=Homo sapiens GN=RNH1 PE=2 SV=1;>tr|E9P 0.90 NaN 1.33 0.33 2.45 2.47 1.49 NaN biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;RNA catabolic process;RNA metabolic process enzyme inhibitor activity;enzyme regulator activity;ribonuclease inhibitor activity + angiogenin-PRI complex;cell part;cytoplasm;extracellular region part;intracellular part;macromolecular complex;protein complex 1.7789E-11 9188000 3

J3KT73;J3QL01;P63173;J3KSP2;M0QYY5;E0CX11;Q9Y2S6;A8MXR1;Q9Y2C4-3;Q9H7B4-2;Q9Y2C4-4;Q9Y2C4;Q9H7B4-3;Q9H7B4;Q15172-2;Q15172;A2A3P3;Q5SZL2;Q5SZL2-4;REV__B8ZZW2 60S ribosomal protein L38

RPL38 >tr|J3KT73|J3KT73_HUMAN 60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=3 SV=1;>tr|J3QL01|J3QL01_HUMAN 60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=3 SV=1;>sp|P63173|RL38_HUMAN 60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2;>tr 1.58 0.71 0.83 0.59 1.60 1.10 1.17 0.75 "anatomical structure morphogenesis;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;cotranslational protein targeting to membrane;covalent chromatin modification;developmental process;embryonic morphogenesis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;histone lysine methylation;histone methylation;histone modification;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;middle ear morphogenesis;mRNA catabolic process;mRNA metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of establishment of protein localization in plasma membrane;negative regulation of kinase activity;negative regulation of lipid kinase activity;negative regulation of lipid metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of transferase activity;neurological system process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;ossification;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of dephosphorylation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;primary metabolic process;protein alkylation;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein methylation;protein modification process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of kinase activity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of transferase activity;reproductive process;response to stimulus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal transduction;small molecule metabolic process;SRP-dependent cotranslational protein targeting to membrane;system process;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" "binding;catalytic activity;cation binding;endonuclease activity;enzyme regulator activity;histone methyltransferase activity;histone-lysine N-methyltransferase activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lysine N-methyltransferase activity;metal ion binding;methyltransferase activity;N-methyltransferase activity;nuclease activity;nucleic acid binding;phosphatase regulator activity;protein methyltransferase activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein-lysine N-methyltransferase activity;RNA binding;S-adenosylmethionine-dependent methyltransferase activity;structural constituent of ribosome;structural molecule activity;transferase activity;transferase activity, transferring one-carbon groups;transition metal ion binding;zinc ion binding" + "cell part;centrosome;chromosomal part;chromosome, centromeric region;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosolic large ribosomal subunit;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;M band;macromolecular complex;membrane;membrane-bounded organelle;microtubule organizing center;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex;ribonucleoprotein complex;ribosome;Z disc" Apoptosis;Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;Ribosome;Wnt signaling pathway 2.1982E-08 22265000 3

P18827;E9PHH3;H7C1K4 Syndecan-1 SDC1 >sp|P18827|SDC1_HUMAN Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3 1.66 1.02 1.37 0.85 1.13 0.62 1.30 1.02 + + "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;canonical Wnt receptor signaling pathway;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell development;cell surface receptor linked signaling pathway;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;developmental process involved in reproduction;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;lipoprotein metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;muscle cell development;myoblast development;nitrogen compound metabolic process;odontogenesis;organ morphogenesis;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to abiotic stimulus;response to calcium ion;response to cAMP;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to light stimulus;response to metal ion;response to organic substance;response to oxidative stress;response to radiation;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;response to toxin;response to wounding;retinoid metabolic process;Sertoli cell development;signal transduction;striated muscle cell development;sulfur compound metabolic process;terpenoid metabolic process;tube development;ureteric bud development;Wnt receptor signaling pathway;wound healing" + adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;external side of plasma membrane;extracellular region;focal adhesion;Golgi apparatus part;Golgi lumen;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane part;protein complex;vacuolar lumen;vacuolar part Cell adhesion molecules (CAMs);ECM-receptor interaction;Malaria 1.6782E-16 18923000 3

O76094-2;O76094;P15514;D6RFX5;D6RDY6;REV__A6NIV6 Signal recognition particle subunit SRP72 SRP72 >sp|O76094-2|SRP72_HUMAN Isoform 2 of Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72;>sp|O76094|SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3 NaN NaN 0.54 NaN 1.53 NaN NaN NaN biological regulation;biosynthetic process;cell communication;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cotranslational protein targeting to membrane;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;G-protein coupled receptor protein signaling pathway;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to chemical stimulus;response to drug;response to stimulus;signal transduction;signaling;SRP-dependent cotranslational protein targeting to membrane;translation;transmembrane receptor protein tyrosine kinase signaling pathway;transport 7S RNA binding;binding;growth factor activity;nucleic acid binding;protein binding;receptor binding;ribonucleoprotein binding;RNA binding;signal recognition particle binding + "cell part;cell surface;cytoplasmic part;cytosol;endoplasmic reticulum;extracellular region part;extracellular space;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;ribonucleoprotein complex;signal recognition particle;signal recognition particle, endoplasmic reticulum targeting" ErbB signaling pathway;Protein export 6.6258E-08 1864500 3

P02786;G3V0E5;F8WBE5;F5H6B1 "Transferrin receptor protein 1;Transferrin receptor protein 1, serum form" TFRC ">sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2;>tr|G3V0E5|G3V0E5_HUMAN Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=2 SV=1" NaN NaN 0.48 NaN 1.16 NaN NaN NaN biological regulation;cation homeostasis;cation transport;cell differentiation;cellular cation homeostasis;cellular chemical homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;chemical homeostasis;developmental process;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;leukocyte differentiation;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;multi-organism process;myeloid cell differentiation;myeloid leukocyte differentiation;osteoclast differentiation;positive regulation of biological process;positive regulation of bone remodeling;positive regulation of bone resorption;positive regulation of homeostatic process;positive regulation of multicellular organismal process;positive regulation of tissue remodeling;primary metabolic process;protein metabolic process;protein transport;proteolysis;regulation of biological process;regulation of biological quality;regulation of bone remodeling;regulation of bone resorption;regulation of homeostatic process;regulation of multicellular organismal process;regulation of tissue remodeling;reproductive process;transferrin transport;transition metal ion transport;transmembrane transport;transport;viral reproductive process;virus-host interaction cargo receptor activity;catalytic activity;hydrolase activity;peptidase activity;receptor activity;transferrin receptor activity + cell part;coated pit;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endosome;external side of plasma membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region;extracellular region part;extracellular vesicular exosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;perinuclear region of cytoplasm;pigment granule;plasma membrane part;vesicle Endocytosis;Hematopoietic cell lineage;Phagosome 1.0744E-07 3022100 3

Q9UHI8 A disintegrin and metalloproteinase with thrombospondin motifs 1 ADAMTS1 >sp|Q9UHI8|ATS1_HUMAN A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Homo sapiens GN=ADAMTS1 PE=1 SV=4 2.02 1.29 0.84 NaN 0.63 NaN 0.84 2.19 + + anatomical structure development;anatomical structure formation involved in morphogenesis;biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;developmental process;heart trabecula formation;integrin-mediated signaling pathway;kidney development;macromolecule metabolic process;metabolic process;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;organ development;ovulation;ovulation cycle process;ovulation from ovarian follicle;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of cell proliferation;regulation of cellular process;reproductive process;response to stimulus;rhythmic process;signal transduction;trabecula formation "binding;carbohydrate binding;catalytic activity;cation binding;endopeptidase activity;glycosaminoglycan binding;heparin binding;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;pattern binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;polysaccharide binding;transition metal ion binding;zinc ion binding" + basement membrane;cell part;cytoplasmic part;cytoplasmic vesicle;extracellular matrix part;extracellular region part;intracellular organelle;intracellular part;organelle;vesicle 1.0242E-13 7293900 4

Q9Y3I0;E7EQS9 tRNA-splicing ligase RtcB homolog C22orf28 >sp|Q9Y3I0|RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=C22orf28 PE=1 SV=1;>tr|E7EQS9|E7EQS9_HUMAN Protein RTCB OS=Homo sapiens GN=RTCB PE=2 SV=2 0.90 0.92 0.59 1.11 1.33 1.43 0.99 0.92 + "anatomical structure development;anatomical structure morphogenesis;biological adhesion;cell adhesion;cell morphogenesis;cell morphogenesis involved in differentiation;cell-matrix adhesion;cell-substrate adhesion;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;in utero embryonic development;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;placenta development;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via endonucleolytic cleavage and ligation;substrate adhesion-dependent cell spreading;tRNA metabolic process;tRNA processing;tRNA splicing, via endonucleolytic cleavage and ligation""adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming phosphoric ester bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA ligase (ATP) activity;RNA ligase activity" cell part;cytoplasm;intracellular part;macromolecular complex;protein complex;tRNA-splicing ligase complex 6.787E-26 22767000 4

J3KTE9;P22223;P22223-2;J3QR60 Cadherin-3 CDH3 >tr|J3KTE9|J3KTE9_HUMAN Cadherin-3 OS=Homo sapiens GN=CDH3 PE=3 SV=1;>sp|P22223|CADH3_HUMAN Cadherin-3 OS=Homo sapiens GN=CDH3 PE=1 SV=2;>sp|P22223-2|CADH3_HUMAN Isoform 2 of Cadherin-3 OS=Homo sapiens GN=CDH3 0.90 1.24 1.23 1.84 0.39 0.18 0.74 1.03 + adherens junction organization;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion;multicellular organismal process;neurological system process;response to stimulus;sensory perception;sensory perception of light stimulus;system process;visual perception binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Cell adhesion molecules (CAMs) 4.7943E-16 21215000 4

P39060-2;H7BXV5;P39060-1;P39060;H7C457 Collagen alpha-1(XVIII) chain;Endostatin COL18A1 >sp|P39060-2|COIA1_HUMAN Isoform 3 of Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1;>tr|H7BXV5|H7BXV5_HUMAN Endostatin (Fragment) OS=Homo sapiens GN=COL18A1 PE=2 SV=1;>sp|P39060-1|COIA1_HUMAN Isoform 2 of Collagen alpha-1(XVIII) chain OS=Homo sa NaN NaN 1.84 NaN 0.23 NaN NaN NaN + + + anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological adhesion;biological regulation;cell adhesion;cell morphogenesis;cell morphogenesis involved in differentiation;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;collagen catabolic process;collagen metabolic process;developmental process;endothelial cell morphogenesis;epithelial cell morphogenesis;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;neurological system process;organ morphogenesis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;positive regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of locomotion;regulation of programmed cell death;sensory perception;sensory perception of light stimulus;system process;visual perception binding;cation binding;ion binding;metal ion binding;structural molecule activity + basement membrane;cell part;collagen;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix;extracellular matrix part;extracellular region part;extracellular space;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Protein digestion and absorption 2.5618E-06 1682500 4

P26232-3;P26232-2;P26232-5;P26232;C9IZ88;C9J144 Catenin alpha-2 CTNNA2>sp|P26232-3|CTNA2_HUMAN Isoform 3 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232-2|CTNA2_HUMAN Isoform 2 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232-5|CTNA2_HUMAN Isoform 5 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232|CTNA2 NaN NaN 1.14 NaN 0.52 NaN NaN NaN + anatomical structure morphogenesis;axonogenesis;biological adhesion;biological regulation;brain morphogenesis;cell adhesion;cell differentiation;cell migration;cell migration in hindbrain;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;dendrite morphogenesis;developmental process;hindbrain radial glia guided cell migration;locomotion;muscle cell differentiation;negative regulation of biological process;negative regulation of response to external stimulus;negative regulation of response to stimulus;neuron projection morphogenesis;organ morphogenesis;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle cell differentiation;prepulse inhibition;radial glia guided migration of Purkinje cell;regulation of biological process;regulation of cell differentiation;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of muscle cell differentiation;regulation of response to external stimulus;regulation of response to stimulus;regulation of synapse organization;regulation of synapse structural plasticity structural constituent of cytoskeleton;structural molecule activity actin cytoskeleton;adherens junction;anchoring junction;axon;basolateral plasma membrane;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane part;neuron projection;non-membrane-bounded organelle;organelle;plasma membrane part Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Endometrial cancer;Leukocyte transendothelial migration;Pathways in cancer;Tight junction 3.6931E-22 3627100 4

O00622 Protein CYR61 CYR61 >sp|O00622|CYR61_HUMAN Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1 1.45 0.55 0.66 0.63 1.57 0.75 0.75 1.41 + + + "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;apoptosis;apoptosis involved in heart morphogenesis;apoptosis involved in morphogenesis;atrial septum morphogenesis;atrioventricular valve morphogenesis;biological adhesion;biological regulation;blood vessel development;cardiac septum development;cardiac septum morphogenesis;cell adhesion;cell death;cell differentiation;cell migration;cell motility;cell proliferation;cell-cell adhesion;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular metabolic process;cellular process;chemotaxis;chondroblast differentiation;chorio-allantoic fusion;death;developmental process;developmental programmed cell death;embryonic organ development;extracellular matrix organization;extracellular structure organization;heart valve morphogenesis;intussusceptive angiogenesis;labyrinthine layer blood vessel development;locomotion;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organ development;osteoblast differentiation;placenta blood vessel development;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of BMP signaling pathway;positive regulation of cartilage development;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of ceramide biosynthetic process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of lipase activity;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of osteoblast differentiation;positive regulation of osteoblast proliferation;positive regulation of peptidase activity;positive regulation of phospholipase activity;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of sphingolipid biosynthetic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;programmed cell death;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of BMP signaling pathway;regulation of cartilage development;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cell-substrate adhesion;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ceramide biosynthetic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of ERK1 and ERK2 cascade;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of lipase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoblast proliferation;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of sphingolipid biosynthetic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to chemical stimulus;response to external stimulus;response to stimulus;taxis;ventricular septum development;wound healing, spreading of cells" binding;carbohydrate binding;extracellular matrix binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding + extracellular region 1.0565E-39 103870000 4

P69905 Hemoglobin subunit alpha HBA1 >sp|P69905|HBA_HUMAN Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2 NaN NaN NaN NaN NaN NaN NaN NaN anion transport;bicarbonate transport;biological regulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;establishment of localization;gas transport;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;inorganic anion transport;ion transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;organic anion transport;oxygen transport;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;reactive oxygen species metabolic process;regulation of biological process;regulation of cell death;regulation of cellular process;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;small molecule metabolic process;transport binding;cation binding;heme binding;ion binding;iron ion binding;metal ion binding;oxygen binding;oxygen transporter activity;substrate-specific transporter activity;tetrapyrrole binding;transition metal ion binding;transporter activity + cell part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytosolic part;cytosolic small ribosomal subunit;endocytic vesicle lumen;extracellular region;haptoglobin-hemoglobin complex;hemoglobin complex;intracellular organelle part;intracellular part;macromolecular complex;membrane-enclosed lumen;organelle lumen;organelle part;protein complex;ribonucleoprotein complex;small ribosomal subunit;vesicle lumen African trypanosomiasis;Malaria 9.9504E-13 7016900 4

P01130-2;P01130-3;P01130-6;P01130-4;P01130-5;P01130;J3KMZ9;H0YM92;H0YMD1;H0YMQ3 Low-density lipoprotein receptor LDLR >sp|P01130-2|LDLR_HUMAN Isoform 2 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR;>sp|P01130-3|LDLR_HUMAN Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR;>sp|P01130-6|LDLR_HUMAN Isoform 6 of Low-density lipoprotein recepto 1.39 1.04 0.96 0.86 5.09 1.19 0.97 1.41 "alcohol metabolic process;biological regulation;catabolic process;cellular catabolic process;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chemical homeostasis;cholesterol homeostasis;cholesterol import;cholesterol metabolic process;cholesterol transport;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;digestive system process;diterpenoid metabolic process;establishment of localization;homeostatic process;interaction with host;interspecies interaction between organisms;intestinal absorption;intestinal cholesterol absorption;isoprenoid metabolic process;lipid homeostasis;lipid metabolic process;lipid transport;lipoprotein catabolic process;lipoprotein metabolic process;low-density lipoprotein particle clearance;macromolecule catabolic process;macromolecule metabolic process;metabolic process;multicellular organismal process;multi-organism process;organic substance transport;phospholipid transport;phototransduction;phototransduction, visible light;plasma lipoprotein particle clearance;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of triglyceride biosynthetic process;positive regulation of triglyceride metabolic process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catabolic process;regulation of cellular amine metabolic process;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of lipid biosynthetic process;regulation of lipid catabolic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of phosphatidylcholine catabolic process;regulation of phospholipid catabolic process;regulation of primary metabolic process;regulation of triglyceride biosynthetic process;regulation of triglyceride metabolic process;reproductive process;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;small molecule metabolic process;steroid metabolic process;sterol homeostasis;sterol import;sterol metabolic process;sterol transmembrane transport;sterol transport;system process;terpenoid metabolic process;transmembrane transport;transport;viral reproductive process;virus-host interaction" binding;calcium ion binding;cargo receptor activity;cation binding;ion binding;lipoprotein particle binding;lipoprotein particle receptor activity;low-density lipoprotein particle binding;low-density lipoprotein receptor activity;metal ion binding;protein-lipid complex binding;receptor activity;very-low-density lipoprotein particle binding;very-low-density lipoprotein particle receptor activity + cell part;clathrin coated vesicle membrane;clathrin-coated endocytic vesicle membrane;coated pit;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;external side of plasma membrane;extracellular region part;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome;low-density lipoprotein particle;lysosome;lytic vacuole;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma lipoprotein particle;plasma membrane part;protein-lipid complex;vacuole;vesicle membrane Bile secretion;Endocytosis;Hepatitis C;Toxoplasmosis 1.1586E-28 14245000 4

Q15646;Q15646-2;Q15646-3;H0YGP3;H0YHL3;H0YI20;F8VXY3;P00973-2;P00973-4;P00973;P00973-3;Q9Y6K5 2-5-oligoadenylate synthase-like protein OASL >sp|Q15646|OASL_HUMAN 2-5-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL PE=1 SV=2;>sp|Q15646-2|OASL_HUMAN Isoform p30 of 2-5-oligoadenylate synthase-like protein OS=Homo sapiens GN=OASL;>sp|Q15646-3|OASL_HUMAN Isoform 3 of 2-5-oligoade NaN NaN 1.20 0.35 4.08 3.02 NaN NaN biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-alpha;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;heterocycle biosynthetic process;heterocycle metabolic process;immune effector process;immune response;immune system process;interferon-gamma-mediated signaling pathway;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multi-organism process;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular process;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of reproductive process;regulation of ribonuclease activity;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-alpha;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;signal transduction;small molecule metabolic process;type I interferon-mediated signaling pathway "2'-5'-oligoadenylate synthetase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;adenylyltransferase activity;ATP binding;binding;catalytic activity;cation binding;DNA binding;double-stranded RNA binding;hormone receptor binding;ion binding;metal ion binding;nuclear hormone receptor binding;nucleic acid binding;nucleotide binding;nucleotidyltransferase activity;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;RNA binding;thyroid hormone receptor binding;transcription factor binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;zinc ion binding" + cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part Hepatitis C;Measles 2.9575E-17 4830200 4

Q15063-4;Q15063-2;Q15063-3;B1ALD9;B1ALD8;Q15063;F5H628;CON__Q2KJC7 Periostin POSTN >sp|Q15063-4|POSTN_HUMAN Isoform 4 of Periostin OS=Homo sapiens GN=POSTN;>sp|Q15063-2|POSTN_HUMAN Isoform 2 of Periostin OS=Homo sapiens GN=POSTN;>sp|Q15063-3|POSTN_HUMAN Isoform 3 of Periostin OS=Homo sapiens GN=POSTN;>tr|B1ALD9|B1ALD9_HUMAN Periostin OS= NaN 1.27 NaN NaN NaN NaN NaN 3.50 + + + anatomical structure development;biological adhesion;biological regulation;cell adhesion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;extracellular matrix organization;extracellular structure organization;regulation of biological process;regulation of cellular process;regulation of Notch signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;skeletal system development;system development;tissue development binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding + cell part;cytoplasmic part;extracellular matrix;extracellular region part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle;proteinaceous extracellular matrix 1.1257E-11 2821500 4

F5H157;Q15286 Ras-related protein Rab-35 RAB35 >tr|F5H157|F5H157_HUMAN Ras-related protein Rab-35 (Fragment) OS=Homo sapiens GN=RAB35 PE=2 SV=1;>sp|Q15286|RAB35_HUMAN Ras-related protein Rab-35 OS=Homo sapiens GN=RAB35 PE=1 SV=1 NaN 1.28 1.19 NaN 0.77 NaN NaN 0.78 biological regulation;cellular process;cellular response to stimulus;cytokinesis;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular signal transduction;intracellular transport;localization;macromolecule localization;protein localization;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;nucleoside-triphosphatase activity;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" + cell part;cell projection membrane;cell projection part;clathrin-coated endocytic vesicle;clathrin-coated vesicle;coated pit;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;endosome;extracellular region part;intercellular bridge;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;pigment granule;plasma membrane part;vesicle 5.199E-36 15338000 4

P06702 Protein S100-A9 S100A9 >sp|P06702|S10A9_HUMAN Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1 0.23 0.32 0.03 0.16 6.38 4.11 1.69 1.61 + + + "actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;activation of caspase activity;autophagy;biological adhesion;biological regulation;catabolic process;cell adhesion;cell chemotaxis;cell communication;cell migration;cell motility;cell-cell adhesion;cell-cell signaling;cellular catabolic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemokine production;chemotaxis;chronic inflammatory response;cytokine production;cytoskeleton organization;defense response;defense response to bacterium;defense response to fungus;homotypic cell-cell adhesion;immune response;immune system process;induction of apoptosis;induction of programmed cell death;inflammatory response;innate immune response;leukocyte aggregation;leukocyte cell-cell adhesion;leukocyte chemotaxis;leukocyte migration;leukocyte migration involved in inflammatory response;locomotion;maintenance of location;metabolic process;multicellular organismal process;multi-organism process;neutrophil aggregation;neutrophil chemotaxis;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular process;positive regulation of defense response;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of inflammatory response;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytoskeleton organization;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of inflammatory response;regulation of integrin biosynthetic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to ethanol;response to external stimulus;response to fungus;response to inorganic substance;response to lipopolysaccharide;response to metal ion;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;response to wounding;response to zinc ion;sequestering of metal ion;sequestering of zinc ion;signaling;taxis" antioxidant activity;arachidonic acid binding;binding;calcium ion binding;carboxylic acid binding;cation binding;cytoskeletal protein binding;fatty acid binding;icosanoid binding;icosatetraenoic acid binding;ion binding;lipid binding;metal ion binding;microtubule binding;molecular transducer activity;monocarboxylic acid binding;protein binding;RAGE receptor binding;receptor binding;signal transducer activity;Toll-like receptor 4 binding;Toll-like receptor binding;transition metal ion binding;tubulin binding;zinc ion binding + cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;plasma membrane 2.7157E-115 119250000 4

Q14108;Q14108-2;D6RDG0 Lysosome membrane protein 2 SCARB2 >sp|Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2;>sp|Q14108-2|SCRB2_HUMAN Isoform 2 of Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 NaN NaN 1.61 NaN 1.30 NaN NaN NaN + biological adhesion;cell adhesion;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;intracellular protein transport;intracellular transport;lysosomal transport;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;transport;vacuolar transport receptor activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;lysosomal membrane;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part;plasma membrane part;vacuolar lumen;vacuolar membrane;vacuolar part;vacuole Lysosome 1.4571E-09 4456600 4

P50454;E9PQ34;E9PJH8;E9PIG2;E9PRS3;E9PKH2;E9PNX1;E9PK86;E9PMI5;E9PR70;E9PPV6;H0YEP8;E9PLA6 Serpin H1 SERPINH1 >sp|P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2;>tr|E9PQ34|E9PQ34_HUMAN Serpin H1 (Fragment) OS=Homo sapiens GN=SERPINH1 PE=2 SV=1;>tr|E9PJH8|E9PJH8_HUMAN Serpin H1 (Fragment) OS=Homo sapiens GN=SERPINH1 PE=2 SV=1;>tr|E9PIG2|E9PIG2_H 0.58 0.59 0.92 1.22 0.89 0.58 1.34 1.02 + + biological regulation;biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen biosynthetic process;collagen fibril organization;collagen metabolic process;extracellular matrix organization;extracellular structure organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;primary metabolic process;protein maturation;protein metabolic process;regulation of biological process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein binding;collagen binding;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;protein binding;serine-type endopeptidase inhibitor activity cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part 3.4063E-20 11712000 4

P02649;E9PEV4;E7ERP7;H0Y7L5 Apolipoprotein E APOE >sp|P02649|APOE_HUMAN Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1;>tr|E9PEV4|E9PEV4_HUMAN Apolipoprotein E (Fragment) OS=Homo sapiens GN=APOE PE=2 SV=1;>tr|E7ERP7|E7ERP7_HUMAN Apolipoprotein E (Fragment) OS=Homo sapiens GN=APOE PE=2 SV=1;>tr|H0Y7L5| 0.56 1.14 1.01 0.89 0.49 0.48 1.00 1.33

"acylglycerol metabolic process;aging;alcohol metabolic process;anatomical structure morphogenesis;artery morphogenesis;axon regeneration;axonogenesis;biological regulation;biosynthetic process;blood vessel morphogenesis;calcium ion homeostasis;catabolic process;cation homeostasis;cell communication;cell death;cell differentiation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cell-cell signaling;cellular biosynthetic process;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to cholesterol;cellular response to cytokine stimulus;cellular response to growth factor stimulus;cellular response to interleukin-1;cellular response to lipid;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cGMP-mediated signaling;chemical homeostasis;cholesterol catabolic process;cholesterol efflux;cholesterol homeostasis;cholesterol metabolic process;cholesterol transport;chylomicron remnant clearance;circulatory system process;cyclic-nucleotide-mediated signaling;cytoskeleton organization;death;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;divalent inorganic cation homeostasis;endocytosis;establishment of localization;establishment of localization in cell;glial cell differentiation;glycerol ether metabolic process;glycerolipid metabolic process;G-protein coupled receptor protein signaling pathway;high-density lipoprotein particle assembly;high-density lipoprotein particle clearance;high-density lipoprotein particle remodeling;homeostatic process;induction of apoptosis;induction of programmed cell death;intracellular signal transduction;intracellular transport;ion homeostasis;isoprenoid metabolic process;lipid catabolic process;lipid homeostasis;lipid metabolic process;lipid transport;lipoprotein biosynthetic process;lipoprotein catabolic process;lipoprotein metabolic process;low-density lipoprotein particle remodeling;macromolecular complex assembly;macromolecular complex remodeling;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maintenance of location;maintenance of location in cell;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of blood coagulation;negative regulation of blood vessel endothelial cell migration;negative regulation of catalytic activity;negative regulation of cell activation;negative regulation of cell death;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of cholesterol biosynthetic process;negative regulation of cholesterol metabolic process;negative regulation of coagulation;negative regulation of defense response;negative regulation of endothelial cell migration;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;negative regulation of inflammatory response;negative regulation of kinase activity;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of locomotion;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of neuron apoptosis;negative regulation of platelet activation;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of steroid biosynthetic process;negative regulation of steroid metabolic process;negative regulation of transferase activity;neuron projection morphogenesis;neuron projection regeneration;neutral lipid metabolic process;nitric oxide mediated signal transduction;oligodendrocyte differentiation;organelle organization;organic ether metabolic process;organic substance transport;peripheral nervous system axon regeneration;phospholipid efflux;phospholipid transport;phototransduction;phototransduction, visible light;plasma lipoprotein particle assembly;plasma lipoprotein particle clearance;plasma lipoprotein particle organization;plasma lipoprotein particle remodeling;positive regulation of apoptosis;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular biosynthetic process;positive regulation of cellular catabolic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cGMP biosynthetic process;positive regulation of cGMP metabolic process;positive regulation of cholesterol efflux;positive regulation of cholesterol esterification;positive regulation of cholesterol transport;positive regulation of cyclic nucleotide biosynthetic process;positive regulation of cyclic nucleotide metabolic process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of lipid metabolic process;positive regulation of lipid transport;positive regulation of low-density lipoprotein particle receptor catabolic process;positive regulation of macromolecule metabolic process;positive regulation of membrane protein ectodomain proteolysis;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of monooxygenase activity;positive regulation of neurogenesis;positive regulation of nitric-oxide synthase activity;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleotide biosynthetic process;positive regulation of nucleotide metabolic process;positive regulation of oxidoreductase activity;positive regulation of programmed cell death;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of proteolysis;positive regulation of receptor catabolic process;positive regulation of steroid metabolic process;positive regulation of sterol transport;positive regulation of transport;primary metabolic process;protein-lipid complex assembly;protein-lipid complex remodeling;protein-lipid complex subunit organization;receptor-mediated endocytosis;regeneration;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of apoptosis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood coagulation;regulation of blood vessel endothelial cell migration;regulation of blood vessel size;regulation of catabolic process;regulation of catalytic activity;regulation of Cdc42 protein signal transduction;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cGMP biosynthetic process;regulation of cGMP metabolic process;regulation of cholesterol biosynthetic process;regulation of cholesterol efflux;regulation of cholesterol esterification;regulation of cholesterol metabolic process;regulation of cholesterol transport;regulation of coagulation;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of defense response;regulation of developmental growth;regulation of developmental process;regulation of endothelial cell migration;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of extent of cell growth;regulation of gene expression;regulation of growth;regulation of inflammatory response;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of lipid transport;regulation of localization;regulation of locomotion;regulation of low-density lipoprotein particle receptor catabolic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of membrane protein ectodomain proteolysis;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron apoptosis;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of oxidoreductase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of platelet activation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of proteolysis;regulation of Ras protein signal transduction;regulation of receptor catabolic process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of sterol transport;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of transport;regulation of tube size;regulation of wound healing;response to abiotic stimulus;response to axon injury;response to chemical stimulus;response to cholesterol;response to cytokine stimulus;response to dietary excess;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to hormone stimulus;response to inorganic substance;response to insulin stimulus;response to interleukin-1;response to light stimulus;response to lipid;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to radiation;response to reactive oxygen species;response to retinoic acid;response to stimulus;response to stress;response to vitamin;response to vitamin A;response to wounding;retinoid metabolic process;reverse cholesterol transport;second-messenger-mediated signaling;signal transduction;signaling;small molecule metabolic process;steroid catabolic process;steroid metabolic process;sterol catabolic process;sterol homeostasis;sterol metabolic process;sterol transport;synaptic transmission;synaptic transmission, cholinergic;system process;terpenoid metabolic process;transport;triglyceride metabolic process;triglyceride-rich lipoprotein particle clearance;triglyceride-rich lipoprotein particle remodeling;vascular process in circulatory system;vasodilation;very-low-density lipoprotein particle clearance;very-low-density lipoprotein particle remodeling;vesicle-mediated transport" antioxidant activity;beta-amyloid binding;binding;carbohydrate binding;cation binding;cholesterol transporter activity;enzyme activator activity;enzyme regulator activity;glycosaminoglycan binding;heparin binding;hydroxyapatite binding;identical protein binding;ion binding;lipid binding;lipid transporter activity;lipoprotein particle binding;lipoprotein particle receptor binding;low-density lipoprotein particle receptor binding;metal chelating activity;metal ion binding;pattern binding;phosphatidylcholine-sterol O-acyltransferase activator activity;phospholipid binding;polysaccharide binding;protein binding;protein dimerization activity;protein homodimerization activity;protein-lipid complex binding;receptor binding;sterol transporter activity;substrate-specific transporter activity;transporter activity;very-low-density lipoprotein particle receptor binding   +   cell body;cell part;cell projection;chylomicron;cytoplasmic part;dendrite;early endosome;endosome;extracellular region;extracellular region part;extrinsic to external side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus;high-density lipoprotein particle;intermediate-density lipoprotein particle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;late endosome;low-density lipoprotein particle;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuron projection;neuronal cell body;organelle;plasma lipoprotein particle;plasma membrane;plasma membrane part;protein-lipid complex;triglyceride-rich lipoprotein particle;very-low-density lipoprotein particle   Alzheimer's disease 8.3791E-96   47538000   5

P62158;H0Y7A7;E7ETZ0;E7EMB3;F8WBR5;M0QZ52;G3V479;G3V361;Q96HY3;G3V226   Calmodulin   CALM1;CALM2;CALM3   >sp|P62158|CALM_HUMAN Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2;>tr|H0Y7A7|H0Y7A7_HUMAN Calmodulin (Fragment) OS=Homo sapiens GN=CALM2 PE=2 SV=1;>tr|E7ETZ0|E7ETZ0_HUMAN Calmodulin OS=Homo sapiens GN=CALM1 PE=2 SV=1;>tr|E7EMB3|E7EMB3_HUMAN Calmodulin OS   1.03 1.43 1.14 2.02 0.28 0.43 0.72 1.05   activation of phospholipase C activity;alcohol metabolic process;biological regulation;calcium-mediated signaling;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell activation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization or biogenesis;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;defense response;detection of calcium ion;detection of chemical stimulus;detection of stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;fibroblast growth factor receptor signaling pathway;generation of precursor metabolites and energy;glucan catabolic process;glucan metabolic process;glucose metabolic process;glycogen catabolic process;glycogen metabolic process;G-protein coupled receptor protein signaling pathway;hexose metabolic process;immune response;immune system process;innate immune response;inositol phosphate metabolic process;intracellular signal transduction;macromolecule catabolic process;macromolecule metabolic process;membrane organization;metabolic process;monosaccharide metabolic process;multicellular organismal process;muscle contraction;muscle system process;negative regulation of biological process;negative regulation of ion transmembrane transporter activity;negative regulation of molecular function;negative regulation of ryanodine-sensitive calcium-release channel activity;negative regulation of transport;negative regulation of transporter activity;nerve growth factor receptor signaling pathway;nitric oxide metabolic process;nitrogen compound metabolic process;organophosphate metabolic process;oxidation-reduction process;platelet activation;platelet degranulation;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cyclic nucleotide metabolic process;positive regulation of cyclic-nucleotide phosphodiesterase activity;positive regulation of dephosphorylation;positive regulation of hydrolase activity;positive regulation of ion transmembrane transporter activity;positive regulation of lipase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleotide metabolic process;positive regulation of phosphatase activity;positive regulation of phosphate metabolic process;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphoprotein phosphatase activity;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of ryanodine-sensitive calcium-release channel activity;positive regulation of transport;positive regulation of transporter activity;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of catalytic activity;regulation of cell division;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclic nucleotide metabolic process;regulation of cyclic-nucleotide phosphodiesterase activity;regulation of cytokinesis;regulation of dephosphorylation;regulation of heart contraction;regulation of heart rate;regulation of homeostatic process;regulation of hydrolase activity;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of lipase activity;regulation of lipoprotein lipase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide metabolic process;regulation of oxidoreductase activity;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to stimulus;response to stress;second-messenger-mediated signaling;secretion;secretion by cell;signal transduction;signaling;small molecule metabolic process;synaptic transmission;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport   "binding;calcium ion binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;ion binding;kinase activity;metal ion binding;phosphatase activator activity;phosphatase regulator activity;protein phosphatase activator activity;protein phosphatase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups"   +   cell part;centrosome;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;plasma membrane;protein complex;sarcomere;spindle microtubule;spindle pole   Alzheimer's disease;Calcium signaling pathway;Gastric acid secretion;Glioma;GnRH signaling pathway;Insulin signaling pathway;ko05152;Long-term potentiation;Melanogenesis;Neurotrophin signaling pathway;Olfactory transduction;Oocyte meiosis;Phosphatidylinositol signaling system;Phototransduction;Phototransduction - fly;Plant-pathogen interaction;Salivary secretion;Vascular smooth muscle contraction   5.5519E-108   486790000   5

P52907   F-actin-capping protein subunit alpha-1 CAPZA1 >sp|P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3   0.85 1.24 1.11 2.77 0.54 0.79 0.60 1.00   actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;defense response;hemostasis;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;protein complex assembly;protein complex subunit organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to stimulus;response to stress   actin binding;binding;cytoskeletal protein binding;protein binding   +   cell part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region;F-actin capping protein complex;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex;WASH complex   1.232E-91   98659000
5

H0YD13;P16070-18;P16070-12;P16070-14;P16070-13;P16070-11;P16070-10;P16070-16;P16070-8;P16070-17;P16070-6;P16070-4;P16070-3;P16070-7;E7EPC6;P16070-5;P16070;H0Y2P0;H0YE40;H0YDW7;H0YCV9;P16070-15;H0Y5E4;P16070-9;E9PKC6;Q86UZ1;P16070-19;H0YDX6;H0YD17;J3KN83   CD44 antigen   CD44   >tr|H0YD13|H0YD13_HUMAN CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1;>sp|P16070-18|CD44_HUMAN Isoform 18 of CD44 antigen OS=Homo sapiens GN=CD44;>sp|P16070-12|CD44_HUMAN Isoform 12 of CD44 antigen OS=Homo sapiens GN=CD44;>sp|P16070-14|CD44_HUM   1.00 1.07 1.52 0.89 0.82 0.54 0.94 1.23   +   "amine metabolic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biological adhesion;biological regulation;branching involved in prostate gland morphogenesis;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;carbohydrate catabolic process;carbohydrate metabolic process;cartilage development;catabolic process;cell adhesion;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-matrix adhesion;cell-substrate adhesion;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;developmental process involved in reproduction;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;homotypic cell-cell adhesion;hyaluronan catabolic process;hyaluronan metabolic process;interferon-gamma-mediated signaling pathway;leukocyte aggregation;leukocyte cell-cell adhesion;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monocyte aggregation;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular process;negative regulation of DNA damage response, signal transduction by p53 class mediator;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nitrogen compound metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell-cell adhesion;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ERK1 and ERK2 cascade;positive regulation of gene expression;positive regulation of heterotypic cell-cell adhesion;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of peptidyl-serine phosphorylation;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;prostate gland epithelium morphogenesis;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell-cell adhesion;regulation of cell-cell adhesion involved in gastrulation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of DNA damage response, signal transduction by p53 class mediator;regulation of embryonic development;regulation of endopeptidase activity;regulation of ERK1 and ERK2 cascade;regulation of gastrulation;regulation of gene expression;regulation of heterotypic cell-cell adhesion;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of peptidase activity;regulation of peptidyl-serine phosphorylation;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to interferon-gamma;response to organic substance;response to stimulus;response to stress;response to wounding;signal transduction;small molecule metabolic process;tissue development;tissue morphogenesis;tube morphogenesis;Wnt receptor signaling pathway;wound healing;wound healing involved in inflammatory response"   "binding;carbohydrate binding;catalytic activity;collagen binding;glycosaminoglycan binding;hexosaminidase activity;hyaluronic acid binding;hyaluronoglucosaminidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;pattern binding;polysaccharide binding;protein binding"   basolateral plasma membrane;cell part;cell surface;cytoplasmic part;external side of plasma membrane;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;organelle;plasma membrane;plasma membrane part   ECM-receptor interaction;Hematopoietic cell lineage;Shigellosis 7.5729E-25   56781000   5

P02452;CON__Q862S4 Collagen alpha-1(I) chain COL1A1 >sp|P02452|CO1A1_HUMAN Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5 NaN NaN 1.79 NaN 3.29 NaN NaN NaN + + "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;biomineral tissue development;biosynthetic process;blood vessel development;bone trabecula formation;cartilage development;cartilage development involved in endochondral bone morphogenesis;cell activation;cell communication;cell differentiation;cell migration;cell motility;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to abiotic stimulus;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to growth factor stimulus;cellular response to mechanical stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to organic nitrogen;cellular response to organic substance;cellular response to retinoic acid;cellular response to stimulus;cellular response to transforming growth factor beta stimulus;cellular response to vitamin;cellular response to vitamin A;collagen biosynthetic process;collagen catabolic process;collagen fibril organization;collagen metabolic process;developmental process;embryonic skeletal system development;endochondral ossification;epidermis morphogenesis;establishment of localization;establishment of protein localization;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;face morphogenesis;immune system process;intramembranous ossification;leukocyte migration;localization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular process;neurological system process;ossification;osteoblast differentiation;platelet activation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cell communication;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell morphogenesis involved in differentiation;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of epithelial to mesenchymal transition;positive regulation of gene expression;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription, DNA-dependent;positive regulation of Wnt receptor signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein localization;protein localization to nucleus;protein localization to organelle;protein oligomerization;protein transport;protein trimerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of cell adhesion;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell-substrate adhesion;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of epithelial to mesenchymal transition;regulation of gene expression;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;response to abiotic stimulus;response to acid;response to amine stimulus;response to amino acid stimulus;response to cAMP;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to mechanical stimulus;response to nutrient;response to nutrient levels;response to organic nitrogen;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to reactive oxygen species;response to retinoic acid;response to steroid hormone stimulus;response to stimulus;response to stress;response to transforming growth factor beta stimulus;response to vitamin;response to vitamin A;sensory perception;sensory perception of light stimulus;sensory perception of mechanical stimulus;sensory perception of sound;skeletal system development;skin morphogenesis;system development;system process;tissue development;tissue morphogenesis;tooth mineralization;trabecula formation;transport;visual perception" binding;cation binding;extracellular matrix structural constituent;growth factor binding;identical protein binding;ion binding;metal ion binding;platelet-derived growth factor binding;protein binding;structural molecule activity + cell part;collagen;collagen type I;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;extracellular space;fibrillar collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Amoebiasis;ECM-receptor interaction;Focal adhesion;Protein digestion and absorption 7.8469E-12 9136700 5

Q14195;Q14195-2;H0YBT4;F5GWI3 Dihydropyrimidinase-related protein 3 DPYSL3 >sp|Q14195|DPYL3_HUMAN Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1;>sp|Q14195-2|DPYL3_HUMAN Isoform LCRMP-4 of Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3;>tr|H0YBT4|H0YBT4_HUMAN Dihydropyrimidinase-related NaN NaN NaN 3.59 NaN 0.72 NaN NaN actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;anatomical structure development;axon guidance;biological regulation;catabolic process;cell development;cellular aromatic compound metabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;heterocycle catabolic process;heterocycle metabolic process;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell projection organization;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of locomotion;negative regulation of neuron projection development;neuron development;nitrogen compound metabolic process;nucleobase catabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;organelle organization;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of filopodium assembly;positive regulation of neuron projection development;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;pyrimidine base catabolic process;pyrimidine base metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of filopodium assembly;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;response to axon injury;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to organic substance;response to stimulus;response to stress;response to wounding;small molecule metabolic process;taxis "binding;carbohydrate binding;catalytic activity;chondroitin sulfate binding;glycosaminoglycan binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides;pattern binding;polysaccharide binding;protein binding;protein domain specific binding;SH3 domain binding" + cell body;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region part;extracellular space;filamentous actin;growth cone;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;organelle part;protein complex;site of polarized growth 6.4427E-13 1436400 5

Q14126 Desmoglein-2 DSG2 >sp|Q14126|DSG2_HUMAN Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2 1.48 1.44 1.07 1.87 0.65 0.44 0.67 1.09 + biological adhesion;cell adhesion;cell-cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;desmosome;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Arrhythmogenic right ventricular cardiomyopathy (ARVC) 1.7463E-12 11999000 5

Q504U8;E9PFD7;P00533;P00533-2;P00533-4;P00533-3;C9JYS6;J3KTI5;H3BLT0;J3QLU9;Q15303-4;Q15303-3;Q15303-2;Q15303 Epidermal growth factor receptor EGFR >tr|Q504U8|Q504U8_HUMAN EGFR protein OS=Homo sapiens GN=EGFR PE=2 SV=1;>tr|E9PFD7|E9PFD7_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=2 SV=2;>sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2 1.19 1.08 1.07 1.04 2.25 0.71 0.89 0.90 + "activation of phospholipase A2 activity;activation of phospholipase A2 activity by calcium-mediated signaling;activation of phospholipase C activity;ameboidal cell migration;anatomical structure development;anatomical structure morphogenesis;apoptosis;axon guidance;biological adhesion;biological regulation;biosynthetic process;body fluid secretion;calcium-mediated signaling;cardiac muscle tissue regeneration;cell adhesion;cell death;cell differentiation;cell fate commitment;cell migration;cell morphogenesis;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;central nervous system morphogenesis;cerebral cortex cell migration;chemotaxis;death;defense response;developmental growth;developmental process;digestive tract morphogenesis;embryonic organ development;embryonic pattern specification;embryonic placenta development;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epidermis development;epithelial cell differentiation;establishment of localization;fibroblast growth factor receptor signaling pathway;forebrain cell migration;gland morphogenesis;growth;hair cycle process;hair follicle development;heart development;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;intracellular signal transduction;lactation;localization;localization within membrane;locomotion;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;macromolecule modification;mammary gland alveolus development;mammary gland epithelial cell differentiation;metabolic process;molting cycle;molting cycle process;morphogenesis of an epithelial fold;morphogenesis of an epithelium;multicellular organismal process;multicellular organismal reproductive process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;neural crest cell migration;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;olfactory bulb interneuron differentiation;organ development;ossification;pattern specification process;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cardiac muscle cell proliferation;positive regulation of catalytic activity;positive regulation of catenin import into nucleus;positive regulation of cell communication;positive regulation of cell cycle;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cyclin-dependent protein kinase activity;positive regulation of cyclin-dependent protein kinase activity involved in G1/S;positive regulation of developmental process;positive regulation of DNA metabolic process;positive regulation of DNA repair;positive regulation of DNA replication;positive regulation of epithelial cell proliferation;positive regulation of ERK1 and ERK2 cascade;positive regulation of fibroblast proliferation;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JAK-STAT cascade;positive regulation of kinase activity;positive regulation of lipase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phospholipase A2 activity;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein import into nucleus;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of protein transport;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of STAT protein import into nucleus;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of tyrosine phosphorylation of STAT protein;positive regulation of tyrosine phosphorylation of Stat5 protein;primary metabolic process;programmed cell death;protein autophosphorylation;protein insertion into membrane;protein localization;protein metabolic process;protein modification process;protein phosphorylation;regeneration;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cardiac muscle cell proliferation;regulation of cardiac muscle tissue development;regulation of cardiac muscle tissue growth;regulation of catabolic process;regulation of catalytic activity;regulation of catenin import into nucleus;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cyclin-dependent protein kinase activity;regulation of cyclin-dependent protein kinase activity involved in G1/S;regulation of developmental growth;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA repair;regulation of DNA replication;regulation of epidermal growth factor receptor signaling pathway;regulation of epithelial cell proliferation;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of fibroblast proliferation;regulation of gene expression;regulation of growth;regulation of heart growth;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of lipase activity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organ growth;regulation of oxidoreductase activity;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phospholipase A2 activity;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of STAT protein import into nucleus;regulation of striated muscle tissue development;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmembrane transport;regulation of transport;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat5 protein;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to light stimulus;response to organic substance;response to radiation;response to stimulus;response to stress;response to UV;response to UV-A;RNA biosynthetic process;RNA metabolic process;salivary gland morphogenesis;second-messenger-mediated signaling;secretion;signal transduction;signal transduction via phosphorylation event;taxis;telencephalon cell migration;tissue development;tissue morphogenesis;tissue regeneration;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;transport" "actin binding;actin filament binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cytoskeletal protein binding;DNA binding;double-stranded DNA binding;epidermal growth factor-activated receptor activity;kinase activity;MAP kinase kinase kinase activity;molecular transducer activity;nucleic acid binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein dimerization activity;protein heterodimerization activity;protein kinase activity;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;receptor signaling protein tyrosine kinase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;signal transducer activity;signaling receptor activity;structure-specific DNA binding;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity" + basolateral plasma membrane;cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endocytic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;endosomal part;endosome;endosome membrane;extracellular region;extracellular region part;extracellular space;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nuclear membrane;nuclear part;nucleoplasm;nucleus;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;Shc-EGFR complex;vesicle Adherens junction;Bladder cancer;Calcium signaling pathway;Cytokine-cytokine receptor interaction;Dorso-ventral axis formation;Endocytosis;Endometrial cancer;Epithelial cell signaling in Helicobacter pylori infection;ErbB signaling pathway;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;Hepatitis C;MAPK signaling pathway;MAPK signaling pathway - fly;Melanoma;Non-small cell lung cancer;Pancreatic cancer;Pathways in cancer;Prostate cancer;Regulation of actin cytoskeleton 1.7806E-19 18250000 5

Q14254;J3QLD9;E7EMK3;K7EKW9 Flotillin-2 FLOT2 >sp|Q14254|FLOT2_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2;>tr|J3QLD9|J3QLD9_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=4 SV=1;>tr|E7EMK3|E7EMK3_HUMAN Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=2 SV=1 NaN NaN 1.73 2.10 0.89 1.33 NaN NaN + anatomical structure development;biological adhesion;cell adhesion;cellular process;developmental process;epidermis development;tissue development acrosomal membrane;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endosome;flotillin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;secretory granule membrane;vesicle;vesicle membrane Insulin signaling pathway 7.5634E-15 6950900 5

P09382;F8WEI7 Galectin-1 LGALS1 >sp|P09382|LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 0.62 0.58 1.25 2.02 0.34 0.24 0.62 0.61 + + apoptosis;B cell activation;B cell activation involved in immune response;B cell differentiation;biological regulation;carbohydrate homeostasis;cell activation;cell activation involved in immune response;cell death;cell differentiation;cellular chemical homeostasis;cellular developmental process;cellular glucose homeostasis;cellular homeostasis;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to monosaccharide stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;death;developmental process;glucose homeostasis;homeostatic process;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;leukocyte differentiation;lymphocyte activation;lymphocyte activation involved in immune response;lymphocyte costimulation;lymphocyte differentiation;mature B cell differentiation;mature B cell differentiation involved in immune response;multicellular organismal process;multicellular organismal response to stress;muscle cell differentiation;myoblast differentiation;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell projection organization;negative regulation of cell-substrate adhesion;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of neuron projection development;plasma cell differentiation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell-cell adhesion;positive regulation of cellular process;positive regulation of erythrocyte aggregation;positive regulation of homotypic cell-cell adhesion;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of T cell activation;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell activation;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell-cell adhesion;regulation of cell-substrate adhesion;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of erythrocyte aggregation;regulation of homotypic cell-cell adhesion;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell activation;response to axon injury;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to glucose stimulus;response to hexose stimulus;response to monosaccharide stimulus;response to organic cyclic compound;response to organic substance;response to stimulus;response to stress;response to wounding;T cell costimulation binding;carbohydrate binding;disaccharide binding;galactoside binding;lactose binding;molecular transducer activity;monosaccharide binding;signal transducer activity;sugar binding + cell part;cell surface;cytoplasm;extracellular matrix;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;proteinaceous extracellular matrix 5.0708E-19 180230000 5

P07237;F5H8J2;H7BZ94;I3L398;H0Y3Z3;I3NI03;I3L312;I3L4M2;I3L3P5;I3L3U6 Protein disulfide-isomerase P4HB >sp|P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3;>tr|F5H8J2|F5H8J2_HUMAN Uncharacterized protein OS=Homo sapiens GN=P4HB PE=2 SV=1;>tr|H7BZ94|H7BZ94_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=2 SV=2;>tr 1.05 0.67 0.58 0.80 1.52 1.17 1.87 1.27 4-hydroxyproline metabolic process;amine metabolic process;biological regulation;carboxylic acid metabolic process;cell redox homeostasis;cellular amine metabolic process;cellular amino acid metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;extracellular matrix organization;extracellular structure organization;glycerol ether metabolic process;heterocycle metabolic process;homeostatic process;lipid metabolic process;lipoprotein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid metabolic process;organic ether metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-proline hydroxylation;peptidyl-proline hydroxylation to 4-hydroxy-L-proline;peptidyl-proline modification;primary metabolic process;protein metabolic process;protein modification process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;peptidyl-proline 4-dioxygenase activity;peptidyl-proline dioxygenase activity;procollagen-proline 4-dioxygenase activity;procollagen-proline dioxygenase activity;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" + cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;plasma membrane;vesicle Protein processing in endoplasmic reticulum 6.0178E-23 14157000 5

P60903 Protein S100-A10 S100A10 >sp|P60903|S10AA_HUMAN Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2 0.92 0.70 0.73 0.14 3.22 2.40 1.42 0.52 + + biological regulation;cellular process;cellular response to acid;cellular response to chemical stimulus;cellular response to stimulus;positive regulation of binding;positive regulation of molecular function;regulation of binding;regulation of biological process;regulation of cellular process;regulation of molecular function;response to acid;response to chemical stimulus;response to stimulus;signal transduction binding;calcium ion binding;cation binding;ion binding;metal ion binding;protein binding;receptor binding cell part;extrinsic to membrane;extrinsic to plasma membrane;membrane part;plasma membrane part 2.1983E-15 226880000 5

P31949 Protein S100-A11 S100A11 >sp|P31949|S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 1.03 0.91 0.75 0.14 3.10 3.04 1.39 0.51 + + biological regulation;cellular process;cellular response to stimulus;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to stimulus;signal transduction binding;calcium ion binding;calcium-dependent protein binding;cation binding;identical protein binding;ion binding;metal ion binding;protein binding;protein dimerization activity;protein homodimerization activity cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;ruffle 6.2403E-32 172640000 5

P05109 "Protein S100-A8;Protein S100-A8, N-terminally processed" S100A8 >sp|P05109|S10A8_HUMAN Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1 0.25 0.29 0.03 0.16 5.56 3.81 1.73 1.63 + + + "activation of caspase activity;acute inflammatory response;autophagy;biological adhesion;biological regulation;catabolic process;cell adhesion;cell chemotaxis;cell migration;cell motility;cell-cell adhesion;cellular catabolic process;cellular component movement;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemokine production;chemotaxis;chronic inflammatory response;cytokine production;defense response;defense response to bacterium;defense response to fungus;homotypic cell-cell adhesion;immune response;immune system process;induction of apoptosis;induction of programmed cell death;inflammatory response;innate immune response;leukocyte aggregation;leukocyte cell-cell adhesion;leukocyte chemotaxis;leukocyte migration;leukocyte migration involved in inflammatory response;locomotion;maintenance of location;metabolic process;multicellular organismal process;multi-organism process;neutrophil aggregation;neutrophil chemotaxis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular process;positive regulation of defense response;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of inflammatory response;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytoskeleton organization;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of inflammatory response;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to ethanol;response to external stimulus;response to fungus;response to inorganic substance;response to lipopolysaccharide;response to metal ion;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;response to wounding;response to zinc ion;sequestering of metal ion;sequestering of zinc ion;taxis;wound healing" arachidonic acid binding;binding;calcium ion binding;carboxylic acid binding;cation binding;cytoskeletal protein binding;fatty acid binding;icosanoid binding;icosatetraenoic acid binding;ion binding;lipid binding;metal ion binding;microtubule binding;monocarboxylic acid binding;protein binding;RAGE receptor binding;receptor binding;Toll-like receptor 4 binding;Toll-like receptor binding;transition metal ion binding;tubulin binding;zinc ion binding + cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;extracellular region part;extracellular space;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;non-membrane-bounded organelle;organelle;plasma membrane 2.3737E-13 96280000 5

B0S7Z4;P30508;B0S7Z5;B0S7Z6;Q5SRN7;P30455;P30443;P16188;P13746;P04439;Q29963;Q07000;P30505;P30501;B0UY12;Q5SRN5;P13746-2;B0UY14;B0UY15;B0UXQ1;A2BDY9;A2ARK8;Q29960-2;Q04826;P30480;P30479;P30460;P01889;P01893;Q31612;P30447;P05534;P30512;P30459;P30457;P30456;P30453;P30450;P18462;P16190;P16189;P10314;B0UXQ0;P30510;P30504;P10321;Q9TNN7;Q29960;A2BF24;Q5SPM3;A2AEA2;A2BF25;A2BF26;F5GXA6;A9R9N8;B0V0C2;Q29940;P30685;P30498;P30495;P30493;P30492;P30491;P30490;P30484;P30464;P18465;P18464;P10319;Q09160;P10316;P01892;P01891;Q29865;P04222;B0V0B9;A9R9N7;B0V0C1;F6U0H7;P17693;Q5RJ85;Q95365;Q29836;Q29718;P30488;P30487;P30485;P30483;P30481;P30475;P30466;P30462;P30461;P18463;P03989;P30499;Q31611;Q5SPT7;B1AZU4 "HLA class I histocompatibility antigen, Cw-12 alpha chain;HLA class I histocompatibility antigen, A-36 alpha chain;HLA class I histocompatibility antigen, A-1 alpha chain;HLA class I histocompatibility antigen, A-30 alpha chain;HLA class I histocompatibility antigen, A-11 alpha chain;HLA class I histocompatibility antigen, A-3 alpha chain;HLA class I histocompatibility antigen, Cw-6 alpha chain;HLA class I histocompatibility antigen, Cw-15 alpha chain;HLA class I histocompatibility antigen, Cw-8 alpha chain;HLA class I histocompatibility antigen, Cw-2 alpha chain;HLA class I histocompatibility antigen, B-40 alpha chain;HLA class I histocompatibility antigen, B-42 alpha chain;HLA class I histocompatibility antigen, B-41 alpha chain;HLA class I histocompatibility antigen, B-8 alpha chain;HLA class I histocompatibility antigen, B-7 alpha chain;Putative HLA class I histocompatibility antigen, alpha chain H;HLA class I histocompatibility antigen, B-73 alpha chain;HLA class I histocompatibility antigen, A-23 alpha chain;HLA class I histocompatibility antigen, A-24 alpha chain;HLA class I histocompatibility antigen, A-29 alpha chain;HLA class I histocompatibility antigen, A-74 alpha chain;HLA class I histocompatibility antigen, A-66 alpha chain;HLA class I histocompatibility antigen, A-43 alpha chain;HLA class I histocompatibility antigen, A-34 alpha chain;HLA class I histocompatibility antigen, A-26 alpha chain;HLA class I histocompatibility antigen, A-25 alpha chain;HLA class I histocompatibility antigen, A-33 alpha chain;HLA class I histocompatibility antigen, A-31 alpha chain;HLA class I histocompatibility antigen, A-32 alpha chain;HLA class I histocompatibility antigen, Cw-14 alpha chain;HLA class I histocompatibility antigen, Cw-4 alpha chain;HLA class I histocompatibility antigen, Cw-7 alpha chain;HLA class I histocompatibility antigen, Cw-5 alpha chain;HLA class I histocompatibility antigen, Cw-16 alpha chain;HLA class I histocompatibility antigen, B-59 alpha chain;HLA class I histocompatibility antigen, B-35 alpha chain;HLA class I histocompatibility antigen, B-78 alpha chain;HLA class I histocompatibility antigen, B-56 alpha chain;HLA class I histocompatibility antigen, B-55 alpha chain;HLA class I histocompatibility antigen, B-54 alpha chain;HLA class I histocompatibility antigen, B-53 alpha chain;HLA class I histocompatibility antigen, B-52 alpha chain;HLA class I histocompatibility antigen, B-46 alpha chain;HLA class I histocompatibility antigen, B-15 alpha chain;HLA class I histocompatibility antigen, B-57 alpha chain;HLA class I histocompatibility antigen, B-51 alpha chain;HLA class I histocompatibility antigen, B-58 alpha chain;HLA class I histocompatibility antigen, A-80 alpha chain;HLA class I histocompatibility antigen, A-69 alpha chain;HLA class I histocompatibility antigen, A-2 alpha chain;HLA class I histocompatibility antigen, A-68 alpha chain;HLA class I histocompatibility antigen, Cw-18 alpha chain;HLA class I histocompatibility antigen, Cw-3 alpha chain" HLA-C;HLA-A;HLA-B;HLA-H ">tr|B0S7Z4|B0S7Z4_HUMAN HLA class I histocompatibility antigen, Cw-14 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=1;>sp|P30508|1C12_HUMAN HLA class I histocompatibility antigen, Cw-12 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=2;>tr|B0S7Z5|B0S7Z5_HUMAN" 0.87 1.08 1.45 1.09 0.46 0.49 0.72 0.91 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;cell surface receptor linked signaling pathway;cellular defense response;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;detection of bacterium;detection of biotic stimulus;detection of external stimulus;detection of stimulus;immune response;immune response-inhibiting cell surface receptor signaling pathway;immune response-inhibiting signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cell activation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of mononuclear cell proliferation;negative regulation of T cell activation;negative regulation of T cell proliferation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of developmental process;positive regulation of immune system process;positive regulation of interleukin-12 production;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of multicellular organismal process;positive regulation of regulatory T cell differentiation;positive regulation of T cell activation;positive regulation of T cell differentiation;positive regulation of T cell tolerance induction;positive regulation of tolerance induction;regulation of biological process;regulation of cell activation;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular process;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of developmental process;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of interleukin-12 production;regulation of interleukin-6 production;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte anergy;regulation of lymphocyte differentiation;regulation of lymphocyte proliferation;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of regulatory T cell differentiation;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of T cell activation;regulation of T cell anergy;regulation of T cell differentiation;regulation of T cell proliferation;regulation of T cell tolerance induction;regulation of tolerance induction;reproductive process;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;signal transduction;type I interferon-mediated signaling pathway;viral reproduction;viral reproductive process;virus-host interaction" binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity + cell part;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome membrane;endocytic vesicle membrane;endoplasmic reticulum part;endosomal part;endosome membrane;ER to Golgi transport vesicle membrane;extracellular region;Golgi apparatus part;Golgi membrane;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;MHC class I protein complex;MHC protein complex;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;plasma membrane part;protein complex;transport vesicle membrane;vesicle membrane Allograft rejection;Antigen processing and presentation;Autoimmune thyroid disease;Cell adhesion molecules (CAMs);Endocytosis;Graft-versus-host disease;Natural killer cell mediated cytotoxicity;Phagosome;Type I diabetes mellitus;Viral myocarditis 4.4264E-85 84379000 6

Q08380;K7EKQ5;K7EP36;K7EQT9;K7ES75;K7EN99;K7ERZ6;K7EJY8;K7EJD3 Galectin-3-binding protein LGALS3BP >sp|Q08380|LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 2.18 1.17 1.37 0.97 0.56 0.46 0.82 0.71 + biological adhesion;biological regulation;cell adhesion;cellular defense response;cellular process;cellular response to stimulus;defense response;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;signal transduction cargo receptor activity;receptor activity;scavenger receptor activity + cell part;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;proteinaceous extracellular matrix;vesicle 2.8784E-21 25818000 6

Q99959-2;Q99959 Plakophilin-2 PKP2 >sp|Q99959-2|PKP2_HUMAN Isoform 1 of Plakophilin-2 OS=Homo sapiens GN=PKP2;>sp|Q99959|PKP2_HUMAN Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2 1.76 1.69 1.31 1.83 0.39 0.34 0.41 0.69 + adherens junction maintenance;adherens junction organization;anatomical structure morphogenesis;biological adhesion;biological regulation;cardiac muscle tissue morphogenesis;cell adhesion;cell junction assembly;cell junction maintenance;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component maintenance;cellular component maintenance at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemical homeostasis;cytoskeleton organization;desmosome assembly;developmental process;gap junction assembly;homeostatic process;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;lipid homeostasis;maintenance of organ identity;muscle tissue morphogenesis;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of developmental process;negative regulation of locomotion;organelle organization;positive regulation of biological process;positive regulation of ion transport;positive regulation of sodium ion transport;positive regulation of transport;regulation of biological process;regulation of biological quality;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of ion transport;regulation of localization;regulation of locomotion;regulation of metal ion transport;regulation of sodium ion transport;regulation of tight junction assembly;regulation of transport;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis binding;channel regulator activity;intermediate filament binding;ion channel binding;protein binding;protein complex binding;protein complex scaffold;sodium channel regulator activity;structural molecule activity adherens junction;anchoring junction;cell junction;cell part;cell-cell contact zone;cell-cell junction;cytoskeletal part;desmosome;integral to membrane;intercalated disc;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC) 2.9445E-18 14702000 6

C9J9K3;P08865;A6NE09;C9JQR9 40S ribosomal protein SA RPSA;RPSAP58 >tr|C9J9K3|C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1;>sp|P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4;>tr|A6NE09|A6NE09_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSAP58 PE=2 0.52 2.23 0.17 1.65 0.61 1.75 0.90 1.01 + "biological adhesion;biosynthetic process;catabolic process;cell adhesion;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cleavage involved in rRNA processing;cotranslational protein targeting to membrane;endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage involved in rRNA processing;endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA);establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;establishment of RNA localization;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA 3'-end processing;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;rRNA 3'-end processing;rRNA export from nucleus;rRNA metabolic process;rRNA processing;rRNA transport;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;laminin receptor activity;receptor activity;ribonucleoprotein binding;ribosome binding;structural constituent of ribosome;structural molecule activity 90S preribosome;cell part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;preribosome;ribonucleoprotein complex;small ribosomal subunit Ribosome 4.8244E-62 85371000 6

Q9HCY8 Protein S100-A14 S100A14 >sp|Q9HCY8|S10AE_HUMAN Protein S100-A14 OS=Homo sapiens GN=S100A14 PE=1 SV=1 1.19 1.59 1.69 1.08 1.03 0.79 0.78 0.87 + + activation of immune response;activation of innate immune response;apoptosis;biological regulation;calcium ion homeostasis;cation homeostasis;cell death;cellular process;cellular response to stimulus;chemical homeostasis;death;defense response;defense response to bacterium;divalent inorganic cation homeostasis;homeostatic process;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response-activating signal transduction;ion homeostasis;metal ion homeostasis;multi-organism process;pattern recognition receptor signaling pathway;positive regulation of behavior;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of defense response;positive regulation of granulocyte chemotaxis;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of monocyte chemotaxis;positive regulation of response to external stimulus;positive regulation of response to stimulus;programmed cell death;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of chemotaxis;regulation of defense response;regulation of granulocyte chemotaxis;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of monocyte chemotaxis;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;signal transduction;toll-like receptor 4 signaling pathway;toll-like receptor signaling pathway binding;calcium ion binding;cation binding;chemokine receptor binding;cytokine receptor binding;G-protein-coupled receptor binding;ion binding;metal ion binding;protein binding;receptor binding cell junction;cell part;cytoplasmic part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;plasma membrane 0 561110000 6

Q9UQE7 Structural maintenance of chromosomes protein 3SMC3 >sp|Q9UQE7|SMC3_HUMAN Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 NaN NaN 1.68 NaN 1.05 NaN NaN NaN anaphase;biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;cytokinesis;cytoskeleton organization;developmental process;DNA metabolic process;DNA repair;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;meiosis;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;mitotic spindle organization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA endoreduplication;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA endoreduplication;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to DNA damage stimulus;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle;signal transduction;sister chromatid cohesion;spindle organization;stem cell maintenance "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;chromatin binding;dynein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" + "basement membrane;cell part;chromatin;chromosomal part;chromosome, centromeric region;cohesin complex;cytoplasmic part;cytoskeletal part;cytosol;extracellular matrix part;extracellular region part;intracellular organelle part;intracellular part;lateral element;macromolecular complex;meiotic cohesin complex;nuclear chromosome part;nuclear cohesin complex;nuclear matrix;nuclear meiotic cohesin complex;nuclear part;nucleoplasm;organelle part;protein complex;spindle pole" Cell cycle;Cell cycle - yeast;Meiosis - yeast;Oocyte meiosis 9.9535E-16 2411000 6

P27797;K7EM77;K7EJB9 Calreticulin CALR >sp|P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1 0.75 0.26 0.52 0.27 2.50 1.48 2.26 1.21 "actin cytoskeleton organization;actin filament-based process;activation of signaling protein activity involved in unfolded protein response;aging;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;carbohydrate metabolic process;cardiac cell differentiation;cardiac muscle cell differentiation;cell aging;cell cycle arrest;cell cycle process;cell differentiation;cellular carbohydrate metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to lithium ion;cellular response to metal ion;cellular response to stimulus;cellular response to stress;cellular senescence;cortical actin cytoskeleton organization;cortical cytoskeleton organization;corticosteroid receptor signaling pathway;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;gamete generation;glucocorticoid receptor signaling pathway;glycosylation;immune system process;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule glycosylation;macromolecule localization;macromolecule metabolic process;macromolecule modification;maintenance of location;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;muscle cell differentiation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of retinoic acid receptor signaling pathway;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;nuclear export;nuclear transport;nucleocytoplasmic transport;organelle organization;peptide antigen assembly with MHC class I protein complex;peptide antigen assembly with MHC protein complex;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell cycle;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of dendritic cell chemotaxis;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of endocytosis;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nuclease activity;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phagocytosis;positive regulation of protein kinase activity;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of transferase activity;positive regulation of transport;posttranscriptional regulation of gene expression;post-translational protein modification;primary metabolic process;protein complex assembly;protein complex subunit organization;protein export from nucleus;protein folding;protein glycosylation;protein localization;protein localization to nucleus;protein localization to organelle;protein maturation;protein maturation by protein folding;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein stabilization;protein targeting;protein transport;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of dendritic cell chemotaxis;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of endocytosis;regulation of gene expression;regulation of hydrolase activity;regulation of immune system process;regulation of kinase activity;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of meiosis;regulation of meiotic cell cycle;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of response to external stimulus;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to hormone stimulus;response to inorganic substance;response to lithium ion;response to metal ion;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;sequestering of calcium ion;sequestering of metal ion;signal transduction;spermatogenesis;steroid hormone receptor signaling pathway;striated muscle cell differentiation;transport" androgen receptor binding;binding;calcium ion binding;carbohydrate binding;cation binding;chaperone binding;complement binding;complement component C1q binding;DNA binding;hormone binding;hormone receptor binding;ion binding;iron ion binding;metal ion binding;mRNA binding;nuclear hormone receptor binding;nucleic acid binding;opsonin binding;peptide binding;protein binding;protein binding involved in protein folding;receptor binding;RNA binding;steroid hormone receptor binding;transition metal ion binding;unfolded protein binding;zinc ion binding + acrosomal vesicle;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;external side of plasma membrane;extracellular matrix;extracellular region part;extracellular space;Golgi apparatus;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;MHC class I peptide loading complex;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane part;polysome;protein complex;proteinaceous extracellular matrix;ribonucleoprotein complex;sarcoplasmic reticulum lumen;stored secretory granule;vesicleAntigen processing and presentation;Chagas disease (American trypanosomiasis);Phagosome;Protein processing in endoplasmic reticulum 3.6084E-21 37782000 7

Q76M96;Q76M96-2;H7C5K4 Coiled-coil domain-containing protein 80 CCDC80 >sp|Q76M96|CCD80_HUMAN Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 PE=1 SV=1;>sp|Q76M96-2|CCD80_HUMAN Isoform 2 of Coiled-coil domain-containing protein 80 OS=Homo sapiens GN=CCDC80 NaN NaN 0.85 NaN 14.95 NaN NaN NaN biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular structure organization;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;regulation of biological process;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular process binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding + basement membrane;extracellular matrix;extracellular matrix part;extracellular region part;interstitial matrix;proteinaceous extracellular matrix 5.5892E-19 8829300 7

Q6YHK3-4;Q6YHK3;Q6YHK3-3;Q6YHK3-2;C9JZB3;Q16821CD109 antigen CD109 >sp|Q6YHK3-4|CD109_HUMAN Isoform 4 of CD109 antigen OS=Homo sapiens GN=CD109;>sp|Q6YHK3|CD109_HUMAN CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2;>sp|Q6YHK3-3|CD109_HUMAN Isoform 3 of CD109 antigen OS=Homo sapiens GN=CD109;>sp|Q6YHK3-2|CD109_HUMAN Isofo 1.00 1.17 1.21 1.40 0.67 0.66 0.75 0.81 + + biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan metabolic process;glycogen metabolic process;macromolecule metabolic process;metabolic process;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;oxidation-reduction process;polysaccharide metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activityendopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity + anchored to membrane;cell part;extracellular region part;extracellular space;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Insulin signaling pathway 4.1548E-53 34716000 7

Q08554-2;Q08554 Desmocollin-1DSC1 >sp|Q08554-2|DSC1_HUMAN Isoform 1B of Desmocollin-1 OS=Homo sapiens GN=DSC1;>sp|Q08554|DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2 0.91 1.29 2.38 1.91 1.89 3.45 1.28 1.12 + biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;desmosome;gap junction;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane 6.8962E-21 15855000 7

Q14574-2;Q14574;J3QRL9 Desmocollin-3DSC3 >sp|Q14574-2|DSC3_HUMAN Isoform 3B of Desmocollin-3 OS=Homo sapiens GN=DSC3;>sp|Q14574|DSC3_HUMAN Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3 1.10 1.30 1.16 1.54 0.77 0.43 0.54 0.63 + biological adhesion;biological regulation;cell adhesion;cell-cell adhesion;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;homophilic cell adhesion;in utero embryonic development;posttranscriptional regulation of gene expression;protein stabilization;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability binding;calcium ion binding;cation binding;ion binding;metal ion binding + anchoring junction;cell junction;cell part;cell-cell junction;cytoplasm;desmosome;extracellular region;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;plasma membrane 1.9046E-16 23106000 7

P29317;Q9UF33-2;J3KR66;D6RAL5;Q5JY90;B3KTB2;Q06187;F8W9W0;C9JXA2;Q96L35;B1AKC9;P54756-3;P29320;P54762;P29323-2;P54760;P29323-3;Q15375-2;Q15375-4;Q15375;P54753;F8VP57;P29322;P54756-2;Q9UF33;P54756;P29323 Ephrin type-A receptor 2 EPHA2 >sp|P29317|EPHA2_HUMAN Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2 1.15 1.30 0.95 1.24 0.86 0.68 0.63 0.70 + "activation of immune response;activation of innate immune response;activation of Rac GTPase activity;activation of Ras GTPase activity;activation of Rho GTPase activity;adaptive immune response;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;antigen receptor-mediated signaling pathway;apoptosis;axial mesoderm formation;axon guidance;axonal fasciculation;axonogenesis;B cell activation;B cell receptor signaling pathway;behavior;biological adhesion;biological regulation;biosynthetic process;blood vessel endothelial cell migration;bone remodeling;brain development;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a nerve;branching morphogenesis of a tube;calcium-mediated signaling;camera-type eye morphogenesis;cAMP-mediated signaling;cell activation;cell adhesion;cell chemotaxis;cell communication;cell death;cell development;cell differentiation;cell maturation;cell migration;cell migration involved in sprouting angiogenesis;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell recognition;cell surface receptor linked signaling pathway;cell-substrate adhesion;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;central nervous system neuron axonogenesis;central nervous system projection neuron axonogenesis;chemotaxis;cognition;commissural neuron axon guidance;corpus callosum development;cranial nerve morphogenesis;cyclic-nucleotide-mediated signaling;death;defense response;dendritic spine morphogenesis;dendritic spine organization;detection of abiotic stimulus;detection of external stimulus;detection of stimulus;detection of stimulus involved in sensory perception;detection of temperature stimulus;detection of temperature stimulus involved in sensory perception;detection of temperature stimulus involved in sensory perception of pain;developmental maturation;developmental process;digestive tract morphogenesis;embryonic morphogenesis;endothelial cell migration;enzyme linked receptor protein signaling pathway;ephrin receptor signaling pathway;epidermal cell differentiation;epithelial cell differentiation;epithelial cell proliferation;establishment of cell polarity;establishment or maintenance of cell polarity;eye morphogenesis;fasciculation of motor neuron axon;fasciculation of sensory neuron axon;formation of primary germ layer;heart morphogenesis;hemopoietic or lymphoid organ development;hippocampus development;I-kappaB kinase/NF-kappaB cascade;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;inner ear morphogenesis;intracellular protein kinase cascade;intracellular signal transduction;keratinocyte differentiation;learning;learning or memory;lens fiber cell morphogenesis;leukocyte activation;leukocyte differentiation;locomotion;lymphocyte activation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;mammary gland epithelial cell proliferation;mesoderm development;mesoderm formation;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;MyD88-dependent toll-like receptor signaling pathway;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of intracellular protein kinase cascade;negative regulation of nervous system development;negative regulation of neurogenesis;negative regulation of protein kinase B signaling cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of synapse assembly;neural precursor cell proliferation;neural tube development;neurological system process;neuron differentiation;neuron maturation;neuron projection morphogenesis;neuron recognition;neuron remodeling;nitrogen compound metabolic process;notochord cell development;notochord formation;nucleic acid metabolic process;nucleobase-containing compound metabolic process;optic nerve morphogenesis;organ development;organ morphogenesis;osteoblast differentiation;osteoclast differentiation;palate development;pattern recognition receptor signaling pathway;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of B cell activation;positive regulation of B cell differentiation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component biogenesis;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of CREB transcription factor activity;positive regulation of defense response;positive regulation of developmental process;positive regulation of establishment of protein localization in plasma membrane;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of long-term neuronal synaptic plasticity;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nervous system development;positive regulation of neurogenesis;positive regulation of neuron apoptosis;positive regulation of neuron projection development;positive regulation of NF-kappaB transcription factor activity;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of programmed cell death;positive regulation of Rac GTPase activity;positive regulation of Ras GTPase activity;positive regulation of response to stimulus;positive regulation of Rho GTPase activity;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of synapse assembly;positive regulation of transferase activity;primary metabolic process;programmed cell death;protein autophosphorylation;protein kinase B signaling cascade;protein metabolic process;protein modification process;protein phosphorylation;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of axonogenesis;regulation of B cell activation;regulation of B cell apoptosis;regulation of B cell cytokine production;regulation of B cell differentiation;regulation of B cell mediated immunity;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood vessel endothelial cell migration;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of Cdc42 GTPase activity;regulation of cell activation;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell-cell adhesion;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of cytokine production involved in immune response;regulation of cytoskeleton organization;regulation of defense response;regulation of developmental process;regulation of endopeptidase activity;regulation of endothelial cell migration;regulation of epithelial to mesenchymal transition;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of focal adhesion assembly;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of homeostatic process;regulation of hormone secretion;regulation of hydrolase activity;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of insulin secretion;regulation of insulin secretion involved in cellular response to glucose stimulus;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of lamellipodium assembly;regulation of leukocyte activation;regulation of leukocyte apoptosis;regulation of leukocyte mediated immunity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of long-term neuronal synaptic plasticity;regulation of lymphocyte activation;regulation of lymphocyte apoptosis;regulation of lymphocyte differentiation;regulation of lymphocyte mediated immunity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron apoptosis;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of production of molecular mediator of immune response;regulation of programmed cell death;regulation of protein autophosphorylation;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Rac GTPase activity;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of secretion;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of synapse assembly;regulation of synapse organization;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of transport;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to retinoic acid;response to stimulus;response to stress;response to temperature stimulus;response to vitamin;response to vitamin A;retinal ganglion cell axon guidance;RNA biosynthetic process;RNA metabolic process;second-messenger-mediated signaling;signal transduction;skeletal system development;substrate adhesion-dependent cell spreading;substrate-dependent cell migration;system development;system process;taxis;thymus development;tissue development;tissue morphogenesis;tissue remodeling;toll-like receptor 2 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor signaling pathway;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;tube morphogenesis;urogenital system development;vasculogenesis" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;axon guidance receptor activity;binding;catalytic activity;cation binding;chemorepellent activity;ephrin receptor activity;GPI-linked ephrin receptor activity;ion binding;kinase activity;lipid binding;metal ion binding;molecular transducer activity;non-membrane spanning protein tyrosine kinase activity;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-3,4,5-trisphosphate binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;ribonucleotide binding;signal transducer activity;signaling receptor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity;transmembrane-ephrin receptor activity" + adherens junction;anchoring junction;axon;cell body;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell surface;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic part;cytoplasmic vesicle;cytosol;dendrite;early endosome;early endosome membrane;endoplasmic reticulum;endosomal part;endosome;endosome membrane;external side of plasma membrane;extracellular region;focal adhesion;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium membrane;leading edge membrane;membrane;membrane part;membrane raft;membrane-bounded organelle;neuromuscular junction;neuron projection;neuronal cell body;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;postsynaptic membrane;rough endoplasmic reticulum;ruffle membrane;synapse;synapse part;synaptic membrane;vesicle Axon guidance;B cell receptor signaling pathway;Fc epsilon RI signaling pathway;Osteoclast differentiation;Primary immunodeficiency 3.5317E-39 22240000 7

P04406;P04406-2;E7EUT5 Glyceraldehyde-3-phosphate dehydrogenase GAPDH >sp|P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3;>sp|P04406-2|G3P_HUMAN Isoform 2 of Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH;>tr|E7EUT5|E7EUT5_HUMAN Glyceraldehyde-3-phosphate dehydr 0.87 0.60 0.47 0.60 1.30 1.56 1.60 0.92 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;apoptosis;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell death;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;death;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;microtubule cytoskeleton organization;microtubule-based process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;neuron apoptosis;neuron death;organelle organization;peptidyl-amino acid modification;peptidyl-cysteine modification;peptidyl-cysteine S-nitrosylation;peptidyl-cysteine S-trans-nitrosylation;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein metabolic process;protein modification process;protein nitrosylation;protein stabilization;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein stability;regulation of translation;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;cytoskeletal protein binding;glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity;microtubule binding;NAD binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;peptidyl-cysteine S-nitrosylase activity;protein binding;transferase activity;transferase activity, transferring nitrogenous groups;tubulin binding" + cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lipid particle;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule cytoskeleton;non-membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane;ribonucleoprotein complex;vesicle Alzheimer's disease;Glycolysis / Gluconeogenesis 2.0119E-71 131470000 7

Q15046;Q15046-2;H3BRC9;H3BVA8 Lysine--tRNA ligase KARS >sp|Q15046|SYK_HUMAN Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3;>sp|Q15046-2|SYK_HUMAN Isoform Mitochondrial of Lysine--tRNA ligase OS=Homo sapiens GN=KARS 1.71 NaN 0.91 NaN 1.10 NaN 2.22 NaN amine metabolic process;amino acid activation;biosynthetic process;bis(5'-nucleosidyl) oligophosphate biosynthetic process;bis(5'-nucleosidyl) oligophosphate metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;diadenosine polyphosphate biosynthetic process;diadenosine polyphosphate metabolic process;diadenosine tetraphosphate biosynthetic process;diadenosine tetraphosphate metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;interaction with host;interspecies interaction between organisms;lysyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;multi-organism process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;reproductive process;ribonucleoside biosynthetic process;ribonucleoside metabolic process;RNA metabolic process;RNA processing;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tRNA processing;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic acid binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;lysine-tRNA ligase activity;metal ion binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding"+ aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-enclosed lumen;microtubule cytoskeleton;mitochondrial matrix;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle lumen;organelle part;plasma membrane;protein complex Aminoacyl-tRNA biosynthesis 1.0882E-14 5671100 7

Q06830;H7C3T4;Q13162 Peroxiredoxin-1 PRDX1 >sp|Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 0.73 0.84 1.15 0.64 1.52 2.15 1.38 0.91 anatomical structure development;biological regulation;catabolic process;cell killing;cell proliferation;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to oxygen radical;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cellular response to superoxide;defense response;developmental process;erythrocyte homeostasis;homeostasis of number of cells;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;I-kappaB phosphorylation;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;leukocyte mediated cytotoxicity;leukocyte mediated immunity;lymphocyte mediated immunity;macromolecule metabolic process;macromolecule modification;metabolic process;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular localization;regulation of cellular process;regulation of cellular response to stress;regulation of establishment of protein localization;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of MAPKKK cascade;regulation of NF-kappaB import into nucleus;regulation of nucleocytoplasmic transport;regulation of programmed cell death;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of transcription factor import into nucleus;regulation of transmembrane transport;regulation of transport;removal of superoxide radicals;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to oxygen radical;response to reactive oxygen species;response to stimulus;response to stress;response to superoxide;skeletal system development;superoxide metabolic process;system development "antioxidant activity;binding;catalytic activity;cation binding;heme binding;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;peroxiredoxin activity;tetrapyrrole binding;thioredoxin peroxidase activity;transition metal ion binding" + cell part;chromatin;chromosomal part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;euchromatin;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microbody lumen;microbody part;mitochondrial matrix;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleolus;nucleus;organelle;organelle lumen;organelle part;peroxisomal matrix;peroxisomal part;pigment granule;vesicle Peroxisome 8.8335E-18 75906000 7

P61026;Q15286-2;P59190-2;P59190;H0YLJ8;H0YL94;C9JB90;E9PI18;C9JFM7;E9PJQ5;Q6MZX6;E9PRF7;E9PNB9;E9PS06;J3QSF4;G3V562;E9PBQ0;Q6MZH2;G3V196;H0YDK7;E9PMJ1;M0R1E0;A6NDJ8;A8MSP2;Q96AX2-4;A8MTC6;A8MZI4;M0R0X1;B7Z3L0;P51153;Q15771;Q86YS6;Q96DA2;P61018;Q96AX2-2;Q14964;P20338;Q96AX2;Q96AX2-3;Q9H082;P61018-2 Ras-related protein Rab-10 RAB10 >sp|P61026|RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 0.83 0.93 0.85 0.41 2.24 2.21 1.24 0.88 + "anatomical structure morphogenesis;autophagy;axonogenesis;biological adhesion;biological regulation;catabolic process;cation homeostasis;cell adhesion;cell differentiation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular metabolic process;cellular monovalent inorganic cation homeostasis;cellular process;cellular protein localization;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;developmental process;endoplasmic reticulum organization;endoplasmic reticulum tubular network organization;endosome transport;epithelial cell differentiation;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of neuroblast polarity;establishment of protein localization;establishment of protein localization in endoplasmic reticulum membrane;establishment of protein localization in membrane;establishment or maintenance of cell polarity;establishment or maintenance of neuroblast polarity;Golgi organization;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;homeostatic process;intracellular pH reduction;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;localization;macromolecule localization;membrane organization;metabolic process;monovalent inorganic cation homeostasis;neuron projection morphogenesis;organelle fusion;organelle organization;pH reduction;phagosome acidification;phagosome maturation;phagosome-lysosome fusion;plasma membrane organization;polarized epithelial cell differentiation;post-Golgi vesicle-mediated transport;protein localization;protein localization in membrane;protein localization in plasma membrane;protein transport;regulation of autophagic vacuole assembly;regulation of autophagy;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular pH;regulation of cellular process;regulation of cellular response to stress;regulation of endocytosis;regulation of intracellular pH;regulation of intracellular transport;regulation of localization;regulation of macroautophagy;regulation of metabolic process;regulation of organelle organization;regulation of pH;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress;regulation of retrograde vesicle-mediated transport, Golgi to ER;regulation of transport;regulation of vacuole organization;regulation of vesicle-mediated transport;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;retrograde transport, plasma membrane to Golgi;signal transduction;small GTPase mediated signal transduction;synapse organization;transport;vesicle-mediated transport" "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transporter activity;transporter activity" cell junction;cell part;cell projection;cell-cell junction;cilium;cis-Golgi network;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum tubular network;endoplasmic reticulum-Golgi intermediate compartment;endosomal part;endosome;endosome membrane;Golgi apparatus;Golgi apparatus part;Golgi cisterna;Golgi lumen;Golgi membrane;insulin-responsive compartment;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;occluding junction;organelle;organelle lumen;organelle membrane;organelle part;organelle subcompartment;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;primary cilium;recycling endosome;recycling endosome membrane;stored secretory granule;tight junction;trans-Golgi network;vesicle;vesicle membrane Endocytosis;Tight junction 5.586E-102 85068000 7

Q96FQ6 Protein S100-A16 S100A16 >sp|Q96FQ6|S10AG_HUMAN Protein S100-A16 OS=Homo sapiens GN=S100A16 PE=1 SV=1 1.26 1.40 1.41 0.96 1.59 1.17 0.78 0.66 + + response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane 1.1324E-41 370180000 7

B4E2V5;P27105;P27105-2 Erythrocyte band 7 integral membrane protein STOM >tr|B4E2V5|B4E2V5_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=2 SV=1;>sp|P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3 0.81 0.83 1.21 1.56 0.68 0.54 1.13 0.99 cellular component assembly;cellular component organization;cellular component organization or biogenesis;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization + cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;pigment granule;plasma membrane part;vesicle 1.2106E-42 62704000 7

P12830;Q9UII8;H3BNC6;H3BVI7;J3QKP1 Cadherin-1;E-Cad/CTF1;E-Cad/CTF2;E-Cad/CTF3 CDH1 ">sp|P12830|CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3;>tr|Q9UII8|Q9UII8_HUMAN Cadherin 1, type 1, E-cadherin (Epithelial), isoform CRA_c OS=Homo sapiens GN=CDH1 PE=2 SV=1;>tr|H3BNC6|H3BNC6_HUMAN Fizzy-related protein homolog OS=Homo sapiens G" 1.19 1.01 1.29 0.98 0.65 0.71 1.07 1.02 + "adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to indole-3-methanol;cellular response to inorganic substance;cellular response to lithium ion;cellular response to metal ion;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cochlea development;developmental process;gland development;homeostatic process;homophilic cell adhesion;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;multicellular organismal process;multicellular organismal water homeostasis;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell-cell adhesion;negative regulation of cellular process;neurological system process;neuron projection development;organ development;pituitary gland development;plasma membrane organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of RNA metabolic process;positive regulation of transcription factor import into nucleus;positive regulation of transcription, DNA-dependent;positive regulation of transmembrane transport;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein localization;protein localization in membrane;protein localization in plasma membrane;protein metabolic process;protein oligomerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of branching involved in salivary gland morphogenesis;regulation of catalytic activity;regulation of cell adhesion;regulation of cell-cell adhesion;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of gene expression;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organ morphogenesis;regulation of peptidase activity;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein localization at cell surface;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of water loss via skin;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to indole-3-methanol;response to inorganic substance;response to lithium ion;response to metal ion;response to organic nitrogen;response to organic substance;response to stimulus;response to toxin;salivary gland cavitation;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;synapse assembly;synapse organization;system process;tight junction assembly;trophectodermal cell differentiation;tube formation;tube lumen cavitation;water homeostasis"beta-catenin binding;binding;calcium ion binding;cation binding;cell adhesion molecule binding;ion binding;metal ion binding;protein binding actin cytoskeleton;adherens junction;aggresome;anchoring junction;apical junction complex;apical part of cell;axon part;axon terminus;basolateral plasma membrane;catenin complex;cell junction;cell part;cell projection part;cell surface;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic part;cytoskeleton;endosome;extrinsic to membrane;extrinsic to plasma membrane;focal adhesion;Golgi apparatus;Golgi apparatus part;inclusion body;integral to membrane;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lateral loop;lateral plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuron projection terminus;node of Ranvier;non-membrane-bounded organelle;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;Schmidt-Lanterman incisure;trans-Golgi networkAdherens junction;Bacterial invasion of epithelial cells;Bladder cancer;Cell adhesion molecules (CAMs);Endometrial cancer;Melanoma;Pathogenic Escherichia coli infection;Pathways in cancer;Thyroid cancer 1.5852E-73 38185000 8

B4DGU4;P35222;P35222-2 Catenin beta-1 CTNNB1 >tr|B4DGU4|B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1;>sp|P35222|CTNB1_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 0.91 1.23 0.84 1.04 0.83 0.80 0.89 0.87 + "adherens junction assembly;adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;anatomical structure morphogenesis;androgen receptor signaling pathway;anterior/posterior axis specification;apoptosis;appendage morphogenesis;axis specification;biological adhesion;biological regulation;biosynthetic process;bone resorption;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling pathway involved in heart development;canonical Wnt receptor signaling pathway involved in negative regulation of apoptosis;canonical Wnt receptor signaling pathway involved in positive regulation of cardiac outflow tract cell proliferation;canonical Wnt receptor signaling pathway involved in positive regulation of epithelial to mesenchymal transition;canonical Wnt receptor signaling pathway involved in regulation of cell proliferation;cell activation;cell adhesion;cell communication;cell death;cell development;cell differentiation;cell fate commitment;cell fate commitment involved in formation of primary germ layers;cell fate determination;cell fate specification;cell junction assembly;cell junction organization;cell maturation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cell surface receptor linked signaling pathway involved in heart development;cell-cell adhesion;cell-cell junction organization;cell-cell signaling;cell-cell signaling involved in cell fate commitment;cell-matrix adhesion;cell-substrate adhesion;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein localization;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to indole-3-methanol;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;central nervous system vasculogenesis;chordate embryonic development;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;death;determination of bilateral symmetry;determination of dorsal/ventral asymmetry;developmental induction;developmental maturation;developmental process;developmental process involved in reproduction;digestive tract development;dorsal/ventral axis specification;ectoderm development;ectodermal placode formation;embryo development;embryo development ending in birth or egg hatching;embryonic appendage morphogenesis;embryonic axis specification;embryonic digit morphogenesis;embryonic epithelial tube formation;embryonic foregut morphogenesis;embryonic forelimb morphogenesis;embryonic heart tube development;embryonic hindlimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic pattern specification;endodermal cell fate commitment;endothelial tube morphogenesis;epidermal cell differentiation;epidermis development;epithelial cell differentiation;epithelial cell differentiation involved in prostate gland development;epithelial cell morphogenesis;epithelial to mesenchymal transition;epithelial tube branching involved in lung morphogenesis;epithelial tube formation;epithelial tube morphogenesis;epithelium development;establishment of localization;forebrain development;forelimb morphogenesis;fungiform papilla formation;gastrulation;gastrulation with mouth forming second;genitalia development;genitalia morphogenesis;germ cell development;glial cell fate determination;glial cell proliferation;hair cell differentiation;hair cycle process;hair follicle morphogenesis;hair follicle placode formation;hemopoietic or lymphoid organ development;hindbrain development;hindlimb morphogenesis;homeostatic process;immune system process;in utero embryonic development;intracellular receptor mediated signaling pathway;lens morphogenesis in camera-type eye;leukocyte activation;leukocyte differentiation;limb morphogenesis;liver development;localization;locomotion;lung cell differentiation;lung induction;lung-associated mesenchyme development;lymphocyte activation;lymphocyte differentiation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;male genitalia development;mesenchymal cell proliferation;mesenchymal cell proliferation involved in lung development;mesenchymal to epithelial transition;mesenchymal to epithelial transition involved in metanephros morphogenesis;mesenchyme development;metabolic process;midgut development;molting cycle;molting cycle process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an endothelium;morphogenesis of an epithelium;multicellular organismal process;muscle cell differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;myoblast differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cardiac cell fate specification;negative regulation of cardioblast cell fate specification;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell fate commitment;negative regulation of cell fate specification;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of chondrocyte differentiation;negative regulation of developmental process;negative regulation of gene expression;negative regulation of glial cell differentiation;negative regulation of gliogenesis;negative regulation of heart induction by canonical Wnt receptor signaling pathway;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte differentiation;negative regulation of neurogenesis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of oligodendrocyte differentiation;negative regulation of osteoclast differentiation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein sumoylation;negative regulation of RNA metabolic process;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nephron tubule formation;neural plate development;neuron migration;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;odontogenesis;odontogenesis of dentine-containing tooth;oocyte development;organ development;organ formation;organ induction;organ morphogenesis;organelle organization;osteoclast differentiation;oviduct development;pancreas development;pattern specification process;patterning of blood vessels;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of branching involved in lung morphogenesis;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of determination of dorsal identity;positive regulation of developmental process;positive regulation of endothelial cell differentiation;positive regulation of epithelial cell differentiation;positive regulation of epithelial cell proliferation;positive regulation of epithelial cell proliferation involved in prostate gland development;positive regulation of fibroblast growth factor receptor signaling pathway;positive regulation of gene expression;positive regulation of glycoprotein biosynthetic process;positive regulation of heparan sulfate proteoglycan biosynthetic process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of muscle cell differentiation;positive regulation of neural precursor cell proliferation;positive regulation of neuroblast proliferation;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of osteoblast differentiation;positive regulation of programmed cell death;positive regulation of reproductive process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of sulfur metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;programmed cell death;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein localization;protein localization at cell surface;protein oligomerization;proximal/distal pattern formation;regionalization;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of branching involved in lung morphogenesis;regulation of calcium ion import;regulation of calcium ion transport;regulation of cardiac cell fate specification;regulation of cardioblast cell fate specification;regulation of cardioblast differentiation;regulation of cardioblast proliferation;regulation of cartilage development;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell fate commitment;regulation of cell fate specification;regulation of cell proliferation;regulation of cell proliferation involved in heart morphogenesis;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of centriole-centriole cohesion;regulation of centromeric sister chromatid cohesion;regulation of chondrocyte differentiation;regulation of chromosome organization;regulation of chromosome segregation;regulation of cytoskeleton organization;regulation of determination of dorsal identity;regulation of developmental process;regulation of embryonic development;regulation of endothelial cell differentiation;regulation of epithelial cell differentiation;regulation of epithelial cell differentiation involved in kidney development;regulation of epithelial cell proliferation;regulation of epithelial cell proliferation involved in prostate gland development;regulation of fibroblast growth factor receptor signaling pathway;regulation of fibroblast proliferation;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of glycoprotein biosynthetic process;regulation of heart induction;regulation of heart morphogenesis;regulation of heparan sulfate proteoglycan biosynthetic process;regulation of homeostatic process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transport;regulation of kidney development;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of localization;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of mesenchymal cell proliferation;regulation of metabolic process;regulation of metal ion transport;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of mononuclear cell proliferation;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of myelination;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nephron tubule epithelial cell differentiation;regulation of nervous system development;regulation of neural precursor cell proliferation;regulation of neurogenesis;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oligodendrocyte differentiation;regulation of organ formation;regulation of organ morphogenesis;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoclast differentiation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein localization;regulation of protein localization at cell surface;regulation of protein metabolic process;regulation of protein modification process;regulation of protein sumoylation;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of secondary heart field cardioblast proliferation;regulation of signal transduction;regulation of signaling;regulation of sister chromatid cohesion;regulation of smooth muscle cell proliferation;regulation of sulfur metabolic process;regulation of system process;regulation of T cell activation;regulation of T cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmission of nerve impulse;regulation of transport;renal inner medulla development;renal outer medulla development;renal vesicle formation;reproductive process;reproductive structure development;response to cadmium ion;response to chemical stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to growth factor stimulus;response to hormone stimulus;response to indole-3-methanol;response to inorganic substance;response to metal ion;response to organic cyclic compound;response to organic substance;response to steroid hormone stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;Schwann cell proliferation;signal transduction;signaling;skin development;smooth muscle cell differentiation;specification of symmetry;steroid hormone receptor signaling pathway;synapse organization;synaptic vesicle transport;T cell activation;T cell differentiation;T cell differentiation in thymus;thymus development;tissue development;tissue homeostasis;tissue morphogenesis;tongue morphogenesis;trachea formation;transcription, DNA-dependent;transport;tube development;tube formation;tube morphogenesis;vasculogenesis;vesicle-mediated transport;Wnt receptor signaling pathway;Wnt receptor signaling pathway involved in heart development" androgen receptor binding;binding;chromatin binding;DNA binding;double-stranded DNA binding;enzyme binding;hormone receptor binding;kinase binding;molecular transducer activity;nuclear hormone receptor binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein binding transcription factor activity;protein kinase binding;receptor binding;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding transcription factor activity;signal transducer activity;steroid hormone receptor binding;structural molecule activity;structure-specific DNA binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;transcription regulatory region DNA binding adherens junction;anchoring junction;apical junction complex;apical part of cell;basolateral plasma membrane;beta-catenin destruction complex;beta-catenin-TCF7L2 complex;catenin complex;catenin-TCF7L2 complex;cell cortex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;dendritic shaft;desmosome;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;internal side of plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;lateral plasma membrane;macromolecular complex;membrane;membrane part;microtubule organizing center;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleoplasm part;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;protein-DNA complex;Scrib-APC-beta-catenin complex;spindle pole;synapse;transcription factor complex;Z disc;zonula adherens Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Basal cell carcinoma;Colorectal cancer;Endometrial cancer;Focal adhesion;Leukocyte transendothelial migration;Melanogenesis;Pathogenic Escherichia coli infection;Pathways in cancer;Prostate cancer;Thyroid cancer;Tight junction;Wnt signaling pathway 6.2099E-18 17731000 8

Q02487-2;Q02487 Desmocollin-2 DSC2 >sp|Q02487-2|DSC2_HUMAN Isoform 2B of Desmocollin-2 OS=Homo sapiens GN=DSC2;>sp|Q02487|DSC2_HUMAN Desmocollin-2 OS=Homo sapiens GN=DSC2 PE=1 SV=1 0.98 0.97 0.78 0.62 1.81 1.66 1.15 1.09 + biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;desmosome;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Arrhythmogenic right ventricular cardiomyopathy (ARVC) 5.265E-44 26635000 8

P62805 Histone H4 HIST1H4A >sp|P62805|H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 1.14 1.42 0.98 3.78 0.43 0.50 0.36 0.33 anatomical structure homeostasis;ATP-dependent chromatin remodeling;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;DNA metabolic process;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;histone exchange;homeostatic process;inositol lipid-mediated signaling;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of megakaryocyte differentiation;negative regulation of myeloid cell differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;phosphatidylinositol-mediated signaling;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biological quality;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of megakaryocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;response to stimulus;signal transduction;telomere maintenance;telomere organization binding;DNA binding;nucleic acid binding + actin cytoskeleton;cell part;chromosomal part;cytoskeleton;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleosome;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus 4.0897E-167 3040700000 8

P07942;G3XAI2;E7EPA6 Laminin subunit beta-1 LAMB1 >sp|P07942|LAMB1_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2;>tr|G3XAI2|G3XAI2_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1 1.52 1.23 1.28 1.00 0.49 0.43 0.81 1.08 + + + anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;cell adhesion;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-substrate adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;chemotaxis;developmental process;embryo implantation;locomotion;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;odontogenesis;organ morphogenesis;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of epithelial cell proliferation;positive regulation of locomotion;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of epithelial cell proliferation;regulation of localization;regulation of locomotion;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;substrate adhesion-dependent cell spreading;taxis binding;extracellular matrix structural constituent;glycolipid binding;glycosphingolipid binding;lipid binding;sphingolipid binding;structural molecule activity + cell part;cytoplasmic part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular part;laminin complex;laminin-1 complex;laminin-10 complex;laminin-2 complex;laminin-8 complex;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;perinuclear region of cytoplasm;plasma membrane part;protein complex;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 1.2512E-61 35002000 8

P47929 Galectin-7 LGALS7 >sp|P47929|LEG7_HUMAN Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2 0.93 1.38 1.55 1.78 0.76 0.89 0.97 1.15 + + + apoptosis;biological adhesion;cell adhesion;cell death;cell-cell adhesion;cellular process;death;heterophilic cell-cell adhesion;programmed cell death binding;carbohydrate binding + cell part;cytoplasm;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.2589E-268 1409100000 8

P06748-2;P06748;P06748-3;E5RGW4;Q9C0A0-2;F5H107;Q9C0A0;E9PDN6 Nucleophosmin NPM1 >sp|P06748-2|NPM_HUMAN Isoform 2 of Nucleophosmin OS=Homo sapiens GN=NPM1;>sp|P06748|NPM_HUMAN Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2;>sp|P06748-3|NPM_HUMAN Isoform 3 of Nucleophosmin OS=Homo sapiens GN=NPM1 1.31 0.99 1.92 1.81 1.02 0.36 0.86 0.65 + "aging;ATP-dependent chromatin remodeling;biological adhesion;biological regulation;cell adhesion;cell aging;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;centrosome cycle;centrosome organization;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;developmental process;DNA metabolic process;DNA repair;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;establishment of localization;establishment of localization in cell;establishment of protein localization;histone exchange;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule organizing center organization;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of centrosome duplication;negative regulation of organelle organization;negative regulation of programmed cell death;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;nucleosome assembly;nucleosome organization;organelle assembly;organelle organization;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein transport;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of centriole replication;regulation of centrosome cycle;regulation of centrosome duplication;regulation of cytoskeleton organization;regulation of deoxyribonuclease activity;regulation of endodeoxyribonuclease activity;regulation of endoribonuclease activity;regulation of gene expression;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of ribonuclease activity;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;signal transduction;transport;viral reproduction;viral reproductive process;virus-host interaction" binding;histone binding;identical protein binding;NF-kappaB binding;nucleic acid binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein heterodimerization activity;protein homodimerization activity;ribonucleoprotein binding;ribosomal large subunit binding;ribosomal small subunit binding;RNA binding;Tat protein binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;unfolded protein binding cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spindle pole centrosome 3.7154E-83 608800000 8

P05120;H7C004;H7BYS2;E7ERB5;E7EPJ9;E9PDK7 Plasminogen activator inhibitor 2 SERPINB2;SERPINB10 >sp|P05120|PAI2_HUMAN Plasminogen activator inhibitor 2 OS=Homo sapiens GN=SERPINB2 PE=1 SV=2;>tr|H7C004|H7C004_HUMAN Serpin B10 (Fragment) OS=Homo sapiens GN=SERPINB10 PE=3 SV=1;>tr|H7BYS2|H7BYS2_HUMAN Serpin B10 (Fragment) OS=Homo sapiens GN=SERPINB10 PE 0.93 0.66 0.55 0.13 3.11 2.96 1.25 0.46 + + biological regulation;blood coagulation;coagulation;fibrinolysis;hemostasis;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood coagulation;negative regulation of cell death;negative regulation of cellular process;negative regulation of coagulation;negative regulation of multicellular organismal process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of blood coagulation;regulation of body fluid levels;regulation of cell death;regulation of cellular process;regulation of coagulation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of proteolysis;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of wound healing;response to stimulus;response to stress;response to wounding;wound healing endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity + cell part;cytoplasm;extracellular region;extracellular region part;extracellular space;intracellular part;membrane;plasma membrane Amoebiasis 2.0486E-43 95338000 8

O60716-24;O60716-23;O60716-21;O60716-19;O60716-22;O60716-20;O60716-16;O60716-18;O60716-15;O60716-17;O60716-13;O60716-11;O60716-14;O60716-12;O60716-10;O60716-8;O60716-9;O60716-7;O60716-5;C9JZR2;O60716-3;O60716-6;O60716-4;O60716-2;O60716;O60716-32;O60716-31;O60716-29;O60716-27;O60716-30;O60716-28;O60716-26;O60716-25;E9PRE2;H0YC95 Catenin delta-1 CTNND1>sp|O60716-24|CTND1_HUMAN Isoform 3 of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716-23|CTND1_HUMAN Isoform 3C of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716-21|CTND1_HUMAN Isoform 3A of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716- 1.06 1.02 1.27 1.11 1.17 1.04 0.99 0.76 + "adherens junction organization;anatomical structure morphogenesis;biological adhesion;biological regulation;biosynthetic process;cell adhesion;cell differentiation;cell differentiation involved in salivary gland development;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell junction organization;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;developmental process;epidermal cell differentiation;epithelial cell differentiation;epithelial cell differentiation involved in salivary gland development;gland morphogenesis;keratinocyte differentiation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;morphogenesis of a polarized epithelium;morphogenesis of an epithelium;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;response to stimulus;RNA biosynthetic process;RNA metabolic process;salivary gland morphogenesis;signal transduction;tissue morphogenesis;transcription, DNA-dependent;Wnt receptor signaling pathway" adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane;membrane-bounded organelle;midbody;nucleus;organelle;plasma membrane Adherens junction;Leukocyte transendothelial migration 6.9215E-25 24491000 9

P05556;P05556-2;P05556-5;P05556-4;P05556-3;C9JPK5;H7C4N8;E7ERX5;Q5T3E6;E9PLR6;E7EUI6;E7EQW5 Integrin beta-1 ITGB1 >sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2;>sp|P05556-2|ITB1_HUMAN Isoform Beta-1B of Integrin beta-1 OS=Homo sapiens GN=ITGB1;>sp|P05556-5|ITB1_HUMAN Isoform Beta-1D of Integrin beta-1 OS=Homo sapiens GN=ITGB1;>sp|P05556-4|IT 1.00 0.93 1.21 0.89 0.86 0.35 1.00 1.14 + actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;anatomical structure homeostasis;axon guidance;B cell activation;B cell differentiation;biological adhesion;biological regulation;blood coagulation;blood vessel endothelial cell migration;calcium ion homeostasis;calcium-independent cell-matrix adhesion;cardiac cell differentiation;cardiac muscle cell differentiation;cation homeostasis;cell activation;cell adhesion;cell adhesion mediated by integrin;cell communication;cell cycle process;cell differentiation;cell fate specification;cell junction assembly;cell junction organization;cell migration;cell migration involved in sprouting angiogenesis;cell motility;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell adhesion mediated by integrin;cell-cell junction assembly;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular defense response;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular membrane organization;cellular metal ion homeostasis;cellular process;cellular process involved in reproduction;cellular response to abiotic stimulus;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to ionizing radiation;cellular response to mechanical stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to radiation;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin D;chemical homeostasis;chemotaxis;chordate embryonic development;coagulation;cytoskeleton organization;defense response;developmental process;divalent inorganic cation homeostasis;embryo development;embryo development ending in birth or egg hatching;endothelial cell migration;establishment of localization;establishment of localization in cell;establishment of protein localization;extracellular matrix organization;extracellular structure organization;G1/S transition of mitotic cell cycle;germ cell migration;hemostasis;homeostatic process;homophilic cell adhesion;immune system process;in utero embryonic development;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;ion homeostasis;leukocyte activation;leukocyte cell-cell adhesion;leukocyte differentiation;leukocyte migration;locomotion;lymphocyte activation;lymphocyte differentiation;maternal process involved in female pregnancy;membrane organization;metal ion homeostasis;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell differentiation;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neuron differentiation;negative regulation of programmed cell death;neuron projection development;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cell-substrate adhesion;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of endocytosis;positive regulation of intracellular protein kinase cascade;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of neuron differentiation;positive regulation of neuron projection development;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transport;protein transport;protein transport within lipid bilayer;regulation of anoikis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cell-substrate adhesion;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of endocytosis;regulation of G-protein coupled receptor protein signaling pathway;regulation of immune response;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to abiotic stimulus;response to activity;response to chemical stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to gonadotropin stimulus;response to growth factor stimulus;response to hormone stimulus;response to ionizing radiation;response to mechanical stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to radiation;response to stimulus;response to stress;response to transforming growth factor beta stimulus;response to vitamin;response to vitamin D;sarcomere organization;signal transduction;striated muscle cell differentiation;taxis;tight junction assembly;tissue homeostasis;transport;viral reproductive process;virus-host interaction actin binding;binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;peptide binding;protein binding;protein dimerization activity;protein heterodimerization activity;receptor activity + acrosomal vesicle;adherens junction;alpha3-beta1 integrin complex;alpha8-beta1 integrin complex;alpha9-beta1 integrin complex;anchoring junction;basement membrane;cell division site part;cell junction;cell part;cell projection;cell surface;cell-cell contact zone;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cleavage furrow;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;external side of plasma membrane;extracellular matrix part;extracellular region part;filopodium;focal adhesion;hemidesmosome;integrin complex;intercalated disc;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;myelin sheath abaxonal region;neuromuscular junction;organelle;pigment granule;plasma membrane;plasma membrane part;protein complex;receptor complex;ruffle;sarcolemma;stored secretory granule;synapse;vesicle Arrhythmogenic right ventricular cardiomyopathy (ARVC);Axon guidance;Bacterial invasion of epithelial cells;Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leishmaniasis;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Shigellosis;Small cell lung cancer;Toxoplasmosis 1.1891E-28 56044000 9

P31947;P31947-2;A2IDB2;F8WEB6;A2IDB1 14-3-3 protein sigma SFN >sp|P31947|1433S_HUMAN 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1;>sp|P31947-2|1433S_HUMAN Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN 1.30 0.33 1.04 0.57 1.83 0.90 3.12 1.19 "anatomical structure development;apoptotic mitochondrial changes;biological regulation;cell differentiation;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to stimulus;cellular response to stress;developmental process;DNA damage response, signal transduction resulting in induction of apoptosis;epidermal cell differentiation;epidermis development;epithelial cell differentiation;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;keratinocyte differentiation;keratinocyte proliferation;membrane organization;mitochondrion organization;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of programmed cell death;positive regulation of protein export from nucleus;positive regulation of protein transport;positive regulation of transport;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of growth;regulation of hydrolase activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nucleocytoplasmic transport;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein export from nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of transferase activity;regulation of transport;release of cytochrome c from mitochondria;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction in response to DNA damage;skin development;tissue development" enzyme inhibitor activity;enzyme regulator activity;kinase inhibitor activity;kinase regulator activity;protein kinase C inhibitor activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity + cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;vesicle membrane Aldosterone-regulated sodium reabsorption;Cell cycle;p53 signaling pathway 1.6488E-31 130910000 9

Q5TCU6;Q9Y490 Talin-1 TLN1 >tr|Q5TCU6|Q5TCU6_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1;>sp|Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 NaN NaN 0.38 NaN 0.48 NaN NaN NaN + actin cytoskeleton organization;actin filament-based process;activation of signaling protein activity involved in unfolded protein response;axon guidance;biological adhesion;biological regulation;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell-cell junction assembly;cell-cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;locomotion;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;metabolic process;multicellular organismal process;muscle contraction;muscle system process;organelle organization;platelet activation;platelet degranulation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to chemical stimulus;response to external stimulus;response to stimulus;secretion;secretion by cell;system process;taxis;transport;vesicle-mediated transport structural constituent of cytoskeleton;structural molecule activity + actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;plasma membrane part;ruffle;ruffle membrane;vesicle Focal adhesion 3.8538E-19 10799000 9

P06733;K7EM90;P06733-2;F5H1C3;F5H5U1;F5GWQ3;E5RI09;E5RG95;K7EPM1;K7EKN2;E5RGZ4;F5H0C8;P13929-3;B7Z2X9;P13929-2;P13929;P09104 Alpha-enolase;Enolase ENO1 >sp|P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2;>tr|K7EM90|K7EM90_HUMAN Enolase (Fragment) OS=Homo sapiens GN=ENO1 PE=3 SV=1;>sp|P06733-2|ENOA_HUMAN Isoform MBP-1 of Alpha-enolase OS=Homo sapiens GN=ENO1 0.28 5.32 0.23 4.58 0.52 1.02 0.52 0.86 "aging;alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental growth;developmental process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;growth;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regeneration;regulation of biological process;regulation of biosynthetic process;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to biotic stimulus;response to chemical stimulus;response to drug;response to other organism;response to stimulus;response to virus;RNA biosynthetic process;RNA metabolic process;skeletal muscle tissue regeneration;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;tissue development;tissue regeneration;transcription, DNA-dependent" binding;carbon-oxygen lyase activity;catalytic activity;cation binding;DNA binding;hydro-lyase activity;ion binding;lyase activity;magnesium ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;phosphopyruvate hydratase activity;protein binding transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity + cell part;contractile fiber part;cytoplasmic part;cytosol;cytosolic part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;M band;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle part;perikaryon;phosphopyruvate hydratase complex;photoreceptor inner segment;plasma membrane;protein complex;vesicle Glycolysis / Gluconeogenesis;Methane metabolism;RNA degradation 4.1871E-67 70418000 10

E7EQR4;P15311 Ezrin EZR >tr|E7EQR4|E7EQR4_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=2 SV=2;>sp|P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 NaN NaN 0.64 NaN 1.06 NaN NaN NaN + actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;axon guidance;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;chemotaxis;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;developmental process;epithelial cell differentiation;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;leukocyte cell-cell adhesion;locomotion;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane docking;membrane to membrane docking;organelle organization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to chemical stimulus;response to external stimulus;response to stimulus;taxis actin binding;actin filament binding;binding;cytoskeletal protein binding;protein binding actin filament;apical part of cell;apical plasma membrane;basolateral plasma membrane;cell cortex part;cell part;cell projection;cell projection membrane;cell projection part;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extrinsic to membrane;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane;membrane part;microtubule basal body;microtubule organizing center;microvillus;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ruffle;ruffle membrane;uropod Gastric acid secretion;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton 4.178E-26 4303600 10

Q9NYQ8 Protocadherin Fat 2 FAT2 >sp|Q9NYQ8|FAT2_HUMAN Protocadherin Fat 2 OS=Homo sapiens GN=FAT2 PE=1 SV=2 NaN NaN 1.96 NaN 1.01 NaN NaN NaN + ameboidal cell migration;biological adhesion;cell adhesion;cell migration;cell motility;cell-cell adhesion;cellular component movement;cellular process;epithelial cell migration;homophilic cell adhesion;locomotion binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane 5.331E-22 7052200 10

P36952;P36952-2;C9JLM5 Serpin B5 SERPINB5 >sp|P36952|SPB5_HUMAN Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2;>sp|P36952-2|SPB5_HUMAN Isoform 2 of Serpin B5 OS=Homo sapiens GN=SERPINB5 0.66 0.37 1.04 0.34 5.25 3.18 1.64 0.97 + + anatomical structure morphogenesis;biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;developmental process involved in reproduction;extracellular matrix organization;extracellular structure organization;gland morphogenesis;morphogenesis of an epithelium;organ morphogenesis;prostate gland morphogenesis;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of epithelial cell proliferation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;reproductive process;tissue morphogenesis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity + cell part;cytoplasm;extracellular region part;extracellular space;intracellular part p53 signaling pathway 4.7485E-42 85852000 10

P67809;H0Y449;C9J5V9;Q9Y2T7 Nuclease-sensitive element-binding protein 1 YBX1 >sp|P67809|YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3;>tr|H0Y449|H0Y449_HUMAN Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens GN=YBX1 PE=4 SV=1;>tr|C9J5V9|C9J5V9_HUMAN Nuclease-sensiti 2.10 0.66 1.17 0.85 0.58 0.39 1.77 1.12 "anatomical structure development;biological regulation;biosynthetic process;cell development;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;chordate embryonic development;CRD-mediated mRNA stabilization;developmental process;developmental process involved in reproduction;embryo development;embryo development ending in birth or egg hatching;gamete generation;germ cell development;in utero embryonic development;macromolecule biosynthetic process;macromolecule metabolic process;male gamete generation;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;multicellular organismal process;multicellular organismal reproductive process;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of muscle cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of RNA metabolic process;negative regulation of striated muscle cell differentiation;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oocyte development;positive regulation of biological process;positive regulation of cell division;positive regulation of cellular process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cell division;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mRNA stability;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of striated muscle cell differentiation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization;spermatid development;spermatogenesis;transcription from RNA polymerase II promoter;transcription, DNA-dependent;translational attenuation" binding;chromatin binding;DNA binding;double-stranded DNA binding;lipid binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;ribonucleoprotein binding;RNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;translation regulator activity + cell part;CRD-mediated mRNA stability complex;cytoplasm;cytoplasmic part;extracellular region;histone pre-mRNA 3'end processing complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;polysome;protein complex;ribonucleoprotein complex;RNA granule;spliceosomal complex;stress granule;U12-type spliceosomal complex 2.4999E-179 167720000 10

P12109 Collagen alpha-1(VI) chain COL6A1 >sp|P12109|CO6A1_HUMAN Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3 NaN NaN 0.47 0.69 31.09 2.39 NaN NaN + + + axon guidance;biological adhesion;cell adhesion;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;chemotaxis;collagen catabolic process;collagen metabolic process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein oligomerization;protein trimerization;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to organic nitrogen;response to organic substance;response to stimulus;taxis binding;growth factor binding;platelet-derived growth factor binding;protein binding + anchoring collagen;cell part;collagen;collagen type VI;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;protein complex;sarcolemma ECM-receptor interaction;Focal adhesion;Protein digestion and absorption 5.5739E-34 48844000 11

P12110;P12110-3;P12110-2;C9JH44;H7C0M5 Collagen alpha-2(VI) chain COL6A2 >sp|P12110|CO6A2_HUMAN Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4;>sp|P12110-3|CO6A2_HUMAN Isoform 2C2A of Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2;>sp|P12110-2|CO6A2_HUMAN Isoform 2C2A of Collagen alpha-2(VI) chain OS=Homo NaN NaN 1.04 NaN 28.76 NaN NaN NaN + + + axon guidance;biological adhesion;cell adhesion;cell-cell adhesion;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;collagen catabolic process;collagen metabolic process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotrimerization;protein oligomerization;protein trimerization;response to chemical stimulus;response to external stimulus;response to stimulus;taxis "binding;binding, bridging;extracellular matrix structural constituent;protein binding;protein binding, bridging;structural molecule activity" + cell part;collagen;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix;extracellular matrix part;extracellular region part;extracellular space;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;protein complex;proteinaceous extracellular matrix;sarcolemma ECM-receptor interaction;Focal adhesion;Protein digestion and absorption 7.8595E-39 22977000 11

P35221;P35221-2;F8W845;G3XAM7;Q8N1C0;E5RIB1;E5RJL0;E5RIE0;E5RHV7;E5RGY7;E5RGY6;E5RG03;E5RIC3;P26232-4;P26232-6;E5RJZ2;E5RIT8;E5RFM3;H0YBB8;E5RJ41;A6NKP0;Q9UI47 Catenin alpha-1 CTNNA1 >sp|P35221|CTNA1_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1;>sp|P35221-2|CTNA1_HUMAN Isoform 2 of Catenin alpha-1 OS=Homo sapiens GN=CTNNA1;>tr|F8W845|F8W845_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=2 SV=1;>tr|G3XAM7|G3XAM7_HUMAN C 1.12 1.05 1.11 1.06 0.75 0.58 1.03 0.79 + adherens junction organization;aging;anatomical structure development;anatomical structure morphogenesis;apical junction assembly;axon regeneration;axonogenesis;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to indole-3-methanol;cellular response to organic substance;cellular response to stimulus;cellular response to stress;developmental process;developmental process involved in reproduction;establishment or maintenance of cell polarity;gap junction assembly;gonad development;macromolecular complex assembly;macromolecular complex subunit organization;male gonad development;muscle cell differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neural precursor cell proliferation;negative regulation of neuroblast proliferation;negative regulation of neurogenesis;negative regulation of programmed cell death;neuron projection morphogenesis;neuron projection regeneration;odontogenesis;odontogenesis of dentine-containing tooth;organ development;organ morphogenesis;ovarian follicle development;ovulation cycle process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle cell differentiation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smoothened signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regeneration;regulation of apoptosis;regulation of biological process;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of nervous system development;regulation of neural precursor cell proliferation;regulation of neurogenesis;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of smoothened signaling pathway;reproductive process;reproductive structure development;response to axon injury;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to indole-3-methanol;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;rhythmic process binding;cadherin binding;cell adhesion molecule binding;protein binding;structural molecule activity acrosomal vesicle;actin cytoskeleton;adherens junction;anchoring junction;catenin complex;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell contact zone;cell-cell junction;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;cytosol;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;intercalated disc;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;plasma membrane;plasma membrane part;protein complex;stored secretory granule;vesicle;zonula adherens Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Endometrial cancer;Leukocyte transendothelial migration;Pathways in cancer;Tight junction 5.0322E-44 78683000 11

Q00341;Q00341-2;H0Y394;H7C0A4;C9JZI8;C9J5E5;C9JIZ1;C9JT62;C9JHS7;C9JK79;C9JHZ8;C9JES8;C9JMQ6;C9JQ82;C9JBS3;C9JEJ8;C9JKQ5;C9JHN6;H7C2D1;C9JHS9;C9J739;H7BZC3 Vigilin HDLBP >sp|Q00341|VIGLN_HUMAN Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2;>sp|Q00341-2|VIGLN_HUMAN Isoform 2 of Vigilin OS=Homo sapiens GN=HDLBP;>tr|H0Y394|H0Y394_HUMAN Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=4 SV=1 1.41 0.49 0.91 0.49 5.76 0.92 2.37 1.40 alcohol metabolic process;cholesterol metabolic process;establishment of localization;lipid metabolic process;lipid transport;metabolic process;organic substance transport;primary metabolic process;small molecule metabolic process;steroid metabolic process;sterol metabolic process;transport binding;lipid binding;nucleic acid binding;RNA binding + cell part;cytoplasm;extracellular region part;high-density lipoprotein particle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;plasma lipoprotein particle;plasma membrane;protein-lipid complex 4.2903E-44 15477000 11

Q92743;H0Y7G9 Serine protease HTRA1 HTRA1 >sp|Q92743|HTRA1_HUMAN Serine protease HTRA1 OS=Homo sapiens GN=HTRA1 PE=1 SV=1 1.07 0.98 1.43 1.21 0.31 0.17 0.36 0.33 + + biological regulation;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of BMP signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of BMP signaling pathway;regulation of cell communication;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity" + cell part;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular part 6.5688E-58 426720000 11

P21589-2;P21589;Q96B60;H0Y7R7 5-nucleotidase NT5E >sp|P21589-2|5NTD_HUMAN Isoform 2 of 5-nucleotidase OS=Homo sapiens GN=NT5E;>sp|P21589|5NTD_HUMAN 5-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1;>tr|Q96B60|Q96B60_HUMAN 5-nucleotidase OS=Homo sapiens GN=NT5E PE=2 SV=1 1.61 2.37 1.02 1.97 0.49 0.50 0.26 0.64 adenosine biosynthetic process;adenosine metabolic process;AMP catabolic process;AMP metabolic process;biological regulation;biosynthetic process;catabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;DNA metabolic process;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of response to external stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside catabolic process;nucleoside metabolic process;nucleoside monophosphate catabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine base metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine nucleoside monophosphate catabolic process;purine nucleoside monophosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine ribonucleoside monophosphate catabolic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;pyrimidine base metabolic process;pyrimidine nucleoside catabolic process;pyrimidine nucleoside metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of defense response;regulation of inflammatory response;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;ribonucleoside biosynthetic process;ribonucleoside metabolic process;ribonucleoside monophosphate catabolic process;ribonucleoside monophosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "5'-nucleotidase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nucleotidase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity" + anchored to membrane;cell part;cytoplasm;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;vesicle Nicotinate and nicotinamide metabolism;Purine metabolism;Pyrimidine metabolism 5.2218E-101 101730000 11

Q13835-2;Q13835 Plakophilin-1 PKP1 >sp|Q13835-2|PKP1_HUMAN Isoform 1 of Plakophilin-1 OS=Homo sapiens GN=PKP1;>sp|Q13835|PKP1_HUMAN Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2 0.80 1.03 1.25 1.48 1.15 1.63 1.00 0.52 + biological adhesion;cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;multicellular organismal development;multicellular organismal process;organelle organization binding;intermediate filament binding;lamin binding;molecular transducer activity;protein binding;protein complex binding;signal transducer activity;structural constituent of epidermis;structural molecule activity anchoring junction;cell junction;cell part;cell-cell junction;cytoskeletal part;desmosome;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex 1.7948E-57 70870000 11

P62269;J3JS69 40S ribosomal protein S18 RPS18 >sp|P62269|RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 1.69 0.91 12.75 0.86 1.13 0.95 1.17 0.70 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity + cell part;collagen;cytosolic small ribosomal subunit;extracellular matrix part;extracellular region part;intracellular organelle part;intracellular part;macromolecular complex;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome 4.8217E-71 196970000 11

Q9Y6C2;H0Y7A0 EMILIN-1 EMILIN1>sp|Q9Y6C2|EMIL1_HUMAN EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=2 NaN NaN 0.97 NaN 42.67 NaN NaN NaN + + + biological adhesion;biological regulation;cell adhesion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular structure organization;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;regulation of biological process;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular process extracellular matrix constituent conferring elasticity;extracellular matrix structural constituent;structural molecule activity + collagen;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;membrane-bounded organelle;membrane-bounded vesicle;organelle;vesicle 2.6241E-39 100390000 12

P06396-2;F5H1A8;P06396-3;P06396;CON__Q3SX14;Q5T0H8;Q5T0H9;Q5T0H7;Q5T0I0;Q5T0I1 Gelsolin GSN >sp|P06396-2|GELS_HUMAN Isoform 2 of Gelsolin OS=Homo sapiens GN=GSN;>tr|F5H1A8|F5H1A8_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=2 SV=1;>sp|P06396-3|GELS_HUMAN Isoform 3 of Gelsolin OS=Homo sapiens GN=GSN;>sp|P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GS 0.26 1.23 0.24 0.93 1.54 3.30 0.98 1.34 actin cytoskeleton organization;actin filament capping;actin filament organization;actin filament polymerization;actin filament severing;actin filament-based process;actin polymerization or depolymerization;aging;anatomical structure development;anatomical structure morphogenesis;apoptosis;barbed-end actin filament capping;biological regulation;cell death;cell development;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to cadmium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;cilium morphogenesis;cytoskeleton organization;death;developmental growth;developmental process;establishment of localization;glial cell development;growth;inositol lipid-mediated signaling;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;oligodendrocyte development;organelle organization;phosphatidylinositol-mediated signaling;programmed cell death;protein complex assembly;protein complex subunit organization;protein polymerization;regeneration;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to acid;response to cadmium ion;response to chemical stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to folic acid;response to inorganic substance;response to metal ion;response to nutrient;response to nutrient levels;response to organic substance;response to stimulus;response to vitamin;signal transduction;tissue development;tissue regeneration;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding + actin cytoskeleton;cell part;cell projection;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;protein complex;ruffle;vesicle Fc gamma R-mediated phagocytosis;Regulation of actin cytoskeleton 3.8955E-30 32961000 12

Q86YZ3;CON__Q86YZ3 Hornerin HRNR >sp|Q86YZ3|HORN_HUMAN Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2;>Q86YZ3 SWISS-PROT:Q86YZ3 Tax_Id=9606 Gene_Symbol=HRNR Hornerin 0.20 4.64 0.08 5.62 0.71 3.43 0.90 1.42 + + developmental process;keratinization binding;calcium ion binding;cation binding;ion binding;metal ion binding + cell part;cornified envelope;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;vesicle 3.2586E-33 45576000 12

P26038;P35241-4;P35241;P35241-5 Moesin MSN >sp|P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 0.58 1.76 0.34 1.86 0.77 0.79 1.19 1.17 + actin filament capping;apical protein localization;asymmetric protein localization;biological adhesion;biological regulation;cell adhesion;cell migration;cell motility;cell projection assembly;cell projection organization;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;immune system process;leukocyte cell-cell adhesion;leukocyte migration;localization;locomotion;macromolecule localization;membrane docking;membrane to membrane docking;microvillus assembly;microvillus organization;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;protein localization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell migration;regulation of cell motility;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of immune system process;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of lymphocyte migration;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization structural constituent of cytoskeleton;structural molecule activity + apical part of cell;apical plasma membrane;basolateral plasma membrane;cell division site part;cell part;cell projection;cell projection membrane;cell projection part;cleavage furrow;cytoplasm;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;extrinsic to membrane;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microvillus;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;plasma membrane part;ruffle;stereocilium;uropod;vesicle Leukocyte transendothelial migration;Measles;Regulation of actin cytoskeleton 3.0315E-71 29683000 12

P38159;P38159-2;H3BT71;Q96E39;H0Y6E7;B3KRG5;H3BUY5;H3BR27;P38159-3;O75526;H3BNC1;Q8IZ40;Q8N7X1 "RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome, N-terminally processed;RNA binding motif protein, X-linked-like-1" RBMX;RBMXL1 ">sp|P38159|RBMX_HUMAN RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3;>sp|P38159-2|RBMX_HUMAN Isoform 2 of RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX;>tr|H3BT71|H3BT71_HUMAN RNA-binding motif protein, X chromo" 1.12 1.24 1.61 3.14 0.42 0.46 0.45 0.47 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interleukin-1;cellular response to organic substance;cellular response to stimulus;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;membrane protein ectodomain proteolysis;membrane protein proteolysis;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein oligomerization;proteolysis;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to cytokine stimulus;response to interleukin-1;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;chromatin binding;core promoter binding;DNA binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleotide binding;protein binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;sequence-specific DNA binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding + catalytic step 2 spliceosome;cell part;chromatin;chromosomal part;euchromatin;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex;transcription factor complex;vesicle Spliceosome 6.2835E-156 324390000 12

P35442;Q5RI53 Thrombospondin-2 THBS2 >sp|P35442|TSP2_HUMAN Thrombospondin-2 OS=Homo sapiens GN=THBS2 PE=1 SV=2 0.50 0.56 1.11 1.00 0.54 0.29 0.88 2.03 + + + biological adhesion;biological regulation;cell adhesion;cellular process;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of developmental process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process binding;calcium ion binding;carbohydrate binding;cation binding;glycosaminoglycan binding;heparin binding;ion binding;metal ion binding;pattern binding;polysaccharide binding+ basement membrane;extracellular matrix part;extracellular region;extracellular region part ECM-receptor interaction;Focal adhesion;Malaria;Phagosome;TGF-beta signaling pathway 8.8536E-207 103720000 12

P13646;K7ERE3;P13646-3;CON__ENSEMBL:ENSP00000377550;CON__P13646-1;P13646-2;K7EMD9;K7EQH6 "Keratin, type I cytoskeletal 13" KRT13 ">sp|P13646|K1C13_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4;>tr|K7ERE3|K7ERE3_HUMAN Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=3 SV=1;>sp|P13646-3|K1C13_HUMAN Isoform 3 of Keratin, type I cytoskeletal 13 OS=Ho" NaN 1.57 0.83 1.71 0.78 0.63 NaN 0.27 anatomical structure development;anatomical structure morphogenesis;cell communication;cellular process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;developmental process;epidermis development;organ morphogenesis;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to radiation;response to retinoic acid;response to stimulus;response to vitamin;response to vitamin A;tissue development;tongue morphogenesis structural molecule activity + cell part;cytoskeletal part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle part;protein complex;vesicle 5.1334E-255 7690800 13

Q9H307;Q9H307-2;G3V5F0;G3V579 Pinin PNN >sp|Q9H307|PININ_HUMAN Pinin OS=Homo sapiens GN=PNN PE=1 SV=4;>sp|Q9H307-2|PININ_HUMAN Isoform 2 of Pinin OS=Homo sapiens GN=PNN 1.36 1.42 0.94 2.86 0.55 0.53 0.52 0.52 + "biological adhesion;biological regulation;biosynthetic process;cell adhesion;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;structural molecule activity anchoring junction;catalytic step 2 spliceosome;cell junction;cell part;cell-cell junction;cytoplasm;cytoskeletal part;desmosome;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;membrane;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;plasma membrane;protein complex;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport 6.1441E-32 55164000 13

P53621;P53621-2 Coatomer subunit alpha;Xenin;Proxenin COPA >sp|P53621|COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2;>sp|P53621-2|COPA_HUMAN Isoform 2 of Coatomer subunit alpha OS=Homo sapiens GN=COPA 0.71 1.08 0.40 0.94 4.73 1.78 1.26 1.33 "biological regulation;body fluid secretion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;digestive system process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;multicellular organismal process;organelle organization;pancreatic juice secretion;protein transport;regulation of biological quality;regulation of body fluid levels;retrograde vesicle-mediated transport, Golgi to ER;secretion;system process;transport;vesicle coating;vesicle organization;vesicle-mediated transport" structural molecule activity + cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;extracellular region part;extracellular space;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;protein complex;vesicle coat Neuroactive ligand-receptor interaction 5.875E-36 19017000 14

P32926 Desmoglein-3 DSG3 >sp|P32926|DSG3_HUMAN Desmoglein-3 OS=Homo sapiens GN=DSG3 PE=1 SV=2 1.19 1.40 0.74 1.03 1.15 1.35 0.89 1.13 + biological adhesion;cell adhesion;cell-cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;desmosome;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;plasma membrane 1.1097E-110 146900000 14

Q9UMD9-2;Q9UMD9;A2A2Y8 Collagen alpha-1(XVII) chain;120 kDa linear IgA disease antigen;97 kDa linear IgA disease antigen COL17A1 >sp|Q9UMD9-2|COHA1_HUMAN Isoform 2 of Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1;>sp|Q9UMD9|COHA1_HUMAN Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1 PE=1 SV=3;>tr|A2A2Y8|A2A2Y8_HUMAN Collagen alpha-1(XVII) chain OS=Homo sapiens GN=C 0.97 1.33 1.29 1.46 0.28 0.20 0.42 0.42 + + + anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;developmental process;epidermis development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;tissue development + basement membrane;cell junction;cell part;cell-cell junction;cell-substrate junction;collagen;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region;extracellular region part;hemidesmosome;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane part Protein digestion and absorption 7.5475E-93 189020000 15

Q15582;G8JLA8;H0Y8L3;H0Y9D7;H0YAB8;D6RBX4;H0YAH8 Transforming growth factor-beta-induced protein ig-h3 TGFBI >sp|Q15582|BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1;>tr|G8JLA8|G8JLA8_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=2 SV=1;>tr|H0Y8L3|H0Y8L3_HUMAN Transfor 0.69 0.66 0.95 0.91 0.46 0.82 1.01 2.71 + + + anatomical structure formation involved in morphogenesis;angiogenesis;biological adhesion;biological regulation;cell adhesion;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;extracellular matrix organization;extracellular structure organization;multicellular organismal process;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;neurological system process;regulation of biological process;regulation of cell adhesion;regulation of cellular process;response to stimulus;sensory perception;sensory perception of light stimulus;system process;visual perception binding;extracellular matrix binding;integrin binding;protein binding;protein complex binding;receptor binding + cell part;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;proteinaceous extracellular matrix;vesicle 8.4574E-89 361680000 15

A8K2U0;F5H2Z2;H0YGG5;H0YH14;F5GXP1 Alpha-2-macroglobulin-like protein 1 A2ML1 >sp|A8K2U0|A2ML1_HUMAN Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens GN=A2ML1 PE=1 SV=3;>tr|F5H2Z2|F5H2Z2_HUMAN Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens GN=A2ML1 PE=2 SV=1;>tr|H0YGG5|H0YGG5_HUMAN Alpha-2-macroglobulin-like protein 1 (Fra 0.61 0.48 0.61 0.30 4.37 3.12 1.31 1.13 + + biological regulation;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity + extracellular region;extracellular region part;extracellular space 1.3063E-50 33570000 16

Q02413;B7Z845 Desmoglein-1 DSG1 >sp|Q02413|DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2 0.59 1.00 0.36 0.70 3.06 2.74 1.59 1.03 + biological adhesion;biological regulation;calcium-dependent cell-cell adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion;maternal process involved in female pregnancy;multicellular organismal process;multicellular organismal reproductive process;posttranscriptional regulation of gene expression;protein stabilization;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to progesterone stimulus;response to steroid hormone stimulus;response to stimulus binding;calcium ion binding;cation binding;ion binding;metal ion binding;toxin binding anchoring junction;apical plasma membrane;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;desmosome;integral to membrane;internal side of plasma membrane;intracellular part;intrinsic to membrane;lateral plasma membrane;membrane part;plasma membrane part Staphylococcus aureus infection 9.1675E-104 237770000 16

A8MUB1;P68366;Q9NY65-2;Q9NY65;C9J2C0;C9JEV8;C9JQ00;C9JJQ8;C9JDL2;C9JDS9;C9K0S6;Q9H853 Tubulin alpha-4A chain;Tubulin alpha-8 chain TUBA4A;TUBA8 >tr|A8MUB1|A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1;>sp|P68366|TBA4A_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1;>sp|Q9NY65-2|TBA8_HUMAN Isoform 2 of Tubulin alpha-8 chain OS=Homo sapiens GN=TUBA8;>sp|Q9N 0.66 0.34 0.55 0.19 3.38 3.08 1.77 1.37 cell activation;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cytoskeleton organization;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;exocytosis;G2/M transition of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;organelle organization;platelet activation;platelet degranulation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;secretion;secretion by cell;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" + cell part;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;protein complex "Aminobenzoate degradation;Benzoate degradation;beta-Alanine metabolism;Butanoate metabolism;Caprolactam degradation;Fatty acid metabolism;Gap junction;Lysine degradation;Pathogenic Escherichia coli infection;Peroxisome;Phagosome;PPAR signaling pathway;Propanoate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 1.2003E-170 244480000 16

P07437;Q5JP53;Q5ST81;E9PBJ4;G3V5W4;G3V2R8;G3V3R4;G3V2N6 Tubulin beta chain TUBB >sp|P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2;>tr|Q5JP53|Q5JP53_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=2 SV=1;>tr|Q5ST81|Q5ST81_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=2 SV=1;>tr|E9PBJ4|E9PBJ4_HUMAN Tub 0.65 0.39 0.56 0.35 2.92 1.88 1.78 1.14 biological regulation;cell cycle process;cell division;cell killing;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytoskeleton organization;cytoskeleton-dependent intracellular transport;defense response;establishment of localization;establishment of localization in cell;G2/M transition of mitotic cell cycle;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;intracellular transport;leukocyte mediated cytotoxicity;leukocyte mediated immunity;lymphocyte mediated immunity;macromolecular complex assembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule-based process;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;organelle assembly;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;protein complex assembly;protein complex subunit organization;protein polymerization;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to stimulus;response to stress;spindle assembly;spindle organization;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;MHC class I protein binding;MHC protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" + cell body;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;nuclear envelope lumen;nuclear part;nucleus;organelle;organelle envelope lumen;organelle part;plasma membrane;protein complex;vesicle Gap junction;Pathogenic Escherichia coli infection;Phagosome 4.7013E-262 298000000 19

P04083;Q5T3N1;Q5T3N0 Annexin A1 ANXA1 >sp|P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2;>tr|Q5T3N1|Q5T3N1_HUMAN Annexin A1 (Fragment) OS=Homo sapiens GN=ANXA1 PE=2 SV=1 1.34 1.13 0.49 0.13 2.92 2.68 1.33 0.46 + + acid secretion;alpha-beta T cell activation;alpha-beta T cell differentiation;anatomical structure development;arachidonic acid secretion;biological regulation;carboxylic acid transport;cell activation;cell cycle;cell differentiation;cell surface receptor linked signaling pathway;cellular component movement;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to corticosteroid stimulus;cellular response to endogenous stimulus;cellular response to glucocorticoid stimulus;cellular response to hormone stimulus;cellular response to hydrogen peroxide;cellular response to organic substance;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to stress;defense response;developmental process;endocrine pancreas development;epidermal cell differentiation;epithelial cell differentiation;establishment of localization;establishment of localization in cell;estrous cycle phase;fatty acid transport;gliogenesis;hepatocyte differentiation;homeostasis of number of cells;homeostatic process;hormone secretion;hormone transport;icosanoid secretion;icosanoid transport;immune system process;inflammatory response;insulin secretion;keratinocyte differentiation;leukocyte activation;leukocyte differentiation;lipid transport;long-chain fatty acid transport;lymphocyte activation;lymphocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid transport;myeloid cell homeostasis;negative regulation of acute inflammatory response;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of programmed cell death;negative regulation of protein secretion;negative regulation of protein transport;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of transport;neurogenesis;neutrophil homeostasis;organic acid transport;organic substance transport;ovulation cycle process;peptide cross-linking;peptide hormone secretion;peptide secretion;peptide transport;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of fatty acid biosynthetic process;positive regulation of fatty acid metabolic process;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of myeloid cell apoptosis;positive regulation of neutrophil apoptosis;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of prostaglandin biosynthetic process;positive regulation of transport;positive regulation of vesicle fusion;primary metabolic process;protein metabolic process;protein modification process;regulation of acute inflammatory response;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of defense response;regulation of establishment of protein localization;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of homeostatic process;regulation of hormone levels;regulation of immune system process;regulation of inflammatory response;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of metabolic process;regulation of myeloid cell apoptosis;regulation of neutrophil apoptosis;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of prostaglandin biosynthetic process;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of transport;regulation of vesicle fusion;regulation of vesicle-mediated transport;response to abiotic stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to interleukin-1;response to ionizing radiation;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to radiation;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;response to X-ray;rhythmic process;secretion;secretion by cell;signal release;signal transduction;T cell activation;T cell differentiation;transport "binding;binding, bridging;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phospholipase A2 inhibitor activity;phospholipase inhibitor activity;phospholipid binding;protein binding;protein binding, bridging;receptor binding;structural molecule activity" + basolateral plasma membrane;cell part;cell projection;cilium;cornified envelope;cytoplasm;cytoplasmic part;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;sarcolemma;vesicle 0 1299900000 20

P68133;P68032;P62736;P63267;Q5T8M8;A6NL76;Q5T8M7;P63267-2;C9JFL5;F6UVQ4;F6QUT6;F8WB63;B8ZZJ2"Actin, alpha skeletal muscle;Actin, alpha cardiac muscle 1;Actin, aortic smooth muscle;Actin, gamma-enteric smooth muscle" ACTA1;ACTC1;ACTA2;ACTG2 ">sp|P68133|ACTS_HUMAN Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1;>sp|P68032|ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1;>sp|P62736|ACTA_HUMAN Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=" 0.94 0.98 0.90 1.66 0.53 1.07 0.81 1.25 actin cytoskeleton organization;actin filament organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;actomyosin structure organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptosis;biological regulation;cardiac muscle contraction;cardiac muscle tissue morphogenesis;cardiac myofibril assembly;cell death;cell development;cell growth;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;circulatory system process;cytoskeleton organization;death;developmental process;glomerular mesangial cell development;growth;heart contraction;heart process;mesangial cell development;multicellular organismal process;multi-organism process;muscle adaptation;muscle cell development;muscle contraction;muscle fiber development;muscle filament sliding;muscle system process;muscle tissue morphogenesis;myofibril assembly;organelle organization;programmed cell death;regulation of anatomical structure size;regulation of biological quality;regulation of blood pressure;regulation of blood vessel size;regulation of tube size;response to abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to inorganic substance;response to lithium ion;response to mechanical stimulus;response to metal ion;response to organic substance;response to other organism;response to steroid hormone stimulus;response to stimulus;response to virus;skeletal muscle adaptation;skeletal muscle fiber adaptation;skeletal muscle fiber development;skeletal muscle thin filament assembly;smooth muscle contraction;striated muscle adaptation;striated muscle cell development;striated muscle contraction;system process;tissue morphogenesis;vascular process in circulatory system;vascular smooth muscle contraction;vasoconstriction "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;myosin binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" + "actin cytoskeleton;actin filament;actin filament bundle;actomyosin;actomyosin, actin part;cell part;cell periphery;contractile fiber;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;I band;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle part;protein complex;smooth muscle contractile fiber;stress fiber;striated muscle thin filament;vesicle" Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM);Vascular smooth muscle contraction0 817500000 21

O00468-6;O00468-3;O00468-7;O00468-2;O00468-5;O00468-4;O00468;H0Y5U1 Agrin;Agrin N-terminal 110 kDa subunit;Agrin C-terminal 110 kDa subunit;Agrin C-terminal 90 kDa fragment;Agrin C-terminal 22 kDa fragment

AGRN >sp|O00468-6|AGRIN_HUMAN Isoform 6 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-3|AGRIN_HUMAN Isoform 3 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-7|AGRIN_HUMAN Isoform 7 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-2|AGRIN_HUMAN Isoform 2 of Agrin OS=Homo 1.27 1.08 1.60 1.12 0.20 0.27 0.54 0.61 + + "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;axon guidance;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular response to stimulus;chemotaxis;chondroitin sulfate metabolic process;clustering of voltage-gated sodium channels;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;G-protein coupled receptor protein signaling pathway;isoprenoid metabolic process;lipid metabolic process;localization;locomotion;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;muscarinic acetylcholine receptor signaling pathway;neuronal ion channel clustering;nitrogen compound metabolic process;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell projection organization;positive regulation of cellular biosynthetic process;positive regulation of cellular component biogenesis;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of filopodium assembly;positive regulation of gene expression;positive regulation of growth;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nervous system development;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;positive regulation of RNA metabolic process;positive regulation of synapse assembly;positive regulation of synaptic growth at neuromuscular junction;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein localization;protein localization in membrane;receptor clustering;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell development;regulation of cell differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of filopodium assembly;regulation of gene expression;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of nervous system development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;regulation of synapse assembly;regulation of synapse organization;regulation of synaptic growth at neuromuscular junction;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;sulfur compound metabolic process;synapse organization;taxis;terpenoid metabolic process"binding;calcium ion binding;carbohydrate binding;cation binding;chondroitin sulfate binding;dystroglycan binding;extracellular matrix binding;glycoprotein binding;glycosaminoglycan binding;heparan sulfate proteoglycan binding;ion binding;laminin binding;metal ion binding;monosaccharide binding;pattern binding;polysaccharide binding;protein binding;proteoglycan binding;sialic acid binding;structural constituent of cytoskeleton;structural molecule activity;sugar binding + basal lamina;cell junction;cell part;cytoplasmic part;extracellular matrix part;extracellular region part;Golgi apparatus part;Golgi lumen;integral to membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal lumen;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;synapse;vacuolar lumen;vacuolar part ECM-receptor interaction 4.5681E-83 151330000 21

Q9NZM1-6;Q9NZM1-3;C9JCN0;Q9NZM1;F8W8J4;Q9NZM1-2;Q9NZM1-5;H0YD14;Q9NZM1-7;Q9NZM1-8;Q9NZM1-4;O75923-15;O75923-3;O75923-9;O75923;O75923-14;O75923-6;O75923-12;O75923-5;O75923-11;O75923-4;O75923-10;O75923-2;O75923-8;O75923-7;O75923-13 Myoferlin MYOF >sp|Q9NZM1-6|MYOF_HUMAN Isoform 6 of Myoferlin OS=Homo sapiens GN=MYOF;>sp|Q9NZM1-3|MYOF_HUMAN Isoform 3 of Myoferlin OS=Homo sapiens GN=MYOF;>tr|C9JCN0|C9JCN0_HUMAN Myoferlin OS=Homo sapiens GN=MYOF PE=2 SV=2;>sp|Q9NZM1|MYOF_HUMAN Myoferlin OS=Homo sapien 1.02 0.69 0.92 0.59 0.81 0.79 1.70 1.91 biological regulation;blood circulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;circulatory system process;membrane fusion;membrane organization;multicellular organismal process;muscle contraction;muscle system process;organelle fusion;organelle organization;plasma membrane organization;plasma membrane repair;regulation of biological process;regulation of cellular process;regulation of cellular response to growth factor stimulus;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of vascular endothelial growth factor receptor signaling pathway;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus;system process;vesicle fusion;vesicle organization binding;calcium-dependent phospholipid binding;lipid binding;phospholipid binding+ caveola;cell part;cell projection;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;envelope;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lamellipodium;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;nuclear envelope;nuclear membrane;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;plasma membrane;plasma membrane part;T-tubule;vesicle;vesicle membrane 2.7134E-134 84360000 21

P07355;P07355-2;H0YN42;H0YMD0;H0YMU9;A6NMY6;H0YKS4;H0YM50;H0YMM1;H0YNP5;H0YKZ7;H0YLV6;H0YMT9;H0YKX9;H0YN28;H0YL33;H0YKV8;H0YKL9;H0YMW4;H0YMD9;H0YNA0;H0YNB8;H0YN52;H0YKN4;H0YLE2 Annexin A2;Annexin;Putative annexin A2-like proteinANXA2;ANXA2P2 >sp|P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2;>sp|P07355-2|ANXA2_HUMAN Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2;>tr|H0YN42|H0YN42_HUMAN Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1;>tr|H0YMD0|H0YMD0_HUMAN Annexin (Fr 1.08 0.57 0.58 0.20 3.84 2.30 1.74 0.92 + + anatomical structure development;anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;body fluid secretion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to chemical stimulus;cellular response to stimulus;collagen fibril organization;developmental process;establishment of localization;extracellular matrix organization;extracellular structure organization;fibrinolysis;multicellular organismal process;negative regulation of biological process;negative regulation of blood coagulation;negative regulation of coagulation;negative regulation of multicellular organismal process;positive regulation of binding;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of transport;positive regulation of vesicle fusion;regulation of binding;regulation of biological process;regulation of biological quality;regulation of blood coagulation;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular process;regulation of coagulation;regulation of localization;regulation of molecular function;regulation of multicellular organismal process;regulation of organelle organization;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of transport;regulation of vesicle fusion;regulation of vesicle-mediated transport;regulation of wound healing;response to acid;response to chemical stimulus;response to stimulus;secretion;skeletal system development;system development;transport "binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipase inhibitor activity;phospholipid binding" + basement membrane;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome;endosome;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;extrinsic to membrane;extrinsic to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lipid particle;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;midbody;myelin sheath adaxonal region;organelle;perinuclear region of cytoplasm;pigment granule;plasma membrane;plasma membrane part;protein complex;sarcolemma;Schmidt-Lanterman incisure;vesicle 0 2607100000 22

Q9Y446;E9PKC4;E9PK71;E9PRW6;E9PJR7;E9PQ15;H0YEY5 Plakophilin-3 PKP3 >sp|Q9Y446|PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1 0.99 1.08 1.18 1.23 1.42 1.69 0.76 0.67 + biological adhesion;cell adhesion;cellular process anchoring junction;cell junction;cell part;cell-cell junction;desmosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.0805E-124 211280000 23

Q6UWP8;Q6UWP8-2;K7ESC4 Suprabasin SBSN >sp|Q6UWP8|SBSN_HUMAN Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2 1.13 0.84 0.51 0.24 3.56 2.27 1.70 1.05 + extracellular region 7.5951E-241 474170000 23

Q6XPR3 Repetin RPTN >sp|Q6XPR3|RPTN_HUMAN Repetin OS=Homo sapiens GN=RPTN PE=1 SV=1 0.24 0.25 0.54 0.22 3.87 3.01 1.86 1.07 + + binding;calcium ion binding;cation binding;ion binding;metal ion binding + cell part;cornified envelope;cytoskeleton;extracellular matrix;extracellular region part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle;proteinaceous extracellular matrix 7.32E-102 155550000 24

P16615-5;P16615-2;P16615-3;P16615;P16615-4;H7C5W9;O14983-2;O14983;B3KY17;Q93084-4;Q93084-2;Q93084-3;Q93084-7;Q93084;Q93084-6;Q93084-5;F8VSH0;H3BVB2 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 ATP2A2 >sp|P16615-5|AT2A2_HUMAN Isoform 5 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2;>sp|P16615-2|AT2A2_HUMAN Isoform 2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2;>sp|P16615-3|AT2A2_HUMAN 1.10 1.00 1.44 0.92 1.55 0.93 1.02 1.06 + anatomical structure development;apoptosis;apoptosis in response to endoplasmic reticulum stress;apoptotic mitochondrial changes;biological adhesion;biological regulation;blood coagulation;calcium ion homeostasis;calcium ion import;calcium ion transmembrane transport;calcium ion transport;cation homeostasis;cation transport;cell adhesion;cell death;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;coagulation;death;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of endoplasmic reticulum calcium ion concentration;elevation of mitochondrial calcium ion concentration;endoplasmic reticulum calcium ion homeostasis;epidermis development;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;hemostasis;homeostatic process;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;maintenance of location;maintenance of location in cell;maintenance of mitochondrion location;maintenance of organelle location;metal ion homeostasis;metal ion transport;mitochondrial calcium ion homeostasis;mitochondrion organization;multicellular organismal process;muscle system process;negative regulation of biological process;negative regulation of cardiac muscle contraction;negative regulation of heart contraction;negative regulation of multicellular organismal process;negative regulation of muscle contraction;negative regulation of striated muscle contraction;organelle organization;positive regulation of biological process;positive regulation of fast-twitch skeletal muscle fiber contraction;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of striated muscle contraction;programmed cell death;reduction of endoplasmic reticulum calcium ion concentration;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cardiac muscle contraction;regulation of cellular process;regulation of fast-twitch skeletal muscle fiber contraction;regulation of heart contraction;regulation of heart rate;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of skeletal muscle contraction;regulation of striated muscle contraction;regulation of system process;regulation of the force of heart contraction;regulation of twitch skeletal muscle contraction;relaxation of cardiac muscle;relaxation of muscle;relaxation of skeletal muscle;response to stimulus;sarcoplasmic reticulum calcium ion transport;signal transduction;system process;tissue development;transmembrane transport;transport"active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;calcium ion binding;calcium ion transmembrane transporter activity;calcium-transporting ATPase activity;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;divalent inorganic cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;metal ion transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" calcium channel complex;cation channel complex;cell part;contractile fiber part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;H zone;I band;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nuclear membrane;nuclear part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;platelet dense tubular network membrane;protein complex;sarcoplasmic reticulum;sarcoplasmic reticulum membrane Alzheimer's disease;Calcium signaling pathway;Pancreatic secretion 6.5691E-154 382620000 26

O00515;E9PDI4;H0Y901 Ladinin-1LAD1 >sp|O00515|LAD1_HUMAN Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2;>tr|E9PDI4|E9PDI4_HUMAN Ladinin-1 OS=Homo sapiens GN=LAD1 PE=2 SV=1 1.05 0.69 0.94 1.31 1.17 1.12 1.17 0.92 structural molecule activity + actin cytoskeleton;basement membrane;cell part;cytoskeleton;extracellular matrix part;extracellular region part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 0 369100000 26

P60709;CON__P60712;G5E9R0;E7EVS6;C9JZR7;C9JTX5;C9JUM1;Q6S8J3;A5A3E0;P0CG38;P0CG39;Q9BYX7;F8WCH0 "Actin, cytoplasmic 1;Actin, cytoplasmic 1, N-terminally processed" ACTB ">sp|P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1;>P60712 SWISS-PROT:P60712 (Bos taurus) Actin, cytoplasmic 1" 1.04 0.99 0.83 1.65 0.73 0.94 0.89 1.14 adherens junction organization;anatomical structure morphogenesis;axon guidance;axonogenesis;biological regulation;blood coagulation;cell activation;cell junction assembly;cell junction organization;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;coagulation;'de novo' posttranslational protein folding;'de novo' protein folding;defense

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response;developmental process;establishment of localization;establishment of localization in cell;exocytosis;hemostasis;immune response;immune system process;innate immune response;locomotion;macromolecule metabolic
process;membrane organization;metabolic process;multicellular organismal process;neuron projection morphogenesis;platelet activation;platelet degranulation;primary metabolic process;protein folding;protein metabolic process;regulation
of biological quality;regulation of body fluid levels;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;secretion;secretion by cell;taxis;transport;vesicle-mediated transport	adenyl
nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural constituent of
cytoskeleton;structural molecule activity	+	axon;cell cortex;cell cortex part;cell part;cell projection;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded
organelle;extracellular organelle;extracellular region;extracellular region part;extracellular vesicular exosome;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;histone methyltransferase complex;intracellular
non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;methyltransferase complex;MLL5-L
complex;neuron projection;non-membrane-bounded organelle;NuA4 histone acetyltransferase complex;nuclear part;nucleoplasm part;organelle;organelle part;postsynaptic density;protein complex;ribonucleoprotein complex;synapse
part;vesicle	Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Dilated cardiomyopathy;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leukocyte transendothelial
migration;Pathogenic Escherichia coli infection;Phagosome;Phototransduction - fly;Regulation of actin cytoskeleton;Shigellosis;Tight junction;Vibrio cholerae infection;Viral myocarditis	0	19896000000	27
P63261;I3L3I0;I3L1U9;K7EM38;I3L3R2;J3KT65	"Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed"	ACTG1	">sp|P63261|ACTG_HUMAN Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1
SV=1;>tr|I3L3I0|I3L3I0_HUMAN Actin, cytoplasmic 2, N-terminally processed (Fragment) OS=Homo sapiens GN=ACTG1 PE=2 SV=1;>tr|I3L1U9|I3L1U9_HUMAN Actin, cytoplasmic 2, N-terminally proc"	1.37 NaN 1.00 1.55 0.57
1.03 0.99 NaN					actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;adherens junction organization;axon guidance;cell junction assembly;cell junction
organization;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular
component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;chemotaxis;cytoskeleton organization;defense response;immune response;immune
system process;innate immune response;locomotion;membrane organization;organelle organization;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;sarcomere organization;taxis	adenyl
nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural constituent of
cytoskeleton;structural molecule activity	+	cell part;contractile fiber;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region
part;extracellular vesicular exosome;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-
bounded vesicle;myofibril;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle	Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Dilated
cardiomyopathy;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Phagosome;Phototransduction - fly;Regulation of actin cytoskeleton;Shigellosis;Tight
junction;Vibrio cholerae infection;Viral myocarditis	0	19952000	27
P22735;B4DWR7;H0YMQ8;H0YN27;H0YNM4;H0YLJ6;H0YKI6;H0YLT9	Protein-glutamine gamma-glutamyltransferase K	TGM1	>sp|P22735|TGM1_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens
GN=TGM1 PE=1 SV=4;>tr|B4DWR7|B4DWR7_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=2 SV=1	1.12 1.24 1.47 0.74 2.64 2.09 0.93 0.40 +				+
anatomical structure morphogenesis;cell differentiation;cell envelope organization;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic
process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;external encapsulating structure organization;keratinization;keratinocyte
differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;organ morphogenesis;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process
"binding;catalytic activity;cation binding;ion binding;metal ion binding;protein-glutamine gamma-glutamyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring amino-acyl
groups"		adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cornified envelope;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular
part;intrinsic to membrane;membrane part;non-membrane-bounded organelle;organelle		1.8537E-293	568000000	28
P14923	Junction plakoglobin	JUP	>sp|P14923|PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	0.83 0.97 0.54 0.75 2.04 2.30 1.25 0.92				+	"adherens junction
organization;anatomical structure development;anatomical structure morphogenesis;atrioventricular valve morphogenesis;biological adhesion;biological regulation;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling
pathway involved in heart development;cell adhesion;cell development;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell motility;cell surface receptor linked signaling pathway;cell surface receptor
linked signaling pathway involved in heart development;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component
morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular
level;cellular developmental process;cellular process;cellular process involved in reproduction;cellular response to chemical stimulus;cellular response to indole-3-methanol;cellular response to organic substance;cellular response to
stimulus;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;desmosome assembly;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection of stimulus;developmental
process;developmental process involved in reproduction;ectoderm development;embryonic morphogenesis;endothelial cell-cell adhesion;epidermis development;epithelial cell-cell adhesion;gastrulation;germ cell development;heart valve
morphogenesis;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in
cell;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;negative regulation of biological process;negative regulation of cardiac cell fate specification;negative regulation of cardioblast cell fate specification;negative
regulation of cell communication;negative regulation of cell differentiation;negative regulation of cell fate commitment;negative regulation of cell fate specification;negative regulation of cellular process;negative regulation of
developmental process;negative regulation of heart induction by canonical Wnt receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative
regulation of Wnt receptor signaling pathway;negative regulation of Wnt receptor signaling pathway involved in heart development;nervous system development;oocyte development;organelle organization;positive regulation of biological
process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cell communication;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular
transport;positive regulation of molecular function;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of response to
stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transmembrane transport;positive regulation of
transport;positive regulation of Wnt receptor signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regulation of apoptosis;regulation of biological
process;regulation of biological quality;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac cell fate specification;regulation of cardioblast cell fate specification;regulation of
cardioblast differentiation;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell fate commitment;regulation of cell fate specification;regulation of cell proliferation;regulation of cellular
biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of
establishment of protein localization;regulation of gene expression;regulation of heart induction;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule
biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal
process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of programmed cell
death;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding
transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of Wnt receptor signaling
pathway;regulation of Wnt receptor signaling pathway involved in heart development;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to indole-3-methanol;response to
mechanical stimulus;response to organic substance;response to stimulus;signal transduction;skin development;system development;tissue development;tissue morphogenesis;Wnt receptor signaling pathway;Wnt receptor signaling pathway
involved in heart development"	binding;enzyme binding;identical protein binding;kinase binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein homodimerization activity;protein kinase
binding;structural constituent of cell wall;structural molecule activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity		actin cytoskeleton;adherens
junction;anchoring junction;apicolateral plasma membrane;basolateral plasma membrane;catenin complex;catenin-TCF7L2 complex;cell junction;cell part;cell-cell adherens junction;cell-cell junction;contractile fiber part;cytoplasmic
part;cytoskeletal part;cytoskeleton;cytosol;cytosolic part;desmosome;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;gamma-catenin-TCF7L2 complex;intermediate filament;internal side of plasma
membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;non-membrane-bounded
organelle;organelle;organelle part;plasma membrane part;protein complex;protein-DNA complex;Z disc;zonula adherens	Acute myeloid leukemia;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Pathways in cancer	3.0942E-
205	292610000	30
Q14764;H3BQK6;H3BRL2;H3BUK7;H3BNF6;H3BP76;H3BPZ2;H3BNF2;H3BUP3;H3BQE7	Major vault protein	MVP	>sp|Q14764|MVP_HUMAN Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	0.87 0.35 0.49
0.38 2.39 1.50 2.18 1.58					biological regulation;establishment of localization;establishment of protein localization;establishment of RNA localization;mRNA transport;negative regulation of biological
process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of kinase activity;negative
regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic
process;negative regulation of phosphorylation;negative regulation of protein autophosphorylation;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification
process;negative regulation of protein phosphorylation;negative regulation of protein tyrosine kinase activity;negative regulation of signaling;negative regulation of transferase activity;nucleic acid transport;nucleobase-containing compound
transport;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase
activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of
phosphorylation;regulation of primary metabolic process;regulation of protein autophosphorylation;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein
phosphorylation;regulation of protein tyrosine kinase activity;regulation of signaling;regulation of transferase activity;RNA transport;transport	binding;enzyme binding;phosphatase binding;protein binding;protein phosphatase binding
+	cell part;cytoplasmic part;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-
bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nuclear
part;nuclear pore;nucleus;organelle;organelle part;perinuclear region of cytoplasm;pore complex;protein complex;ribonucleoprotein complex;vesicle		2.5385E-189	215030000	30
O00159-3;F5H6E2;O00159;O00159-2;I3L501;I3L204;I3L4D4;I3L3Y6;I3L168;I3L3F5	Unconventional myosin-Ic	MYO1C	>sp|O00159-3|MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens
GN=MYO1C;>tr|F5H6E2|F5H6E2_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=2 SV=1;>sp|O00159|MYO1C_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4;>	0.97 1.32
1.22 1.83 0.75 0.77 0.58 0.78					biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;defense
response;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;immune response;immune system process;innate immune response;intracellular protein
transport;intracellular transport;membrane organization;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;positive regulation of biological process;positive regulation of intracellular protein transport;positive
regulation of intracellular transport;positive regulation of protein targeting to membrane;positive regulation of protein transport;positive regulation of transport;protein targeting;protein targeting to membrane;protein transport;regulation of
biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of
intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of protein localization;regulation of protein targeting to membrane;regulation of protein transport;regulation of tight junction
assembly;regulation of transport;response to stimulus;response to stress;RNA transport;transport	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity,
acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate
binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	+	basal plasma membrane;brush border;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic part;cytoskeletal
part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;filamentous actin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded
organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded
vesicle;microvillus;microvillus membrane;myosin complex;myosin I complex;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleolus;nucleoplasm;nucleus;organelle;organelle part;plasma membrane part;pore
complex;protein complex;stereocilium;stereocilium membrane;unconventional myosin complex;vesicle		2.2714E-176	245730000	30
P14618;P14618-3;H3BQ34;H3BUW1;H3BTJ2;H3BT25;H3BU13;H3BN34;H3BQZ3;P30613-2;P30613	Pyruvate kinase isozymes M1/M2;Pyruvate kinase	PKM	>sp|P14618|KPYM_HUMAN Pyruvate kinase PKM OS=Homo
sapiens GN=PKM PE=1 SV=4;>sp|P14618-3|KPYM_HUMAN Isoform 3 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM;>tr|H3BQ34|H3BQ34_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM PE=2 SV=1	0.24 3.53 0.15
3.57 0.54 1.92 0.54 1.06					alcohol catabolic process;alcohol metabolic process;anatomical structure development;ATP biosynthetic process;ATP metabolic process;biological regulation;biosynthetic
process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;catabolic process;cell death;cellular biosynthetic process;cellular carbohydrate catabolic
process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response
to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response
to stimulus;death;developmental process;endocrine pancreas development;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucose catabolic
process;glucose metabolic process;glycolysis;heterocycle biosynthetic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide
catabolic process;monosaccharide metabolic process;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-
containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic
process;organic acid biosynthetic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of
cellular process;positive regulation of metabolic process;primary metabolic process;programmed cell death;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic
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process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyruvate biosynthetic process;pyruvate metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;response to abiotic stimulus;response to ATP;response to biotic stimulus;response to cAMP;response to carbohydrate stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to glucose stimulus;response to heat;response to hexose stimulus;response to hormone stimulus;response to hypoxia;response to inorganic substance;response to insulin stimulus;response to lithium ion;response to metal ion;response to monosaccharide stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to other organism;response to oxygen levels;response to peptide hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;alkali metal ion binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;potassium ion binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyruvate kinase activity;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups"+ cell part;cytoplasmic part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;nucleus;organelle;plasma membrane;vesicle Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis;Insulin signaling pathway;Maturity onset diabetes of the young;Purine metabolism;Pyruvate metabolism;Type II diabetes mellitus 0 1159200000 32

P10809;E7ESH4;E7EXB4;B7Z712;C9JL25;C9JL19;C9JCQ4;C9J0S9 "60 kDa heat shock protein, mitochondrial" HSPD1 ">sp|P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2" 1.20 1.01 1.81 0.65 1.29 0.92 1.32 1.26 activation of caspase activity;activation of immune response;activation of innate immune response;adaptive immune response;adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;B cell activation;B cell activation involved in immune response;B cell cytokine production;B cell mediated immunity;B cell proliferation;biological regulation;cell activation;cell activation involved in immune response;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;chaperone-mediated protein complex assembly;cytokine production;cytokine production involved in immune response;'de novo' protein folding;DNA metabolic process;DNA recombination;immune effector process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response-activating signal transduction;interaction with host;interspecies interaction between organisms;isotype switching;isotype switching to IgG isotypes;leukocyte activation;leukocyte activation involved in immune response;leukocyte mediated immunity;leukocyte proliferation;lymphocyte activation;lymphocyte activation involved in immune response;lymphocyte mediated immunity;lymphocyte proliferation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mononuclear cell proliferation;multicellular organismal process;multi-organism process;MyD88-dependent toll-like receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;pattern recognition receptor signaling pathway;positive regulation of adaptive immune response;positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell death;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of hydrolase activity;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune response to tumor cell;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of interferon-alpha production;positive regulation of interferon-gamma production;positive regulation of interleukin-10 production;positive regulation of interleukin-12 production;positive regulation of interleukin-6 production;positive regulation of leukocyte activation;positive regulation of leukocyte mediated immunity;positive regulation of lymphocyte activation;positive regulation of lymphocyte mediated immunity;positive regulation of macrophage activation;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of response to biotic stimulus;positive regulation of response to stimulus;positive regulation of response to tumor cell;positive regulation of T cell activation;positive regulation of T cell mediated immune response to tumor cell;positive regulation of T cell mediated immunity;positive regulation of type I interferon production;posttranscriptional regulation of gene expression;primary metabolic process;production of molecular mediator of immune response;protein complex assembly;protein complex subunit organization;protein folding;protein maturation;protein metabolic process;protein refolding;protein stabilization;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell activation;regulation of cell death;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of immune effector process;regulation of immune response;regulation of immune response to tumor cell;regulation of immune system process;regulation of innate immune response;regulation of interferon-alpha production;regulation of interferon-gamma production;regulation of interleukin-10 production;regulation of interleukin-12 production;regulation of interleukin-6 production;regulation of leukocyte activation;regulation of leukocyte mediated immunity;regulation of lymphocyte activation;regulation of lymphocyte mediated immunity;regulation of macromolecule metabolic process;regulation of macrophage activation;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of peptidase activity;regulation of programmed cell death;regulation of protein stability;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of response to tumor cell;regulation of T cell activation;regulation of T cell mediated immune response to tumor cell;regulation of T cell mediated immunity;regulation of type I interferon production;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;signal transduction;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response;T cell activation;toll-like receptor signaling pathway;viral reproductive process;virus-host interaction"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cell surface binding;DNA binding;DNA replication origin binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipopolysaccharide binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;sequence-specific DNA binding;single-stranded DNA binding;structure-specific DNA binding;unfolded protein binding" + cell part;cell surface;coated pit;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;early endosome;endosome;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lipopolysaccharide receptor complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane part;protein complex;receptor complex;stored secretory granule;vesicle ko05152;RNA degradation;Type I diabetes mellitus 0 1213600000 33

P11142;E9PKE3;P11142-2;E9PNE6;E9PN89;A8K7Q2;E9PLF4;E9PQQ4;E9PQK7;E9PK54;E9PPY6;E9PS65;E9PI65;E9PN25;E9PM13 Heat shock cognate 71 kDa protein HSPA8 >sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1;>tr|E9PKE3|E9PKE3_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=2 SV=1;>sp|P11142-2|HSP7C_HUMAN Isoform 2 of Heat shock cognate 71 kDa protein 1.10 1.17 0.97 1.69 0.46 0.51 1.01 0.97 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chaperone mediated protein folding requiring cofactor;chaperone-mediated protein folding;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;gene expression;Golgi vesicle transport;interaction with host;interspecies interaction between organisms;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;membrane organization;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;post-Golgi vesicle-mediated transport;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of neurotransmitter levels;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;secretion;secretion by cell;signal release;transcription, DNA-dependent;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" + cell part;cell surface;clathrin coated vesicle membrane;clathrin sculpted gamma-aminobutyric acid transport vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;protein complex;Prp19 complex;ribonucleoprotein complex;spliceosomal complex;vesicle;vesicle membrane Antigen processing and presentation;Endocytosis;MAPK signaling pathway;Measles;Protein processing in endoplasmic reticulum;Spliceosome;Toxoplasmosis 0 1139700000 34

P23229-7;C9JXX7 >sp|P23229-7|ITA6_HUMAN Isoform 7 of Integrin alpha-6 OS=Homo sapiens GN=ITGA6 NaN 1.54 NaN NaN NaN NaN NaN 0.34 + anatomical structure morphogenesis;biological adhesion;biological regulation;brown fat cell differentiation;cell adhesion;cell adhesion mediated by integrin;cell communication;cell differentiation;cell migration;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to stimulus;developmental process;fat cell differentiation;filopodium assembly;immune system process;integrin-mediated signaling pathway;leukocyte migration;locomotion;microspike assembly;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-cell adhesion;positive regulation of cellular process;regulation of biological process;regulation of cell adhesion;regulation of cell-cell adhesion;regulation of cellular process;response to external stimulus;response to extracellular stimulus;response to stimulus;signal transduction + basal plasma membrane;basement membrane;cell junction;cell part;cell-substrate junction;external side of plasma membrane;extracellular matrix part;extracellular region part;hemidesmosome;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex 0 3098100 34

P11021;O95399;Q5H8X8;O95399-2 78 kDa glucose-regulated protein HSPA5 >sp|P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=21.50 0.77 0.67 0.49 0.92 0.51 1.84 1.41 "activation of signaling protein activity involved in unfolded protein response;anatomical structure arrangement;anatomical structure development;behavior;biological regulation;calcium ion homeostasis;catabolic process;cation homeostasis;cell activation;cell communication;cell-cell signaling;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to biotic stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;cerebellar Purkinje cell layer development;cerebellum structural organization;chemical homeostasis;circadian behavior;circadian rhythm;circadian sleep/wake cycle process;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion concentration;ER overload response;ER-associated protein catabolic process;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;homeostatic process;ion homeostasis;macromolecule catabolic process;macromolecule metabolic process;metabolic process;metal ion homeostasis;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multicellular organismal process;muscle contraction;muscle system process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood pressure;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular process;negative regulation of glomerular filtration;negative regulation of heart contraction;negative regulation of heart rate;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of multicellular organismal process;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of programmed cell death;negative regulation of renal sodium excretion;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of transport;negative regulation of urine volume;platelet activation;platelet degranulation;positive regulation of angiogenesis;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of blood pressure;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of circadian rhythm;positive regulation of circadian sleep/wake cycle, REM sleep;positive regulation of circadian sleep/wake cycle, sleep;positive regulation of circadian sleep/wake cycle, wakefulness;positive regulation of collagen biosynthetic process;positive regulation of collagen metabolic process;positive regulation of developmental process;positive regulation of fibroblast migration;positive regulation of fibroblast proliferation;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal metabolic process;positive regulation of multicellular organismal process;positive regulation of neurological system process;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of response to stimulus;positive regulation of signaling;positive regulation of synaptic transmission;positive regulation of synaptic transmission, cholinergic;positive regulation of transferase activity;positive regulation of transmission of nerve impulse;positive regulation of vasodilation;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of body fluid levels;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of circadian rhythm;regulation of circadian sleep/wake cycle;regulation of circadian sleep/wake cycle, REM sleep;regulation of circadian sleep/wake cycle, sleep;regulation of circadian sleep/wake cycle, wakefulness;regulation of collagen biosynthetic process;regulation of collagen metabolic process;regulation of developmental process;regulation of excretion;regulation of fibroblast migration;regulation of fibroblast proliferation;regulation of glomerular filtration;regulation of heart contraction;regulation of heart rate;regulation of homeostatic process;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of ion homeostasis;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of nuclease activity;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein folding in endoplasmic reticulum;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein ubiquitination;regulation of renal sodium excretion;regulation of response to stimulus;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of synaptic transmission;regulation of synaptic transmission, cholinergic;regulation of system process;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmission of nerve impulse;regulation of transport;regulation of urine volume;regulation of vasodilation;renal system process;renal system process involved in regulation of blood volume;renal system process involved in regulation of systemic arterial blood pressure;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to endoplasmic reticulum stress;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to hypoxia;response to nutrient levels;response to organic substance;response to oxygen levels;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;rhythmic behavior;rhythmic process;secretion;secretion by cell;signal transduction;signaling;synaptic transmission;system process;transport;ubiquitin-dependent protein catabolic process;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;binding, bridging;calcium ion binding;catalytic activity;cation binding;chaperone binding;hormone activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;misfolded protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleoprotein binding;ribonucleotide binding;ribosome binding;unfolded protein binding" + cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum chaperone complex;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;extracellular region part;extracellular space;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;midbody;nucleus;organelle;organelle lumen;organelle part;pigment granule;protein complex;vesicle Neuroactive ligand-receptor interaction;Prion diseases;Protein export;Protein processing in endoplasmic reticulum 0 919280000 36

Q00610-2;Q00610;J3KS13;K7EJJ5;J3KSQ2;J3KRF5;F5H5N6 Clathrin heavy chain 1 CLTC >sp|Q00610-2|CLH1_HUMAN Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC;>sp|Q00610|CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 1.01 0.83 0.40 0.88 1.18 1.26 1.67 1.36 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cation transport;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;ferric iron transport;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;ion transport;iron ion transport;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;metal ion transport;mitosis;nuclear division;organelle fission;organelle organization;post-Golgi vesicle-mediated transport;protein transport;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;transferrin transport;transition metal ion transport;transport;vesicle-mediated transport structural molecule activity + cell part;clathrin coat;clathrin coat of coated pit;clathrin coat of trans-Golgi network vesicle;clathrin coated vesicle membrane;clathrin vesicle coat;clathrin-coated endocytic vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endocytic vesicle membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane coat;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;protein complex;spindle;trans-Golgi network membrane;vesicle;vesicle coat;vesicle membrane Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease;Lysosome 0 400550000 37

P23229-4;P23229-2;P23229-9;P23229-6;P23229-5;P23229-3;P23229;H7BZ97 Integrin alpha-6;Integrin alpha-6 heavy chain;Integrin alpha-6 light chain ITGA6 >sp|P23229-4|ITA6_HUMAN Isoform Alpha-6X2A of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;>sp|P23229-2|ITA6_HUMAN Isoform Alpha-6X1A of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;>sp|P23229-9|ITA6_HUMAN Isoform 9 of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;> 1.47 1.27 0.99 1.14 0.52 0.17 0.35 0.39 + "biological adhesion;biological regulation;blood coagulation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;coagulation;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;hemostasis;immune system process;integrin-mediated signaling pathway;leukocyte migration;locomotion;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;signal transduction" binding;cation binding;ion binding;metal ion binding cell part;integrin complex;macromolecular complex;membrane;membrane part;plasma membrane;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer;Toxoplasmosis 0 1552800000 37

P24821;P24821-3 Tenascin TNC >sp|P24821|TENA_HUMAN Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3;>sp|P24821-3|TENA_HUMAN Isoform 3 of Tenascin OS=Homo sapiens GN=TNC 0.27 0.37 0.73 0.67 1.03 1.52 1.23 3.42 + + + anatomical structure morphogenesis;axon regeneration;axonogenesis;biological adhesion;biological regulation;cell adhesion;cell communication;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell signaling;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular process involved in reproduction;cellular response to stimulus;cellular response to stress;developmental process;developmental process involved in reproduction;mesenchymal-epithelial cell signaling;mesenchymal-epithelial cell signaling involved in prostate gland development;morphogenesis of an epithelium;neuromuscular junction development;neuron projection morphogenesis;neuron projection regeneration;peripheral nervous system axon regeneration;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;prostate gland epithelium morphogenesis;regeneration;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;reproductive process;response to axon injury;response to stimulus;response to stress;response to wounding;signaling;synapse organization;tissue morphogenesis + basement membrane;extracellular matrix;extracellular matrix part;extracellular region part;extracellular space;interstitial matrix;proteinaceous extracellular matrix ECM-receptor interaction;Focal adhesion 3.1105E-178 266750000 37

O43707;D6PXK4;F5GXS2;H7C144;K7EJH8;K7EP19;D6RH00;Q9H254-2;C9JRP8;M0QZQ3;Q9H254-4;Q9H254 Alpha-actinin-4 ACTN4 >sp|O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2;>tr|D6PXK4|D6PXK4_HUMAN Alpha actinin 4 short isoform OS=Homo sapiens GN=ACTN4 PE=2 SV=1 1.69 0.55 1.07 1.26 1.44 0.81 1.85 1.20 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament capping;actin filament organization;actin filament-based process;adult behavior;adult locomotory behavior;adult walking behavior;anatomical structure morphogenesis;axon guidance;axonogenesis;behavior;biological regulation;cardiac conduction;cell activation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;central nervous system neuron axonogenesis;central nervous system projection neuron axonogenesis;chemotaxis;circulatory system process;clustering of voltage-gated sodium channels;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;exocytosis;fertilization;heart process;locomotion;locomotory behavior;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane organization;multicellular organismal process;multicellular organismal signaling;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of heart contraction;negative regulation of heart rate;negative regulation of multicellular organismal process;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;neurological system process;neuron projection morphogenesis;neuronal ion channel clustering;organelle organization;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of growth;positive regulation of ion transmembrane transporter activity;positive regulation of molecular function;positive regulation of multicellular organism growth;positive regulation of multicellular organismal process;positive regulation of pinocytosis;positive regulation of sodium ion transmembrane transporter activity;positive regulation of sodium:hydrogen antiporter activity;positive regulation of transport;positive regulation of transporter activity;protein transport;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cardiac muscle contraction;regulation of cell death;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of endocytosis;regulation of growth;regulation of heart contraction;regulation of heart rate;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of organelle organization;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of pinocytosis;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of proton transport;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of sodium:hydrogen antiporter activity;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to external stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signaling;system process;taxis;transmission of nerve impulse;transport;vesicle-mediated transport actin binding;actin filament binding;ankyrin binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;identical protein binding;integrin binding;ion binding;lipid binding;metal ion binding;nucleoside binding;phospholipid binding;protein binding;protein complex binding;protein dimerization activity;protein homodimerization activity;receptor binding;spectrin binding;structural constituent of cytoskeleton;structural molecule activity + adherens junction;anchoring junction;axon hillock;axon part;cell body fiber;cell cortex part;cell junction;cell part;cell projection;cell projection part;contractile fiber part;cortical cytoskeleton;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;initial segment;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;neuron projection;node of Ranvier;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear part;nucleoplasm part;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane;platelet alpha granule lumen;PML body;protein complex;pseudopodium;ribonucleoprotein complex;secretory granule lumen;spectrin;vesicle;vesicle lumen;Z disc Adherens junction;Amoebiasis;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Systemic lupus erythematosus;Tight junction 0 298020000 41

Q14517;D6RCE4 "Protocadherin Fat 1;Protocadherin Fat 1, nuclear form" FAT1 >sp|Q14517|FAT1_HUMAN Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2 0.99 0.94 1.27 1.25 0.42 0.61 0.68 1.05 + actin cytoskeleton organization;actin filament organization;actin filament-based process;anatomical structure morphogenesis;biological adhesion;cell adhesion;cell communication;cell migration;cell motility;cell-cell adhesion;cell-cell signaling;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;establishment or maintenance of cell polarity;homophilic cell adhesion;locomotion;organelle organization;signaling binding;calcium ion binding;cation binding;ion binding;metal ion binding cell junction;cell part;cell projection;cell-cell junction;cytoplasmic part;filopodium;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium;membrane part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane part 3.5369E-200 371580000 41

P98160;Q5SZJ2;Q5SZJ1;Q5SZI9 Basement membrane-specific heparan sulfate proteoglycan core protein;Endorepellin;LG3 peptide HSPG2 >sp|P98160|PGBM_HUMAN Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4 0.52 0.68 0.76 0.78 0.50 1.18 0.78 1.69 + + "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological regulation;biosynthetic process;brain development;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;cardiac muscle tissue development;cartilage development;cartilage development involved in endochondral bone morphogenesis;catabolic process;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chondrocyte differentiation;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;embryonic morphogenesis;embryonic organ morphogenesis;embryonic skeletal system morphogenesis;endochondral ossification;extracellular matrix organization;extracellular structure organization;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;lipoprotein metabolic process;localization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;metabolic process;multicellular organismal process;muscle tissue development;nitrogen compound metabolic process;organ development;organ morphogenesis;ossification;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;protein localization;regulation of biological process;regulation of cellular process;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;skeletal system morphogenesis;striated muscle tissue development;sulfur compound metabolic process;terpenoid metabolic process;tissue development" binding;cation binding;ion binding;metal ion binding + basal lamina;cell part;cytoplasmic part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;Golgi apparatus part;Golgi lumen;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;vacuolar lumen;vacuolar part;vesicle ECM-receptor interaction 5.4322E-193 181130000 42

P12814;P12814-3;P12814-2;B7TY16;H9KV75;H7C5W8;H0YJW3;G3V2W4;G3V2N5;H0YJ11;Q08043;G3V5M4;G3V2X9;G3V2E8;G3V380 Alpha-actinin-1 ACTN1 >sp|P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2;>sp|P12814-3|ACTN1_HUMAN Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1;>sp|P12814-2|ACTN1_HUMAN Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1;>tr|B7TY16|B7TY16_HUMAN 1.39 0.48 1.08 1.17 1.31 0.85 1.88 1.32 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;biological regulation;cell activation;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;focal adhesion assembly;muscle filament sliding;negative regulation of biological process;negative regulation of cellular component movement;negative regulation of cellular process;organelle organization;platelet activation;platelet degranulation;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of programmed cell death;secretion;secretion by cell;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;identical protein binding;integrin binding;ion binding;metal ion binding;protein binding;protein complex binding;protein dimerization activity;protein homodimerization activity;receptor binding;structural constituent of muscle;structural molecule activity + actin filament;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;dendritic spine;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;fascia adherens;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;neuron projection;neuron spine;non-membrane-bounded organelle;nucleus;organelle;organelle lumen;organelle part;plasma membrane;platelet alpha granule lumen;protein complex;pseudopodium;ruffle;secretory granule lumen;vesicle;vesicle lumen;Z disc Adherens junction;Amoebiasis;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Systemic lupus erythematosus;Tight junction 0 644220000 43

Q07283;Q5VUA4-2;Q5VUA4;REV__Q6ZQQ6;REV__Q6ZQQ6-2;REV__E7ESW6 Trichohyalin TCHH >sp|Q07283|TRHY_HUMAN Trichohyalin OS=Homo sapiens GN=TCHH PE=1 SV=2 0.26 0.34 0.74 0.34 1.69 4.52 1.25 3.15 + + "biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;keratinization;macromolecule biosynthetic process;macromolecule metabolic process;meiosis;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;calcium ion binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane 0 188960000 44

Q5D862;CON__Q5D862 Filaggrin-2 FLG2 >sp|Q5D862|FILA2_HUMAN Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1;>Q5D862 SWISS-PROT:Q5D862 Tax_Id=9606 Gene_Symbol=FLG2 Filaggrin-2 0.40 0.43 0.52 0.24 3.43 3.37 1.90 1.08 + + binding;calcium ion binding;cation binding;ion binding;metal ion binding;structural molecule activity 9.9629E-277 485000000 46

P07996;CON__Q28194;A8MZG1 Thrombospondin-1 THBS1 >sp|P07996|TSP1_HUMAN Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2;>Q28194 TREMBL:Q28194 (Bos taurus) Thrombospondin-1 1.27 0.88 1.58 1.17 0.39 0.20 0.49 0.60 + + + "activation of MAPK activity;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological adhesion;biological regulation;blood vessel morphogenesis;cartilage development;cartilage development involved in endochondral bone morphogenesis;cell activation;cell adhesion;cell cycle arrest;cell cycle process;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to heat;cellular response to stimulus;cellular response to stress;chronic inflammatory response;defense response;developmental process;endocardial cushion development;engulfment of apoptotic cell;establishment of localization;establishment of localization in cell;exocytosis;growth plate cartilage development;immune response;immune system process;induction of apoptosis;induction of programmed cell death;inflammatory response;locomotion;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;mesenchyme development;metabolic process;negative regulation of angiogenesis;negative regulation of antigen processing and presentation;negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood vessel endothelial cell migration;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell adhesion;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cell-matrix adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cGMP-mediated signaling;negative regulation of cytokine production;negative regulation of dendritic cell antigen processing and presentation;negative regulation of developmental process;negative regulation of endothelial cell migration;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;negative regulation of fatty acid transport;negative regulation of fibrinolysis;negative regulation of fibroblast growth factor receptor signaling pathway;negative regulation of focal adhesion assembly;negative regulation of hydrolase activity;negative regulation of immune system process;negative regulation of interleukin-12 production;negative regulation of lipid transport;negative regulation of locomotion;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of nitric oxide mediated signal transduction;negative regulation of organic acid transport;negative regulation of peptidase activity;negative regulation of plasma membrane long-chain fatty acid transport;negative regulation of plasminogen activation;negative regulation of programmed cell death;negative regulation of protein processing;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transmembrane transport;negative regulation of transport;outflow tract morphogenesis;peptide cross-linking;phagocytosis, engulfment;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;platelet degranulation;positive regulation of angiogenesis;positive regulation of apoptosis;positive regulation of behavior;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of blood coagulation;positive regulation of blood vessel endothelial cell migration;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemotaxis;positive regulation of coagulation;positive regulation of cytokine biosynthetic process;positive regulation of cytokine production;positive regulation of developmental process;positive regulation of endothelial cell migration;positive regulation of eukaryotic cell surface binding;positive regulation of fibroblast migration;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of macrophage activation;positive regulation of macrophage chemotaxis;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein serine/threonine kinase activity;positive regulation of reactive oxygen species metabolic process;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transferase activity;positive regulation of transforming growth factor beta production;positive regulation of transforming growth factor beta receptor signaling pathway;positive regulation of transforming growth factor beta1 production;positive regulation of translation;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;positive regulation of tumor necrosis factor biosynthetic process;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of antigen processing and presentation;regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;regulation of apoptosis;regulation of behavior;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of blood coagulation;regulation of blood vessel endothelial cell migration;regulation of catalytic activity;regulation of cell activation;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cGMP-mediated signaling;regulation of chemotaxis;regulation of coagulation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of dendritic cell antigen processing and presentation;regulation of developmental process;regulation of endopeptidase activity;regulation of endothelial cell migration;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of eukaryotic cell surface binding;regulation of fatty acid transport;regulation of fibrinolysis;regulation of fibroblast growth factor receptor signaling pathway;regulation of fibroblast migration;regulation of focal adhesion assembly;regulation of gene expression;regulation of granulocyte chemotaxis;regulation of hydrolase activity;regulation of immune system process;regulation of interleukin-12 production;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of lipid transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of macrophage activation;regulation of macrophage chemotaxis;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell migration;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitric oxide mediated signal transduction;regulation of organic acid transport;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of plasma membrane long-chain fatty acid transport;regulation of plasminogen activation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein processing;regulation of protein serine/threonine kinase activity;regulation of reactive oxygen species metabolic process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of transforming growth factor beta production;regulation of transforming growth factor beta receptor signaling pathway;regulation of transforming growth factor beta1 production;regulation of translation;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmembrane transport;regulation of transport;regulation of tumor necrosis factor biosynthetic process;regulation of tumor necrosis factor production;regulation of wound healing;response to abiotic stimulus;response to calcium ion;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to glucose stimulus;response to heat;response to hexose stimulus;response to hormone stimulus;response to hypoxia;response to inorganic substance;response to magnesium ion;response to metal ion;response to monosaccharide stimulus;response to organic substance;response to oxygen levels;response to progesterone stimulus;response to steroid hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;response to wounding;secretion;secretion by cell;sprouting angiogenesis;tissue development;transport;vesicle-mediated transport" binding;calcium ion binding;carbohydrate binding;cation binding;cell surface binding;collagen binding;collagen V binding;cytokine binding;eukaryotic cell surface binding;extracellular matrix binding;fibrinogen binding;fibroblast growth factor binding;fibronectin binding;glycoprotein binding;glycosaminoglycan binding;growth factor binding;heparin binding;identical protein binding;integrin binding;ion binding;laminin binding;lipid binding;lipoprotein particle binding;low-density lipoprotein particle binding;metal ion binding;pattern binding;phosphatidylserine binding;phospholipid binding;polysaccharide binding;protein binding;protein complex binding;protein-lipid complex binding;proteoglycan binding;receptor binding;transforming growth factor beta binding +

cell part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;external side of plasma membrane;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;fibrinogen complex;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane part;platelet alpha granule lumen;protein complex;secretory granule lumen;vesicle;vesicle lumen ECM-receptor interaction;Focal adhesion;Malaria;Phagosome;TGF-beta signaling pathway 0 7819100000 46

Q14204 Cytoplasmic dynein 1 heavy chain 1 DYNC1H1 >sp|Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 0.81 0.88 0.46 0.80 1.31 1.82 1.32 1.31 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cell cycle process;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cytoplasmic mRNA processing body assembly;cytoskeleton organization;death;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;macromolecular complex assembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;mitotic spindle organization;organelle organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;spindle organization;stress granule assembly;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" + cell part;centrosome;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle Phagosome;Vasopressin-regulated water reabsorption 7.4393E-174 92487000 51

P08670;B0YJC4;B0YJC5;Q5JVS8;P17661;H7C5W5;P41219;P41219-2;K7EKH6;F8W835;Q16352;P07197-2;P07196;E7EMV2;E7ESP9;P07197 Vimentin VIM>sp|P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4;>tr|B0YJC4|B0YJC4_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=2 SV=1 0.47 0.20 0.60 0.75 2.74 1.53 1.23 1.34 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;anatomical structure development;anterograde axon cargo transport;astrocyte development;astrocyte differentiation;axon cargo transport;axon transport of mitochondrion;Bergmann glial cell differentiation;biological regulation;cell communication;cell development;cell differentiation;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;establishment of localization;establishment of localization in cell;glial cell development;glial cell differentiation;interaction with host;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;interspecies interaction between organisms;intracellular transport;lens fiber cell development;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;multi-organism process;muscle filament sliding;negative regulation of biological process;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of neuron projection development;nervous system development;neurofilament bundle assembly;neurofilament cytoskeleton organization;organelle organization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of axon diameter;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cell projection size;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of developmental process;regulation of heart contraction;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of system process;reproductive process;retrograde axon cargo transport;signaling;synaptic transmission;system development;transport;viral reproductive process;virus-host interaction structural constituent of cytoskeleton;structural constituent of eye lens;structural molecule activity + adherens junction;anchoring junction;axon;axon part;cell junction;cell leading edge;cell part;cell projection;cell projection part;cell-cell adherens junction;cell-cell junction;C-fiber;cilium part;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;fascia adherens;intermediate filament;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;microbody;neurofilament;neuromuscular junction;neuron projection;non-membrane-bounded organelle;organelle;organelle part;peroxisome;photoreceptor outer segment membrane;plasma membrane;protein complex;sarcolemma;synapse;vesicle;Z disc Amyotrophic lateral sclerosis (ALS);Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM) 0 4649900000 51

F5GWP8;C9JTX4;C9J826;C9JK18;C9JKY1;C9JPI2;K7ERP3 JUP >tr|F5GWP8|F5GWP8_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=2 SV=1 0.87 0.94 0.56 0.67 2.15 1.96 1.30 0.91 + anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;desmosome assembly;developmental process;epidermis development;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;skin development;tissue development structural molecule activity adherens junction;anchoring junction;apicolateral plasma membrane;cell junction;cell part;cell-cell adherens junction;cell-cell junction;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;desmosome;fascia adherens;intermediate filament;internal side of plasma membrane;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;organelle part;plasma membrane part;protein complex;Z disc 0 365010000 52

Q13751;Q5THA1;REV__H0YLF6;REV__Q9BVR6;REV__H3BPU4;REV__Q9UGJ1-2;REV__Q9UGJ1;F5H149;Q9P1Z9;Q9P1Z9-2 Laminin subunit beta-3 LAMB3 >sp|Q13751|LAMB3_HUMAN Laminin subunit beta-3 OS=Homo sapiens GN=LAMB3 PE=1 SV=1 1.13 0.81 1.69 1.22 0.23 0.16 0.53 0.78 + + + anatomical structure development;biological adhesion;brown fat cell differentiation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;fat cell differentiation;hemidesmosome assembly;tissue development structural molecule activity + cell part;extracellular matrix part;extracellular region;extracellular region part;integral to membrane;intrinsic to membrane;laminin complex;laminin-5 complex;macromolecular complex;membrane part;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 0 8068700000 53

Q9P2E9;Q9P2E9-2;Q9P2E9-3;F8W7S5;A2A2S5;H0YBV2;B8ZZA5;G3V112;REV__Q9P2M7;A8K944;Q8NE09;Q8N4C6-6;F8W6D3;H0YDJ4;E9PN67;Q8N4C6-4;C9J066;P00451 Ribosome-binding protein 1 RRBP1 >sp|Q9P2E9|RRBP1_HUMAN Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4;>sp|Q9P2E9-2|RRBP1_HUMAN Isoform 1 of Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1;>sp|Q9P2E9-3|RRBP1_HUMAN Isoform 2 of Ribosome-binding protein 1 OS=Homo sapiens 1.25 0.98 1.27 0.94 0.76 0.58 1.21 1.23 + "acute inflammatory response;acute-phase response;biological adhesion;biological regulation;biosynthetic process;blood coagulation, intrinsic pathway;cell activation;cell adhesion;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;inflammatory response;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;platelet activation;platelet degranulation;primary metabolic process;protein activation cascade;protein metabolic process;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of G-protein coupled receptor protein signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;response to stress;response to wounding;secretion;secretion by cell;signal transduction;termination of G-protein coupled receptor signaling pathway;termination of signal transduction;translation;transport;vesicle-mediated transport" binding;calcium ion binding;catalytic activity;cation binding;copper ion binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;oxidoreductase activity;receptor activity;transition metal ion binding + cell part;cytoplasm;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;endoplasmic reticulum;endoplasmic reticulum part;extracellular region;extracellular region part;extracellular space;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;non-membrane-bounded organelle;organelle;organelle lumen;organelle part;plasma membrane;platelet alpha granule lumen;ribonucleoprotein complex;ribosome;secretory granule lumen;vesicle lumen Complement and coagulation cascades;Protein processing in endoplasmic reticulum 0 707260000 55

P16144-4;P16144-2;P16144-3;P16144;P16144-5;J3QS11;J3QRK0;J3QQL2;J3KSH9 Integrin beta-4 ITGB4 >sp|P16144-4|ITB4_HUMAN Isoform Beta-4D of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp|P16144-2|ITB4_HUMAN Isoform Beta-4A of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp|P16144-3|ITB4_HUMAN Isoform Beta-4B of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp| 1.49 1.18 1.17 1.15 0.24 0.17 0.40 0.43 + biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;developmental process;extracellular matrix organization;extracellular structure organization;filopodium assembly;hemidesmosome assembly;integrin-mediated signaling pathway;locomotion;microspike assembly;multicellular organismal development;multicellular organismal process;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;response to wounding;signal transduction receptor activity + basal plasma membrane;basement membrane;cell junction;cell leading edge;cell part;cell surface;cell-substrate junction;extracellular matrix part;extracellular region part;hemidesmosome;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Regulation of actin cytoskeleton 0 2939100000 57

Q13753;Q13753-2;REV__A6PVS8-3;REV__A6PVS8-2;REV__A6PVS8 Laminin subunit gamma-2 LAMC2 >sp|Q13753|LAMC2_HUMAN Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 PE=1 SV=2;>sp|Q13753-2|LAMC2_HUMAN Isoform Short of Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 1.14 0.83 1.55 1.22 0.25 0.15 0.52 0.77 + + + anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;tissue development binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding + extracellular matrix part;extracellular region;extracellular region part;laminin complex;laminin-5 complex;macromolecular complex;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 0 8832400000 57

P12111-2;P12111;E9PCV6;E7ENL6;P12111-4;P12111-5;P12111-3;C9JNG9;I3L392 Collagen alpha-3(VI) chain COL6A3 >sp|P12111-2|CO6A3_HUMAN Isoform 2 of Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3;>sp|P12111|CO6A3_HUMAN Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5;>tr|E9PCV6|E9PCV6_HUMAN Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE 1.11 1.00 1.08 1.36 2.76 1.69 1.01 0.97 + + + anatomical structure development;axon guidance;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;collagen catabolic process;collagen metabolic process;developmental process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;locomotion;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;muscle organ development;muscle structure development;organ development;response to chemical stimulus;response to external stimulus;response to stimulus;taxisendopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity + anchoring collagen;cell part;collagen;collagen type VI;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;extracellular space;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;sarcolemma ECM-receptor interaction;Focal adhesion;Protein digestion and absorption 0 916790000 64

P02751;P02751-3;P02751-8;P02751-15;P02751-5;P02751-14;P02751-17;P02751-7;P02751-6;F8W7G7;P02751-10;P02751-9;P02751-11;P02751-4;P02751-13;P02751-12;H0Y7Z1;P02751-16;P02751-2;H0Y4K8 Fibronectin;Anastellin;Ugl-Y1;Ugl-Y2;Ugl-Y3 FN1 >sp|P02751|FINC_HUMAN Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4;>sp|P02751-3|FINC_HUMAN Isoform 3 of Fibronectin OS=Homo sapiens GN=FN1;>sp|P02751-8|FINC_HUMAN Isoform 8 of Fibronectin OS=Homo sapiens GN=FN1;>sp|P02751-15|FINC_HUMAN Isoform 15 of Fibron 0.09 0.12 0.42 0.14 3.65 4.49 0.52 2.67 + + + acute inflammatory response;acute-phase response;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological adhesion;biological regulation;calcium-independent cell-matrix adhesion;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;defense response;developmental process;establishment of localization;establishment of localization in cell;exocytosis;extracellular matrix organization;extracellular structure organization;immune system process;inflammatory response;leukocyte migration;locomotion;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;platelet activation;platelet degranulation;primary metabolic process;protein metabolic process;protein modification process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to stimulus;response to stress;response to wounding;secretion;secretion by cell;substrate adhesion-dependent cell spreading;transport;vesicle-mediated transport binding;carbohydrate binding;collagen binding;enzyme activator activity;enzyme regulator activity;extracellular matrix structural constituent;glycosaminoglycan binding;heparin binding;pattern binding;peptidase activator activity;peptidase regulator activity;polysaccharide binding;protein binding;structural molecule activity + apical plasma membrane;basement membrane;cell part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;endoplasmic reticulum-Golgi intermediate compartment;extracellular matrix;extracellular matrix part;extracellular region;extracellular region part;fibrinogen complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane part;platelet alpha granule lumen;protein complex;proteinaceous extracellular matrix;secretory granule lumen;vesicle lumen Amoebiasis;Bacterial invasion of epithelial cells;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer 0 3140500000 76

P21333-2;P21333;Q5HY54;E9PHF0;F8WE98;H0Y5C6;H0Y5F3;H7C2E7 Filamin-A FLNA >sp|P21333-2|FLNA_HUMAN Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA;>sp|P21333|FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4;>tr|Q5HY54|Q5HY54_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1 1.12 0.52 0.94 0.95 1.02 0.80 1.65 1.07 "actin crosslink formation;actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament organization;actin filament-based process;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;cAMP-mediated signaling;cell activation;cell cycle process;cell junction assembly;cell junction organization;cell morphogenesis;cell morphogenesis involved in differentiation;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cellular response to stimulus;cilium assembly;cyclic-nucleotide-mediated signaling;cytoplasmic sequestering of protein;cytoskeleton organization;developmental process;dopamine receptor signaling pathway;early endosome to late endosome transport;endosome transport;epithelial to mesenchymal transition;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;inhibition of adenylate cyclase activity by dopamine receptor signaling pathway;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;intracellular transport;localization;macromolecule localization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane organization;microtubule cytoskeleton organization;microtubule-based process;mitotic spindle organization;negative regulation of adenylate cyclase activity;negative regulation of biological process;negative regulation of catabolic process;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of protein transport;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of transport;organelle assembly;organelle organization;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription factor import into nucleus;positive regulation of transmembrane transport;positive regulation of transport;posttranscriptional regulation of gene expression;protein localization;protein localization at cell surface;protein localization in membrane;protein stabilization;receptor clustering;regulation of adenylate cyclase activity;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of establishment of protein localization;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of lyase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein stability;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;response to stimulus;second-messenger-mediated signaling;secretion;secretion by cell;signal transduction;spindle assembly;spindle assembly involved in mitosis;spindle organization;transport;vesicle-mediated transport"actin binding;actin filament binding;binding;cytoskeletal protein binding;enzyme binding;Fc-gamma receptor I complex binding;glycoprotein binding;GTPase binding;identical protein binding;immunoglobulin receptor binding;molecular transducer activity;protein binding;protein dimerization activity;protein homodimerization activity;Rac GTPase binding;Ral GTPase binding;Ras GTPase binding;receptor binding;Rho GTPase binding;signal transducer activity;small GTPase binding + actin cytoskeleton;cell cortex;cell part;chromosomal part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;Myb complex;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex;trans-Golgi network;vesicle Focal adhesion;MAPK signaling pathway 0 1365700000 92

Q16787-1;B0YJ33;Q16787;Q16787-4;Q16787-3;K7EIP4;K7ERM0 Laminin subunit alpha-3 LAMA3 >sp|Q16787-1|LAMA3_HUMAN Isoform 1 of Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3;>tr|B0YJ33|B0YJ33_HUMAN Laminin alpha-3 chain variant 2 OS=Homo sapiens GN=LAMA3 PE=2 SV=1;>sp|Q16787|LAMA3_HUMAN Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3 PE=1 S 1.11 0.81 1.48 1.19 0.29 0.16 0.52 0.80 + + + anatomical structure development;biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of developmental process;regulation of embryonic development;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;tissue development structural molecule activity + basement membrane;extracellular matrix part;extracellular region part;laminin complex;laminin-1 complex;laminin-5 complex;macromolecular complex;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 0 12433000000 94

P20930;CON__P20930 Filaggrin FLG >sp|P20930|FILA_HUMAN Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3;>P20930 SWISS-PROT:P20930 Tax_Id=9606 Gene_Symbol=FLG Filaggrin 0.32 0.24 0.62 0.17 5.01 3.88 1.89 1.05 + + cell differentiation;cellular developmental process;cellular process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinocyte differentiation binding;calcium ion binding;cation binding;ion binding;metal ion binding;structural molecule activity cell part;cornified envelope;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle 0 3098600000 118

P15924;P15924-2 Desmoplakin DSP >sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3;>sp|P15924-2|DESP_HUMAN Isoform DPII of Desmoplakin OS=Homo sapiens GN=DSP 0.97 0.73 0.52 0.55 2.73 2.63 1.47 1.02 + adherens junction organization;anatomical structure development;anatomical structure morphogenesis;biological adhesion;cardiac muscle tissue morphogenesis;cell adhesion;cell differentiation;cell junction organization;cell-cell adhesion;cell-cell junction organization;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cytoskeleton organization;developmental process;epidermal cell differentiation;epidermis development;epithelial cell differentiation;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;keratinocyte differentiation;localization;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;muscle tissue morphogenesis;organelle organization;peptide cross-linking;primary metabolic process;protein localization;protein localization to adherens junction;protein metabolic process;protein modification process;skin development;tissue development;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis;ventricular compact myocardium morphogenesis "binding;binding, bridging;protein binding;protein binding, bridging;structural constituent of cytoskeleton;structural molecule activity" anchoring junction;basolateral plasma membrane;cell junction;cell part;cell-cell contact zone;cell-cell junction;cornified envelope;cytoplasmic part;cytoskeletal part;cytoskeleton;desmosome;intercalated disc;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;plasma membrane part;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC) 0 3521700000 161

P35579;P35579-2;Q5BKV1;B1AH99;Q7Z406;Q7Z406-6;F2Z2U8;Q7Z406-2;G8JLL9;Q7Z406-5;Q7Z406-4;M0QY43Myosin-9 MYH9 >sp|P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4;>sp|P35579-2|MYH9_HUMAN Isoform 2 of Myosin-9 OS=Homo sapiens GN=MYH9 0.97 0.65 0.80 0.77 1.24 1.50 1.27 1.72 + actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based movement;actin filament-based process;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;axon guidance;biological adhesion;biological regulation;blood vessel endothelial cell migration;cell adhesion;cell cycle phase;cell cycle process;cell differentiation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;chemotaxis;chordate embryonic development;cytokinesis;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;endothelial cell migration;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of lymphocyte polarity;establishment of meiotic spindle localization;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;establishment of T cell polarity;establishment or maintenance of cell polarity;immune system process;in utero embryonic development;integrin-mediated signaling pathway;leukocyte differentiation;leukocyte migration;locomotion;macromolecule metabolic process;meiotic metaphase I;meiotic spindle organization;membrane protein ectodomain proteolysis;membrane protein proteolysis;metabolic process;metaphase;microtubule cytoskeleton organization;microtubule-based process;monocyte differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;myoblast fusion;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle organization;platelet formation;primary metabolic process;protein metabolic process;protein transport;proteolysis;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of G-protein coupled receptor protein signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;spindle organization;syncytium formation;syncytium formation by plasma membrane fusion;taxis;termination of G-protein coupled receptor signaling pathway;termination of signal transduction;transport;uropod organization "actin binding;actin filament binding;actin-dependent ATPase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein anchor;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" + actin filament bundle;actomyosin;actomyosin contractile ring;adherens junction;anchoring junction;cell cortex part;cell division site part;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cleavage furrow;contractile ring;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;immunological synapse;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;myosin complex;myosin II complex;neuromuscular junction;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ruffle;spindle;stress fiber;synapse;uropod;vesicle Tight junction;Viral myocarditis 0 11297000000 180

Supplemental Table S8 - significantly regulated proteases

Protein names Gene names Protein IDs Fasta headers c1 intr5 p1 intr5 c2 intr6 p2 intr6 c1 intr7 p1 intr7 c2 intr8 p2 intr8 Proteases Cysteinproteasen Aspartatproteasen Metalloproteasen Serinproteasen Threoninproteasen welch Significant welch Difference (-Log welch p value) PEP Intensity Number of proteins Peptides Razor + unique peptides Unique peptides Sequence coverage [%]

U4/U6.U5 tri-snRNP-associated protein 2 USP39 B9A018;Q53GS9;Q53GS9-2;Q53GS9-3;F8WC91 >tr|B9A018|B9A018_HUMAN U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=2 SV=1;>sp|Q53GS9|SNUT2_HUMAN U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=1 SV=2;>sp|Q53GS9-2|SNUT2_HUMAN Isoform 2 of U4/U6.U5 tri-snRNP-as 0.09 -0.84 -0.02 -0.09 0.05 -0.82 0.05 -0.40 + + + 0.582867431 1.308656448 7.79E-23 31030000 5 4 4 4 10.1

Ubiquitin carboxyl-terminal hydrolase isozyme L5 UCHL5 Q9Y5K5-2;Q9Y5K5-4;Q9Y5K5-3;Q9Y5K5;Q5LJA5;Q5LJA9;Q5LJB0;B4DW59;B7Z9U9;H0Y6Y4;H0Y4E0;H0Y4K0;H0Y636 >sp|Q9Y5K5-2|UCHL5_HUMAN Isoform 2 of Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCHL5;>sp|Q9Y5K5-4|UCHL5_HUMAN Isoform 4 of Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCHL5;>sp|Q9Y5K5-3|UCHL5_HUMAN Isoform 0.07 -0.39 0.39 -0.32 0.01 -0.65 0.12 -0.49 + + + 0.612832662 1.949615861 5.01E-51 128690000 13 8 8 8 29.7

Ubiquitin carboxyl-terminal hydrolase 10 USP10 Q14694;Q14694-3;Q14694-2;J3KT19;H3BQP1;H3BNS8;H3BQC6;H3BNA1;H3BVF1 >sp|Q14694|UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2;>sp|Q14694-3|UBP10_HUMAN Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10;>sp|Q14694-2|UBP10_HUMAN Isoform 2 of Ubiquitin carbo 0.03 -0.24 -0.02 -0.17 0.13 -0.16 -0.03 -0.26 + + + 0.237240963 1.897833508 7.96E-55 257400000 9 12 12 12 23.1

Puromycin-sensitive aminopeptidase NPEPPS E9PLK3;P55786;B7Z463;E5RJ24;E7EWZ2;A6NEC2;F5GZY4;H0YAQ6;E9PP11;A6NEC2-2;H0YDG0;H0YCQ5;E9PJY4;E9PJ74;E9PPD4;A6NEC2-3;L7N488;E9PRQ5;E9PI82;E9PJF9;E9PPZ2>tr|E9PLK3|E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1;>sp|P55786|PSA_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2;>tr|B7Z463|B7Z463_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sa 0.03 0.53 -0.11 0.27 -0.03 0.22 -0.01 0.66 + + + -0.444781196 1.577901586 5.37E-260 2139300000 21 38 38 38 48.4

Probable ubiquitin carboxyl-terminal hydrolase FAF-X USP9X Q93008-1;Q93008;O00507;O00507-2;E9PFG1;H7C2M9 >sp|Q93008-1|USP9X_HUMAN Isoform 2 of Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X;>sp|Q93008|USP9X_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 0.15 0.61 -0.09 0.40 -0.10 0.10 -0.22 0.34 + + + -0.424455091 1.33310072 1.34E-85 199470000 6 21 21 21 10.7

Cathepsin Z CTSZ Q9UBR2 >sp|Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 0.04 0.50 0.14 0.49 -0.33 0.65 -0.05 0.28 + + + -0.529800428 1.604037118 3.97E-64 284200000 1 5 5 5 21.5

Ubiquitin carboxyl-terminal hydrolase 5 USP5 P45974-2;P45974;F5H571;REV__Q9UPY3-2;REV__Q9UPY3 >sp|P45974-2|UBP5_HUMAN Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5;>sp|P45974|UBP5_HUMAN Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 0.04 0.54 0.00 0.18 -0.05 0.22 0.00 0.44 + + + -0.346566794 1.543815654 2.33E-262 1463500000 5 30 30 28 44.1

"Presequence protease, mitochondrial" PITRM1 Q5JRX3;Q5JRX3-2;C9JSL2;Q5JRX3-3;H0Y7L7;B1APQ0;B1APQ1">sp|Q5JRX3|PREP_HUMAN Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3;>sp|Q5JRX3-2|PREP_HUMAN Isoform 2 of Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1;>tr|C9JSL2|C9JSL2_HUMAN Uncharacterized protein OS=Homo sapiens" -0.60 0.46 0.02 0.41 -0.60 0.29 0.08 0.48 + + + -0.686190275 1.422601192 4.97E-98 346990000 7 18 18 18 23.3

Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain CTSB P07858;E9PR54;E9PJ67;E9PCB3;E9PKQ7;E9PNL5;E9PHZ5;E9PLY3;E9PSG5;E9PQM1;R4GMQ5;E9PS78 >sp|P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 -0.97 1.29 -1.42 0.49 -0.37 2.09 -0.38 0.98 + + + -1.993415907 1.749178258 1.80E-62 687110000 12 10 10 10 33.9

Supplemental Table S6: Intracellular proteome of primary human keratinocytes
(SILAC ratios of WCL isolated from primary human keratinocytes derived from two RDEB and two healthy donors)

Protein IDs Protein names Gene names Fasta headers log2 Ctrl1_1 log2 Ctrl1_2 log2 Ctrl2_1 log2 Ctrl2_2 log2 RDEB1_1 log2 RDEB1_2 log2 RDEB2_1 log2 RDEB2_2 welch Significant (Permutation based) (-Log10 P value) welch Difference GOBP name GOMF name GOCC name KEGG name PEP Number of proteins Peptides Unique peptides Sequence coverage [%]

CON__P08727;P08727;C9JM50;K7EMS3;Q99456;CON__Q99456;K7EQH6 "Keratin, type I cytoskeletal 19" KRT19 ">P08727 SWISS-PROT:P08727 Tax_Id=9606 Gene_Symbol=KRT19 Keratin, type I cytoskeletal 19;>sp|P08727|K1C19_HUMAN Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4;>tr|C9JM50|C9JM50_HUMAN Keratin, type I cytoskeletal 19 (Fragment) OS=Homo sap" 0.81 1.21 0.97 0.96 -3.03 -1.51 -1.88 -0.29 + 1.730535397 2.660733968 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;anatomical structure development;cell differentiation;cell differentiation involved in embryonic placenta development;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cornea development in camera-type eye;cytoskeleton organization;developmental process;epithelium development;interaction with host;interspecies interaction between organisms;multicellular organismal process;multi-organism process;neurological system process;organelle organization;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus;sarcomere organization;sensory perception;sensory perception of light stimulus;system process;tissue development;viral reproductive process;virus-host interaction;visual perception structural constituent of cytoskeleton;structural constituent of muscle;structural molecule activity cell part;cell periphery;contractile fiber part;costamere;cytoplasmic part;cytoskeletal part;dystrophin-associated glycoprotein complex;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;organelle part;plasma membrane;plasma membrane part;protein complex;sarcolemma;Z disc 0 7 35 17 77.5

P06396-2;F5H1A8;P06396-3;P06396;Q5T0H9;CON__Q3SX14;Q5T0H8;Q5T0H7;Q5T0I0;Q5T0I1;REV__F5H555;REV__H0YJM7;REV__Q6TDU7-4;REV__Q6TDU7-2;REV__Q6TDU7-3;REV__Q6TDU7;REV__F8W8F9 Gelsolin GSN >sp|P06396-2|GELS_HUMAN Isoform 2 of Gelsolin OS=Homo sapiens GN=GSN;>tr|F5H1A8|F5H1A8_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=2 SV=1;>sp|P06396-3|GELS_HUMAN Isoform 3 of Gelsolin OS=Homo sapiens GN=GSN;>sp|P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GS -0.58 -0.44 -0.06 -0.03 0.97 1.20 1.02 0.85 + 2.43423804 -1.288441374 actin cytoskeleton organization;actin filament capping;actin filament organization;actin filament polymerization;actin filament severing;actin filament-based process;actin polymerization or depolymerization;aging;anatomical structure development;anatomical structure morphogenesis;apoptosis;barbed-end actin filament capping;biological regulation;cell death;cell development;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to cadmium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;cilium morphogenesis;cytoskeleton organization;death;developmental growth;developmental process;establishment of localization;glial cell development;growth;inositol lipid-mediated signaling;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;oligodendrocyte development;organelle organization;phosphatidylinositol-mediated signaling;programmed cell death;protein complex assembly;protein complex subunit organization;protein polymerization;regeneration;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to acid;response to cadmium ion;response to chemical stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to folic acid;response to inorganic substance;response to metal ion;response to nutrient;response to nutrient levels;response to organic substance;response to stimulus;response to vitamin;signal transduction;tissue development;tissue regeneration;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding actin cytoskeleton;cell part;cell projection;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;protein complex;ruffle;vesicle Fc gamma R-mediated phagocytosis;Regulation of actin cytoskeleton 0 17 33 33 53.5

Q9NQT5-2;Q9NQT5 Exosome complex component RRP40 EXOSC3 >sp|Q9NQT5-2|EXOS3_HUMAN Isoform 2 of Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3;>sp|Q9NQT5|EXOS3_HUMAN Exosome complex component RRP40 OS=Homo sapiens GN=EXOSC3 PE=1 SV=3 0.38 0.20 0.23 0.18 -0.07 -0.61 -0.20 -0.16 + 1.558439255 0.50781309 "B cell activation;B cell activation involved in immune response;catabolic process;cell activation;cell activation involved in immune response;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;CUT catabolic process;CUT metabolic process;DNA deamination;DNA metabolic process;DNA modification;DNA recombination;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;immune effector process;immune system process;isotype switching;leukocyte activation;leukocyte activation involved in immune response;lymphocyte activation;lymphocyte activation involved in immune response;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA catabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response" "3'-5' exonuclease activity;3'-5'-exoribonuclease activity;binding;catalytic activity;exonuclease activity;exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;exoribonuclease activity;exoribonuclease activity, producing 5'-phosphomonoesters;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding;ribonuclease activity;RNA binding" cell part;chromatin;chromosomal part;cytoplasmic exosome (RNase complex);cytoplasmic part;cytosol;exosome (RNase complex);intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear exosome (RNase complex);nuclear part;nucleolus;organelle;organelle part;protein complex;transcriptionally active chromatin RNA degradation 1.26E-09 2 1 1 9.1

O75607 Nucleoplasmin-3 NPM3 >sp|O75607|NPM3_HUMAN Nucleoplasmin-3 OS=Homo sapiens GN=NPM3 PE=1 SV=3 -0.14 0.22 0.16 0.32 -0.40 -1.04 -1.20 -0.48 + 1.596891513 0.920942225 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;rRNA transcription;transcription, DNA-dependent" binding;nucleic acid binding cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 4.79E-42 1 1 1 9

P09110;H7C131;P09110-2;H0Y4D4;B4E072;B4DVF4;F2Z2Q6;F2Z3P7 "3-ketoacyl-CoA thiolase, peroxisomal" ACAA1 ">sp|P09110|THIK_HUMAN 3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2;>tr|H7C131|H7C131_HUMAN 3-ketoacyl-CoA thiolase, peroxisomal (Fragment) OS=Homo sapiens GN=ACAA1 PE=3 SV=1;>sp|P09110-2|THIK_HUMAN Isoform 2 of 3-ketoacyl-CoA thi" -0.01 -0.13 0.00 0.03 0.15 0.37 0.23 0.30 + 1.772116998 -0.289376396 bile acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid beta-oxidation using acyl-CoA oxidase;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;steroid metabolic process;very long-chain fatty acid metabolic process "acetyl-CoA C-acyltransferase activity;acyl-CoA oxidase activity;C-acyltransferase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, oxygen as acceptor;palmitoyl-CoA oxidase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;microbody lumen;microbody part;organelle lumen;organelle part;peroxisomal matrix;peroxisomal part "Benzoate degradation;Biosynthesis of unsaturated fatty acids;Fatty acid metabolism;Peroxisome;PPAR signaling pathway;Valine, leucine and isoleucine degradation" 1.91E-98 8 8 1 28.8

P62913;Q5VVC8;Q5VVC9 60S ribosomal protein L11 RPL11 >sp|P62913|RL11_HUMAN 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2;>tr|Q5VVC8|Q5VVC8_HUMAN 60S ribosomal protein L11 (Fragment) OS=Homo sapiens GN=RPL11 PE=2 SV=1 -0.01 0.03 0.06 0.09 -0.63 -0.74 -0.16 -0.39 + 1.54574581 0.520672476 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein localization;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;localization;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein localization;protein localization to nucleus;protein localization to organelle;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 5.76E-112 3 9 1 41

Q96AE4;B4DT31 Far upstream element-binding protein 1 FUBP1 >sp|Q96AE4|FUBP1_HUMAN Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3;>tr|B4DT31|B4DT31_HUMAN Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=2 SV=1 -0.01 0.17 0.00 0.10 -0.43 -0.57 -0.68 -0.53 + 2.575820623 0.620526824 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;primary metabolic process;regulation of biological process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;RNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.78E-267 2 22 1 43.3

Q71U36-2;Q71U36;Q13748;Q13748-2;Q6PEY2;F8VQQ4;F8VRZ4;F8VS66;F8VWV9;F8VX09;A6NHL2-2;A6NHL2;C9K0S6;F8VRK0;F8VXZ7;F8W0F6 Tubulin alpha-1A chain;Tubulin alpha-3C/D chain;Tubulin alpha-3E chain TUBA1A;TUBA3C;TUBA3E >sp|Q71U36-2|TBA1A_HUMAN Isoform 2 of Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A;>sp|Q71U36|TBA1A_HUMAN Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1;>sp|Q13748|TBA3C_HUMAN Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3;>sp -0.93 -1.34 -1.71 -0.66 1.83 1.89 1.22 2.05 + 2.664465383 -2.90741463 cell cycle process;cell division;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;G2/M transition of mitotic cell cycle;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 16 27 1 66.8

Q01518;Q5T0R1;Q5T0R4;Q5T0R3;Q5T0R2;Q5T0R5;Q5T0R7;Q5T0R6;Q5T0S3;Q5T0R8;E9PDI2;P40123;F8WDB9;B7Z214;B7Z385;B7Z1C4 Adenylyl cyclase-associated protein 1 CAP1 >sp|Q01518|CAP1_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5;>tr|Q5T0R1|Q5T0R1_HUMAN Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens GN=CAP1 PE=2 SV=1 0.18 -0.13 -0.12 -0.02 0.24 0.51 0.49 0.68 + 1.632490288 -0.498811269 actin cytoskeleton organization;actin filament-based process;activation of adenylate cyclase activity;ameboidal cell migration;anatomical structure morphogenesis;axon guidance;biological regulation;cell activation;cell migration;cell morphogenesis;cell motility;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;endocytosis;establishment of localization;establishment of localization in cell;establishment or maintenance of cell polarity;exocytosis;locomotion;membrane invagination;membrane organization;organelle organization;platelet activation;platelet degranulation;positive regulation of adenylate cyclase activity;positive regulation of catalytic activity;positive regulation of cyclase activity;positive regulation of lyase activity;positive regulation of molecular function;receptor-mediated endocytosis;regulation of adenylate cyclase activity;regulation of biological process;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;response to chemical stimulus;response to external stimulus;response to stimulus;secretion;secretion by cell;signal transduction;taxis;transport;vesicle-mediated transport cell cortex part;cell part;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane 0 16 37 1 68.4

Q01518-2;Q5T0R9 CAP1 >sp|Q01518-2|CAP1_HUMAN Isoform 2 of Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1;>tr|Q5T0R9|Q5T0R9_HUMAN Adenylyl cyclase-associated protein 1 (Fragment) OS=Homo sapiens GN=CAP1 PE=2 SV=1 0.05 -0.12 -0.20 -0.10 0.30 0.31 0.56 0.27 + 1.893610372 -0.450249587 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization 0 2 37 1 68.4

Q9BTE6;C9J5N1;Q9BTE6-2;Q9BTE6-3;L7N2F4 Alanyl-tRNA editing protein Aarsd1 AARSD1;PTGES3L-AARSD1 >sp|Q9BTE6|AASD1_HUMAN Alanyl-tRNA editing protein Aarsd1 OS=Homo sapiens GN=AARSD1 PE=1 SV=2;>tr|C9J5N1|C9J5N1_HUMAN Protein PTGES3L-AARSD1 OS=Homo sapiens GN=PTGES3L-AARSD1 PE=2 SV=1;>sp|Q9BTE6-2|AASD1_HUMAN Isoform 2 of Alanyl-tRNA editing protein Aarsd 0.15 0.14 0.10 0.15 -0.17 -0.39 -0.27 -0.44 + 2.268709856 0.455427852 alanyl-tRNA aminoacylation;amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;alanine-tRNA ligase activity;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;metal ion binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;intracellular part 2.71E-14 5 2 2 8.5

Q8NDH2 Coiled-coil domain-containing protein 168 CCDC168 >sp|Q8NDH2|CC168_HUMAN Coiled-coil domain-containing protein 168 OS=Homo sapiens GN=CCDC168 PE=2 SV=2 0.11 0.14 -0.07 0.13 -0.23 -0.22 -0.35 -0.28 + 2.067853704 0.348249648 1.09E-07 1 2 2 1.2

Q0VDF9 Heat shock 70 kDa protein 14 HSPA14 >sp|Q0VDF9|HSP7E_HUMAN Heat shock 70 kDa protein 14 OS=Homo sapiens GN=HSPA14 PE=1 SV=1 0.24 0.40 0.03 0.02 -0.23 -0.34 -0.02 -0.40 + 1.36148289 0.417597903 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' cotranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic part;cytosol;intracellular part 3.62E-18 1 2 2 7.1

E9PJW9;Q96SU4-7;Q96SU4-2;Q96SU4;B1AKJ6;J3KPA3;H0YE19;Q96SU4-5;Q96SU4-4;Q96SU4-3;Q96SU4-6 Oxysterol-binding protein;Oxysterol-binding protein-related protein 9 OSBPL9 >tr|E9PJW9|E9PJW9_HUMAN Oxysterol-binding protein OS=Homo sapiens GN=OSBPL9 PE=2 SV=1;>sp|Q96SU4-7|OSBL9_HUMAN Isoform 7 of Oxysterol-binding protein-related protein 9 OS=Homo sapiens GN=OSBPL9;>sp|Q96SU4-2|OSBL9_HUMAN Isoform 2 of Oxysterol-binding protei 0.19 0.14 0.33 0.04 -0.53 -0.11 -0.08 -0.30 + 1.426136476 0.429536834 establishment of localization;lipid transport;organic substance transport;transport binding;lipid binding;phospholipid binding 2.83E-05 11 2 2 4.9

F5H3C5;B3KUK2;F5H4R2;F5GYZ5;P04179;G8JLJ2;B4E3K9;P04179-2 "Superoxide dismutase;Superoxide dismutase [Mn], mitochondrial" SOD2 ">tr|F5H3C5|F5H3C5_HUMAN Superoxide dismutase [Mn], mitochondrial (Fragment) OS=Homo sapiens GN=SOD2 PE=2 SV=1;>tr|B3KUK2|B3KUK2_HUMAN Superoxide dismutase OS=Homo sapiens GN=SOD2 PE=2 SV=1;>tr|F5H4R2|F5H4R2_HUMAN Superoxide dismutase [Mn], mitochondrial (F" -0.83 -0.14 -0.97 -0.36 1.75 1.92 0.56 0.93 + 1.792515125 -1.864305682 "age-dependent response to oxidative stress;age-dependent response to reactive oxygen species;amine metabolic process;anatomical structure development;apoptotic mitochondrial changes;behavior;biological regulation;biosynthetic process;carboxylic acid metabolic process;cation homeostasis;cell development;cell differentiation;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to ethanol;cellular response to organic substance;cellular response to oxidative stress;cellular response to oxygen radical;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cellular response to superoxide;chemical homeostasis;circulatory system process;detection of chemical stimulus;detection of oxygen;detection of stimulus;developmental process;electron transport chain;erythrophore differentiation;gas homeostasis;generation of precursor metabolites and energy;glutathione metabolic process;heart development;hemopoiesis;hemopoietic or lymphoid organ development;homeostatic process;hydrogen peroxide biosynthetic process;hydrogen peroxide metabolic process;ion homeostasis;iron ion homeostasis;liver development;locomotory behavior;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;mitochondrion organization;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood pressure;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of fat cell differentiation;negative regulation of fibroblast proliferation;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of systemic arterial blood pressure;neuron development;nitrogen compound metabolic process;organ development;organelle organization;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;oxygen homeostasis;peptide metabolic process;pigment cell differentiation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;post-embryonic development;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;reactive oxygen species metabolic process;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of blood vessel size;regulation of catalytic activity;regulation of cell death;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of fat cell differentiation;regulation of fibroblast proliferation;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of mitochondrial membrane potential;regulation of molecular function;regulation of neuron apoptosis;regulation of nitric oxide biosynthetic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of tube size;release of cytochrome c from mitochondria;removal of superoxide radicals;respiratory electron transport chain;response to abiotic stimulus;response to activity;response to axon injury;response to biotic stimulus;response to cadmium ion;response to chemical stimulus;response to drug;response to electrical stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to gamma radiation;response to hydrogen peroxide;response to hyperoxia;response to hypoxia;response to inorganic substance;response to ionizing radiation;response to L-ascorbic acid;response to lipopolysaccharide;response to manganese ion;response to metal ion;response to molecule of bacterial origin;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to oxygen levels;response to oxygen radical;response to radiation;response to reactive oxygen species;response to selenium ion;response to silicon dioxide;response to stimulus;response to stress;response to superoxide;response to vitamin;response to wounding;response to zinc ion;small molecule metabolic process;sulfur compound metabolic process;superoxide anion generation;superoxide metabolic process;system process;vascular process in circulatory system;vasodilation;vasodilation by acetylcholine involved in regulation of systemic arterial blood pressure" "antioxidant activity;binding;catalytic activity;cation binding;DNA binding;ion binding;manganese ion binding;metal ion binding;nucleic acid binding;oxidoreductase activity;oxidoreductase activity, acting on superoxide radicals as acceptor;oxygen binding;superoxide dismutase activity;transition metal ion binding" cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part Huntington's disease;Peroxisome 2.66E-19 8 2 2 18.9

B4DK69;P52895;P52895-2 Aldo-keto reductase family 1 member C2 AKR1C2 >tr|B4DK69|B4DK69_HUMAN Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=2 SV=1;>sp|P52895|AK1C2_HUMAN Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 -0.86 -0.75 -0.39 -0.26 1.58 1.96 1.44 1.02 + 2.484382087 -2.067053229 biological regulation;C21-steroid hormone metabolic process;carboxylic acid metabolic process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to jasmonic acid stimulus;cellular response to organic substance;cellular response to stimulus;digestion;fatty acid metabolic process;hormone metabolic process;icosanoid metabolic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of protein kinase B signaling cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;progesterone metabolic process;prostaglandin metabolic process;prostanoid metabolic process;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell proliferation;regulation of cellular process;regulation of hormone levels;regulation of intracellular protein kinase cascade;regulation of protein kinase B signaling cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to jasmonic acid stimulus;response to lipid;response to organic substance;response to prostaglandin stimulus;response to stimulus;small molecule metabolic process;steroid metabolic process;unsaturated fatty acid metabolic process "alcohol dehydrogenase (NADP+) activity;alditol:NADP+ 1-oxidoreductase activity;aldo-keto reductase (NADP) activity;androsterone dehydrogenase (A-specific) activity;androsterone dehydrogenase activity;bile acid binding;binding;carboxylic acid binding;catalytic activity;G-protein coupled receptor activity;icosanoid receptor activity;ketosteroid monooxygenase activity;lipid binding;molecular transducer activity;monocarboxylic acid binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;phenanthrene 9,10-monooxygenase activity;prostaglandin F receptor activity;prostaglandin receptor activity;prostanoid receptor activity;receptor activity;signal transducer activity;signaling receptor activity;steroid binding;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity;transmembrane signaling receptor activity" cell part;cytoplasm;intracellular part Metabolism of xenobiotics by cytochrome P450;Steroid hormone biosynthesis 8.41E-53 3 10 2 34.3

Q01105 Protein SET SET >sp|Q01105|SET_HUMAN Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 -0.06 0.09 -0.13 0.03 -1.00 -0.53 -0.33 -0.33 + 1.324324367 0.532556712 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;DNA metabolic process;DNA replication;establishment of localization;establishment of localization in cell;gene expression;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of histone acetylation;negative regulation of histone modification;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron apoptosis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of peptidyl-lysine acetylation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;nucleosome assembly;nucleosome disassembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of gene expression;regulation of histone acetylation;regulation of histone modification;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-lysine acetylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA metabolic process;transport" binding;DNA binding;enzyme inhibitor activity;enzyme regulator activity;histone binding;nucleic acid binding;phosphatase inhibitor activity;phosphatase regulator activity;protein binding;protein phosphatase inhibitor activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity cell part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;perinuclear region of cytoplasm;protein complex 1.95E-92 1 10 2 34.5

P62277;E9PS50 40S ribosomal protein S13 RPS13 >sp|P62277|RS13_HUMAN 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 0.02 0.00 0.11 0.02 -0.23 -0.68 -0.23 -0.37 + 1.518296472 0.416365732 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 3.26E-99 2 12 2 53.6

Q16851;E7EUC7;C9JQU9;C9J6Q0 UTP--glucose-1-phosphate uridylyltransferase UGP2 >sp|Q16851|UGPA_HUMAN UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5;>tr|E7EUC7|E7EUC7_HUMAN UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=2 SV=1 -0.26 -0.26 -0.14 -0.02 1.02 0.99 0.63 0.34 + 1.889007209 -0.911933925 alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular ketone metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan biosynthetic process;glucan metabolic process;glucose metabolic process;glucuronate biosynthetic process;glucuronate metabolic process;glycogen biosynthetic process;glycogen metabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;UDP-glucose metabolic process;UDP-glucuronate biosynthetic process;UDP-glucuronate metabolic process;uronic acid metabolic process;xenobiotic metabolic process "binding;catalytic activity;cation binding;ion binding;metal ion binding;nucleotidyltransferase activity;transferase activity;transferase activity, transferring phosphorus-containing groups;uridylyltransferase activity;UTP:glucose-1-phosphate uridylyltransferase activity;UTP-monosaccharide-1-phosphate uridylyltransferase activity" cell part;cytoplasmic part;cytosol;intracellular part Amino sugar and nucleotide sugar metabolism;Galactose metabolism;Pentose and glucuronate interconversions;Starch and sucrose metabolism 0 4 30 2 67.7

A6NN80;E5RK69 Annexin ANXA6 >tr|A6NN80|A6NN80_HUMAN Annexin OS=Homo sapiens GN=ANXA6 PE=2 SV=3;>tr|E5RK69|E5RK69_HUMAN Annexin OS=Homo sapiens GN=ANXA6 PE=2 SV=1 -1.33 -1.24 -0.64 -0.15 1.93 1.54 1.22 0.83 + 2.059817497 -2.221436784 binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;ion binding;lipid binding;metal ion binding;phospholipid binding 0 2 58 2 78.4

H0YAN8;O15013-7;O15013-4;O15013-5;O15013-6;O15013 Rho guanine nucleotide exchange factor 10 ARHGEF10 >tr|H0YAN8|H0YAN8_HUMAN Rho guanine nucleotide exchange factor 10 (Fragment) OS=Homo sapiens GN=ARHGEF10 PE=2 SV=1;>sp|O15013-7|ARHGA_HUMAN Isoform 3 of Rho guanine nucleotide exchange factor 10 OS=Homo sapiens GN=ARHGEF10;>sp|O15013-4|ARHGA_HUMAN Isoform 0.15 0.52 0.03 -0.15 -0.31 -0.85 -0.37 -0.69 + 1.4466894 0.694976982 axon ensheathment;biological regulation;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;centrosome duplication;centrosome organization;cytoskeleton organization;ensheathment of neurons;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based process;mitotic spindle organization;myelination;myelination in peripheral nervous system;organelle assembly;organelle organization;peripheral nervous system axon ensheathment;positive regulation of actin filament bundle assembly;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of GTP catabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleotide catabolic process;positive regulation of nucleotide metabolic process;positive regulation of organelle organization;positive regulation of purine nucleotide catabolic process;positive regulation of stress fiber assembly;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of GTP catabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of stress fiber assembly;spindle assembly;spindle assembly involved in mitosis;spindle organization enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity;Ras guanyl-nucleotide exchange factor activity;Rho guanyl-nucleotide exchange factor activity;small GTPase regulator activity cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part 1.11E-08 6 3 3 4.9

Q8NHH9-3;B5MCN0;B7Z7X8;Q8NHH9-4;Q8NHH9-2;Q8NHH9;C9JQQ5 Atlastin-2ATL2 >sp|Q8NHH9-3|ATLA2_HUMAN Isoform 3 of Atlastin-2 OS=Homo sapiens GN=ATL2;>tr|B5MCN0|B5MCN0_HUMAN Atlastin-2 OS=Homo sapiens GN=ATL2 PE=2 SV=1;>tr|B7Z7X8|B7Z7X8_HUMAN Atlastin-2 OS=Homo sapiens GN=ATL2 PE=2 SV=1;>sp|Q8NHH9-4|ATLA2_HUMAN Isoform 4 of Atlasti 0.32 0.04 0.26 0.07 -0.41 -0.12 0.00 -0.32 + 1.352223989 0.387000427 catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;endoplasmic reticulum organization;Golgi organization;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 5.02E-75 7 3 3 9.7

Q6PD62 RNA polymerase-associated protein CTR9 homolog CTR9 >sp|Q6PD62|CTR9_HUMAN RNA polymerase-associated protein CTR9 homolog OS=Homo sapiens GN=CTR9 PE=1 SV=1 0.08 0.24 0.19 -0.12 -0.47 -0.35 -0.83 -0.12 + 1.300882057 0.539671579 "biological regulation;biosynthetic process;cell fate commitment;cell fate commitment involved in formation of primary germ layers;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interleukin-6;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to organic substance;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;cytokine-mediated signaling pathway;developmental process;endodermal cell fate commitment;histone H2B ubiquitination;histone H3-K4 methylation;histone H3-K4 trimethylation;histone lysine methylation;histone methylation;histone modification;histone monoubiquitination;histone ubiquitination;interleukin-6-mediated signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of myeloid cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine methylation;peptidyl-lysine modification;peptidyl-lysine trimethylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of histone H3-K4 methylation;positive regulation of histone methylation;positive regulation of histone modification;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of RNA metabolic process;positive regulation of transcription elongation from RNA polymerase II promoter;positive regulation of transcription elongation, DNA-dependent;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein ubiquitination;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of developmental process;regulation of gene expression;regulation of histone H3-K4 methylation;regulation of histone methylation;regulation of histone modification;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of RNA metabolic process;regulation of transcription elongation from RNA polymerase II promoter;regulation of transcription elongation, DNA-dependent;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interleukin-6;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;small molecule metabolic process;stem cell maintenance;transcription, DNA-dependent;Wnt receptor signaling pathway" Cdc73/Paf1 complex;cell part;chromatin;chromosomal part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex;transcription elongation factor complex;transcriptionally active chromatin 9.81E-12 1 3 3 4

K7EQ02;Q96EP5-2;Q96EP5;K7EJ88 DAZ-associated protein 1 DAZAP1 >tr|K7EQ02|K7EQ02_HUMAN DAZ-associated protein 1 (Fragment) OS=Homo sapiens GN=DAZAP1 PE=4 SV=1;>sp|Q96EP5-2|DAZP1_HUMAN Isoform 2 of DAZ-associated protein 1 OS=Homo sapiens GN=DAZAP1;>sp|Q96EP5|DAZP1_HUMAN DAZ-associated protein 1 OS=Homo sapiens GN=DAZA -0.16 0.12 -0.23 0.26 -0.28 -0.57 -0.70 -0.59 + 1.454279544 0.530809259 cell differentiation;cellular developmental process;cellular process;developmental process;gamete generation;male gamete generation;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;reproductive process;spermatogenesis binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle mRNA surveillance pathway 1.16E-12 4 3 3 20.9

O94992 Protein HEXIM1 HEXIM1 >sp|O94992|HEXI1_HUMAN Protein HEXIM1 OS=Homo sapiens GN=HEXIM1 PE=1 SV=1 0.18 0.10 0.28 -0.05 -0.39 -0.48 -0.60 -0.49 + 2.30068213 0.619794434 "anatomical structure development;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;heart development;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cyclin-dependent protein kinase activity;negative regulation of gene expression;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of gene expression;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cyclin-dependent protein kinase inhibitor activity;cyclin-dependent protein kinase regulator activity;enzyme inhibitor activity;enzyme regulator activity;kinase inhibitor activity;kinase regulator activity;nucleic acid binding;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity;RNA binding;snRNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.54E-12 1 3 3 15.6

Q3ZCW2;F8WF17;B9A055 Galectin-related protein LGALSL >sp|Q3ZCW2|LEGL_HUMAN Galectin-related protein OS=Homo sapiens GN=LGALSL PE=1 SV=2 -0.28 0.09 0.05 0.05 0.43 1.04 0.89 0.24 + 1.321947418 -0.6703706 binding;carbohydrate binding cell part;intracellular 6.11E-15 3 3 3 18.6

P43121;P43121-2 Cell surface glycoprotein MUC18 MCAM >sp|P43121|MUC18_HUMAN Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM PE=1 SV=2;>sp|P43121-2|MUC18_HUMAN Isoform 2 of Cell surface glycoprotein MUC18 OS=Homo sapiens GN=MCAM -0.52 -0.43 -0.28 0.03 0.15 0.69 0.09 0.71 + 1.380054754 -0.707483018 anatomical structure formation involved in morphogenesis;angiogenesis;angiogenesis involved in wound healing;biological adhesion;cell adhesion;cellular process;developmental process;glomerular filtration;multicellular organismal process;renal system process;system process;vascular wound healing cell part;external side of plasma membrane;integral to membrane;intrinsic to membrane;membrane part;plasma membrane part 8.26E-11 2 3 3 6

P82914 "28S ribosomal protein S15, mitochondrial" MRPS15 ">sp|P82914|RT15_HUMAN 28S ribosomal protein S15, mitochondrial OS=Homo sapiens GN=MRPS15 PE=1 SV=1" -0.10 0.11 -0.35 0.08 -0.49 -0.53 -0.99 -0.48 + 1.382282015 0.556909973 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial part;mitochondrial small ribosomal subunit;nuclear membrane;nuclear part;organellar small ribosomal subunit;organelle membrane;organelle part;ribonucleoprotein complex;small ribosomal subunit 1.31E-22 1 3 3 11.3

Q96CV9-3;Q96CV9-2;Q96CV9 Optineurin OPTN >sp|Q96CV9-3|OPTN_HUMAN Isoform 3 of Optineurin OS=Homo sapiens GN=OPTN;>sp|Q96CV9-2|OPTN_HUMAN Isoform 2 of Optineurin OS=Homo sapiens GN=OPTN;>sp|Q96CV9|OPTN_HUMAN Optineurin OS=Homo sapiens GN=OPTN PE=1 SV=2 -0.45 -0.33 -0.14 -0.09 0.30 0.56 0.70 0.83 + 2.03547095 -0.851814931 "biological regulation;cell cycle process;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;death;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;G2/M transition of mitotic cell cycle;Golgi organization;Golgi ribbon formation;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;organelle organization;post-Golgi vesicle-mediated transport;protein targeting;protein targeting to Golgi;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;retrograde transport, vesicle recycling within Golgi;signal transduction;transport;vesicle-mediated transport" cell part;cytoplasmic part;cytosol;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;membrane;nuclear part;nucleoplasm;organelle membrane;organelle part;perinuclear region of cytoplasm;trans-Golgi network 3.10E-29 3 3 3 7.9

O60828-5;O60828-4;O60828-2;O60828;H7C053;O60828-10;O60828-9;O60828-8;O60828-7;O60828-6;C9JQA1;O60828-3 Polyglutamine-binding protein 1 PQBP1 >sp|O60828-5|PQBP1_HUMAN Isoform 5 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1;>sp|O60828-4|PQBP1_HUMAN Isoform 4 of Polyglutamine-binding protein 1 OS=Homo sapiens GN=PQBP1;>sp|O60828-2|PQBP1_HUMAN Isoform 2 of Polyglutamine-binding protei 0.21 0.37 0.20 0.55 -0.05 -0.29 -0.68 -0.24 + 1.59123308 0.644580293 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA biosynthetic process;RNA metabolic process;stress granule assembly;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;cell projection part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;neuronal RNA granule;non-membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex;RNA granule;stress granule Spliceosome 6.42E-09 12 3 3 31.5

P62854;Q5JNZ5 40S ribosomal protein S26;Putative 40S ribosomal protein S26-like 1 RPS26;RPS26P11 >sp|P62854|RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3;>sp|Q5JNZ5|RS26L_HUMAN Putative 40S ribosomal protein S26-like 1 OS=Homo sapiens GN=RPS26P11 PE=5 SV=1 0.07 0.07 0.16 0.11 -0.59 -0.47 -0.24 -0.27 + 1.995994202 0.492002379 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 9.16E-24 2 3 3 27

O00401 Neural Wiskott-Aldrich syndrome protein WASL >sp|O00401|WASL_HUMAN Neural Wiskott-Aldrich syndrome protein OS=Homo sapiens GN=WASL PE=1 SV=2 0.11 -0.06 0.14 -0.08 -0.20 -0.17 -0.19 -0.25 + 1.503701263 0.231040556 "actin cytoskeleton organization;actin filament organization;actin filament-based movement;actin filament-based process;actin polymerization or depolymerization;axon guidance;biological regulation;biosynthetic process;cell cycle process;cellular biosynthetic process;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex localization;cellular protein localization;chemotaxis;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;localization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;membrane budding;membrane organization;metabolic process;multi-organism process;nitric oxide metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle localization;organelle organization;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of clathrin-mediated endocytosis;positive regulation of endocytosis;positive regulation of filopodium assembly;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex localization;protein complex subunit organization;protein localization;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of clathrin-mediated endocytosis;regulation of endocytosis;regulation of filopodium assembly;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oxidoreductase activity;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of transport;regulation of vesicle-mediated transport;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to external stimulus;response to other organism;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;spindle localization;taxis;transcription, DNA-dependent;vesicle localization;vesicle organization;vesicle transport along actin filament" enzyme regulator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;small GTPase regulator activity actin cap;actin cytoskeleton;cell cortex part;cell part;cell projection;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;endocytic vesicle membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;plasma membrane;vesicle membrane   Adherens junction;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis   1.11E-07 1   3   3   9.1

O75886;O75886-2 Signal transducing adapter molecule 2   STAM2   >sp|O75886|STAM2_HUMAN Signal transducing adapter molecule 2 OS=Homo sapiens GN=STAM2 PE=1 SV=1;>sp|O75886-2|STAM2_HUMAN Isoform 2 of Signal transducing adapter molecule 2 OS=Homo sapiens GN=STAM2 0.13 -0.20   0.05 -0.24   0.31 0.18 0.53 0.49 +   1.450683222   -0.443310362 biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;endosome transport;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport   cell part;cytoplasmic part;cytosol;early endosome membrane;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part   Endocytosis;Jak-STAT signaling pathway   2.44E-16   2   4   3   9.5

P18085;C9JPM4;C9JAK5   ADP-ribosylation factor 4   ARF4   >sp|P18085|ARF4_HUMAN ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3;>tr|C9JPM4|C9JPM4_HUMAN ADP-ribosylation factor 4 (Fragment) OS=Homo sapiens GN=ARF4 PE=2 SV=1;>tr|C9JAK5|C9JAK5_HUMAN ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=2 0.04 -0.07   -0.17   -0.13   0.71 0.41 0.55 0.54 +   2.438605103   -0.640213391 anatomical structure development;biological regulation;brain development;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;developmental process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of protein localization;intracellular signal transduction;organ development;protein transport;regulation of biological process;regulation of cellular process;response to axon injury;response to stimulus;response to stress;response to wounding;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport   "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"   cell part;cytoplasm;cytoplasmic part;Golgi apparatus;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle;plasma membrane   1.20E-30 3   5   3   27.2

E9PC52;Q16576;Q16576-2;H0YF10;Q5JP01;Q5JP02;H0YCT5;H0YDK2;H0YEU5;B4DRT0;Q5JNZ6 Histone-binding protein RBBP7   RBBP7;RBBP4   >tr|E9PC52|E9PC52_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=2 SV=1;>sp|Q16576|RBBP7_HUMAN Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1;>sp|Q16576-2|RBBP7_HUMAN Isoform 2 of Histone-binding protein RBBP7 OS=Homo sap   0.30 0.03 -0.03   0.13 -0.29   -0.54   -0.65   -0.80   +   1.856269608   0.673401366   "ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cell proliferation;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular heat acclimation;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;developmental process;DNA metabolic process;DNA replication;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;heat acclimation;histone exchange;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent"   cell part;chromatin remodeling complex;ESC/E(Z) complex;histone deacetylase complex;histone methyltransferase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;methyltransferase complex;nuclear part;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;PcG protein complex;protein complex;transcriptional repressor complex   1.73E-38 11   10   3   21.9

O96019-2;O96019;H7C5S0;C9JQT2   Actin-like protein 6A   ACTL6A >sp|O96019-2|ACL6A_HUMAN Isoform 2 of Actin-like protein 6A OS=Homo sapiens GN=ACTL6A;>sp|O96019|ACL6A_HUMAN Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1;>tr|H7C5S0|H7C5S0_HUMAN Actin-like protein 6A (Fragment) OS=Homo sapiens GN=ACTL6A PE=4 S   0.19 0.41 0.09 0.15 0.10 -0.40   -0.52   -0.43   +   1.368523125   0.526618157   "anatomical structure development;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;covalent chromatin modification;developmental process;DNA metabolic process;DNA recombination;DNA repair;histone acetylation;histone H2A acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nervous system development;neural retina development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;system development;transcription, DNA-dependent" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;chromatin binding;nucleotide binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;chromatin remodeling complex;chromosomal part;DNA helicase complex;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;Ino80 complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;npBAF complex;NuA4 histone acetyltransferase complex;nuclear chromosome part;nuclear part;nucleoplasm part;organelle part;plasma membrane;protein complex;SWI/SNF complex;SWI/SNF-type complex 4.38E-26 4 4 4 13.4

Q9BRF8;B4DQ68;Q9BRF8-2 Calcineurin-like phosphoesterase domain-containing protein 1 CPPED1 >sp|Q9BRF8|CPPED_HUMAN Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3;>tr|B4DQ68|B4DQ68_HUMAN Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=2 SV=1;>sp|Q9BRF8-2|CP -0.66 -0.05 -0.71 -0.47 1.45 1.53 0.52 0.71 + 1.843421889 -1.525995003 binding;catalytic activity;cation binding;hydrolase activity;ion binding;metal ion binding 1.38E-35 3 4 4 14.6

P51398-2;P51398-3;P51398 "28S ribosomal protein S29, mitochondrial" DAP3 ">sp|P51398-2|RT29_HUMAN Isoform 2 of 28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3;>sp|P51398-3|RT29_HUMAN Isoform 3 of 28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3;>sp|P51398|RT29_HUMAN 28S ribosomal protein S29, mit" -0.31 0.22 0.34 0.09 -0.35 -0.84 -1.30 -0.73 + 1.459385492 0.891178126 apoptotic mitochondrial changes;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;mitochondrion organization;organelle organization cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial part;mitochondrial ribosome;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit 1.70E-73 3 4 4 14.6

Q96LJ7;H0YNC2 Dehydrogenase/reductase SDR family member 1 DHRS1 >sp|Q96LJ7|DHRS1_HUMAN Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 -0.20 0.01 0.48 0.50 -1.22 -0.91 -1.09 -1.26 + 2.201767202 1.31795417 metabolic process;oxidation-reduction process catalytic activity;oxidoreductase activity cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle membrane;organelle part 1.11E-57 2 4 4 16.3

Q5RKV6 Exosome complex component MTR3 EXOSC6 >sp|Q5RKV6|EXOS6_HUMAN Exosome complex component MTR3 OS=Homo sapiens GN=EXOSC6 PE=1 SV=1 0.11 0.22 0.24 0.28 -0.21 -0.53 -1.19 -0.86 + 1.617736238 0.907981733 "B cell activation;B cell activation involved in immune response;catabolic process;cell activation;cell activation involved in immune response;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA deamination;DNA metabolic process;DNA modification;DNA recombination;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;gene expression;immune effector process;immune system process;isotype switching;leukocyte activation;leukocyte activation involved in immune response;lymphocyte activation;lymphocyte activation involved in immune response;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response" binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;exosome (RNase complex);intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex RNA degradation 2.94E-31 1 4 4 25.7

O15357;O15357-2;F5H588;H7BXR2;F5H3D8;H0YFZ4 "Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2" INPPL1 ">sp|O15357|SHIP2_HUMAN Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Homo sapiens GN=INPPL1 PE=1 SV=2;>sp|O15357-2|SHIP2_HUMAN Isoform 2 of Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Homo sapiens GN=INPPL1" -0.43 -0.14 -0.79 -0.01 0.89 1.24 0.69 0.66 + 1.9381217 -1.213667535 actin cytoskeleton organization;actin filament organization;actin filament-based process;alcohol metabolic process;anatomical structure development;biological adhesion;biological regulation;biosynthetic process;brain development;carbohydrate metabolic process;cell adhesion;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cytoskeleton organization;dephosphorylation;developmental process;endocytosis;establishment of localization;glucose metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;hexose metabolic process;inositol phosphate metabolic process;inositol trisphosphate metabolic process;lipid biosynthetic process;lipid metabolic process;lipid modification;membrane invagination;membrane organization;metabolic process;monosaccharide metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell projection organization;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of gene expression;negative regulation of insulin receptor signaling pathway;negative regulation of insulin-like growth factor receptor signaling pathway;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of neuron projection development;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of platelet-derived growth factor receptor signaling pathway;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transferase activity;organ development;organelle organization;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol dephosphorylation;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid dephosphorylation;phospholipid metabolic process;phosphorus metabolic process;post-embryonic development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of gene expression;regulation of insulin receptor signaling pathway;regulation of insulin-like growth factor receptor signaling pathway;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of platelet-derived growth factor receptor signaling pathway;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transferase activity;response to chemical stimulus;response to drug;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;small molecule metabolic process;transport;vesicle-mediated transport "binding;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;inositol or phosphatidylinositol phosphatase activity;inositol phosphate phosphatase activity;inositol trisphosphate phosphatase activity;inositol-polyphosphate 5-phosphatase activity;lipid binding;phosphatase activity;phosphatidylinositol binding;phosphatidylinositol-3,4,5-trisphosphate binding;phospholipid binding;phosphoric ester hydrolase activity" cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;filopodium;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane;membrane-bounded organelle;non-membrane-bounded organelle;organelle;plasma membrane Inositol phosphate metabolism;Phosphatidylinositol signaling system 1.03E-15 6 4 4 4.5

B4E2S7;P13473-2;P13473;P13473-3;B7Z2R9;H0YCG2 Lysosome-associated membrane glycoprotein 2 LAMP2 >tr|B4E2S7|B4E2S7_HUMAN Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=2 SV=1;>sp|P13473-2|LAMP2_HUMAN Isoform LAMP-2B of Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2;>sp|P13473|LAMP2_HUMAN Lysosome-associat -0.46 -0.21 -0.17 -0.04 0.89 1.06 0.42 0.59 + 1.959762535 -0.963071723 cell activation;cellular process;establishment of localization;establishment of localization in cell;exocytosis;platelet activation;platelet degranulation;secretion;secretion by cell;transport;vesicle-mediated transport cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosomal part;endosome membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;late endosome membrane;lysosomal membrane;membrane;membrane part;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;platelet dense granule membrane;secretory granule membrane;vacuolar membrane;vacuolar part;vesicle membrane ko05152;Lysosome;Phagosome 6.22E-19 6 4 4 9.9

Q8IWT6 Leucine-rich repeat-containing protein 8A LRRC8A >sp|Q8IWT6|LRC8A_HUMAN Leucine-rich repeat-containing protein 8A OS=Homo sapiens GN=LRRC8A PE=1 SV=1 -0.01 0.17 0.17 0.34 -0.94 -0.65 -0.76 -0.59 + 2.479213365 0.901074079 B cell activation;B cell differentiation;cell activation;cell differentiation;cellular developmental process;cellular process;developmental process;immature B cell differentiation;immune system process;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;pre-B cell differentiation cell part;integral to membrane;intrinsic to membrane;membrane part 5.68E-13 1 4 4 7.3

O95232;J3KPP4;D6RDI2;B4DJ96;D6RHH0;E7EN55;O95232-2;C9JL41 Luc7-like protein 3 LUC7L3 ">sp|O95232|LC7L3_HUMAN Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2;>tr|J3KPP4|J3KPP4_HUMAN Cisplatin resistance-associated overexpressed protein, isoform CRA_b OS=Homo sapiens GN=LUC7L3 PE=4 SV=1;>tr|D6RDI2|D6RDI2_HUMAN Luc7-like protein 3 (Fra" 0.12 0.09 -0.01 0.08 -0.15 -0.42 -0.33 -0.47 + 1.937249654 0.414977804 apoptosis;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;response to stimulus;response to stress;RNA metabolic process;RNA processing;RNA splicing binding;DNA binding;mRNA binding;nucleic acid binding;RNA binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;focal adhesion;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part;plasma membrane 4.66E-43 8 4 4 13.2

Q8TDZ2;Q8TDZ2-4;Q8TDZ2-2;H0Y6Z4;Q8TDZ2-3 Protein-methionine sulfoxide oxidase MICAL1 MICAL1 >sp|Q8TDZ2|MICA1_HUMAN Protein-methionine sulfoxide oxidase MICAL1 OS=Homo sapiens GN=MICAL1 PE=1 SV=2;>sp|Q8TDZ2-4|MICA1_HUMAN Isoform 4 of Protein-methionine sulfoxide oxidase MICAL1 OS=Homo sapiens GN=MICAL1;>sp|Q8TDZ2-2|MICA1_HUMAN Isoform 2 of Protein 0.21 -0.21 -0.08 -0.29 1.08 0.65 1.04 0.30 + 1.565215753 -0.860960808 actin cytoskeleton organization;actin filament depolymerization;actin filament organization;actin filament-based process;actin polymerization or depolymerization;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex disassembly;cellular response to stimulus;cytoskeleton organization;macromolecular complex disassembly;macromolecular complex subunit organization;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of hydrolase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;organelle organization;protein complex disassembly;protein complex subunit organization;protein depolymerization;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;response to stimulus;signal transduction "actin binding;binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;cytoskeletal protein binding;FAD binding;flavin adenine dinucleotide binding;ion binding;metal ion binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;protein binding;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex 1.16E-12 5 4 4 5.4

Q14554;Q9BV43 Protein disulfide-isomerase A5 PDIA5 >sp|Q14554|PDIA5_HUMAN Protein disulfide-isomerase A5 OS=Homo sapiens GN=PDIA5 PE=1 SV=1 -0.43 -0.36 -0.44 -0.04 0.97 0.64 0.66 0.42 + 2.173180983 -0.988778546 activation of signaling protein activity involved in unfolded protein response;biological regulation;cell redox homeostasis;cellular homeostasis;cellular process;glycerol ether metabolic process;homeostatic process;metabolic process;organic ether metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle membrane;organelle part 3.87E-24 2 4 4 11.4

Q8IV08;M0QZI4;M0R3G9;M0R1F7 Phospholipase D3 PLD3 >sp|Q8IV08|PLD3_HUMAN Phospholipase D3 OS=Homo sapiens GN=PLD3 PE=1 SV=1;>tr|M0QZI4|M0QZI4_HUMAN Phospholipase D3 (Fragment) OS=Homo sapiens GN=PLD3 PE=4 SV=1 -0.39 -0.02 -0.03 0.15 0.15 0.42 0.38 0.57 + 1.299016755 -0.45607375 biosynthetic process;catabolic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;metabolic process;organophosphate metabolic process;phosphatidylglycerol biosynthetic process;phosphatidylglycerol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;small molecule metabolic process "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;NAPE-specific phospholipase D activity;phospholipase activity;phospholipase D activity;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part 3.17E-12 4 4 4 11.6

O43172-2;O43172 U4/U6 small nuclear ribonucleoprotein Prp4 PRPF4 >sp|O43172-2|PRP4_HUMAN Isoform 2 of U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens GN=PRPF4;>sp|O43172|PRP4_HUMAN U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens GN=PRPF4 PE=1 SV=2 0.04 0.16 0.07 0.16 -0.22 -0.50 -1.07 -0.79 + 1.567499133 0.752813492 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" Cajal body;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U4/U6 snRNP Spliceosome 3.02E-17 2 4 4 11.1

P20936-2;B4DTL2;E9PGC0;P20936;Q68CU6 Ras GTPase-activating protein 1 RASA1 >sp|P20936-2|RASA1_HUMAN Isoform 2 of Ras GTPase-activating protein 1 OS=Homo sapiens GN=RASA1;>tr|B4DTL2|B4DTL2_HUMAN Ras GTPase-activating protein 1 OS=Homo sapiens GN=RASA1 PE=2 SV=1;>tr|E9PGC0|E9PGC0_HUMAN Ras GTPase-activating protein 1 OS=Homo sapien 0.21 -0.02 -0.11 -0.14 0.24 0.59 0.31 0.44 + 1.469709902 -0.413025683 biological regulation;cell differentiation;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;cellular response to stimulus;cytokinesis;developmental process;embryo development;intracellular signal transduction;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell-matrix adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of Ras protein signal transduction;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of small GTPase mediated signal transduction;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell morphogenesis;regulation of cell shape;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein polymerization;regulation of purine nucleotide catabolic process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;signal transduction;vasculogenesis binding;channel inhibitor activity;channel regulator activity;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion channel inhibitor activity;lipid binding;nucleoside-triphosphatase regulator activity;phospholipid binding;potassium channel inhibitor activity;potassium channel regulator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;cell projection;cytoplasmic part;cytosol;intracellular;intracellular part;intrinsic to internal side of plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part;ruffle Axon guidance;MAPK signaling pathway 2.69E-29 5 4 4 7.6

P62899;H7C2W9;C9JU56;B7Z4E3;P62899-3;P62899-2;B7Z4C8;B8ZZK4 60S ribosomal protein L31 RPL31 >sp|P62899|RL31_HUMAN 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1;>tr|H7C2W9|H7C2W9_HUMAN 60S ribosomal protein L31 (Fragment) OS=Homo sapiens GN=RPL31 PE=4 SV=1;>tr|C9JU56|C9JU56_HUMAN 60S ribosomal protein L31 (Fragment) OS=Homo sapiens 0.09 0.00 0.17 0.16 -0.32 -0.43 -0.22 -0.40 + 2.275307511 0.444778523 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.25E-46 8 4 4 32.8

O15126;O15126-2 Secretory carrier-associated membrane protein 1 SCAMP1 >sp|O15126|SCAM1_HUMAN Secretory carrier-associated membrane protein 1 OS=Homo sapiens GN=SCAMP1 PE=1 SV=2;>sp|O15126-2|SCAM1_HUMAN Isoform 2 of Secretory carrier-associated membrane protein 1 OS=Homo sapiens GN=SCAMP1 0.01 0.01 -0.48 -0.12 0.59 0.82 0.21 0.72 + 1.580548166 -0.733097478 cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;post-Golgi vesicle-mediated transport;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;endosomal part;endosome membrane;Golgi apparatus;Golgi apparatus part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;recycling endosome membrane;trans-Golgi network 3.47E-23 2 4 4 23.4

Q9BWU0;H7C256 Kanadaptin SLC4A1AP >sp|Q9BWU0|NADAP_HUMAN Kanadaptin OS=Homo sapiens GN=SLC4A1AP PE=1 SV=1 0.24 0.09 0.14 -0.10 -0.15 -0.33 -0.58 -0.43 + 1.587799756 0.46696456 binding;double-stranded RNA binding;nucleic acid binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.11E-09 2 4 4 8.4

Q13148;Q13148-2;K7EJM5;K7EN94;B1AKP7;G3V162;B4DJ45;K7EJ99;Q13148-3 TAR DNA-binding protein 43 TARDBP>sp|Q13148|TADBP_HUMAN TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1;>sp|Q13148-2|TADBP_HUMAN Isoform 2 of TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP;>tr|K7EJM5|K7EJM5_HUMAN TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens G0.13 0.16 -0.06 0.21 -0.12 -0.36 -0.66 -0.38 + 1.523389709 0.491832551 "3'-UTR-mediated mRNA stabilization;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;interaction with symbiont;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;mRNA metabolic process;mRNA processing;mRNA stabilization;multi-organism process;negative regulation by host of viral transcription;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of reproductive process;negative regulation of RNA metabolic process;negative regulation of viral transcription;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of viral reproduction;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of RNA stability;regulation of viral reproduction;regulation of viral transcription;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA stabilization;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;DNA binding;double-stranded DNA binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleotide binding;RNA binding;sequence-specific DNA binding transcription factor activity;structure-specific DNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.74E-86 9 4 4 15.2

Q8WWA1-2;Q8WWA1;B4DXI0;C9JID5 Transmembrane protein 40 TMEM40 >sp|Q8WWA1-2|TMM40_HUMAN Isoform 2 of Transmembrane protein 40 OS=Homo sapiens GN=TMEM40;>sp|Q8WWA1|TMM40_HUMAN Transmembrane protein 40 OS=Homo sapiens GN=TMEM40 PE=1 SV=2;>tr|B4DXI0|B4DXI0_HUMAN Transmembrane protein 40 OS=Homo sapiens GN=TMEM40 PE=2 SV= 0.38 0.24 -0.47 -0.30 0.69 1.17 0.44 0.94 + 1.329727591 -0.846771345 cell part;integral to membrane;intrinsic to membrane;membrane part 1.31E-76 4 4 4 30.5

B9A018;Q53GS9;Q53GS9-2;Q53GS9-3;F8WC91 U4/U6.U5 tri-snRNP-associated protein 2 USP39 >tr|B9A018|B9A018_HUMAN U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=2 SV=1;>sp|Q53GS9|SNUT2_HUMAN U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=1 SV=2;>sp|Q53GS9-2|SNUT2_HUMAN Isoform 2 of U4/U6.U5 tri-snRNP-as 0.09 0.05 -0.02 0.05 -0.09 -0.40 -0.84 -0.82 + 1.308656448 0.582867431 catabolic process;cell cycle;cell division;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;spliceosome assembly;ubiquitin-dependent protein catabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;thiolester hydrolase activity;transition metal ion binding;ubiquitin thiolesterase activity;zinc ion binding" cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 7.79E-23 5 4 4 10.1

Q9H269;Q5JUA8;Q9H269-2;Q5JUB0;Q5JUA9 Vacuolar protein sorting-associated protein 16 homolog VPS16 >sp|Q9H269|VPS16_HUMAN Vacuolar protein sorting-associated protein 16 homolog OS=Homo sapiens GN=VPS16 PE=1 SV=2;>tr|Q5JUA8|Q5JUA8_HUMAN Vacuolar protein sorting-associated protein 16 homolog OS=Homo sapiens GN=VPS16 PE=2 SV=1;>sp|Q9H269-2|VPS16_HUMAN Isof -0.25 -0.01 -0.20 -0.14 0.25 0.36 0.34 0.40 + 2.368502366 -0.486283718 establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;transport actin filament;axon;cell body;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeletal part;early endosome;endosomal part;endosome;endosome membrane;HOPS complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;late endosome membrane;lysosomal membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuron projection;neuronal cell body;organelle;organelle membrane;organelle part;protein complex;recycling endosome;vacuolar membrane;vacuolar part 4.37E-12 5 4 4 6.7

P31350;P31350-2;C9JXC1 Ribonucleoside-diphosphate reductase subunit M2 RRM2 >sp|P31350|RIR2_HUMAN Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens GN=RRM2 PE=1 SV=1;>sp|P31350-2|RIR2_HUMAN Isoform 2 of Ribonucleoside-diphosphate reductase subunit M2 OS=Homo sapiens GN=RRM2;>tr|C9JXC1|C9JXC1_HUMAN Ribonucleoside-diph 0.56 0.23 -0.03 0.59 -0.37 -1.22 -0.39 -1.44 + 1.492241621 1.193673094 "biological regulation;biosynthetic process;cell cycle process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;deoxyribonucleoside diphosphate metabolic process;deoxyribonucleotide biosynthetic process;deoxyribonucleotide metabolic process;DNA metabolic process;DNA replication;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside diphosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription involved in G1/S phase of mitotic cell cycle;regulation of transcription, DNA-dependent;small molecule metabolic process" "binding;catalytic activity;cation binding;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on CH or CH2 groups;oxidoreductase activity, acting on CH or CH2 groups, disulfide as acceptor;ribonucleoside-diphosphate reductase activity;transition metal ion binding" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part Glutathione metabolism;p53 signaling pathway;Purine metabolism;Pyrimidine metabolism 7.76E-35 3 5 4 19.8

Q13188;B3KYA7;E5RFQ9 Serine/threonine-protein kinase 3;Serine/threonine-protein kinase 3 36kDa subunit;Serine/threonine-protein kinase 3 20kDa subunit STK3 >sp|Q13188|STK3_HUMAN Serine/threonine-protein kinase 3 OS=Homo sapiens GN=STK3 PE=1 SV=2;>tr|B3KYA7|B3KYA7_HUMAN Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK3 PE=2 SV=1 0.32 0.05 0.25 -0.02 -0.89 -0.56 -0.16 -0.54 + 1.568884189 0.689509864 anatomical structure development;anatomical structure formation involved in morphogenesis;apoptosis;biological regulation;cell death;cell differentiation;cell differentiation involved in embryonic placenta development;cellular developmental process;cellular process;cellular response to stimulus;central nervous system development;death;developmental process;embryonic epithelial tube formation;embryonic hemopoiesis;embryonic organ development;endocardium development;epithelial tube formation;hemopoiesis;hemopoietic or lymphoid organ development;hippo signaling cascade;intracellular protein kinase cascade;intracellular signal transduction;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of growth;negative regulation of organ growth;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;neural tube formation;organ development;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of JNK cascade;positive regulation of MAPKKK cascade;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;primitive hemopoiesis;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of cellular response to stress;regulation of growth;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of MAPKKK cascade;regulation of organ growth;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of Wnt receptor signaling pathway;response to stimulus;signal transduction;system development;tube formation "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;ion binding;kinase activator activity;kinase activity;kinase regulator activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein dimerization activity;protein kinase activator activity;protein kinase activity;protein kinase regulator activity;protein serine/threonine kinase activator activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle MAPK signaling pathway 1.07E-34 3 6 4 15.3

P36507;G5E9C7 Dual specificity mitogen-activated protein kinase kinase 2 MAP2K2 >sp|P36507|MP2K2_HUMAN Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 0.04 -0.15 -0.10 -0.38 0.57 0.52 0.51 0.18 + 1.749719256 -0.591350708 activation of immune response;activation of innate immune response;activation of MAPK activity;activation of MAPKK activity;activation of protein kinase activity;axon guidance;biological regulation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chemotaxis;defense response;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;ERK1 and ERK2 cascade;fibroblast growth factor receptor signaling pathway;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;insulin receptor signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;locomotion;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;nerve growth factor receptor signaling pathway;pattern recognition receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of response to stimulus;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regulation of biological process;regulation of catalytic activity;regulation of cell motility;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of defense response;regulation of early endosome to late endosome transport;regulation of Golgi inheritance;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;small GTPase mediated signal transduction;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;taxis;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;TRIF-dependent toll-like receptor signaling pathway "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;kinase activator activity;kinase activity;kinase regulator activity;MAP kinase kinase activity;nucleotide binding;PDZ domain binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein domain specific binding;protein kinase activator activity;protein kinase activity;protein kinase regulator activity;protein serine/threonine kinase activator activity;protein serine/threonine kinase activity;protein serine/threonine/tyrosine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;cell cortex;cell junction;cell part;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytosol;early endosome;endoplasmic reticulum;endosome;extracellular region;focal adhesion;Golgi apparatus;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;microtubule;mitochondrion;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;peroxisomal membrane;peroxisomal part;plasma membrane part;protein complex Acute myeloid leukemia;B cell receptor signaling pathway;Bladder cancer;Chronic myeloid leukemia;Endometrial cancer;ErbB signaling pathway;Fc epsilon RI signaling pathway;Gap junction;Glioma;GnRH signaling pathway;Insulin signaling pathway;Long-term depression;Long-term potentiation;MAPK signaling pathway;Melanogenesis;Melanoma;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Non-small cell lung cancer;Pathways in cancer;Prion diseases;Prostate cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;T cell receptor signaling pathway;Thyroid cancer;Toll-like receptor signaling pathway;Vascular smooth muscle contraction;VEGF signaling pathway 3.20E-41 2 7 4 16.2

B4DR80;Q9Y6E0-2;Q9Y6E0;H0Y630;Q5JV98;Q5JV99;C9JDH9;C9J6L2;C9JCC0;C9J232;H7C279;B7Z9K1;A8K6Z3;O00506;C9JJV0 Serine/threonine-protein kinase 24;Serine/threonine-protein kinase 24 36 kDa subunit;Serine/threonine-protein kinase 24 12 kDa subunit STK24 >tr|B4DR80|B4DR80_HUMAN Serine/threonine-protein kinase 24 12 kDa subunit OS=Homo sapiens GN=STK24 PE=2 SV=1;>sp|Q9Y6E0-2|STK24_HUMAN Isoform A of Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24;>sp|Q9Y6E0|STK24_HUMAN Serine/threonine-protein k0.15 0.03 0.01 -0.12 -0.37 -0.55 -0.17 -0.26 + 1.433906995 0.355178707 biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;establishment or maintenance of cell polarity;Golgi localization;induction of apoptosis;induction of apoptosis by intracellular signals;induction of apoptosis by oxidative stress;induction of programmed cell death;localization;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;organelle localization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of neurogenesis;positive regulation of programmed cell death;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of axon regeneration;regulation of axonogenesis;regulation of biological process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of cellular response to stress;regulation of developmental process;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuron projection regeneration;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part 7.41E-56 15 8 4 25

P42330;B4DL37;A6NHU4;P17516;P51857-2;P51857 Aldo-keto reductase family 1 member C3 AKR1C3;AKR1C1 >sp|P42330|AK1C3_HUMAN Aldo-keto reductase family 1 member C3 OS=Homo sapiens GN=AKR1C3 PE=1 SV=4;>tr|B4DL37|B4DL37_HUMAN Aldo-keto reductase family 1 member C3 OS=Homo sapiens GN=AKR1C3 PE=2 SV=1;>tr|A6NHU4|A6NHU4_HUMAN Aldo-keto reductase family 1 member -0.14 -0.33 -0.43 -0.50 1.95 1.81 1.30 0.70 + 2.053036971 -1.788621407 "alcohol catabolic process;alcohol metabolic process;anatomical structure development;androgen biosynthetic process;androgen metabolic process;apocarotenoid metabolic process;arachidonic acid metabolic process;bile acid biosynthetic process;bile acid catabolic process;bile acid metabolic process;biological regulation;biosynthetic process;C21-steroid hormone metabolic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell communication;cell differentiation;cellular aldehyde metabolic process;cellular biosynthetic process;cellular catabolic process;cellular developmental process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to cadmium ion;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to corticosteroid stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to hormone stimulus;cellular response to inorganic substance;cellular response to jasmonic acid stimulus;cellular response to lipid;cellular response to metal ion;cellular response to nutrient levels;cellular response to organic substance;cellular response to oxidative stress;cellular response to prostaglandin stimulus;cellular response to reactive oxygen species;cellular response to starvation;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to stress;cholesterol catabolic process;cholesterol metabolic process;cyclooxygenase pathway;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;developmental process involved in reproduction;digestion;diterpenoid metabolic process;epidermal cell differentiation;epithelial cell differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;farnesol catabolic process;farnesol metabolic process;fat-soluble vitamin metabolic process;fatty acid metabolic process;gonad development;hormone biosynthetic process;hormone metabolic process;icosanoid metabolic process;intracellular protein transport;intracellular transport;isoprenoid catabolic process;isoprenoid metabolic process;keratinocyte differentiation;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;macromolecule metabolic process;male gonad development;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;organ development;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;phototransduction;phototransduction, visible light;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of endothelial cell apoptosis;positive regulation of intracellular protein kinase cascade;positive regulation of metabolic process;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of reactive oxygen species metabolic process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary alcohol catabolic process;primary alcohol metabolic process;primary metabolic process;progesterone metabolic process;protein import into nucleus, translocation;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of endothelial cell apoptosis;regulation of hormone biosynthetic process;regulation of hormone levels;regulation of hormone metabolic process;regulation of intracellular protein kinase cascade;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of reactive oxygen species metabolic process;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of signal transduction;regulation of signaling;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of testosterone biosynthetic process;renal absorption;renal system process;reproductive process;reproductive structure development;response to abiotic stimulus;response to cadmium ion;response to calcium ion;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to inorganic substance;response to jasmonic acid stimulus;response to light stimulus;response to lipid;response to metal ion;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to prostaglandin stimulus;response to radiation;response to reactive oxygen species;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;retinal metabolic process;retinoid metabolic process;sesquiterpene catabolic process;sesquiterpene metabolic process;sesquiterpenoid catabolic process;sesquiterpenoid metabolic process;signal transduction;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;steroid biosynthetic process;steroid catabolic process;steroid metabolic process;sterol catabolic process;sterol metabolic process;system process;terpene catabolic process;terpene metabolic process;terpenoid catabolic process;terpenoid metabolic process;testosterone biosynthetic process;transport;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process;vitamin A metabolic process;vitamin metabolic process" "15-hydroxyprostaglandin-D dehydrogenase (NADP+) activity;alcohol dehydrogenase (NADP+) activity;alditol:NADP+ 1-oxidoreductase activity;aldo-keto reductase (NADP) activity;androsterone dehydrogenase (A-specific) activity;androsterone dehydrogenase (B-specific) activity;androsterone dehydrogenase activity;bile acid transmembrane transporter activity;binding;carboxylic acid transmembrane transporter activity;catalytic activity;chlordecone reductase activity;delta4-3-oxosteroid 5beta-reductase activity;dihydrotestosterone 17-beta-dehydrogenase activity;electron carrier activity;enone reductase activity;geranylgeranyl reductase activity;G-protein coupled receptor activity;icosanoid receptor activity;indanol dehydrogenase activity;ketoreductase activity;ketosteroid monooxygenase activity;lipid binding;molecular transducer activity;monocarboxylic acid transmembrane transporter activity;monooxygenase activity;organic acid transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;phenanthrene 9,10-monooxygenase activity;prostaglandin F receptor activity;prostaglandin receptor activity;prostaglandin-F synthase activity;prostanoid receptor activity;receptor activity;retinal dehydrogenase activity;retinol dehydrogenase activity;signal transducer activity;signaling receptor activity;steroid binding;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;testosterone 17-beta-dehydrogenase (NADP+) activity;testosterone dehydrogenase (NAD+) activity;trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity;transmembrane signaling receptor activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Arachidonic acid metabolism;Metabolism of xenobiotics by cytochrome P450;Primary bile acid biosynthesis;Steroid hormone biosynthesis 8.47E-125 6 14 4 50.5

Q15067-2;Q15067;Q15067-3;I3L2U4;K7ELT1;I3L0T4 Peroxisomal acyl-coenzyme A oxidase 1 ACOX1 >sp|Q15067-2|ACOX1_HUMAN Isoform 2 of Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1;>sp|Q15067|ACOX1_HUMAN Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3;>sp|Q15067-3|ACOX1_HUMAN Isoform 3 of Peroxisomal acyl-coen -0.12 -0.23 -0.31 -0.06 1.20 1.33 1.02 0.74 + 2.540500502 -1.255567146 biological regulation;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;chemical homeostasis;fatty acid beta-oxidation;fatty acid beta-oxidation using acyl-CoA oxidase;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;gamete generation;generation of precursor metabolites and energy;homeostatic process;icosanoid metabolic process;lipid catabolic process;lipid homeostasis;lipid metabolic process;lipid modification;lipid oxidation;male gamete generation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;multicellular organismal process;multicellular organismal reproductive process;organelle fission;organelle organization;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;peroxisome fission;positive regulation of biological process;positive regulation of cholesterol homeostasis;positive regulation of homeostatic process;primary metabolic process;prostaglandin metabolic process;prostanoid metabolic process;regulation of biological process;regulation of biological quality;regulation of cholesterol homeostasis;regulation of homeostatic process;reproductive process;small molecule catabolic process;small molecule metabolic process;spermatogenesis;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process "acyl-CoA dehydrogenase activity;acyl-CoA oxidase activity;binding;carboxylic acid binding;catalytic activity;coenzyme binding;cofactor binding;FAD binding;fatty acid binding;flavin adenine dinucleotide binding;lipid binding;monocarboxylic acid binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, oxygen as acceptor;palmitoyl-CoA oxidase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part;peroxisome alpha-Linolenic acid metabolism;Biosynthesis of unsaturated fatty acids;Fatty acid metabolism;Peroxisome;PPAR signaling pathway 1.20E-20 6 5 5 13.9

P00568;Q5T9B7;H0Y4J6;H0YID2 Adenylate kinase isoenzyme 1 AK1>sp|P00568|KAD1_HUMAN Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3;>tr|Q5T9B7|Q5T9B7_HUMAN Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=2 SV=1;>tr|H0Y4J6|H0Y4J6_HUMAN Adenylate kinase isoenzyme 1 (Fragment) OS=Homo sapiens GN=AK1 -0.04 -0.01 -0.22 0.01 0.50 0.65 0.60 0.29 + 2.02739901 -0.57409124 ATP metabolic process;biological regulation;cell cycle arrest;cell cycle process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of cell cycle;regulation of cellular process;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;adenylate kinase activity;ATP binding;binding;catalytic activity;kinase activity;nucleobase-containing compound kinase activity;nucleotide binding;nucleotide kinase activity;phosphotransferase activity, phosphate group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" axoneme part;cell part;cell projection part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;organelle part;outer dense fiber;plasma membrane Purine metabolism 1.49E-25 4 5 5 25.8

E7ERV9;E7EMM4;Q13510-3;Q13510;Q13510-2 Acid ceramidase;Acid ceramidase subunit alpha;Acid ceramidase subunit beta ASAH1 >tr|E7ERV9|E7ERV9_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=2 SV=1;>tr|E7EMM4|E7EMM4_HUMAN Acid ceramidase OS=Homo sapiens GN=ASAH1 PE=2 SV=1;>sp|Q13510-3|ASAH1_HUMAN Isoform 3 of Acid ceramidase OS=Homo sapiens GN=ASAH1;>sp|Q13510|ASAH1_HUMAN Acid -0.49 -0.25 -0.64 -0.03 1.39 1.93 0.59 0.65 + 1.636043497 -1.494720411 anatomical structure development;cell death;cellular lipid metabolic process;cellular metabolic process;cellular process;ceramide metabolic process;death;developmental process;glycolipid metabolic process;glycosphingolipid metabolic process;lipid metabolic process;lung development;membrane lipid metabolic process;metabolic process;organ development;primary metabolic process;response to chemical stimulus;response to organic substance;response to stimulus;small molecule metabolic process;sphingoid metabolic process;sphingolipid metabolic process "catalytic activity;ceramidase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;lysosome;lytic vacuole;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vacuolar lumen;vacuolar part;vacuole Lysosome;Sphingolipid metabolism 1.30E-19 5 5 5 21

Q53RT3 Retroviral-like aspartic protease 1 ASPRV1 >sp|Q53RT3|APRV1_HUMAN Retroviral-like aspartic protease 1 OS=Homo sapiens GN=ASPRV1 PE=1 SV=1 -0.34 0.78 -1.11 -0.33 2.15 2.80 1.74 1.06 + 1.575912014 -2.182722695 anatomical structure development;developmental process;epidermis development;macromolecule metabolic process;metabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;skin development;tissue development "aspartic-type endopeptidase activity;aspartic-type peptidase activity;catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;integral to membrane;intrinsic to membrane;membrane part 1.44E-28 1 5 5 18.4

P30085;Q5T0D2;P30085-2 UMP-CMP kinase CMPK1 >sp|P30085|KCY_HUMAN UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3;>tr|Q5T0D2|Q5T0D2_HUMAN UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=2 SV=1 -0.09 -0.13 -0.26 -0.13 0.29 0.38 0.76 0.53 + 2.021975858 -0.642746922 2'-deoxyribonucleotide biosynthetic process;2'-deoxyribonucleotide metabolic process;benzene-containing compound metabolic process;biosynthetic process;carboxylic acid metabolic process;CDP biosynthetic process;CDP metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;dCDP biosynthetic process;dCDP metabolic process;deoxyribonucleoside diphosphate biosynthetic process;deoxyribonucleoside diphosphate metabolic process;deoxyribonucleotide biosynthetic process;deoxyribonucleotide metabolic process;dicarboxylic acid metabolic process;dUDP biosynthetic process;dUDP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside diphosphate biosynthetic process;nucleoside diphosphate metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid metabolic process;ovulation cycle process;oxoacid metabolic process;phthalate metabolic process;primary metabolic process;pyrimidine deoxyribonucleoside diphosphate biosynthetic process;pyrimidine deoxyribonucleoside diphosphate metabolic process;pyrimidine deoxyribonucleotide biosynthetic process;pyrimidine deoxyribonucleotide metabolic process;pyrimidine nucleoside diphosphate biosynthetic process;pyrimidine nucleoside diphosphate metabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside diphosphate biosynthetic process;pyrimidine ribonucleoside diphosphate metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;rhythmic process;ribonucleoside diphosphate biosynthetic process;ribonucleoside diphosphate metabolic process;ribonucleoside metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;UDP biosynthetic process;UDP metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cytidylate kinase activity;kinase activity;nucleobase-containing compound kinase activity;nucleoside kinase activity;nucleotide binding;nucleotide kinase activity;phosphotransferase activity, phosphate group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups;UMP kinase activity;uridine kinase activity;uridylate kinase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Pyrimidine metabolism 2.93E-52 3 5 5 23

Q9UBR2 Cathepsin Z CTSZ >sp|Q9UBR2|CATZ_HUMAN Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 0.04 -0.33 0.14 -0.05 0.49 0.28 0.50 0.65 + 1.604037118 -0.529800428 anatomical structure morphogenesis;angiotensin maturation;biological regulation;branching morphogenesis of a tube;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epithelial tube branching involved in lung morphogenesis;epithelial tube morphogenesis;hormone metabolic process;macromolecule metabolic process;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;peptide hormone processing;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;regulation of biological quality;regulation of hormone levels;tissue morphogenesis;tube morphogenesis "catalytic activity;cysteine-type peptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;endoplasmic reticulum;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane;membrane-bounded organelle;organelle;plasma membrane;vacuole Lysosome 3.97E-64 1 5 5 21.5

Q6BCY4;E9PIV9;E9PMI2;E9PQW2;Q6BCY4-2;E9PRM4NADH-cytochrome b5 reductase 2CYB5R2 >sp|Q6BCY4|NB5R2_HUMAN NADH-cytochrome b5 reductase 2 OS=Homo sapiens GN=CYB5R2 PE=1 SV=1;>tr|E9PIV9|E9PIV9_HUMAN NADH-cytochrome b5 reductase 2 (Fragment) OS=Homo sapiens GN=CYB5R2 PE=2 SV=1;>tr|E9PMI2|E9PMI2_HUMAN NADH-cytochrome b5 reductase 2 (Fragment 0.15 -0.10 -0.24 -0.12 0.48 0.86 0.99 0.49 + 1.831397632 -0.782785298 alcohol metabolic process;biosynthetic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "catalytic activity;cytochrome-b5 reductase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle Amino sugar and nucleotide sugar metabolism 1.06E-21 6 5 5 21.7

Q6PI48 "Aspartate--tRNA ligase, mitochondrial" DARS2 ">sp|Q6PI48|SYDM_HUMAN Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1" 0.19 0.11 0.18 -0.01 -0.31 -0.52 -0.14 -0.49 + 1.777890922 0.479035466 amine metabolic process;amino acid activation;asparaginyl-tRNA aminoacylation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mitochondrial asparaginyl-tRNA aminoacylation;mitochondrial RNA metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for mitochondrial protein translation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;aspartate-tRNA ligase activity;aspartate-tRNA(Asn) ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nucleus;organelle;organelle lumen;organelle part Aminoacyl-tRNA biosynthesis 4.15E-37 1 5 5 10.9

B7Z817;Q15392;F5H0H1;H7C4B7 Delta(24)-sterol reductase DHCR24 >tr|B7Z817|B7Z817_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 SV=1;>sp|Q15392|DHC24_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2;>tr|F5H0H1|F5H0H1_HUMAN Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=2 S 0.17 -0.17 -0.68 -0.77 1.12 1.12 0.86 0.44 + 1.707756795 -1.24894128 alcohol metabolic process;amyloid precursor protein catabolic process;amyloid precursor protein metabolic process;anatomical structure development;biological regulation;biosynthetic process;catabolic process;cell cycle arrest;cell cycle process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular response to stimulus;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;developmental process involved in reproduction;epidermis development;genitalia development;glycoprotein catabolic process;glycoprotein metabolic process;intracellular signal transduction;lipid biosynthetic process;lipid metabolic process;localization;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;male genitalia development;membrane organization;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;organ development;plasminogen activation;primary metabolic process;protein localization;protein maturation;protein metabolic process;protein processing;Ras protein signal transduction;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of programmed cell death;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to oxidative stress;response to stimulus;response to stress;signal transduction;skin development;small GTPase mediated signal transduction;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;tissue development;zymogen activation"antigen binding;binding;catalytic activity;coenzyme binding;cofactor binding;delta24-sterol reductase activity;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;peptide antigen binding;peptide binding;UDP-N-acetylmuramate dehydrogenase activity" cell part;cytoplasmic part;cytoskeleton;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part Steroid biosynthesis 1.30E-26 4 5 5 10.7

Q14512 Fibroblast growth factor-binding protein 1 FGFBP1 >sp|Q14512|FGFP1_HUMAN Fibroblast growth factor-binding protein 1 OS=Homo sapiens GN=FGFBP1 PE=1 SV=1 -0.27 0.14 0.23 0.20 -2.61 -2.27 -1.55 -1.84 + 2.422843831 2.143640351 biological regulation;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of fibroblast growth factor receptor signaling pathway;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cell proliferation;regulation of cellular process;regulation of fibroblast growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;signaling binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding cell part;cell surface;extracellular region part;extracellular space;membrane;plasma membrane 3.60E-91 1 5 5 20.9

P48507 Glutamate--cysteine ligase regulatory subunit GCLM >sp|P48507|GSH0_HUMAN Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1 0.07 -0.40 -0.44 -0.35 1.86 1.01 0.99 0.68 + 1.826305329 -1.413148284 amine biosynthetic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;circulatory system process;cysteine metabolic process;glutamate metabolic process;glutamine family amino acid metabolic process;glutathione biosynthetic process;glutathione metabolic process;metabolic process;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptide biosynthetic process;peptide metabolic process;positive regulation of catalytic activity;positive regulation of glutamate-cysteine ligase activity;positive regulation of ligase activity;positive regulation of molecular function;primary metabolic process;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of blood vessel size;regulation of catalytic activity;regulation of cell death;regulation of cellular process;regulation of glutamate-cysteine ligase activity;regulation of homeostatic process;regulation of ion homeostasis;regulation of ligase activity;regulation of membrane depolarization;regulation of metabolic process;regulation of mitochondrial depolarization;regulation of molecular function;regulation of neuron apoptosis;regulation of programmed cell death;regulation of tube size;response to chemical stimulus;response to drug;response to nitrosative stress;response to oxidative stress;response to stimulus;response to stress;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;system process;vascular process in circulatory system;xenobiotic metabolic process cell part;cytoplasmic part;cytosol;glutamate-cysteine ligase complex;intracellular part;macromolecular complex;protein complex Glutathione metabolism 1.05E-49 1 5 5 24.8

P17900;H0YBY3;E5RJD0 Ganglioside GM2 activator;Ganglioside GM2 activator isoform short GM2A >sp|P17900|SAP3_HUMAN Ganglioside GM2 activator OS=Homo sapiens GN=GM2A PE=1 SV=4 -0.35 -0.12 -0.85 -0.53 1.07 1.22 1.01 0.63 + 2.266152484 -1.442858886 behavior;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular catabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;ceramide metabolic process;cognition;ganglioside catabolic process;ganglioside metabolic process;glycolipid catabolic process;glycolipid metabolic process;glycosphingolipid catabolic process;glycosphingolipid metabolic process;learning or memory;lipid catabolic process;lipid localization;lipid metabolic process;lipid storage;localization;macromolecule localization;membrane lipid catabolic process;membrane lipid metabolic process;metabolic process;multicellular organismal process;neurological system process;neuromuscular process;neuromuscular process controlling balance;oligosaccharide catabolic process;oligosaccharide metabolic process;primary metabolic process;response to stimulus;small molecule metabolic process;sphingoid metabolic process;sphingolipid catabolic process;sphingolipid metabolic process;system process "beta-N-acetylhexosaminidase activity;catalytic activity;enzyme activator activity;enzyme regulator activity;hexosaminidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;sphingolipid activator protein activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-bounded organelle;membrane-enclosed lumen;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle lumen;organelle part;vacuolar lumen;vacuolar part Lysosome 1.63E-16 3 5 5 23.8

Q13823;H0YG10 Nucleolar GTP-binding protein 2 GNL2 >sp|Q13823|NOG2_HUMAN Nucleolar GTP-binding protein 2 OS=Homo sapiens GN=GNL2 PE=1 SV=1 0.10 0.44 0.14 0.25 -0.16 -0.34 -0.92 -0.21 + 1.361341748 0.638780482 cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes 1.06E-10 2 5 5 8.5

Q9HAV7;CON__Q3MHN2 "GrpE protein homolog 1, mitochondrial" GRPEL1 ">sp|Q9HAV7|GRPE1_HUMAN GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2" -0.01 0.11 0.42 0.04 -0.43 -0.12 -0.39 -0.20 + 1.4046048 0.427646324 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transmembrane transport;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein folding;protein import;protein import into mitochondrial matrix;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transmembrane transport;protein transport;transmembrane transport;transport adenyl nucleotide binding;adenyl-nucleotide exchange factor activity;ATPase regulator activity;binding;enzyme regulator activity;nucleoside-triphosphatase regulator activity;nucleotide binding;protein binding;purine nucleotide binding;unfolded protein binding cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part 8.93E-44 2 5 5 23

Q5JR04;Q9HCE1;Q9HCE1-2 Putative helicase MOV-10 MOV10 ">tr|Q5JR04|Q5JR04_HUMAN Mov10, Moloney leukemia virus 10, homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=MOV10 PE=2 SV=1;>sp|Q9HCE1|MOV10_HUMAN Putative helicase MOV-10 OS=Homo sapiens GN=MOV10 PE=1 SV=2;>sp|Q9HCE1-2|MOV10_HUMAN Isoform 2 of Putative he" 0.20 0.02 0.12 0.00 -0.53 -0.73 -0.29 -0.34 + 1.846119894 0.557319746 "biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;defense response;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA cleavage;mRNA cleavage involved in gene silencing by miRNA;mRNA metabolic process;mRNA processing;nerve growth factor receptor signaling pathway;nitrogen compound metabolic process;Notch signaling pathway;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;phosphatidylinositol-mediated signaling;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;RNA processing;signal transduction;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding" cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;RNA granule 2.95E-31 3 5 5 5.9

Q00653-4;Q00653;Q00653-3 Nuclear factor NF-kappa-B p100 subunit;Nuclear factor NF-kappa-B p52 subunit NFKB2 >sp|Q00653-4|NFKB2_HUMAN Isoform 4 of Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens GN=NFKB2;>sp|Q00653|NFKB2_HUMAN Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens GN=NFKB2 PE=1 SV=4 0.29 -0.09 0.07 -0.25 0.56 0.82 0.59 0.71 + 1.836648042 -0.667538244 "activation of immune response;activation of innate immune response;adaptive immune response;adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;anatomical structure development;biological regulation;biosynthetic process;cell activation;cell differentiation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;defense response;developmental process;extracellular matrix organization;extracellular structure organization;follicular dendritic cell activation;follicular dendritic cell differentiation;germinal center formation;hemopoietic or lymphoid organ development;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;pattern recognition receptor signaling pathway;positive regulation of biological process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of NF-kappaB transcription factor activity;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of type I interferon production;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of defense response;regulation of gene expression;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;regulation of type I interferon production;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;spleen development;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transcription, DNA-dependent;TRIF-dependent toll-like receptor signaling pathway" binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity Bcl3/NF-kappaB2 complex;cell part;cytoplasmic part;cytosol;I-kappaB/NF-kappaB complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;protein complex MAPK signaling pathway;Osteoclast differentiation;Pathways in cancer 1.47E-13 3 5 5 10.3

Q86TB9-4;Q86TB9;Q86TB9-2;Q86TB9-3 Protein PAT1 homolog 1 PATL1 >sp|Q86TB9-4|PATL1_HUMAN Isoform 4 of Protein PAT1 homolog 1 OS=Homo sapiens GN=PATL1;>sp|Q86TB9|PATL1_HUMAN Protein PAT1 homolog 1 OS=Homo sapiens GN=PATL1 PE=1 SV=2;>sp|Q86TB9-2|PATL1_HUMAN Isoform 2 of Protein PAT1 homolog 1 OS=Homo sapiens GN=PATL1 -0.02 -0.15 0.26 0.13 -0.24 -0.28 -0.29 -0.44 + 1.483775683 0.371349283 "catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoplasmic mRNA processing body assembly;deadenylation-dependent decapping of nuclear-transcribed mRNA;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;gene expression;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA catabolic process;RNA metabolic process" binding;nucleic acid binding;poly(G) RNA binding;poly(U) RNA binding;poly-purine tract binding;poly-pyrimidine tract binding;RNA binding;single-stranded RNA binding cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part;PML body;ribonucleoprotein complex;RNA granule RNA degradation 2.81E-51 4 5 5 11.7

E7EVX8;Q8WWY3;E7EU94;E7ESX0;Q8WWY3-3;E7EN72;Q8WWY3-2;E7ESA8 U4/U6 small nuclear ribonucleoprotein Prp31 PRPF31 >tr|E7EVX8|E7EVX8_HUMAN U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=2 SV=1;>sp|Q8WWY3|PRP31_HUMAN U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2;>tr|E7EU94|E7EU94_HUMAN U4/U6 small nuclear ribon -0.03 0.09 0.05 0.09 -0.12 -0.87 -0.73 -0.87 + 1.499704504 0.693066696 assembly of spliceosomal tri-snRNP;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization binding;nucleic acid binding;ribonucleoprotein binding;RNA binding;snRNP binding Cajal body;cell part;histone methyltransferase complex;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL1 complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U2-type spliceosomal complex;U4 snRNP;U4/U6 x U5 tri-snRNP complex;U4atac snRNP Spliceosome 5.26E-27 8 5 5 17.6

B8ZZQ6;P06454-2;P06454;B8ZZA1;B8ZZW7;H7C2N1 Prothymosin alpha;Thymosin alpha-1 PTMA >tr|B8ZZQ6|B8ZZQ6_HUMAN Thymosin alpha-1 OS=Homo sapiens GN=PTMA PE=2 SV=1;>sp|P06454-2|PTMA_HUMAN Isoform 2 of Prothymosin alpha OS=Homo sapiens GN=PTMA;>sp|P06454|PTMA_HUMAN Prothymosin alpha OS=Homo sapiens GN=PTMA PE=1 SV=2;>tr|B8ZZA1|B8ZZA1_HUMAN Thym 0.18 -0.03 -0.41 0.01 -0.54 -0.96 -0.37 -0.81 + 1.363120726 0.607818255 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.22E-189 6 5 5 36.4

Q12923-2;Q12923-3;Q12923;Q12923-4 Tyrosine-protein phosphatase non-receptor type 13 PTPN13 >sp|Q12923-2|PTN13_HUMAN Isoform 2 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13;>sp|Q12923-3|PTN13_HUMAN Isoform 3 of Tyrosine-protein phosphatase non-receptor type 13 OS=Homo sapiens GN=PTPN13;>sp|Q12923|PTN13_HUMAN Tyros 0.33 0.18 0.15 -0.07 -0.86 -1.35 -0.65 -1.14 + 2.135539812 1.148858353 "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein tyrosine phosphatase activity" cell part;cell projection;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;plasma membrane 1.47E-18 4 5 5 2.5

Q9NTZ6;A6PVI1;A6PVI0;Q5JX62 RNA-binding protein 12 RBM12 >sp|Q9NTZ6|RBM12_HUMAN RNA-binding protein 12 OS=Homo sapiens GN=RBM12 PE=1 SV=1 0.09 -0.01 0.03 0.03 -0.07 -0.31 -0.39 -0.29 + 1.632352026 0.301473039 binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 9.52E-20 4 5 5 6.4

P62829;C9JD32;B9ZVP7;J3KT29;J3KTJ3 60S ribosomal protein L23 RPL23 >sp|P62829|RL23_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1;>tr|C9JD32|C9JD32_HUMAN 60S ribosomal protein L23 (Fragment) OS=Homo sapiens GN=RPL23 PE=2 SV=1;>tr|B9ZVP7|B9ZVP7_HUMAN 60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE -0.04 0.01 -0.06 0.11 -0.94 -0.94 -0.30 -0.47 + 1.54092502 0.666784749 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear import;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein import;protein import into nucleus;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribosomal protein import into nucleus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 3.87E-63 5 5 5 44.3

P00441;H7BYH4 Superoxide dismutase [Cu-Zn] SOD1 >sp|P00441|SODC_HUMAN Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2;>tr|H7BYH4|H7BYH4_HUMAN Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=2 SV=1 -0.03 -0.12 -0.30 -0.16 0.57 0.38 0.52 0.06 + 1.603839529 -0.534128931 "activation of MAPK activity;aging;amine metabolic process;anatomical structure development;anatomical structure homeostasis;anterograde axon cargo transport;auditory receptor cell stereocilium organization;axon cargo transport;behavior;biological regulation;biosynthetic process;carboxylic acid metabolic process;catabolic process;cation homeostasis;cell activation;cell aging;cell projection organization;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular ketone metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to oxygen radical;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cellular response to superoxide;chemical homeostasis;circulatory system process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;DNA repair;double-strand break repair;embryo implantation;establishment of localization;establishment of localization in cell;exocytosis;gamete generation;glutathione metabolic process;heart contraction;heart process;hemopoietic or lymphoid organ development;homeostasis of number of cells;homeostatic process;hydrogen peroxide biosynthetic process;hydrogen peroxide metabolic process;immune system process;inner ear receptor stereocilium organization;intermediate filament cytoskeleton organization;intermediate filament-based process;intracellular transport;ion homeostasis;iron ion homeostasis;locomotory behavior;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;male gamete generation;membrane organization;metabolic process;metal ion homeostasis;microtubule-based movement;microtubule-based process;microtubule-based transport;multicellular organismal process;multicellular organismal reproductive process;muscle cell homeostasis;muscle system process;myelin maintenance;myeloid cell homeostasis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular process;negative regulation of cholesterol biosynthetic process;negative regulation of cholesterol metabolic process;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of metabolic process;negative regulation of multicellular organismal process;negative regulation of muscle contraction;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of smooth muscle contraction;negative regulation of steroid biosynthetic process;negative regulation of steroid metabolic process;neurofilament cytoskeleton organization;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;organ development;organelle organization;organic acid metabolic process;ovarian follicle development;ovulation cycle process;oxoacid metabolic process;peptide metabolic process;peripheral nervous system myelin maintenance;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;placenta development;plasma membrane organization;platelet activation;platelet degranulation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of kinase activity;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of catalytic activity;regulation of cell activation;regulation of cell death;regulation of cell differentiation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cholesterol biosynthetic process;regulation of cholesterol metabolic process;regulation of cytokine production;regulation of developmental process;regulation of growth;regulation of immune system process;regulation of kinase activity;regulation of leukocyte activation;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of membrane potential;regulation of metabolic process;regulation of mitochondrial membrane potential;regulation of molecular function;regulation of multicellular organism growth;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of neuron apoptosis;regulation of organ growth;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of smooth muscle contraction;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of system process;regulation of T cell activation;regulation of T cell differentiation;regulation of T cell differentiation in thymus;regulation of transferase activity;relaxation of muscle;relaxation of vascular smooth muscle;removal of superoxide radicals;reproductive process;response to abiotic stimulus;response to amine stimulus;response to amphetamine;response to axon injury;response to chemical stimulus;response to copper ion;response to DNA damage stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to heat;response to hydrogen peroxide;response to inorganic substance;response to metal ion;response to nutrient levels;response to organic nitrogen;response to organic substance;response to oxidative stress;response to oxygen radical;response to reactive oxygen species;response to stimulus;response to stress;response to superoxide;response to temperature stimulus;response to wounding;retina homeostasis;retrograde axon cargo transport;rhythmic process;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;small molecule metabolic process;spermatogenesis;sulfur compound metabolic process;superoxide anion generation;superoxide metabolic process;system process;thymus development;tissue homeostasis;transport;vesicle-mediated transport" "antioxidant activity;binding;catalytic activity;cation binding;copper ion binding;enzyme binding;identical protein binding;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on superoxide radicals as acceptor;phosphatase binding;protein binding;protein dimerization activity;protein homodimerization activity;protein phosphatase 2B binding;protein phosphatase binding;superoxide dismutase activity;transition metal ion binding;zinc ion binding" cell body;cell part;cell projection cytoplasm;cell projection part;cytoplasmic part;cytoplasmic vesicle;cytosol;dendrite cytoplasm;extracellular matrix;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-enclosed lumen;microbody;mitochondrial matrix;mitochondrial part;neuronal cell body;nucleus;organelle;organelle lumen;organelle part;peroxisome;protein complex;vesicle Amyotrophic lateral sclerosis (ALS);Huntington's disease;Peroxisome;Prion diseases 2.26E-71 2 5 5 37

E7EW69;Q9P0V9;E7EX04;Q9P0V9-2;B5ME97;Q9P0V9-3;B7Z371;B7Z277;F5GYV2;C9JEW2;C9JNR7;F5H1F2 Septin-10 10-Sep >tr|E7EW69|E7EW69_HUMAN Septin-10 OS=Homo sapiens GN=SEPT10 PE=2 SV=1;>sp|Q9P0V9|SEP10_HUMAN Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2;>tr|E7EX04|E7EX04_HUMAN Septin-10 OS=Homo sapiens GN=SEPT10 PE=2 SV=1;>sp|Q9P0V9-2|SEP10_HUMAN Isoform 2 of Septin-10 -0.01 0.06 -0.04 -0.10 -0.54 -0.42 -0.40 -0.73 + 2.042473205 0.497559944 cell cycle;cell division;cellular process binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell cortex part;cell part;cytoplasmic part;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex;septin complex 6.20E-19 12 6 5 14.2

Q9P265;Q14689-3;Q14689-2;Q14689-4;Q14689-5 Disco-interacting protein 2 homolog B DIP2B >sp|Q9P265|DIP2B_HUMAN Disco-interacting protein 2 homolog B OS=Homo sapiens GN=DIP2B PE=1 SV=3 0.07 0.04 -0.55 -0.37 0.52 0.99 0.97 0.58 + 1.789127733 -0.968973595 catalytic activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.58E-21 5 6 5 5.7

P50452;H7BXK7;P50452-2;C9JVA8;B4DTW2;C9JTJ8;C9J7N5;P50453;O75830 Serpin B8 SERPINB8 >sp|P50452|SPB8_HUMAN Serpin B8 OS=Homo sapiens GN=SERPINB8 PE=1 SV=2;>tr|H7BXK7|H7BXK7_HUMAN Serpin B8 (Fragment) OS=Homo sapiens GN=SERPINB8 PE=3 SV=1;>sp|P50452-2|SPB8_HUMAN Isoform 2 of Serpin B8 OS=Homo sapiens GN=SERPINB8 -0.12 -0.12 0.09 0.04 0.51 0.46 0.77 0.31 + 1.786935689 -0.538771375 biological regulation;cellular component movement;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to estrogen stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to steroid hormone stimulus;cellular response to stimulus;immune effector process;immune response;immune system process;leukocyte mediated immunity;mast cell mediated immunity;myeloid leukocyte mediated immunity;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of proteolysis;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus caspase inhibitor activity;caspase regulator activity;cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasmic part;cytosol;extracellular region;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Amoebiasis 1.96E-52 9 7 5 20.3

Q92804-2;Q92804;K7EPT6;K7EL85;K7ENI1;K7EKB2 TATA-binding protein-associated factor 2N TAF15 >sp|Q92804-2|RBP56_HUMAN Isoform Short of TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15;>sp|Q92804|RBP56_HUMAN TATA-binding protein-associated factor 2N OS=Homo sapiens GN=TAF15 PE=1 SV=1;>tr|K7EPT6|K7EPT6_HUMAN TATA-binding protein-as 0.01 0.04 0.19 0.20 -0.24 -0.66 -0.41 -0.25 + 1.68929707 0.497768189 "biological regulation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelleBasal transcription factors 4.04E-90 6 7 5 20.7

Q13247-3;Q13247;Q13247-2;F6T1J1;B4DJK0;B4DUA4 Serine/arginine-rich splicing factor 6 SRSF6 >sp|Q13247-3|SRSF6_HUMAN Isoform SRP55-3 of Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6;>sp|Q13247|SRSF6_HUMAN Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2 -0.08 0.11 0.12 0.04 -0.15 -0.63 -0.90 -0.71 + 1.511118881 0.643800928 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA splice site selection;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part Spliceosome 2.16E-23 6 8 5 21.8

Q9UKY7;Q9UKY7-2;H0Y8K3;D6RAV0 Protein CDV3 homolog CDV3 >sp|Q9UKY7|CDV3_HUMAN Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 SV=1;>sp|Q9UKY7-2|CDV3_HUMAN Isoform 2 of Protein CDV3 homolog OS=Homo sapiens GN=CDV3;>tr|H0Y8K3|H0Y8K3_HUMAN Protein CDV3 homolog (Fragment) OS=Homo sapiens GN=CDV3 PE=4 SV=1-0.01 0.02 -0.14 -0.09 0.40 0.31 0.30 0.04 + 1.456283296 -0.318320394 cell proliferation cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 1.00E-86 4 10 5 72.1

P62140;C9JP48;C9J9S3;E7ETD8 Serine/threonine-protein phosphatase PP1-beta catalytic subunit;Serine/threonine-protein phosphatase PPP1CB >sp|P62140|PP1B_HUMAN Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3;>tr|C9JP48|C9JP48_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CB PE=2 SV=1 0.03 0.20 0.09 0.28 -0.26 -0.07 -0.12 -0.17 + 1.66273523 0.303283971 acylglycerol catabolic process;acylglycerol metabolic process;biological regulation;carbohydrate metabolic process;catabolic process;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular carbohydrate metabolic process;cellular catabolic process;cellular glucan metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;dephosphorylation;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;G2/M transition of mitotic cell cycle;generation of precursor metabolites and energy;glucan metabolic process;glycerol ether catabolic process;glycerol ether metabolic process;glycerolipid catabolic process;glycerolipid metabolic process;glycogen metabolic process;lipid catabolic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;neutral lipid catabolic process;neutral lipid metabolic process;organic ether metabolic process;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;polysaccharide metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of cell adhesion;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen biosynthetic process;regulation of glycogen catabolic process;regulation of glycogen metabolic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to stimulus;signal transduction;small molecule metabolic process;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;triglyceride catabolic process;triglyceride metabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;myosin phosphatase activity;myosin-light-chain-phosphatase activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity" cell part;cytoplasmic part;glycogen granule;histone methyltransferase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL5-L complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;organelle;organelle part;protein complex;protein phosphatase type 1 complex;protein serine/threonine phosphatase complex;PTW/PP1 phosphatase complex Focal adhesion;Insulin signaling pathway;Long-term potentiation;Meiosis - yeast;Oocyte meiosis;Regulation of actin cytoskeleton;Vascular smooth muscle contraction 3.07E-89 4 12 5 44.6

P39687;H0YN26;O95626;O43423;H7BZ09;REV__F8WED0;REV__Q96LZ3;REV__Q17RF5-2;REV__P52849-2 Acidic leucine-rich nuclear phosphoprotein 32 family member A ANP32A >sp|P39687|AN32A_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1;>tr|H0YN26|H0YN26_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=2 SV=10.17 -0.01 0.05 0.01 -0.32 -0.70 -0.13 -0.69 + 1.409386649 0.515402223 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;gene expression;intracellular signal transduction;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription, DNA-dependent;transport" cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;perinuclear region of cytoplasm 9.37E-106 9 13 5 38.6

Q13509;A8K854;G3V2A3;G3V5W4;G3V2R8;G3V3R4;G3V2N6 Tubulin beta-3 chain TUBB3 ">sp|Q13509|TBB3_HUMAN Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2;>tr|A8K854|A8K854_HUMAN HCG1983504, isoform CRA_f OS=Homo sapiens GN=TUBB3 PE=2 SV=1" -0.92 -0.17 -0.57 -0.13 0.25 1.05 1.07 1.25 + 1.732882028 -1.353632174 axon guidance;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chemotaxis;'de novo' posttranslational protein folding;'de novo' protein folding;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;mitosis;nuclear division;organelle fission;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;taxis "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;peptide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" axon;cell part;cell projection;cytoplasm;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule cytoskeleton;neuron projection;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 7 24 5 51.3

Q13885;Q9BVA1 Tubulin beta-2A chain;Tubulin beta-2B chain TUBB2A;TUBB2B >sp|Q13885|TBB2A_HUMAN Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1;>sp|Q9BVA1|TBB2B_HUMAN Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1-0.17 0.04 -0.87 -0.16 0.66 0.83 0.34 0.76 + 1.598701131 -0.939047645 cell migration;cell motility;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;neuron migration;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;organelle part;plasma membrane;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 2 30 5 69.4

P07741;P07741-2;H3BQZ9;H3BQF1;H3BQB1;H3BSW3 Adenine phosphoribosyltransferase APRT >sp|P07741|APT_HUMAN Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2;>sp|P07741-2|APT_HUMAN Isoform 2 of Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT;>tr|H3BQZ9|H3BQZ9_HUMAN Adenine phosphoribosyltransferase OS=Homo sapiens -0.18 -0.12 0.00 -0.03 0.43 0.17 0.68 0.17 + 1.403264402 -0.449187246 adenine biosynthetic process;adenine metabolic process;adenine salvage;AMP biosynthetic process;AMP metabolic process;AMP salvage;behavior;biological regulation;biosynthetic process;body fluid secretion;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;establishment of localization;grooming behavior;heterocycle biosynthetic process;heterocycle metabolic process;lactation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside salvage;nucleotide biosynthetic process;nucleotide metabolic process;nucleotide salvage;pigment biosynthetic process;pigment metabolic process;primary metabolic process;purine base biosynthetic process;purine base metabolic process;purine base salvage;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine nucleotide salvage;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleoside salvage;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;purine-containing compound salvage;regulation of biological quality;regulation of body fluid levels;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside biosynthetic process;ribonucleoside metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;small molecule metabolic process;transport "adenine binding;adenine phosphoribosyltransferase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;AMP binding;binding;catalytic activity;nucleobase binding;nucleotide binding;purine base binding;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups"cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Purine metabolism 9.81E-36 6 6 6 34.4

Q12996;Q12996-2;E9PLP8;Q12996-3;E9PJ06;H0YE74 Cleavage stimulation factor subunit 3 CSTF3 >sp|Q12996|CSTF3_HUMAN Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1 0.08 0.12 0.10 0.29 -0.09 -0.24 -0.77 -0.35 + 1.342094234 0.510220217 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA cleavage;mRNA metabolic process;mRNA polyadenylation;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA metabolic process;RNA polyadenylation;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;termination of RNA polymerase II transcription;transcription termination, DNA-dependent" binding;nucleic acid binding;RNA binding cell part;intracellular;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part mRNA surveillance pathway 3.65E-41 6 6 6 13.8

O95302;B7Z230;B7Z6H3;B7Z1G9;Q75LS8;C9J4P8 Peptidyl-prolyl cis-trans isomerase FKBP9 FKBP9 >sp|O95302|FKBP9_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens GN=FKBP9 PE=1 SV=2;>tr|B7Z230|B7Z230_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens GN=FKBP9 PE=2 SV=1;>tr|B7Z6H3|B7Z6H3_HUMAN Peptidyl-prolyl cis-trans isome -0.23 -0.40 -0.09 -0.12 0.48 0.31 0.48 0.16 + 1.919183437 -0.565946518 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-proline modification;primary metabolic process;protein folding;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization binding;calcium ion binding;catalytic activity;cation binding;cis-trans isomerase activity;drug binding;FK506 binding;ion binding;isomerase activity;macrolide binding;metal ion binding;peptidyl-prolyl cis-trans isomerase activity cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle 5.50E-22 6 6 6 12.6

J3KQG4;P04062-2;P04062;F5H241;J3KQK9;P04062-3 Glucosylceramidase GBA >tr|J3KQG4|J3KQG4_HUMAN Glucosylceramidase OS=Homo sapiens GN=GBA PE=4 SV=1;>sp|P04062-2|GLCM_HUMAN Isoform Short of Glucosylceramidase OS=Homo sapiens GN=GBA;>sp|P04062|GLCM_HUMAN Glucosylceramidase OS=Homo sapiens GN=GBA PE=1 SV=3;>tr|F5H241|F5H241_HUMAN -0.80 -0.30 -0.25 0.01 1.30 1.53 0.15 0.63 + 1.390976756 -1.236498679 alcohol biosynthetic process;alcohol metabolic process;amine metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;catabolic process;cell death;cellular biosynthetic process;cellular catabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to tumor necrosis factor;ceramide biosynthetic process;ceramide catabolic process;ceramide metabolic process;death;glucosylceramide catabolic process;glucosylceramide metabolic process;glycolipid catabolic process;glycolipid metabolic process;glycosphingolipid catabolic process;glycosphingolipid metabolic process;glycosylceramide catabolic process;glycosylceramide metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;membrane lipid biosynthetic process;membrane lipid catabolic process;membrane lipid metabolic process;metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of interleukin-6 production;negative regulation of kinase activity;negative regulation of MAP kinase activity;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transferase activity;nitrogen compound metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of dephosphorylation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cell communication;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of defense response;regulation of dephosphorylation;regulation of inflammatory response;regulation of interleukin-6 production;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transferase activity;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;response to tumor necrosis factor;small molecule biosynthetic process;small molecule metabolic process;sphingoid biosynthetic process;sphingoid catabolic process;sphingoid metabolic process;sphingolipid biosynthetic process;sphingolipid catabolic process;sphingolipid metabolic process;sphingosine biosynthetic process;sphingosine metabolic process;termination of signal transduction "binding;catalytic activity;ceramidase activity;glucosylceramidase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;protein binding;receptor binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;lysosomal membrane;membrane;membrane-enclosed lumen;organelle lumen;organelle membrane;organelle part;vacuolar lumen;vacuolar membrane;vacuolar part Lysosome;Other glycan degradation;Sphingolipid metabolism 2.22E-20 6 6 6 15.1

P11279;B4DWL3 Lysosome-associated membrane glycoprotein 1 LAMP1 >sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1

SV=3;>tr|B4DWL3|B4DWL3_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=2 SV=1 -0.38 -0.20 -0.21 0.02 0.53 0.66 0.15 0.39 + 1.716016779 -0.628397547 autophagic cell death;autophagy;catabolic process;cell death;cellular catabolic process;cellular metabolic process;cellular process;death;metabolic process;programmed cell death cell body;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;dendrite;endosomal part;endosome;endosome membrane;external side of plasma membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome;lysosomal membrane;lysosome;lytic vacuole;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;multivesicular body;neuron projection;neuronal cell body;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;plasma membrane part;sarcolemma;vacuolar membrane;vacuolar part;vacuole;vesicle ko05152;Lysosome;Phagosome 3.54E-63 2 6 6 13.7

P49916;P49916-2;K7EQB6;K7ERZ5;K7ENR9 DNA ligase 3 LIG3 >sp|P49916|DNLI3_HUMAN DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2;>sp|P49916-2|DNLI3_HUMAN Isoform Beta of DNA ligase 3 OS=Homo sapiens GN=LIG3;>tr|K7EQB6|K7EQB6_HUMAN Leucine-rich repeats and immunoglobulin-like domains protein 3 (Fragment) OS=Homo sa 0.11 -0.21 0.08 0.04 -0.19 -0.47 -0.64 -0.87 + 1.361735528 0.543602325 base-excision repair;biological regulation;cell cycle process;cell division;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA ligation;DNA ligation involved in DNA repair;DNA metabolic process;DNA recombination;DNA repair;DNA strand elongation;DNA strand elongation involved in DNA replication;double-strand break repair;double-strand break repair via nonhomologous end joining;gamete generation;lagging strand elongation;macromolecule metabolic process;male gamete generation;metabolic process;mitochondrial DNA metabolic process;mitochondrial DNA repair;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA recombination;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;primary metabolic process;reciprocal DNA recombination;reciprocal meiotic recombination;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA recombination;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;spermatogenesis "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;DNA binding;DNA ligase (ATP) activity;DNA ligase activity;ion binding;ligase activity;ligase activity, forming phosphoric ester bonds;metal ion binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transition metal ion binding;zinc ion binding" cell part;chromosomal part;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoplasm;organelle;organelle part;synaptonemal complex Base excision repair 7.66E-22 5 6 6 6.9

Q6XQN6-3;Q6XQN6;C9JC60;Q6XQN6-2;G5E977;C9J8U2;H0YDA6;H0YF31 Nicotinate phosphoribosyltransferase NAPRT1 >sp|Q6XQN6-3|PNCB_HUMAN Isoform 3 of Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT1;>sp|Q6XQN6|PNCB_HUMAN Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT1 PE=1 SV=2;>tr|C9JC60|C9JC60_HUMAN Nicotinate phosphoribosyltransferase 0.17 0.09 0.19 0.09 -0.29 -0.78 -0.40 -0.89 + 1.790915839 0.72494974 alkaloid metabolic process;biosynthetic process;cellular amide metabolic process;cellular biosynthetic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;NAD biosynthetic process;NAD metabolic process;nicotinamide metabolic process;nicotinamide nucleotide biosynthetic process;nicotinamide nucleotide metabolic process;nicotinate nucleotide biosynthetic process;nicotinate nucleotide metabolic process;nicotinate nucleotide salvage;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;nucleotide salvage;oxidoreduction coenzyme metabolic process;primary metabolic process;pyridine nucleotide biosynthetic process;pyridine nucleotide metabolic process;pyridine nucleotide salvage;pyridine-containing compound biosynthetic process;pyridine-containing compound metabolic process;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "catalytic activity;nicotinate phosphoribosyltransferase activity;nicotinate-nucleotide diphosphorylase (carboxylating) activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasmic part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Nicotinate and nicotinamide metabolism 2.88E-35 8 6 6 11.8

Q15274 Nicotinate-nucleotide pyrophosphorylase [carboxylating] QPRT >sp|Q15274|NADC_HUMAN Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 0.00 -0.18 -0.31 -0.24 0.51 0.23 0.69 0.37 + 1.897242402 -0.635314567 biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;dicarboxylic acid catabolic process;dicarboxylic acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;NAD biosynthetic process;NAD metabolic process;nicotinamide nucleotide biosynthetic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid catabolic process;organic acid metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;pyridine nucleotide biosynthetic process;pyridine nucleotide metabolic process;pyridine-containing compound biosynthetic process;pyridine-containing compound metabolic process;quinolinate catabolic process;quinolinate metabolic process;small molecule catabolic process;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "binding;catalytic activity;identical protein binding;nicotinate-nucleotide diphosphorylase (carboxylating) activity;protein binding;protein dimerization activity;protein homodimerization activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasmic part;cytosol;intracellular part Nicotinate and nicotinamide metabolism 1.10E-29 1 6 6 21.9

P61353;K7ELC7;K7EQQ9;K7ERY7 60S ribosomal protein L27 RPL27 >sp|P61353|RL27_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2;>tr|K7ELC7|K7ELC7_HUMAN 60S ribosomal protein L27 (Fragment) OS=Homo sapiens GN=RPL27 PE=3 SV=1;>tr|K7EQQ9|K7EQQ9_HUMAN 60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE -0.16 0.03 0.08 -0.10 -0.74 -0.35 -0.39 -0.45 + 1.626924004 0.443969901 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 3.92E-14 4 6 6 41.2

P46776;E9PJD9;E9PLL6;E9PLX7 60S ribosomal protein L27a RPL27A >sp|P46776|RL27A_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2;>tr|E9PJD9|E9PJD9_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1;>tr|E9PLL6|E9PLL6_HUMAN 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 S -0.05 0.08 0.37 0.05 -0.29 -0.57 -0.41 -0.30 + 1.687858953 0.503922003 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 9.03E-46 4 6 6 39.2

P32969;D6RAN4;H0Y9V9;E7ESE0;H0Y9R4;REV__B4DZN5;REV__O75648-5;REV__O75648-2;REV__O75648 60S ribosomal protein L9 RPL9 >sp|P32969|RL9_HUMAN 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1;>tr|D6RAN4|D6RAN4_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL9 PE=2 SV=1;>tr|H0Y9V9|H0Y9V9_HUMAN 60S ribosomal protein L9 (Fragment) OS=Homo sapiens GN=RPL 0.05 0.00 0.24 0.04 -0.44 -0.77 -0.22 -0.18 + 1.356130878 0.485034874 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 2.13E-94 9 6 6 29.7

Q9NQG5;A2A2M0 Regulation of nuclear pre-mRNA domain-containing protein 1B RPRD1B >sp|Q9NQG5|RPR1B_HUMAN Regulation of nuclear pre-mRNA domain-containing protein 1B OS=Homo sapiens GN=RPRD1B PE=1 SV=1;>tr|A2A2M0|A2A2M0_HUMAN Regulation of nuclear pre-mRNA domain-containing protein 1B (Fragment) OS=Homo sapiens GN=RPRD1B PE=2 SV=1 0.24 0.15 -0.07 0.20 -0.49 -0.47 -0.26 -0.40 + 2.06993151 0.534737954 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;dephosphorylation;dephosphorylation of RNA polymerase II C-terminal domain;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" basal RNA polymerase II transcription machinery binding;basal transcription machinery binding;binding;enzyme binding;protein binding;RNA polymerase binding;RNA polymerase core enzyme binding;RNA polymerase II core binding "cell part;DNA-directed RNA polymerase II, holoenzyme;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm part;organelle part;protein complex" 1.65E-89 2 6 6 31

P21912 "Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial" SDHB ">sp|P21912|DHSB_HUMAN Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3" -0.06 -0.01 0.29 0.11 -0.32 -0.36 -1.03 -0.58 + 1.437649509 0.657190721 acetyl-CoA catabolic process;acetyl-CoA metabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;electron transport chain;generation of precursor metabolites and energy;metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;respiratory electron transport chain;small molecule metabolic process;succinate metabolic process;tricarboxylic acid cycle "2 iron, 2 sulfur cluster binding;3 iron, 4 sulfur cluster binding;4 iron, 4 sulfur cluster binding;binding;catalytic activity;cation binding;cofactor binding;electron carrier activity;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor;quinone binding;succinate dehydrogenase (ubiquinone) activity;succinate dehydrogenase activity;ubiquinone binding" cell part;cytoplasmic part;fumarate reductase complex;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex II;organelle part;protein complex;succinate dehydrogenase complex;succinate dehydrogenase complex (ubiquinone) Alzheimer's disease;Citrate cycle (TCA cycle);Huntington's disease;Oxidative phosphorylation;Parkinson's disease 3.07E-20 1 6 6 22.5

O94855;O94855-2;E9PDM8;E9PC44 Protein transport protein Sec24D SEC24D >sp|O94855|SC24D_HUMAN Protein transport protein Sec24D OS=Homo sapiens GN=SEC24D PE=1 SV=2;>sp|O94855-2|SC24D_HUMAN Isoform 2 of Protein transport protein Sec24D OS=Homo sapiens GN=SEC24D;>tr|E9PDM8|E9PDM8_HUMAN Protein transport protein Sec24D OS=Homo sa -0.14 -0.24 -0.43 -0.14 1.14 0.86 0.30 0.24 + 1.49813724 -0.870805029 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;small molecule metabolic process;transport;vesicle coating;vesicle organization;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;COPII vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;vesicle coat Protein processing in endoplasmic reticulum 1.64E-18 4 6 6 7.2

O95721;C9JAF7 Synaptosomal-associated protein 29;Synaptosomal-associated protein SNAP29 >sp|O95721|SNP29_HUMAN Synaptosomal-associated protein 29 OS=Homo sapiens GN=SNAP29 PE=1 SV=1;>tr|C9JAF7|C9JAF7_HUMAN Synaptosomal-associated protein (Fragment) OS=Homo sapiens GN=SNAP29 PE=2 SV=1 0.25 -0.03 -0.05 0.05 0.78 0.98 0.43 0.33 + 1.395427693 -0.575664917 autophagic vacuole fusion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;membrane fusion;membrane organization;organelle fusion;organelle membrane fusion;organelle organization;protein transport;secretion;secretion by cell;transport;vesicle targeting;vesicle-mediated transport binding;protein binding;SNAP receptor activity cell junction;cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuron projection;nucleus;organelle;plasma membrane;protein complex;SNARE complex;synapse SNARE interactions in vesicular transport 1.82E-32 2 6 6 31.4

Q8IYB3-2;Q8IYB3;A9Z1X7;E9PCT1;M0R088;M0QXG5;M0R1E7;B4DED5 Serine/arginine repetitive matrix protein 1 SRRM1 >sp|Q8IYB3-2|SRRM1_HUMAN Isoform 2 of Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1;>sp|Q8IYB3|SRRM1_HUMAN Serine/arginine repetitive matrix protein 1 OS=Homo sapiens GN=SRRM1 PE=1 SV=2;>tr|A9Z1X7|A9Z1X7_HUMAN Serine/arginine repetit -0.24 0.15 0.22 0.02 -0.32 -0.66 -0.97 -0.82 + 1.628471283 0.731747348 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;DNA binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear matrix;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport 1.03E-60 8 6 6 9.6

Q8WU90;B4DMW2;H7C466;F8WB26 Zinc finger CCCH domain-containing protein 15 ZC3H15 >sp|Q8WU90|ZC3HF_HUMAN Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens GN=ZC3H15 PE=1 SV=1 -0.09 0.01 0.21 0.18 -0.30 -0.27 -0.11 -0.39 + 1.491843194 0.34504674 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part 4.17E-57 4 6 6 18.8

P11166;C9JIM8 "Solute carrier family 2, facilitated glucose transporter member 1" SLC2A1 ">sp|P11166|GTR1_HUMAN Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2;>tr|C9JIM8|C9JIM8_HUMAN Solute carrier family 2, facilitated glucose transporter member 1 (Fragment) OS=Homo sapiens GN=SLC2A1 PE=2" 0.02 0.30 0.17 0.30 -1.38 -1.16 -1.50 -1.06 + 2.930103608 1.471746533 biological regulation;carboxylic acid metabolic process;cell communication;cellular ketone metabolic process;cellular metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;L-ascorbic acid metabolic process;metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;response to abiotic stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient levels;response to osmotic stress;response to starvation;response to stimulus;response to stress;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process carbohydrate transmembrane transporter activity;dehydroascorbic acid transporter activity;D-glucose transmembrane transporter activity;glucose transmembrane transporter activity;hexose transmembrane transporter activity;monosaccharide transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;sugar transmembrane transporter activity;transmembrane transporter activity;transporter activity;vitamin transporter activity;xenobiotic transporter activity basolateral plasma membrane;caveola;cell junction;cell part;cell-cell junction;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;female pronucleus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;midbody;nucleus;organelle;pigment granule;plasma membrane;plasma membrane part;pronucleus;vesicle Adipocytokine signaling pathway;Bile secretion;Pathways in cancer;Renal cell carcinoma 7.12E-40 2 7 6 13.4

A1X283;G3V144 SH3 and PX domain-containing protein 2B SH3PXD2B >sp|A1X283|SPD2B_HUMAN SH3 and PX domain-containing protein 2B OS=Homo sapiens GN=SH3PXD2B PE=1 SV=3;>tr|G3V144|G3V144_HUMAN SH3 and PX domain-containing protein 2B OS=Homo sapiens GN=SH3PXD2B PE=2 SV=1 -0.07 0.03 -0.09 -0.09 1.26 1.01 0.28 0.89 + 1.653675892 -0.914487053 adipose tissue development;anatomical structure development;biological regulation;bone development;cell communication;cell differentiation;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;developmental process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;eye development;heart development;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;membrane organization;metabolic process;organ development;podosome assembly;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of fat cell differentiation;protein complex assembly;protein complex subunit organization;protein localization;protein localization in membrane;reactive oxygen species metabolic process;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of fat cell differentiation;sensory organ development;superoxide metabolic process;tissue development "binding;lipid binding;phosphatidylinositol binding;phosphatidylinositol-3,5-bisphosphate binding;phosphatidylinositol-3-phosphate binding;phosphatidylinositol-4-phosphate binding;phosphatidylinositol-5-phosphate binding;phospholipid binding;protein binding;protein domain specific binding;SH2 domain binding" cell junction;cell part;cell projection;cytoplasm;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;podosome;protein complex 3.20E-34 2 8 6 11.2

P61163;R4GMT0;B4DXP9;F5H3I4 Alpha-centractin ACTR1A >sp|P61163|ACTZ_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1;>tr|R4GMT0|R4GMT0_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=4 SV=1;>tr|B4DXP9|B4DXP9_HUMAN Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=2 SV=1;>tr|F5H3I4|F5H3I4_HUMAN Alp -0.08 -0.04 -0.21 -0.05 0.14 0.25 0.14 0.20 + 2.020244167 -0.281097527 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cell cycle process;cellular process;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;transport;vesicle-mediated transport adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;dynactin complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex 6.87E-180 4 13 6 53.2

Q9UIV8;Q9UIV8-2;C9JL93;H7BZS9 Serpin B13 SERPINB13 >sp|Q9UIV8|SPB13_HUMAN Serpin B13 OS=Homo sapiens GN=SERPINB13 PE=1 SV=2;>sp|Q9UIV8-2|SPB13_HUMAN Isoform 2 of Serpin B13 OS=Homo sapiens GN=SERPINB13 -0.34 0.24 -0.37 -0.28 1.02 1.49 1.18 0.44 + 1.726341713 -1.220135495 biological regulation;regulation of biological process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;response to abiotic stimulus;response to light stimulus;response to radiation;response to stimulus;response to UV endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasm;extracellular region;intracellular part Amoebiasis 1.00E-79 4 15 6 45.8

P61160;P61160-2 Actin-related protein 2 ACTR2 >sp|P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1;>sp|P61160-2|ARP2_HUMAN Isoform 2 of Actin-related protein 2 OS=Homo sapiens GN=ACTR2 -0.15 0.06 -0.24 0.15 0.23 0.26 0.27 0.21 + 1.297104546 -0.286819569 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin nucleation;Arp2/3 complex-mediated actin nucleation;biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stress adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding Arp2/3 protein complex;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex 3.89E-134 2 16 6 37.1

Q9Y2T2;H0YBM0;E5RJ52;P53677 AP-3 complex subunit mu-1 AP3M1 >sp|Q9Y2T2|AP3M1_HUMAN AP-3 complex subunit mu-1 OS=Homo sapiens GN=AP3M1 PE=1 SV=1 -0.03 -0.04 -0.23 -0.20 0.06 0.01 0.22 0.09 + 1.330642928 -0.222570359 anterograde axon cargo transport;anterograde synaptic vesicle transport;axon cargo transport;cellular component movement;cellular process;cytoskeleton-dependent intracellular transport;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;intracellular protein transport;intracellular transport;lysosomal transport;microtubule-based movement;microtubule-based process;microtubule-based transport;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;synaptic vesicle transport;transport;vacuolar transport;vesicle-mediated transport AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;macromolecular complex;membrane part;membrane-bounded organelle;organelle;protein complex;vacuole Lysosome 1.94E-71 4 7 7 24.6

J3QT28;O43684-2;O43684;B4DDM6;J3QSX4 Mitotic checkpoint protein BUB3 BUB3 >tr|J3QT28|J3QT28_HUMAN Mitotic checkpoint protein BUB3 (Fragment) OS=Homo sapiens GN=BUB3 PE=4 SV=1;>sp|O43684-2|BUB3_HUMAN Isoform 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3;>sp|O43684|BUB3_HUMAN Mitotic checkpoint protein BUB3 OS=Homo 0.19 0.08 -0.11 0.06 -0.05 -0.40 -0.41 -0.45 + 1.40127953 0.386810643 anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;attachment of spindle microtubules to chromosome;attachment of spindle microtubules to kinetochore;biological regulation;catabolic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell division;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;chromosome organization;chromosome segregation;cytoskeleton organization;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;meiosis;metabolic process;microtubule anchoring;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic cell cycle checkpoint;mitotic cell cycle spindle assembly checkpoint;mitotic cell cycle spindle checkpoint;mitotic prometaphase;mitotic sister chromatid segregation;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cellular component organization;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitosis;negative regulation of mitotic metaphase/anaphase transition;negative regulation of molecular function;negative regulation of nuclear division;negative regulation of organelle organization;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;organelle organization;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome segregation;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic metaphase/anaphase transition;regulation of molecular function;regulation of nuclear division;regulation of organelle organization;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;sister chromatid segregation;spindle assembly checkpoint;spindle checkpoint;ubiquitin-dependent protein catabolic process cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex Cell cycle;Cell cycle - yeast 1.13E-67 5 7 7 30.6

Q9Y295;H0YI06;F8WEE0 Developmentally-regulated GTP-binding protein 1 DRG1 >sp|Q9Y295|DRG1_HUMAN Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1 0.17 0.06 -0.04 0.01 -0.28 -0.46 -0.08 -0.45 + 1.450702095 0.3670595 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transcription factor binding cell part;cytoplasm;cytoskeleton;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;polysome;ribonucleoprotein complex 9.63E-66 3 7 7 27

P35269;E7EUG6;M0QXD6;M0R0R9;M0R0Z3 General transcription factor IIF subunit 1 GTF2F1 >sp|P35269|T2FA_HUMAN General transcription factor IIF subunit 1 OS=Homo sapiens GN=GTF2F1 PE=1 SV=2;>tr|E7EUG6|E7EUG6_HUMAN General transcription factor IIF subunit 1 OS=Homo sapiens GN=GTF2F1 PE=2 SV=1;>tr|M0QXD6|M0QXD6_HUMAN General transcription factor 0.18 0.09 0.11 -0.03 -0.23 -0.43 -0.26 -0.12 + 1.68421049 0.348677211 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA capping;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to biotic stimulus;response to other organism;response to stimulus;response to virus;RNA biosynthetic process;RNA capping;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;viral reproductive process" binding;catalytic activity;DNA binding;enzyme activator activity;enzyme regulator activity;nucleic acid binding;phosphatase activator activity;phosphatase regulator activity;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell junction;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;transcription factor complex;transcription factor TFIIF complex Basal transcription factors 3.57E-42 5 7 7 20.3

G5E9W7;G5E9V5;P82650;H7C5F2;Q9H3I1;H7C5H3;H7C5L9;C9J5D8 "28S ribosomal protein S22, mitochondrial" MRPS22 ">tr|G5E9W7|G5E9W7_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1;>tr|G5E9V5|G5E9V5_HUMAN 28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=2 SV=1;>sp|P82650|RT22_HUMAN 28S ribosomal protein S22, mitoc" -0.38 0.13 0.14 0.26 -0.50 -0.47 -1.21 -0.61 + 1.325608477 0.735679988 structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial part;mitochondrial small ribosomal subunit;mitochondrion;non-membrane-bounded organelle;organellar small ribosomal subunit;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit 3.51E-54 8 7 7 25.1

Q92597;E9PDL6;Q92597-3;Q92597-2;E7ESM1;E5RJY1;E5RIR1;E5RGM5;E5RIV1;E5RIM2;E5RI76;E5RH82;E5RK17;E5RJ98;E5RG99 Protein NDRG1 NDRG1 >sp|Q92597|NDRG1_HUMAN Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1;>tr|E9PDL6|E9PDL6_HUMAN Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=2 SV=2;>sp|Q92597-3|NDRG1_HUMAN Isoform 3 of Protein NDRG1 OS=Homo sapiens GN=NDRG1;>sp|Q92597-2|NDRG1_HUMAN Isoform 2 -0.73 -0.50 -0.09 -0.01 0.11 0.35 0.90 0.57 + 1.362816132 -0.812809139 "biological regulation;cell activation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to hypoxia;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;DNA damage response, signal transduction by p53 class mediator;immune system process;intracellular signal transduction;leukocyte activation;mast cell activation;membrane organization;myelin maintenance;myeloid leukocyte activation;peripheral nervous system myelin maintenance;plasma membrane organization;positive regulation of biological process;positive regulation of spindle checkpoint;regulation of biological process;regulation of cellular process;regulation of spindle checkpoint;response to chemical stimulus;response to DNA damage stimulus;response to hypoxia;response to inorganic substance;response to metal ion;response to oxygen levels;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage" binding;cadherin binding;cell adhesion molecule binding;cytoskeletal protein binding;enzyme binding;gamma-tubulin binding;GTPase binding;microtubule binding;protein binding;Rab GTPase binding;Ras GTPase binding;small GTPase binding;tubulin binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule;microtubule cytoskeleton;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex;recycling endosome membrane 2.17E-87 15 7 7 30.2

Q9NR12;Q9NR12-2;Q9NR12-5;Q9NR12-6;Q9NR12-4;D6RH06;Q9NR12-3;D6RF83;H7BYK4;D6RAN1 PDZ and LIM domain protein 7 PDLIM7 >sp|Q9NR12|PDLI7_HUMAN PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1;>sp|Q9NR12-2|PDLI7_HUMAN Isoform 2 of PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7;>sp|Q9NR12-5|PDLI7_HUMAN Isoform 5 of PDZ and LIM domain protein 7 OS=Homo -0.13 -0.10 -0.20 -0.01 0.31 0.29 0.16 0.41 + 2.067900127 -0.401822703 actin cytoskeleton organization;actin filament-based process;biological regulation;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cytoskeleton organization;developmental process;endocytosis;establishment of localization;membrane invagination;membrane organization;multicellular organismal development;multicellular organismal process;organelle organization;ossification;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of osteoblast differentiation;receptor-mediated endocytosis;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal process;regulation of ossification;regulation of osteoblast differentiation;transport;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding actin cytoskeleton;actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeletal part;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;ruffle;stress fiber 5.65E-29 10 7 7 18.2

Q86UU1-3;Q86UU1-2;Q86UU1;H0YCP1;E9PKC1;E9PMZ5 Pleckstrin homology-like domain family B member 1 PHLDB1 >sp|Q86UU1-3|PHLB1_HUMAN Isoform 3 of Pleckstrin homology-like domain family B member 1 OS=Homo sapiens GN=PHLDB1;>sp|Q86UU1-2|PHLB1_HUMAN Isoform 2 of Pleckstrin homology-like domain family B member 1 OS=Homo sapiens GN=PHLDB1;>sp|Q86UU1|PHLB1_HUMAN Pleck -0.34 -0.66 -0.71 -0.42 1.40 0.35 0.75 -0.06 + 1.410522184 -1.143171949 binding;lipid binding;phospholipid binding 5.38E-23 6 7 7 11.2

P17480-2;E9PKP7;P17480;E9PMM2;E9PLT2 Nucleolar transcription factor 1 UBTF >sp|P17480-2|UBF1_HUMAN Isoform UBF2 of Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF;>tr|E9PKP7|E9PKP7_HUMAN Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=2 SV=1;>sp|P17480|UBF1_HUMAN Nucleolar transcription factor 1 OS=Homo sapie -0.21 0.26 0.25 0.39 -0.10 -0.52 -1.00 -0.76 + 1.349602022 0.769935435 "biological regulation;biosynthetic process;blastocyst growth;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental growth;developmental process;embryo implantation;growth;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase I promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase I promoter;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;termination of RNA polymerase I transcription;transcription elongation from RNA polymerase I promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase I promoter;transcription initiation, DNA-dependent;transcription termination, DNA-dependent" binding;DNA binding;nucleic acid binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part 9.52E-17 5 7 7 10.6

Q92890;Q92890-1;Q92890-3;A6NJ11;C9J6N9;C9JNP9;C9IZG3 Ubiquitin fusion degradation protein 1 homolog UFD1L >sp|Q92890|UFD1_HUMAN Ubiquitin fusion degradation protein 1 homolog OS=Homo sapiens GN=UFD1L PE=1 SV=3;>sp|Q92890-1|UFD1_HUMAN Isoform Long of Ubiquitin fusion degradation protein 1 homolog OS=Homo sapiens GN=UFD1L;>sp|Q92890-3|UFD1_HUMAN Isoform 3 of Ubi 0.02 0.07 0.15 -0.15 0.14 0.46 0.39 0.34 + 1.323459146 -0.308628935 anatomical structure development;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;developmental process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;skeletal system development;system development;ubiquitin-dependent protein catabolic process "catalytic activity;cysteine-type peptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;small conjugating protein-specific protease activity;ubiquitin-specific protease activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Protein processing in endoplasmic reticulum 3.88E-23 7 7 7 29.3

Q6ZSR9;I3L097 Uncharacterized protein FLJ45252 >sp|Q6ZSR9|YJ005_HUMAN Uncharacterized protein FLJ45252 OS=Homo sapiens PE=2 SV=2;>tr|I3L097|I3L097_HUMAN Uncharacterized protein OS=Homo sapiens PE=4 SV=1 -0.27 -0.02 -0.19 -0.08 0.43 0.64 0.50 0.59 + 2.59242169 -0.676835246 4.98E-40 2 7 7 33.8

Q9H2U2;Q9H2U2-2;Q9H2U2-3;E2QRM6;Q9H2U2-6;D6RGV9;B4DFH3;H0Y9D8;Q9H2U2-4;D6R967;H0YAK2;D6RGI1;D6RAD3 "Inorganic pyrophosphatase 2, mitochondrial" PPA2 ">sp|Q9H2U2|IPYR2_HUMAN Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2;>sp|Q9H2U2-2|IPYR2_HUMAN Isoform 2 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2;>sp|Q9H2U2-3|IPYR2_HUMAN Isoform 3 of Inorganic pyr" -0.23 -0.03 0.11 0.23 -0.35 -0.42 -0.37 -0.47 + 1.60271245 0.423121389 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;diphosphate metabolic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic diphosphatase activity;ion binding;magnesium ion binding;metal ion binding;pyrophosphatase activity" cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Oxidative phosphorylation 5.65E-79 13 8 7 31.1

B4E241;P84103 Serine/arginine-rich splicing factor 3 SRSF3 >tr|B4E241|B4E241_HUMAN Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1;>sp|P84103|SRSF3_HUMAN Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 -0.14 0.20 0.13 0.31 -0.16 -0.43 -1.02 -0.47 + 1.296369292 0.644574042 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part Spliceosome 2.11E-46 2 8 7 54

Q2M2I8-2;Q2M2I8;E9PG46 AP2-associated protein kinase 1 AAK1 >sp|Q2M2I8-2|AAK1_HUMAN Isoform 2 of AP2-associated protein kinase 1 OS=Homo sapiens GN=AAK1;>sp|Q2M2I8|AAK1_HUMAN AP2-associated protein kinase 1 OS=Homo sapiens GN=AAK1 PE=1 SV=3;>tr|E9PG46|E9PG46_HUMAN AP2-associated protein kinase 1 OS=Homo sapiens GN= -0.18 -0.19 -0.08 -0.26 0.69 0.71 0.63 0.39 + 2.616835872 -0.782153703 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;endocytosis;establishment of localization;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of Notch signaling pathway;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;posttranscriptional regulation of gene expression;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;protein stabilization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular component organization;regulation of cellular process;regulation of clathrin-mediated endocytosis;regulation of endocytosis;regulation of gene expression;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of Notch signaling pathway;regulation of protein localization;regulation of protein stability;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of vesicle-mediated transport;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;AP-2 adaptor complex binding;ATP binding;binding;catalytic activity;kinase activity;Notch binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein complex binding;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" axon part;cell leading edge;cell part;cell projection part;clathrin-coated vesicle;coated pit;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extrinsic to membrane;extrinsic to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane part;synapse part;terminal button;vesicle 4.58E-52 3 8 8 17.6

O43747;O43747-2;J3KQU9;B3KXW5;H3BR36;H3BUN9;H3BNR4;B3KNW1 AP-1 complex subunit gamma-1 AP1G1 >sp|O43747|AP1G1_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=1 SV=5;>sp|O43747-2|AP1G1_HUMAN Isoform 2 of AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1;>tr|J3KQU9|J3KQU9_HUMAN AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 0.02 -0.12 0.06 -0.02 0.08 0.26 0.27 0.16 + 1.390357706 -0.206579037 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;membrane invagination;membrane organization;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;transport;vesicle-mediated transport;viral reproduction protein transporter activity;substrate-specific transporter activity;transporter activity AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;clathrin coated vesicle membrane;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endosome;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lysosomal membrane;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;recycling endosome;trans-Golgi network;trans-Golgi network membrane;vacuolar membrane;vacuolar part;vesicle membrane Lysosome 1.60E-38 8 8 8 13.7

Q9HDC9;Q9HDC9-2;H0Y512 Adipocyte plasma membrane-associated protein APMAP >sp|Q9HDC9|APMAP_HUMAN Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2;>sp|Q9HDC9-2|APMAP_HUMAN Isoform 2 of Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP;>tr|H0Y512|H0Y512_HUMAN Adipocyte plasma memb -0.34 -0.23 -0.08 -0.08 0.90 0.49 0.28 0.28 + 1.60950356 -0.670215482 biosynthetic process;metabolic process "amine-lyase activity;arylesterase activity;carbon-nitrogen lyase activity;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;lyase activity;strictosidine synthase activity" cell part;cell surface;integral to membrane;intrinsic to membrane;membrane;membrane part 1.50E-49 3 8 8 24.8

P13807-2;P13807;B7Z806;F5H1N8;P54840;M0QYU1 "Glycogen [starch] synthase, muscle" GYS1 ">sp|P13807-2|GYS1_HUMAN Isoform 2 of Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1;>sp|P13807|GYS1_HUMAN Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2;>tr|B7Z806|B7Z806_HUMAN Glycogen [starch] synthase, muscle OS=Homo sa" -0.13 -0.14 -0.41 -0.36 0.13 0.28 -0.05 0.19 + 1.541842717 -0.400573916 alcohol metabolic process;anatomical structure development;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;developmental process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan biosynthetic process;glucan metabolic process;glucose metabolic process;glycogen biosynthetic process;glycogen metabolic process;heart development;hexose metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;organ development;oxidation-reduction process;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process;response to carbohydrate stimulus;response to chemical stimulus;response to glucose stimulus;response to hexose stimulus;response to monosaccharide stimulus;response to organic substance;response to stimulus;small molecule metabolic process "binding;carbohydrate binding;catalytic activity;glucose binding;glucosyltransferase activity;glycogen (starch) synthase activity;identical protein binding;monosaccharide binding;protein binding;protein dimerization activity;protein homodimerization activity;sugar binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;UDP-glucosyltransferase activity;UDP-glycosyltransferase activity" cell cortex part;cell part;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;ectoplasm;inclusion body;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part Insulin signaling pathway;Starch and sucrose metabolism 2.51E-27 6 8 8 15.6

O14879 Interferon-induced protein with tetratricopeptide repeats 3 IFIT3 >sp|O14879|IFIT3_HUMAN Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens GN=IFIT3 PE=1 SV=1 0.16 0.31 -0.06 -0.24 -1.19 -1.07 -0.43 -0.42 + 1.388720789 0.821276603 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-alpha;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;immune effector process;immune system process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of programmed cell death;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-alpha;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;signal transduction;type I interferon-mediated signaling pathway cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 1.41E-34 1 8 8 18.4

B4DT35;Q7Z3B4;E7EUM5;Q7Z3B4-2Nucleoporin p54 NUP54 >tr|B4DT35|B4DT35_HUMAN Nucleoporin p54 OS=Homo sapiens GN=NUP54 PE=2 SV=1;>sp|Q7Z3B4|NUP54_HUMAN Nucleoporin p54 OS=Homo sapiens GN=NUP54 PE=1 SV=2;>tr|E7EUM5|E7EUM5_HUMAN Nucleoporin p54 OS=Homo sapiens GN=NUP54 PE=2 SV=2;>sp|Q7Z3B4-2|NUP54_HUMAN Isoform 0.30 0.06 0.18 0.09 -0.10 -0.22 -0.45 -0.42 + 1.713477422 0.453054765 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular protein transport;intracellular transport;metabolic process;monosaccharide transport;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;organic substance transport;primary metabolic process;protein targeting;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process nucleocytoplasmic transporter activity;transporter activity cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear pore;nucleoplasm;organelle membrane;organelle part;pore complex;protein complex RNA transport 3.45E-93 4 8 8 23.1

P50479;P50479-2;C9J542 PDZ and LIM domain protein 4 PDLIM4 >sp|P50479|PDLI4_HUMAN PDZ and LIM domain protein 4 OS=Homo sapiens GN=PDLIM4 PE=1 SV=2;>sp|P50479-2|PDLI4_HUMAN Isoform 2 of PDZ and LIM domain protein 4 OS=Homo sapiens GN=PDLIM4 -0.18 -0.15 0.02 0.11 0.51 0.63 0.27 0.76 + 1.757098011 -0.592516823 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding 1.22E-59 3 8 8 33.6

P46779;P46779-2;P46779-3;H0YKD8;P46779-4;P46779-5;H0YMF4;H0YLP6 60S ribosomal protein L28 RPL28 >sp|P46779|RL28_HUMAN 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3;>sp|P46779-2|RL28_HUMAN Isoform 2 of 60S ribosomal protein L28 OS=Homo sapiens GN=RPL28;>sp|P46779-3|RL28_HUMAN Isoform 3 of 60S ribosomal protein L28 OS=Homo sapiens GN=RPL -0.11 0.00 0.01 0.00 -0.14 -0.40 -0.32 -0.30 + 1.653300236 0.265489195 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 2.55E-62 8 8 8 40.1

O14745;B3KY21;J3QRP6 Na(+)/H(+) exchange regulatory cofactor NHE-RF1 SLC9A3R1 >sp|O14745|NHRF1_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4;>tr|B3KY21|B3KY21_HUMAN Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=2 SV=1;>tr|J3QRP6|J3QRP6_HUMAN Na(+)/H(+) ex 0.25 -0.10 0.56 0.22 -0.83 -0.88 -0.23 -0.24 + 1.386099198 0.775830325 "acid secretion;actin cytoskeleton organization;actin filament-based process;activation of adenylate cyclase activity;activation of adenylate cyclase activity by dopamine receptor signaling pathway;activation of adenylate cyclase activity by G-protein signaling pathway;activation of phospholipase C activity;activation of phospholipase C activity by dopamine receptor signaling pathway;activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger;amine transport;amino acid transport;anion homeostasis;apoptosis;bile acid secretion;biological regulation;cAMP-mediated signaling;carboxylic acid transport;cation transport;cell death;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular anion homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule localization;cellular phosphate ion homeostasis;cellular process;cellular protein localization;cellular response to stimulus;cellular trivalent inorganic anion homeostasis;chemical homeostasis;cyclic-nucleotide-mediated signaling;cytoskeleton organization;death;dopamine receptor signaling pathway;establishment of localization;glutathione transport;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;homeostatic process;inositol phosphate-mediated signaling;intracellular signal transduction;ion homeostasis;ion transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;metal ion transport;microvillus assembly;microvillus organization;modified amino acid transport;monovalent inorganic cation transport;multicellular organismal process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of ERK1 and ERK2 cascade;negative regulation of intracellular protein kinase cascade;negative regulation of ion transmembrane transporter activity;negative regulation of ion transport;negative regulation of locomotion;negative regulation of MAPKKK cascade;negative regulation of molecular function;negative regulation of phosphatidylinositol 3-kinase cascade;negative regulation of platelet-derived growth factor receptor signaling pathway;negative regulation of protein kinase B signaling cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of sodium ion transmembrane transporter activity;negative regulation of sodium ion transport;negative regulation of sodium:hydrogen antiporter activity;negative regulation of transport;negative regulation of transporter activity;nitrogen compound transport;oligopeptide transport;organelle organization;organic acid transport;organic substance transport;peptide transport;phosphate ion homeostasis;positive regulation of adenylate cyclase activity;positive regulation of adenylate cyclase activity by G-protein signaling pathway;positive regulation of catalytic activity;positive regulation of cyclase activity;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of lyase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;programmed cell death;protein complex assembly;protein complex subunit organization;protein localization;regulation of adenylate cyclase activity;regulation of adenylate cyclase activity involved in G-protein signaling pathway;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of ERK1 and ERK2 cascade;regulation of excretion;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of kinase activity;regulation of lipase activity;regulation of localization;regulation of locomotion;regulation of lyase activity;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase cascade;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of platelet-derived growth factor receptor signaling pathway;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of proton transport;regulation of response to stimulus;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of sodium:hydrogen antiporter activity;regulation of system process;regulation of transferase activity;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;renal absorption;renal sodium ion transport;renal system process;response to stimulus;second-messenger-mediated signaling;secretion;signal transduction;sodium ion transport;system process;transport;tripeptide transport;trivalent inorganic anion homeostasis;Wnt receptor signaling pathway" binding;channel regulator activity;chloride channel regulator activity;protein binding;protein self-association actin cytoskeleton;apical plasma membrane;brush border membrane;cell part;cell projection;cell projection membrane;cell projection part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;endomembrane system;filopodium;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane part;membrane-bounded organelle;microtubule organizing center;microvillus membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;ruffle 3.09E-63 3 8 8 35.2

Q92797;Q92797-2;M0R3C7;M0R1C2;M0R180;M0QXP5 Symplekin SYMPK >sp|Q92797|SYMPK_HUMAN Symplekin OS=Homo sapiens GN=SYMPK PE=1 SV=2;>sp|Q92797-2|SYMPK_HUMAN Isoform 2 of Symplekin OS=Homo sapiens GN=SYMPK;>tr|M0R3C7|M0R3C7_HUMAN Symplekin OS=Homo sapiens GN=SYMPK PE=4 SV=1 -0.05 0.28 0.10 0.26 -0.37 -0.51 -1.08 -0.68 + 1.737943142 0.810867662 biological adhesion;biological regulation;cell adhesion;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA metabolic process;mRNA polyadenylation;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of dephosphorylation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;RNA 3'-end processing;RNA metabolic process;RNA polyadenylation;RNA processing cell junction;cell part;cell-cell junction;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear part;nucleoplasm;occluding junction;organelle;organelle part;plasma membrane;tight junction mRNA surveillance pathway;Tight junction 4.34E-85 6 8 8 10.1

Q99426;K7EK42;Q6FGY5;A8MVD5;K7ELT5;K7EP07;K7ENS2;K7EL99;K7EQH0;K7ER04 Tubulin-folding cofactor B TBCB;CKAP1 >sp|Q99426|TBCB_HUMAN Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2;>tr|K7EK42|K7EK42_HUMAN Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=4 SV=1;>tr|Q6FGY5|Q6FGY5_HUMAN CKAP1 protein OS=Homo sapiens GN=CKAP1 PE=2 SV=1;>tr|A8MVD5|A8MV 0.11 -0.08 0.06 -0.02 0.55 0.47 0.32 0.15 + 1.427453546 -0.353334015 anatomical structure development;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;developmental process;macromolecule metabolic process;metabolic process;nervous system development;primary metabolic process;protein folding;protein metabolic process;system development cell part;cytoplasm;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;protein complex 3.65E-70 10 8 8 40.2

O60784;O60784-3;E7EPD0;O60784-2;O60784-4;B0QY01;B3KUU1;F8WB30;F8WAW7;F8WE29;F8WBB0;H7BYN7;B0QY02 Target of Myb protein 1 TOM1 >sp|O60784|TOM1_HUMAN Target of Myb protein 1 OS=Homo sapiens GN=TOM1 PE=1 SV=2;>sp|O60784-3|TOM1_HUMAN Isoform 3 of Target of Myb protein 1 OS=Homo sapiens GN=TOM1;>tr|E7EPD0|E7EPD0_HUMAN Target of Myb protein 1 OS=Homo sapiens GN=TOM1 PE=2 SV=1;>sp|O6078 -0.50 0.16 -0.36 -0.17 0.96 1.30 1.16 0.49 + 1.875645808 -1.197984543 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;membrane invagination;membrane organization;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;cytosol;early endosome;endosome;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle 9.53E-54 13 8 8 26

Q01081;Q01081-2;Q01081-4;Q8WU68-3;Q8WU68;K7EJH3;K7EJM7;M0QYK5;Q01081-3;K7ERY8;M0R2N4;Q8WU68-2;K7EPL9 Splicing factor U2AF 35 kDa subunit U2AF1 >sp|Q01081|U2AF1_HUMAN Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3;>sp|Q01081-2|U2AF1_HUMAN Isoform 2 of Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1;>sp|Q01081-4|U2AF1_HUMAN Isoform 4 of Splicing factor U2AF 35 k 0.11 0.10 -0.06 0.24 -0.14 -0.35 -0.73 -0.23 + 1.314106574 0.461286525 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding Cajal body;catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Shigellosis;Spliceosome 8.34E-44 13 8 8 41.7

Q9Y5K5-2;Q9Y5K5-4;Q9Y5K5-3;Q9Y5K5;Q5LJA5;Q5LJA9;Q5LJB0;B4DW59;B7Z9U9;H0Y6Y4;H0Y4E0;H0Y4K0;H0Y636 Ubiquitin carboxyl-terminal hydrolase isozyme L5 UCHL5 >sp|Q9Y5K5-2|UCHL5_HUMAN Isoform 2 of Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCHL5;>sp|Q9Y5K5-4|UCHL5_HUMAN Isoform 4 of Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCHL5;>sp|Q9Y5K5-3|UCHL5_HUMAN Isoform 0.07 0.01 0.39 0.12 -0.32 -0.49 -0.39 -0.65 + 1.949615861 0.612832662 "anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;DNA recombination;DNA repair;enzyme linked receptor protein signaling pathway;forebrain morphogenesis;lateral ventricle development;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;midbrain development;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of proteolysis;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;ubiquitin-dependent protein catabolic process" "binding;catalytic activity;cysteine-type peptidase activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;exopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;omega peptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;peptidase inhibitor activity;peptidase regulator activity;proteasome binding;protein binding;protein complex binding;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" cell part;chromatin remodeling complex;chromosomal part;cytoplasm;cytoplasmic part;cytosol;DNA helicase complex;Ino80 complex;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleus;organelle;organelle part;proteasome complex;protein complex 5.01E-51 13 8 8 29.7

P43034;I3L495;B4DF38;I3L3N5;P43034-2 Platelet-activating factor acetylhydrolase IB subunit alpha PAFAH1B1 >sp|P43034|LIS1_HUMAN Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2 0.19 -0.04 -0.31 -0.26 0.39 0.42 0.58 0.15 + 1.368202009 -0.48871247 acrosome assembly;actin cytoskeleton organization;actin filament-based process;adult behavior;adult locomotory behavior;alcohol metabolic process;ameboidal cell migration;amine metabolic process;anaphase;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;axon cargo transport;axonogenesis;behavior;biological regulation;brain morphogenesis;catabolic process;cell communication;cell cycle phase;cell cycle process;cell differentiation;cell division;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell-cell signaling;cellular amine metabolic process;cellular biogenic amine metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular localization;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular process involved in reproduction in multicellular organism;central nervous system neuron axonogenesis;central nervous system neuron differentiation;central nervous system projection neuron axonogenesis;cerebral cortex neuron differentiation;cognition;corpus callosum morphogenesis;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;developmental process involved in reproduction;establishment of centrosome localization;establishment of localization;establishment of localization in cell;establishment of mitotic spindle localization;establishment of mitotic spindle orientation;establishment of nucleus localization;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;establishment of spindle orientation;ethanolamine-containing compound metabolic process;G2/M transition of mitotic cell cycle;glycerolipid metabolic process;glycerophospholipid metabolic process;hippocampus development;intracellular transport;layer formation in cerebral cortex;learning or memory;lipid catabolic process;lipid metabolic process;localization;locomotion;locomotory behavior;M phase;M phase of mitotic cell cycle;membrane disassembly;membrane organization;metabolic process;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based movement;microtubule-based process;microtubule-based transport;mitosis;mitotic anaphase;mitotic prometaphase;multicellular organismal process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of intracellular protein kinase cascade;negative regulation of JNK cascade;negative regulation of MAPKKK cascade;negative regulation of neuron projection development;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of stress-activated protein kinase signaling cascade;neural precursor cell proliferation;neuroblast proliferation;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;neuron migration;neuron projection morphogenesis;nitrogen compound metabolic process;nuclear division;nuclear envelope disassembly;nuclear envelope organization;nuclear migration;organ morphogenesis;organelle fission;organelle localization;organelle organization;organelle transport along microtubule;organophosphate metabolic process;phospholipid metabolic process;platelet activating factor metabolic process;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell cycle;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytokine-mediated signaling pathway;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of mitotic cell cycle;positive regulation of neurogenesis;positive regulation of response to cytokine stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein secretion;protein transport;regulation of anatomical structure morphogenesis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of cytokine-mediated signaling pathway;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of MAPKKK cascade;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to cytokine stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;reproductive process;response to stimulus;retrograde axon cargo transport;secretion;secretion by cell;signaling;small molecule metabolic process;stem cell division;synaptic transmission;system process;transport;vesicle localization;vesicle transport along microtubule binding;carbohydrate binding;catalytic activity;cytoskeletal protein binding;dynactin binding;dynein binding;enzyme binding;glycosaminoglycan binding;heparin binding;hydrolase activity;identical protein binding;microtubule binding;pattern binding;phospholipase binding;phosphoprotein binding;polysaccharide binding;protein binding;protein dimerization activity;protein homodimerization activity;tubulin binding astral microtubule;axon part;cell body;cell cortex;cell leading edge;cell part;cell projection;cell projection part;centrosome;chromosomal part;cilium;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytosol;envelope;growth cone;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinesin complex;kinetochore;macromolecular complex;membrane;microtubule;microtubule associated complex;microtubule organizing center;motile primary cilium;neuronal cell body;non-membrane-bounded organelle;nuclear envelope;nuclear membrane;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;perinuclear region of cytoplasm;primary cilium;protein complex;site of polarized growth;spindle microtubule;vesicle Ether lipid metabolism 1.47E-64 5 9 8 27.6

P35237 Serpin B6 SERPINB6 >sp|P35237|SPB6_HUMAN Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 0.10 -0.26 -0.02 -0.08 0.62 0.72 0.74 0.19 + 1.615269233 -0.635948949 biological regulation;regulation of biological process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex Amoebiasis 4.10E-116 1 9 8 33.2

E9PCY7;P31943;G8JLB6;D6RBM0;D6RIT2;D6RIU0;E7EQJ0;D6RAM1;D6R9T0;D6RFM3;D6RDU3;D6RJ04;D6RIH9;E5RGV0;E7EN40;H0YB39;D6RDL0;H0YBD7;D6RF17;E5RGH4;H0YBG7;D6R9D3;H0YAQ2;F5GZT4;E5RJ94;H7C2J6;Q9NQA5 "Heterogeneous nuclear ribonucleoprotein H;Heterogeneous nuclear ribonucleoprotein H, N-terminally processed"HNRNPH1 >tr|E9PCY7|E9PCY7_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1;>sp|P31943|HNRH1_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4;>tr|G8JLB6|G8JLB6_HUMAN Heterogeneous nuclear ribon 0.17 0.35 -0.04 0.34 -0.14 -0.34 -0.72 -0.20 + 1.401518166 0.557794196 "biological regulation;calcium ion transmembrane transport;calcium ion transport;cation transport;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;ion transmembrane transport;ion transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;metal ion transport;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein tetramerization;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transmembrane transport;transport" binding;calcium channel activity;cation channel activity;cation transmembrane transporter activity;channel activity;ion channel activity;ion transmembrane transporter activity;nucleic acid binding;nucleotide binding;passive transmembrane transporter activity;poly(U) RNA binding;poly-pyrimidine tract binding;RNA binding;single-stranded RNA binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity actin cytoskeleton;apical plasma membrane;catalytic step 2 spliceosome;cell part;cytoplasm;cytoskeleton;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane part;ribonucleoprotein complex;spliceosomal complex Endocrine and other factor-regulated calcium reabsorption 9.47E-277 27 15 8 45.7

Q9Y305-2;Q9Y305;Q9Y305-4;Q9Y305-3;H7C5Q2;C9J7L8 "Acyl-coenzyme A thioesterase 9, mitochondrial"ACOT9 ">sp|Q9Y305-2|ACOT9_HUMAN Isoform 2 of Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9;>sp|Q9Y305|ACOT9_HUMAN Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2;>sp|Q9Y305-4|ACOT9_HUMAN Isoform 4 of Acyl-"0.01 -0.12 -0.19 -0.27 0.15 0.37 0.21 0.69 + 1.452948203 -0.495815006 acyl-CoA metabolic process;cellular metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;metabolic process;thioester metabolic process "acetyl-CoA hydrolase activity;carboxylesterase activity;carboxylic ester hydrolase activity;catalytic activity;CoA hydrolase activity;hydrolase activity;hydrolase activity, acting on ester bonds;thiolester hydrolase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 2.34E-32 6 9 9 26.4

Q96CW1-2;Q96CW1;E9PFW3;C9JJ47;C9JTK4;C9JGT8;C9JJD3;C9JPV8;H7C4C3 AP-2 complex subunit mu AP2M1 >sp|Q96CW1-2|AP2M1_HUMAN Isoform 2 of AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1;>sp|Q96CW1|AP2M1_HUMAN AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2;>tr|E9PFW3|E9PFW3_HUMAN AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=2 SV=1;>tr|0.12 -0.19 -0.52 -0.26 0.52 0.46 0.26 0.45 + 1.684744086 -0.633991748 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;immune system process;intracellular protein transport;intracellular transport;locomotion;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of epidermal growth factor receptor signaling pathway;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;synaptic transmission;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport;viral reproduction binding;lipid binding;transporter activity AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;clathrin coat;clathrin coat of coated pit;clathrin coated vesicle membrane;clathrin-coated endocytic vesicle membrane;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endocytic vesicle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lysosomal membrane;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;vacuolar membrane;vacuolar part;vesicle membrane Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease 5.03E-29 9 9 9 22.9

Q16850;Q16850-2;H7C0D0;C9IYR8 Lanosterol 14-alpha demethylase CYP51A1 >sp|Q16850|CP51A_HUMAN Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1 PE=1 SV=3;>sp|Q16850-2|CP51A_HUMAN Isoform 2 of Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1 -0.04 0.00 0.05 0.19 -0.48 -0.74 -0.33 -0.38 + 1.83159766 0.529579794 "alcohol metabolic process;biosynthetic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol biosynthetic process via 24,25-dihydrolanosterol;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;xenobiotic metabolic process" "binding;catalytic activity;cation binding;demethylase activity;electron carrier activity;heme binding;ion binding;iron ion binding;metal ion binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;sterol 14-demethylase activity;tetrapyrrole binding;transition metal ion binding" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Steroid biosynthesis 2.08E-33 4 9 9 22.7

Q71RC2;Q71RC2-4;Q71RC2-7;Q71RC2-5;Q71RC2-3;Q96J85;Q71RC2-2;Q71RC2-6;F8W1I4;F8VY40;F8W1Z5 La-related protein 4LARP4 >sp|Q71RC2|LARP4_HUMAN La-related protein 4 OS=Homo sapiens GN=LARP4 PE=1 SV=3;>sp|Q71RC2-4|LARP4_HUMAN Isoform 4 of La-related protein 4 OS=Homo sapiens GN=LARP4;>sp|Q71RC2-7|LARP4_HUMAN Isoform 7 of La-related protein 4 OS=Homo sapiens GN=LARP4;>sp|Q71RC 0.46 0.21 0.02 -0.02 -0.40 -0.27 -0.27 -0.09 + 1.367603353 0.425804484 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of cell morphogenesis;regulation of cellular component organization;regulation of cellular process;regulation of developmental process binding;nucleic acid binding;RNA binding 2.82E-44 11 9 9 16.9

Q08380;K7EKQ5;K7EP36;K7ERZ6;K7EJD3;K7EQT9;K7ES75;K7EN99;K7EJY8;REV__H0YD26;REV__J3QL17;REV__Q9UHL0 Galectin-3-binding protein LGALS3BP >sp|Q08380|LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 0.07 0.13 0.24 0.36 -1.77 -1.27 -1.68 -0.93 + 2.370633138 1.611451432 biological adhesion;biological regulation;cell adhesion;cellular defense response;cellular process;cellular response to stimulus;defense response;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;signal transduction cargo receptor activity;receptor activity;scavenger receptor activity cell part;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;proteinaceous extracellular matrix;vesicle 9.58E-48 12 9 9 17.4

Q8TCS8;H7BXF6;F8WBI3 "Polyribonucleotide nucleotidyltransferase 1, mitochondrial" PNPT1 ">sp|Q8TCS8|PNPT1_HUMAN Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Homo sapiens GN=PNPT1 PE=1 SV=2" 0.02 0.23 0.22 -0.04 -0.53 -0.67 -0.43 -0.41 + 2.19130873 0.613656547 anatomical structure morphogenesis;biological regulation;catabolic process;cell cycle arrest;cell cycle process;cell part morphogenesis;cellular catabolic process;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-beta;cellular response to organic substance;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;developmental process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mitochondrial mRNA catabolic process;mitochondrial RNA 3'-end processing;mitochondrial RNA 5'-end processing;mitochondrial RNA catabolic process;mitochondrial RNA metabolic process;mitochondrial RNA processing;mitochondrial transport;mitochondrion morphogenesis;mitochondrion organization;mitotic cell cycle arrest;modification-dependent macromolecule catabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;negative regulation of growth;nitrogen compound metabolic process;nuclear polyadenylation-dependent mRNA catabolic process;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;organelle organization;polyadenylation-dependent mRNA catabolic process;polyadenylation-dependent RNA catabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of miRNA catabolic process;positive regulation of miRNA metabolic process;positive regulation of mitochondrial RNA catabolic process;positive regulation of mRNA catabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotrimerization;protein oligomerization;protein trimerization;regulation of biological process;regulation of catabolic process;regulation of cell aging;regulation of cell cycle;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular respiration;regulation of cellular response to stress;regulation of cellular senescence;regulation of developmental process;regulation of generation of precursor metabolites and energy;regulation of growth;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of miRNA catabolic process;regulation of miRNA metabolic process;regulation of mitochondrial RNA catabolic process;regulation of mRNA catabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;response to chemical stimulus;response to cytokine stimulus;response to interferon-beta;response to organic substance;response to oxidative stress;response to stimulus;response to stress;RNA 3'-end processing;RNA 5'-end processing;RNA catabolic process;RNA import into mitochondrion;RNA metabolic process;RNA processing;RNA transport;rRNA import into mitochondrion;rRNA transport;transport "3'-5' exonuclease activity;3'-5'-exoribonuclease activity;binding;catalytic activity;exonuclease activity;exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;exoribonuclease activity;exoribonuclease activity, producing 5'-phosphomonoesters;hydrolase activity;hydrolase activity, acting on ester bonds;miRNA binding;nuclease activity;nucleic acid binding;nucleotidyltransferase activity;poly(G) RNA binding;poly(U) RNA binding;poly-purine tract binding;poly-pyrimidine tract binding;polyribonucleotide nucleotidyltransferase activity;ribonuclease activity;RNA binding;single-stranded RNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic exosome (RNase complex);cytoplasmic part;exosome (RNase complex);intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-enclosed lumen;mitochondrial degradosome;mitochondrial intermembrane space;mitochondrial part;organelle envelope lumen;organelle part;plasma membrane;protein complex Purine metabolism;Pyrimidine metabolism;RNA degradation 1.25E-52 3 9 9 14.6

O75400-2;O75400;O75400-3;F5H578;H7C2N3 Pre-mRNA-processing factor 40 homolog A PRPF40A >sp|O75400-2|PR40A_HUMAN Isoform 2 of Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A;>sp|O75400|PR40A_HUMAN Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2;>sp|O75400-3|PR40A_HUMAN Isoform 3 of Pre-mRNA-proc 0.02 0.15 -0.10 0.03 -0.31 -0.51 -0.71 -0.32 + 1.712367216 0.486988566 biological regulation;cell cycle;cell division;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoskeleton organization;locomotion;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell division;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of cytokinesis;regulation of developmental process;RNA metabolic process;RNA processing;RNA splicing cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear matrix;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part Spliceosome 6.50E-58 5 9 9 11.7

P61289;P61289-2;B3KQ25;K7ESG5;K7ENH2;K7EMD0;K7EPX6;K7EKR3;B7Z8D3;REV__Q9NXL9-2;REV__Q9NXL9-4;REV__Q9UJA3-2;REV__Q9UJA3-3;REV__Q9UJA3;REV__P33991;REV__Q9UJA3-4;REV__Q9NXL9 Proteasome activator complex subunit 3 PSME3 >sp|P61289|PSME3_HUMAN Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1;>sp|P61289-2|PSME3_HUMAN Isoform 2 of Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3;>tr|B3KQ25|B3KQ25_HUMAN Proteasome activator complex subu 0.19 0.05 0.04 0.04 -0.22 -0.48 -0.40 -0.40 +

2.191382639 0.451587519 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular catabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of proteolysis;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" binding;endopeptidase activator activity;endopeptidase regulator activity;enzyme activator activity;enzyme regulator activity;p53 binding;peptidase activator activity;peptidase regulator activity;protein binding cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome activator complex;proteasome complex;protein complex Antigen processing and presentation;Hepatitis C;Proteasome 1.39E-81 17 9 9 36.2

P61313;E7EQV9;E7ENU7;E7EX53;P61313-2;E7ERA2 60S ribosomal protein L15;Ribosomal protein L15 RPL15 >sp|P61313|RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2;>tr|E7EQV9|E7EQV9_HUMAN Ribosomal protein L15 (Fragment) OS=Homo sapiens GN=RPL15 PE=2 SV=1;>tr|E7ENU7|E7ENU7_HUMAN Ribosomal protein L15 (Fragment) OS=Homo sapiens GN=RPL15 -0.11 0.07 0.67 0.13 -0.70 -0.41 -0.42 -0.37 + 1.438913117 0.668779053 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 6.62E-59 6 9 9 45.6

Q2NL82;I3L4E8 Pre-rRNA-processing protein TSR1 homolog TSR1 >sp|Q2NL82|TSR1_HUMAN Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=10.13 0.15 0.08 0.17 -0.05 -0.22 -0.44 -0.28 + 1.730823807 0.380434052 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;organelle assembly;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 2.22E-69 2 9 9 16.4

Q9UN86-2;Q9UN86;D6RAC7;D6RB17;D6RGJ4;D6RBM9;D6REX8;D6RBR0;D6RE13;D6RBW8;D6R9X5;D6R9A4 Ras GTPase-activating protein-binding protein 2 G3BP2 >sp|Q9UN86-2|G3BP2_HUMAN Isoform B of Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2;>sp|Q9UN86|G3BP2_HUMAN Ras GTPase-activating protein-binding protein 2 OS=Homo sapiens GN=G3BP2 PE=1 SV=2;>tr|D6RAC7|D6RAC7_HUMAN Ras GTPase-acti 0.15 0.04 -0.15 0.07 -0.34 -0.45 -0.34 -0.29 + 1.9025469 0.38159248 biological regulation;cellular process;cellular response to stimulus;cytoplasmic sequestering of NF-kappaB;cytoplasmic sequestering of protein;cytoplasmic sequestering of transcription factor;establishment of localization;establishment of RNA localization;intracellular signal transduction;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;mRNA transport;negative regulation of biological process;negative regulation of cellular process;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of NF-kappaB import into nucleus;negative regulation of nucleocytoplasmic transport;negative regulation of protein import into nucleus;negative regulation of protein transport;negative regulation of transcription factor import into nucleus;negative regulation of transmembrane transport;negative regulation of transport;nucleic acid transport;nucleobase-containing compound transport;Ras protein signal transduction;regulation of biological process;regulation of biological quality;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of NF-kappaB import into nucleus;regulation of nucleocytoplasmic transport;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription factor import into nucleus;regulation of transmembrane transport;regulation of transport;response to stimulus;RNA transport;signal transduction;small GTPase mediated signal transduction;transport binding;nucleic acid binding;nucleotide binding;protein binding;protein complex scaffold;receptor signaling complex scaffold activity;RNA binding;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosol;intracellular;intracellular part 7.68E-64 12 10 9 29.8

P42285;F5H7E2;H0YAC4;H0Y8U3;D6REC7;REV__P0CJ87;REV__Q9UBX2;REV__P0CJ90;REV__P0CJ89;REV__P0CJ88;REV__P0CJ86;REV__P0CJ85;REV__E9PEK5;REV__F5GZ66;REV__CON__Q3MHN2;REV__F5GZ84;REV__Q96AE4;REV__O94887-2;REV__Q96AE4-2;REV__E9PEB5;REV__B4DT31;O43151-3;J3KNF3;REV__O94887;O43151-2;O43151;REV__Q8NF91-8;REV__Q8NF91-2 Superkiller viralicidic activity 2-like 2 SKIV2L2>sp|P42285|SK2L2_HUMAN Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3;>tr|F5H7E2|F5H7E2_HUMAN Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=2 SV=1 0.26 0.39 0.01 0.03 -0.18 -0.45 -0.85 -0.25 + 1.379549222 0.602303085 "biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular

component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;demethylation;DNA dealkylation;DNA demethylation;DNA metabolic process;DNA modification;glycosylation;histone H3-K4 methylation;histone H3-K4 trimethylation;histone lysine methylation;histone methylation;histone modification;macromolecule glycosylation;macromolecule metabolic process;macromolecule methylation;macromolecule modification;maturation of 5.8S rRNA;metabolic process;methylation;mRNA metabolic process;mRNA processing;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine methylation;peptidyl-lysine modification;peptidyl-lysine trimethylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein alkylation;protein glycosylation;protein metabolic process;protein methylation;protein modification process;protein O-linked glycosylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;rRNA metabolic process;rRNA processing;small molecule metabolic process"	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;cation binding;dioxygenase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;methylcytosine dioxygenase activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	catalytic step 2 spliceosome;cell part;cytoplasm;female pronucleus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;male pronucleus;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;pronucleus;ribonucleoprotein complex;spliceosomal complex	RNA degradation	6.49E-50	28	10	9	11.7
P06493;P06493-2;E5RIU6;K7ELV5;Q00526;G3V317;F8VXD2;H0YE20;F8VYH9;B4DNF9;F8VZZ0;F8VTV8;F8VWX7;F8VZ51;Q8IZL9-2;H0YAZ9;Q8IZL9-3;H0Y9P2;B3KUS6;Q9UPZ9-2;P11802;Q8IZL9-5;Q8IZL9-4;E7EUK8;Q8IZL9;Q96Q40-2;H7C265;Q96Q40-4;E5RGN0;Q96Q40-3;O94921-3;Q96Q40-5;E9PJX5;Q96Q40;O94921-2;Q8IXN4;F5H3M4;O94921;F5H6Z0;Q07002;Q07002-2;Q00536;Q00536-3;Q07002-3;P51451;Q00537-2;Q00537;P09769;Q00536-2;P20794-3;P20794;Q9UPZ9;P20794-2;P11362-6;P11362-5;H7BXU9;P21802-22;P21802-4;P22607-3;P21802-20;P21802-15;P21802-21;E7EVR7;P21802-23;P11362-4;P11362-14;P11362-3;E7EU09;J3KPQ0;P22455-2;P21802-8;P21802-2;P21802-13;P21802-17;P21802-12;P21802-6;P22607-4;F8W9L4;P22455;P22607;P22607-2;P11362-20;P21802-7;P21802-9;P21802-5;P21802-10;P21802-18;P11362-7;P11362-2;P21802;P21802-3;P21802-16;P11362-19;P11362;J3KNT4;P21802-11;P11362-21;J3QSD7;Q9NYV4-3	Cyclin-dependent kinase 1	CDK1	>sp|P06493|CDK1_HUMAN Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3;>sp|P06493-2|CDK1_HUMAN Isoform 2 of Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1;>tr|E5RIU6|E5RIU6_HUMAN Cyclin-dependent kinase 1 (Fragment) OS=Homo sapiens GN=CDK1 PE	0.67	0.12	-0.02	-0.02	-0.44	-1.19	-0.77	-0.96	+	1.692326359	1.030372874	"activation of immune response;activation of innate immune response;activation of MAPK activity;activation of MAPKK activity;activation of protein kinase activity;aging;alveolar secondary septum development;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure maturation;anatomical structure morphogenesis;angiogenesis;anion homeostasis;antigen receptor-mediated signaling pathway;apoptosis;appendage morphogenesis;auditory receptor cell development;axis elongation;axon ensheathment;axon ensheathment in central nervous system;axon guidance;axonogenesis;axonogenesis involved in innervation;B cell receptor signaling pathway;biological regulation;biomineral tissue development;biosynthetic process;blood coagulation;bone maturation;bone mineralization;bone morphogenesis;branch elongation involved in salivary gland morphogenesis;branch elongation of an epithelium;branching involved in embryonic placenta morphogenesis;branching involved in prostate gland morphogenesis;branching involved in salivary gland morphogenesis;branching morphogenesis of a nerve;bud elongation involved in lung branching;carbohydrate homeostasis;cardiac cell development;cardiac muscle cell development;cardiac muscle tissue morphogenesis;cardiac septum morphogenesis;catabolic process;cation transport;cell aging;cell communication;cell cycle checkpoint;cell cycle phase;cell cycle process;cell death;cell development;cell differentiation;cell division;cell fate commitment;cell maturation;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cell-cell signaling involved in cell fate commitment;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component disassembly;cellular component disassembly at cellular level;cellular component maintenance;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to hydrogen peroxide;cellular response to insulin stimulus;cellular response to organic substance;cellular response to oxidative stress;cellular response to peptide hormone stimulus;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;central nervous system myelination;central nervous system neuron development;centrosome cycle;centrosome organization;chemical homeostasis;chemotaxis;chondrocyte differentiation;chondrocyte proliferation;chordate embryonic development;chromosome condensation;chromosome organization;circadian rhythm;coagulation;cochlea development;columnar/cuboidal epithelial cell differentiation;coronal suture morphogenesis;cranial suture morphogenesis;craniofacial suture morphogenesis;death;defense response;defense response to bacterium;defense response to Gram-positive bacterium;developmental growth;developmental growth involved in morphogenesis;developmental induction;developmental maturation;developmental process;developmental process involved in reproduction;digestive tract morphogenesis;DNA conformation change;DNA damage checkpoint;DNA integrity checkpoint;DNA metabolic process;DNA packaging;DNA repair;DNA replication;embryo development;embryo development ending in birth or egg hatching;embryonic appendage morphogenesis;embryonic cranial skeleton morphogenesis;embryonic digestive tract morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;embryonic pattern specification;embryonic skeletal system morphogenesis;endochondral bone growth;endochondral ossification;endodermal digestive tract morphogenesis;ensheathment of neurons;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epithelial cell differentiation;epithelial cell differentiation involved in prostate gland development;epithelial cell fate commitment;epithelial cell proliferation;epithelial cell proliferation involved in salivary gland morphogenesis;epithelium development;establishment of localization;establishment of localization in cell;exocytosis;fibroblast growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway involved in hemopoiesis;fibroblast growth factor receptor signaling pathway involved in mammary gland specification;fibroblast growth factor receptor signaling pathway involved in negative regulation of apoptosis in bone marrow;fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development;fibroblast growth factor receptor signaling pathway involved in positive regulation of cell proliferation in bone marrow;forebrain neuroblast division;forebrain neuron development;forebrain ventricular zone progenitor cell division;G0 to G1 transition;G1 phase;G1 phase of mitotic cell cycle;G1/S transition of mitotic cell cycle;G2/M transition checkpoint;G2/M transition DNA damage checkpoint;G2/M transition of mitotic cell cycle;gamete generation;gland development;glandular epithelial cell differentiation;glucose homeostasis;growth;growth hormone secretion;hair cycle process;hair follicle morphogenesis;hemostasis;homeostatic process;hormone secretion;hormone transport;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;in utero embryonic development;innate immune response;innate immune response-activating signal transduction;inner ear morphogenesis;inner ear receptor cell development;inner ear receptor cell differentiation;inositol lipid-mediated signaling;insulin receptor signaling pathway;integrin-mediated signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;ion homeostasis;ion transport;JAK-STAT cascade;karyogamy;lacrimal gland development;lateral sprouting from an epithelium;lens fiber cell development;lens morphogenesis in camera-type eye;limb bud formation;limb morphogenesis;localization;locomotion;lung alveolus development;lung epithelium development;lung lobe morphogenesis;lung-associated mesenchyme development;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;macromolecule modification;male gamete generation;mammary gland bud formation;MAPKKK cascade;mechanoreceptor differentiation;membrane disassembly;membrane organization;membranous septum morphogenesis;mesenchymal cell differentiation;mesenchymal cell differentiation involved in lung development;mesenchymal cell proliferation;mesenchymal cell proliferation involved in lung development;mesenchymal-

epithelial cell signaling;mesenchyme development;mesoderm development;metabolic process;metal ion transport;microtubule organizing center organization;midbrain development;middle ear morphogenesis;mitosis;mitotic cell cycle checkpoint;mitotic cell cycle G2/M transition checkpoint;mitotic cell cycle G2/M transition DNA damage checkpoint;mitotic nuclear envelope disassembly;mitotic prometaphase;mitotic prophase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;molting cycle;molting cycle process;monovalent inorganic cation transport;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;multicellular organism growth;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell development;muscle tissue morphogenesis;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;myelination;negative regulation of apoptosis;negative regulation of astrocyte differentiation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental growth;negative regulation of developmental process;negative regulation of epithelial cell proliferation;negative regulation of gene expression;negative regulation of glial cell differentiation;negative regulation of gliogenesis;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitosis;negative regulation of neurogenesis;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear division;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of programmed cell death;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of smoothened signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nerve growth factor receptor signaling pathway;neuroblast division;neurological system process;neuromuscular junction development;neuron development;neuron differentiation;neuron migration;neuron projection development;neuron projection morphogenesis;nitrogen compound metabolic process;nuclear division;nuclear envelope disassembly;nuclear envelope organization;nucleic acid metabolic process;nucleobase-containing compound metabolic process;odontogenesis;organ development;organ growth;organ induction;organ morphogenesis;organ regeneration;organelle fission;organelle fusion;organelle organization;ossification;otic vesicle formation;outer ear morphogenesis;outflow tract septum morphogenesis;paraxial mesoderm development;pattern recognition receptor signaling pathway;pattern specification process;peptide hormone secretion;peptide secretion;peptide transport;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate ion homeostasis;phosphate-containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;photoreceptor cell maintenance;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cardiac muscle cell proliferation;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell cycle;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cell size;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokine secretion;positive regulation of defense response;positive regulation of developmental process;positive regulation of DNA biosynthetic process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of DNA-dependent DNA replication initiation;positive regulation of endothelial cell proliferation;positive regulation of epithelial cell proliferation;positive regulation of epithelial cell proliferation involved in lung morphogenesis;positive regulation of ERK1 and ERK2 cascade;positive regulation of exocytosis;positive regulation of fibroblast proliferation;positive regulation of gene expression;positive regulation of hormone secretion;positive regulation of hydrolase activity;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of insulin secretion;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JAK-STAT cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of leukocyte degranulation;positive regulation of ligase activity;positive regulation of lipase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway;positive regulation of mast cell activation;positive regulation of mast cell activation involved in immune response;positive regulation of mast cell degranulation;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of metalloenzyme activity;positive regulation of mitotic cell cycle;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of neuron differentiation;positive regulation of neuron projection development;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein import into nucleus, translocation;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein secretion;positive regulation of protein serine/threonine kinase activity;positive regulation of protein transport;positive regulation of protein ubiquitination;positive regulation of proteolysis;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of secretion;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of translation;positive regulation of transport;positive regulation of tyrosine phosphorylation of STAT protein;positive regulation of tyrosine phosphorylation of Stat1 protein;positive regulation of tyrosine phosphorylation of Stat3 protein;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;positive regulation of Wnt receptor signaling pathway;post-embryonic development;posttranscriptional regulation of gene expression;potassium ion transport;primary metabolic process;programmed cell death;pronuclear fusion;prophase;prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis;prostate epithelial cord elongation;prostate gland epithelium morphogenesis;prostate gland growth;prostate gland morphogenetic growth;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein autophosphorylation;protein complex assembly;protein complex subunit organization;protein localization;protein localization to chromosome;protein localization to kinetochore;protein localization to organelle;protein metabolic process;protein modification process;protein phosphorylation;proteolysis;proteolysis involved in cellular protein catabolic process;pyramidal neuron development;Ras protein signal transduction;re-entry into mitotic cell cycle;regeneration;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of apoptosis;regulation of astrocyte differentiation;regulation of bile acid biosynthetic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of branching involved in prostate gland morphogenesis;regulation of branching involved in salivary gland morphogenesis;regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac muscle cell proliferation;regulation of cardiac muscle tissue development;regulation of cardiac muscle tissue growth;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell division;regulation of cell fate commitment;regulation of cell fate specification;regulation of cell migration;regulation of cell morphogenesis;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cell shape;regulation of cell size;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cholesterol homeostasis;regulation of cytokine production;regulation of cytokine secretion;regulation of defense response;regulation of developmental growth;regulation of developmental process;regulation of DNA biosynthetic process;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of DNA-dependent DNA replication initiation;regulation of embryonic development;regulation of endocytosis;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of epithelial cell proliferation involved in lung morphogenesis;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of exocytosis;regulation of extracellular matrix disassembly;regulation of fibroblast growth factor receptor signaling pathway;regulation of fibroblast proliferation;regulation of G2/M transition of mitotic cell cycle;regulation of gastrulation;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of growth;regulation of heart growth;regulation of homeostatic process;regulation of hormone levels;regulation of hormone secretion;regulation of hydrolase activity;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of insulin secretion;regulation of insulin secretion involved in cellular response to glucose stimulus;regulation of interphase of mitotic cell cycle;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of lateral mesodermal cell fate specification;regulation of leukocyte activation;regulation of leukocyte degranulation;regulation of leukocyte mediated immunity;regulation of ligase activity;regulation of lipase activity;regulation of lipid biosynthetic process;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of mast cell activation;regulation of mast cell activation involved in immune response;regulation of mast cell degranulation;regulation of mesenchymal cell proliferation;regulation of mesoderm development;regulation of mesodermal cell fate specification;regulation of metabolic process;regulation of metalloenzyme activity;regulation of mitosis;regulation of mitotic cell cycle;regulation of molecular function;regulation of morphogenesis of a branching structure;regulation of multicellular organism growth;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of myeloid leukocyte mediated immunity;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organ formation;regulation of organ growth;regulation of organ morphogenesis;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoblast proliferation;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of peptidyl-tyrosine phosphorylation;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphatidylinositol 3-kinase cascade;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein secretion;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of protein ubiquitination;regulation of proteolysis;regulation of reproductive process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of Schwann cell differentiation;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of smooth muscle cell differentiation;regulation of smoothened signaling pathway;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of striated muscle tissue development;regulation of transcription from RNA polymerase II promoter;regulation of transcription involved in G1/S phase of mitotic cell cycle;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of transmembrane transport;regulation of transport;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat1 protein;regulation of tyrosine phosphorylation of Stat3 protein;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;regulation of vesicle-mediated transport;regulation of Wnt receptor signaling pathway;reproductive process;response to activity;response to amine stimulus;response to axon injury;response to bacterium;response to biotic stimulus;response to cadmium ion;response to chemical stimulus;response to copper ion;response to DNA damage stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to hydrogen peroxide;response to hyperoxia;response to inorganic substance;response to insulin stimulus;response to lead ion;response to metal ion;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to other organism;response to oxidative stress;response to oxygen levels;response to peptide hormone stimulus;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;response to toxin;response to virus;response to wounding;rhythmic process;RNA biosynthetic process;RNA metabolic process;S phase;S phase of mitotic cell cycle;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal release;signal transduction;signaling;skeletal system morphogenesis;small GTPase mediated signal transduction;somatic stem cell division;somatic stem cell maintenance;spermatogenesis;squamous basal epithelial stem cell differentiation involved in prostate gland acinus development;stem cell division;stem cell maintenance;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;substantia nigra development;synapse organization;synaptic vesicle transport;system process;taxis;tissue development;tissue morphogenesis;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;transport;TRIF-dependent toll-like receptor signaling pathway;trivalent inorganic anion homeostasis;tube development;ubiquitin-dependent protein catabolic process;ureteric bud development;ventricular cardiac muscle cell development;ventricular cardiac muscle tissue morphogenesis;ventricular zone neuroblast division;vesicle-mediated transport;Wnt receptor signaling pathway" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate binding;catalytic activity;cation binding;cyclin-dependent protein kinase activity;enzyme binding;Fc-gamma receptor I complex binding;fibroblast growth factor binding;fibroblast growth factor-activated receptor activity;glycosaminoglycan binding;growth factor binding;heparin binding;histone kinase activity;immunoglobulin receptor binding;ion binding;kinase activity;kinase binding;magnesium ion binding;metal ion binding;molecular transducer activity;non-membrane spanning protein tyrosine kinase activity;nucleotide binding;pattern binding;phosphoprotein binding;phosphotransferase activity, alcohol group as acceptor;phosphotyrosine binding;polysaccharide binding;protein binding;protein binding transcription factor activity;protein kinase activity;protein kinase binding;protein phosphorylated amino acid binding;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;receptor binding;ribonucleotide binding;RNA polymerase II carboxy-terminal domain kinase activity;signal transducer activity;signaling receptor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity""actin cytoskeleton;cell cortex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell surface;cell-cell junction;centrosome;chromatin;chromosomal part;chromosome;chromosome, telomeric region;cilium;condensed chromosome;cyclin-dependent protein kinase holoenzyme complex;cytoplasm;cytoplasmic cyclin-dependent protein kinase holoenzyme complex;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;cytosol;endoplasmic reticulum;endosome;excitatory synapse;extracellular region;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus;integral to membrane;integral to plasma membrane;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;leading edge membrane;lysosome;lytic vacuole;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microtubule;microtubule organizing center;midbody;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial part;mitochondrion;mitotic spindle;neuron projection;non-membrane-bounded organelle;nonmotile primary cilium;nuclear membrane;nuclear part;nucleolus;nucleoplasm;nucleoplasm part;nucleus;occluding junction;organelle;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part;perinuclear region of cytoplasm;photoreceptor inner segment;photoreceptor outer segment;plasma membrane;plasma membrane part;primary cilium;protein complex;ruffle membrane;sex chromosome;spindle;spindle microtubule;synapse;tight junction;transcription factor complex;transport vesicle;vacuole;vesicle;X chromosome;Y chromosome" Adherens junction;Bladder cancer;Cell cycle;Chemokine signaling pathway;Chronic myeloid leukemia;Endocytosis;Gap junction;Glioma;MAPK signaling pathway;Measles;Melanoma;Non-small cell lung cancer;Oocyte meiosis;p53 signaling pathway;Pancreatic cancer;Pathways in cancer;Progesterone-mediated oocyte maturation;Prostate cancer;Regulation of actin cytoskeleton;Small cell lung cancer;T cell receptor signaling pathway;Tight junction 2.81E-147 99 11 9 40.7

Q8NB90;Q8NB90-2;Q8NB90-3;O14544 Spermatogenesis-associated protein 5 SPATA5 >sp|Q8NB90|SPAT5_HUMAN Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5 PE=1 SV=3;>sp|Q8NB90-2|SPAT5_HUMAN Isoform 2 of Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SPATA5;>sp|Q8NB90-3|SPAT5_HUMAN Isoform 3 of Spermatogenesis-assoc 0.13 0.20 0.16 0.13 -0.22 -0.15 -0.18 0.05 + 1.688346946 0.279950553 biological regulation;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;defense response;developmental process;gamete generation;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cell activation;negative regulation of cell communication;negative regulation of cellular process;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of lymphocyte activation;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of T cell activation;primary metabolic process;proteasomal protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cell activation;regulation of cell communication;regulation of cellular process;regulation of growth;regulation of immune system process;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell activation;reproductive process;response to stimulus;response to stress;signal transduction;spermatogenesis "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;immunological synapse;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane part;membrane-bounded organelle;mitochondrion;organelle;plasma membrane part Ribosome biogenesis in eukaryotes 4.45E-40 4 11 9 16.3

P07858;E9PR54;E9PJ67;E9PCB3;E9PKQ7;E9PNL5;E9PHZ5;E9PLY3;E9PSG5;E9PQM1;R4GMQ5;E9PS78 Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain CTSB >sp|P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3 -0.97 -0.37 -1.42 -0.38 0.49 0.98 1.29 2.09 + 1.749178258 -1.993415907 activation of immune response;activation of innate immune response;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to thyroid hormone stimulus;collagen catabolic process;collagen metabolic process;defense response;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;pattern recognition receptor signaling pathway;positive regulation of biological process;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of response to stimulus;primary metabolic process;protein metabolic process;proteolysis;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular process;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of metabolic process;regulation of molecular function;regulation of programmed cell death;regulation of response to stimulus;regulation of response to stress;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;response to stress;response to thyroid hormone stimulus;signal transduction;toll-like receptor signaling pathway "catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lysosome;lytic vacuole;melanosome;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;perinuclear region of cytoplasm;pigment granule;vacuole;vesicle Antigen processing and presentation;Lysosome 1.80E-62 12 10 10 33.9

Q8IWE2;Q6MZV4 Protein NOXP20 FAM114A1;DKFZp686F20250 >sp|Q8IWE2|NXP20_HUMAN Protein NOXP20 OS=Homo sapiens GN=FAM114A1 PE=1 SV=2;>tr|Q6MZV4|Q6MZV4_HUMAN Protein NOXP20 OS=Homo sapiens GN=DKFZp686F20250 PE=2 SV=1 -0.38 -0.30 -0.17 -0.10 1.29 0.95 0.62 0.66 + 2.167742044 -1.115191795 cell part;cytoplasm;intracellular part 4.50E-72 2 10 10 25.8

P50213;H0YL72;H0YMU3;H0YLI6;P50213-2;B7Z9J8;H0YKD0;H0YM64 "Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial" IDH3A ">sp|P50213|IDH3A_HUMAN Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1;>tr|H0YL72|H0YL72_HUMAN Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=2 SV=1;>tr|H0YMU3|H0YMU3_H"0.14 -0.02 0.06 0.02 -0.19 -0.09 -0.08 -0.10 + 1.45083901 0.16340522 acetyl-CoA catabolic process;acetyl-CoA metabolic process;carbohydrate metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;tricarboxylic acid cycle "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;ion binding;isocitrate dehydrogenase (NAD+) activity;isocitrate dehydrogenase activity;magnesium ion binding;metal ion binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Citrate cycle (TCA cycle) 1.88E-57 8 10 10 30.9

B4DLR8;P15559-3;P15559-2;P15559;H3BNV2;H3BRK3 NAD(P)H dehydrogenase [quinone] 1 NQO1 >tr|B4DLR8|B4DLR8_HUMAN NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=2 SV=1;>sp|P15559-3|NQO1_HUMAN Isoform 3 of NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1;>sp|P15559-2|NQO1_HUMAN Isoform 2 of NAD(P)H dehydrogenase [quinone] 0.38 -0.03 -1.45 -1.05 2.05 1.35 1.06 0.50 + 1.346366814 -1.781812842 "aging;biological regulation;biosynthetic process;cell communication;cell-cell signaling;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;developmental process;metabolic process;negative regulation of catalytic activity;negative regulation of molecular function;nitric oxide biosynthetic process;nitric oxide metabolic process;nitrogen compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of neuron apoptosis;positive regulation of programmed cell death;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;response to chemical stimulus;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to steroid hormone stimulus;response to stimulus;response to stress;response to toxin;signaling;small molecule metabolic process;superoxide metabolic process;synaptic transmission;synaptic transmission, cholinergic;xenobiotic metabolic process" "antioxidant activity;catalytic activity;cytochrome-b5 reductase activity;NAD(P)H dehydrogenase (quinone) activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;oxidoreductase activity, acting on superoxide radicals as acceptor;superoxide dismutase activity" cell body;cell part;cytoplasmic part;cytosol;intracellular part;neuronal cell body 5.66E-60 6 10 10 43.1

Q15738;C9JDR0 "Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating" NSDHL ">sp|Q15738|NSDHL_HUMAN Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2;>tr|C9JDR0|C9JDR0_HUMAN Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating (Fragment) OS=Homo sapiens GN=NSDHL PE=2 SV=1" 0.04 0.05 -0.06 -0.09 0.21 0.30 0.33 0.13 + 1.684429134 -0.257062351 alcohol metabolic process;anatomical structure development;biological regulation;biosynthetic process;blood vessel development;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;embryonic organ development;epidermis development;hair cycle process;hair follicle development;labyrinthine layer blood vessel development;lipid biosynthetic process;lipid metabolic process;metabolic process;molting cycle;molting cycle process;multicellular organismal process;organ development;placenta blood vessel development;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small molecule metabolic process;smoothened signaling pathway;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;tissue development "3-beta-hydroxy-delta5-steroid dehydrogenase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) activity" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lipid particle;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Steroid biosynthesis 1.14E-100 2 10 10 35.4

Q9Y263;E5RIM3;H0YBW4;H0YC16 Phospholipase A-2-activating protein PLAA >sp|Q9Y263|PLAP_HUMAN Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2;>tr|E5RIM3|E5RIM3_HUMAN Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=2 SV=1;>tr|H0YBW4|H0YBW4_HUMAN Phospholipase A-2-activating protein (Fragme 0.34 0.01 -0.13 -0.18 0.43 0.41 0.41 0.62 + 1.422237113 -0.456068239 biological regulation;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;defense response;inflammatory response;lipid metabolic process;metabolic process;organophosphate metabolic process;phospholipid metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;response to wounding;signal transduction enzyme activator activity;enzyme regulator activity;lipase activator activity;phospholipase A2 activator activity;phospholipase activator activity extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;membrane-bounded organelle;membrane-bounded vesicle;organelle;vesicle Protein processing in endoplasmic reticulum 4.17E-72 4 10 10 20.4

O15160;O15160-2;E7EQB9;D6RDJ3;H0Y723 DNA-directed RNA polymerases I and III subunit RPAC1 POLR1C >sp|O15160|RPAC1_HUMAN DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens GN=POLR1C PE=1 SV=1;>sp|O15160-2|RPAC1_HUMAN Isoform 2 of DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens GN=POLR1C;>tr|E7EQB9|E7EQB9_HUMAN DNA 0.14 0.21 0.14 0.14 -0.42 -0.38 -0.27 -0.21 + 2.554955661 0.476926811 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;termination of RNA polymerase I transcription;termination of RNA polymerase III transcription;transcription elongation from RNA polymerase I promoter;transcription elongation from RNA polymerase III promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase I promoter;transcription initiation, DNA-dependent;transcription termination, DNA-dependent;transcription, DNA-dependent" "binding;catalytic activity;DNA binding;DNA-directed RNA polymerase activity;nucleic acid binding;nucleotidyltransferase activity;RNA polymerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;DNA-directed RNA polymerase complex;DNA-directed RNA polymerase I complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear DNA-directed RNA polymerase complex;nuclear part;nucleolar part;nucleoplasm;organelle part;protein complex;RNA polymerase complex Cytosolic DNA-sensing pathway;Purine metabolism;Pyrimidine metabolism;RNA polymerase 1.01E-65 5 10 10 36.7

E1P5S2;Q14498-3;Q14498-2;Q14498;G3XAC6;H0Y4X3;Q5QP23;G3V546;G3V5Z6;Q5QP22;Q5QP21;H0YJJ3;G3XAP0;Q86U06-3;Q86U06-4;Q86U06-5;Q86U06-2;Q86U06 RNA-binding protein 39 RBM39 >tr|E1P5S2|E1P5S2_HUMAN RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=2 SV=1;>sp|Q14498-3|RBM39_HUMAN Isoform 3 of RNA-binding protein 39 OS=Homo sapiens GN=RBM39;>sp|Q14498-

2|RBM39_HUMAN Isoform 2 of RNA-binding protein 39 OS=Homo sapiens GN=RBM39;>s 0.14 0.11 0.12 0.16 -0.27 -0.52 -0.84 -0.61 + 2.00121311 0.695330925 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;transcription, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;centrosome;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part 3.83E-91 18 10 10 35.9

Q07020;J3QQ67;F8VWC5;G3V203;H0YHA7;F8VYV2;F8VUA6;F8VXR6 60S ribosomal protein L18 RPL18 >sp|Q07020|RL18_HUMAN 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2;>tr|J3QQ67|J3QQ67_HUMAN 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=3 SV=1;>tr|F8VWC5|F8VWC5_HUMAN 60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE -0.07 0.02 0.16 0.14 -0.24 -0.57 -0.33 -0.36 + 1.811623075 0.436680604 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.05E-140 8 10 10 49.5

C9JNW5;P83731;C9JXB8 60S ribosomal protein L24 RPL24 >tr|C9JNW5|C9JNW5_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1;>sp|P83731|RL24_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1;>tr|C9JXB8|C9JXB8_HUMAN 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=2 SV=1 -0.22 0.03 0.11 0.06 -0.12 -0.49 -0.43 -0.38 + 1.295882301 0.349232246 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 2.52E-42 3 10 10 52.7

M0QZC5;P62280;M0R1H6 40S ribosomal protein S11 RPS11 >tr|M0QZC5|M0QZC5_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=4 SV=1;>sp|P62280|RS11_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3;>tr|M0R1H6|M0R1H6_HUMAN 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=4 SV=1-0.08 -0.03 0.14 -0.06 -0.84 -0.97 -0.23 -0.38 + 1.313375584 0.594066154 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 1.19E-41 3 10 10 55.1

P62241;Q5JR95 40S ribosomal protein S8 RPS8 >sp|P62241|RS8_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2;>tr|Q5JR95|Q5JR95_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=2 SV=1 -0.07 0.08 -0.02 -0.02 -0.08 -0.39 -0.36 -0.21 + 1.301914472 0.248839898 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maturation of SSU-rRNA;maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 1.76E-202 2 10 10 52.4

Q15404;Q15404-2 Ras suppressor protein 1 RSU1 >sp|Q15404|RSU1_HUMAN Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 PE=1 SV=3;>sp|Q15404-2|RSU1_HUMAN Isoform 2 of Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 -0.20 -0.04 -0.35 -0.07 0.87 0.67 0.27 0.17 + 1.467624576 -0.660637023 biological regulation;cell junction assembly;cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;intracellular signal transduction;Ras protein signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction cell part;cytoplasmic part;cytosol;intracellular part 1.21E-55 2 10 10 41.5

B7ZKM0;Q15020;F8VV04;Q15020-2;Q15020-3;H0YHU8;F8W667 Squamous cell carcinoma antigen recognized by T-cells 3 SART3 >tr|B7ZKM0|B7ZKM0_HUMAN SART3 protein OS=Homo sapiens GN=SART3 PE=2 SV=1;>sp|Q15020|SART3_HUMAN Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens GN=SART3 PE=1 SV=1;>tr|F8VV04|F8VV04_HUMAN Squamous cell carcinoma antigen recognized by -0.06 0.10 0.16 0.14 -0.12 -0.54 -0.83 -0.85 + 1.48259734 0.669947641 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part 1.60E-60 7 10 10 16.1

O95793-2;O95793;Q5JW30;O95793-3;Q5JW28;F6UDC6 Double-stranded RNA-binding protein Staufen homolog 1 STAU1 >sp|O95793-2|STAU1_HUMAN Isoform Short of Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1;>sp|O95793|STAU1_HUMAN Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens GN=STAU1 PE=1 SV=2;>tr|Q5JW30|Q5JW30_HUMAN 0.07 0.10 -0.04 0.05 -0.17 -0.29 -0.18 -0.10 + 1.7037825 0.229992146 cellular localization;cellular macromolecule localization;cellular process;intracellular mRNA localization;localization;macromolecule localization;RNA localizationbinding;double-stranded RNA binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule associated complex;non-membrane-bounded organelle;organelle;organelle part;protein complex;ribonucleoprotein complex;RNA granule;rough endoplasmic reticulum;stress granule 7.30E-89 6 10 10 26.6

Q9UH65;E7EMB1;E9PJK8;E9PJM7 Switch-associated protein 70 SWAP70 >sp|Q9UH65|SWP70_HUMAN Switch-associated protein 70 OS=Homo sapiens GN=SWAP70 PE=1 SV=1;>tr|E7EMB1|E7EMB1_HUMAN Switch-associated protein 70 OS=Homo sapiens GN=SWAP70 PE=2 SV=1 0.08 0.20 0.03 -0.12 0.25 0.29 0.43 0.37 + 1.451528221 -0.286444411 B cell activation;B cell activation involved in immune response;cell activation;cell activation involved in immune response;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA metabolic process;DNA recombination;immune effector process;immune system process;isotype switching;leukocyte activation;leukocyte activation involved in immune response;lymphocyte activation;lymphocyte activation involved in immune response;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;cation binding;DNA binding;ion binding;lipid binding;metal ion binding;nucleic acid binding;nucleotide binding;phospholipid binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 4.51E-29 4 10 10 17.3

P15121;E9PCX2;E9PEF9;C9JRZ8-2;C9JRZ8 Aldose reductase AKR1B1 >sp|P15121|ALDR_HUMAN Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3;>tr|E9PCX2|E9PCX2_HUMAN Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=2 SV=1;>tr|E9PEF9|E9PEF9_HUMAN Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=2 SV=1 -0.23 -0.24 -0.52 -0.14 2.09 1.59 0.71 0.50 + 1.534777076 -1.50475318 biological regulation;biosynthetic process;C21-steroid hormone biosynthetic process;C21-steroid hormone metabolic process;carbohydrate metabolic process;cellular biosynthetic process;cellular hormone metabolic process;cellular metabolic process;cellular process;hormone biosynthetic process;hormone metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;regulation of biological quality;regulation of hormone levels;response to stimulus;response to stress;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process "alcohol dehydrogenase (NADP+) activity;alditol:NADP+ 1-oxidoreductase activity;aldo-keto reductase (NADP) activity;catalytic activity;electron carrier activity;glyceraldehyde oxidoreductase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasm;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Fructose and mannose metabolism;Galactose metabolism;Glycerolipid metabolism;Pentose and glucuronate interconversions;Pyruvate metabolism 9.25E-63 5 11 10 41.1

P30050;P30050-2;Q86SU0-3;Q86SU0-2;Q86SU0 60S ribosomal protein L12 RPL12 >sp|P30050|RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1;>sp|P30050-2|RL12_HUMAN Isoform 2 of 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 0.02 0.00 -0.11 0.06 -0.20 -0.49 -0.17 -0.29 + 1.414611262 0.279088538 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosol;cytosolic large ribosomal subunit;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;large ribosomal subunit;macromolecular complex;membrane;membrane part;organelle part;plasma membrane;ribonucleoprotein complex Ribosome 4.12E-156 5 11 10 71.5

O94804;H0YB71 Serine/threonine-protein kinase 10 STK10 >sp|O94804|STK10_HUMAN Serine/threonine-protein kinase 10 OS=Homo sapiens GN=STK10 PE=1 SV=1 0.00 -0.08 -0.43 -0.32 0.45 0.32 0.63 0.40 + 1.90435531 -0.653604009 biological adhesion;biological regulation;cell adhesion;cell cycle;cell-cell adhesion;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;homotypic cell-cell adhesion;leukocyte aggregation;leukocyte cell-cell adhesion;lymphocyte aggregation;macromolecule metabolic process;macromolecule modification;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of immune system process;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of lymphocyte migration "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;identical protein binding;kinase activity;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;polo kinase kinase activity;protein binding;protein dimerization activity;protein homodimerization activity;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;membrane;plasma membrane 1.26E-68 2 11 10 15.7

Q86W92-4;Q86W92-2;Q86W92;Q86W92-3;H0YFE4;F5GZP6;E9PP16;Q8ND30-3;Q8ND30-2;F5H6Q7;F5H0E0;F5H495;Q86W92-5 Liprin-beta-1 PPFIBP1 >sp|Q86W92-4|LIPB1_HUMAN Isoform 4 of Liprin-beta-1 OS=Homo sapiens GN=PPFIBP1;>sp|Q86W92-2|LIPB1_HUMAN Isoform 2 of Liprin-beta-1 OS=Homo sapiens GN=PPFIBP1;>sp|Q86W92|LIPB1_HUMAN Liprin-beta-1 OS=Homo sapiens GN=PPFIBP1 PE=1 SV=2;>sp|Q86W92-3|LIPB1_HUMAN 0.15 0.02 -0.17 -0.13 0.47 0.40 0.31 0.12 + 1.368851804 -0.357672641 biological adhesion;cell adhesion;cellular process binding;catalytic activity;DNA binding;integrase activity;nucleic acid binding cell part;membrane;plasma membrane 3.65E-37 13 12 10 16.4

P17301;D6RG08 Integrin alpha-2 ITGA2 >sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1 0.35 -0.18 0.37 0.01 -0.87 -0.89 -0.37 -0.27 + 1.389794245 0.73264574 anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular process;cellular response to stimulus;chemotaxis;coagulation;developmental process;hemostasis;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;locomotion;multicellular organismal process;multi-organism process;organ morphogenesis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis;viral reproductive process;virus-host interaction binding;cation binding;collagen binding;ion binding;metal ion binding;protein binding basal part of cell;cell part;cell surface;external side of plasma membrane;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Small cell lung cancer0 2 28 10 32.1

Q9NR19;Q9NR19-2;E7EWU3;F8WCJ4;C9IYL0;B4DEH9;C9JY31;F8WDJ9;C9JXD9;C9J7L5 "Acetyl-coenzyme A synthetase, cytoplasmic" ACSS2 ">sp|Q9NR19|ACSA_HUMAN Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens GN=ACSS2 PE=1 SV=1;>sp|Q9NR19-2|ACSA_HUMAN Isoform 2 of Acetyl-coenzyme A synthetase, cytoplasmic OS=Homo sapiens GN=ACSS2;>tr|E7EWU3|E7EWU3_HUMAN Acetyl-coenzyme A synthetase," -0.14 -0.18 0.29 0.18 -1.03 -1.13 -0.14 -0.76 + 1.308240605 0.803503551 acetate biosynthetic process;acetate metabolic process;acetyl-CoA biosynthetic process;acetyl-CoA biosynthetic process from acetate;acetyl-CoA metabolic process;alcohol metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;ethanol metabolic process;ethanol oxidation;lipid biosynthetic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary alcohol metabolic process;primary metabolic process;propionate biosynthetic process;propionate metabolic process;small molecule biosynthetic process;small molecule metabolic process;xenobiotic metabolic process "acetate-CoA ligase activity;acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;AMP binding;ATP binding;binding;catalytic activity;CoA-ligase activity;ligase activity;ligase activity, forming carbon-sulfur bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Carbon fixation pathways in prokaryotes;Glycolysis / Gluconeogenesis;Methane metabolism;Propanoate metabolism;Pyruvate metabolism1.06E-47 10 11 11 19.4

P11766;H0YAG8;D6RFE4;D6RAY0;D6R9G2 Alcohol dehydrogenase class-3 ADH5 >sp|P11766|ADHX_HUMAN Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4 -0.25 -0.58 -0.44 -0.38 0.32 0.02 0.99 0.21 + 1.436170722 -0.795872211 aging;alcohol catabolic process;alcohol metabolic process;aldehyde catabolic process;biological regulation;catabolic process;cellular aldehyde metabolic process;cellular catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;diterpenoid metabolic process;ethanol catabolic process;ethanol metabolic process;ethanol oxidation;formaldehyde catabolic process;formaldehyde metabolic process;isoprenoid metabolic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;oxidation-reduction process;peptidyl-amino acid modification;peptidyl-cysteine modification;peptidyl-cysteine S-nitrosylation;positive regulation of blood pressure;primary alcohol catabolic process;primary alcohol metabolic process;primary metabolic process;protein metabolic process;protein modification process;protein nitrosylation;regulation of biological quality;regulation of blood pressure;respiratory gaseous exchange;respiratory system process;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to nitrosative stress;response to organic substance;response to redox state;response to stimulus;response to stress;retinoid metabolic process;small molecule catabolic process;small molecule metabolic process;system process;terpenoid metabolic process "alcohol dehydrogenase (NAD) activity;binding;carboxylic acid binding;catalytic activity;cation binding;electron carrier activity;fatty acid binding;formaldehyde dehydrogenase activity;ion binding;lipid binding;metal ion binding;monocarboxylic acid binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;S-(hydroxymethyl)glutathione dehydrogenase activity;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle Chloroalkane and chloroalkene degradation;Drug metabolism - cytochrome P450;Fatty acid metabolism;Glycolysis / Gluconeogenesis;Metabolism of xenobiotics by cytochrome P450;Methane metabolism;Naphthalene degradation;Retinol metabolism;Tyrosine metabolism 9.12E-36 5 11 11 29.9

O15143;C9JBJ7;C9K057;C9J4Z7;C9JEY1;C9JQM8;C9JFG9;C9J6C8;C9JTT6;F8VXW2;C9JM51;F8WEB3 Actin-related protein 2/3 complex subunit 1B ARPC1B >sp|O15143|ARC1B_HUMAN Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3;>tr|C9JBJ7|C9JBJ7_HUMAN Actin-related protein 2/3 complex subunit 1B (Fragment) OS=Homo sapiens GN=ARPC1B PE=2 SV=1;>tr|C9K057|C9K057_HUMAN Actin-relate 0.06 0.10 -0.39 -0.28 0.69 0.63 0.55 0.53 + 1.975601476 -0.726381914 biological regulation;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular process;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization structural constituent of cytoskeleton;structural molecule activity Arp2/3 protein complex;cell part;cytoplasm;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis 3.97E-61 12 11 11 35.8

Q96AY3;K7ESG6;H0Y827;K7ELI6;Q9H6J3;C9JPC3;K7EM43;Q86V35 Peptidyl-prolyl cis-trans isomerase FKBP10 FKBP10 >sp|Q96AY3|FKB10_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1 -0.87 -0.85 -0.59 -0.06 3.19 2.96 0.49 0.77 + 1.348111491 -2.443260107 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-proline modification;primary metabolic process;protein folding;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization binding;calcium ion binding;catalytic activity;cation binding;cis-trans isomerase activity;drug binding;FK506 binding;ion binding;isomerase activity;macrolide binding;metal ion binding;peptidyl-prolyl cis-trans isomerase activity cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;Golgi apparatus;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;trans-Golgi network membrane 8.72E-50 8 11 11 20.8

Q13418;B7Z1I0;B7Z418;E9PM54;E9PNR4 Integrin-linked protein kinase ILK >sp|Q13418|ILK_HUMAN Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2;>tr|B7Z1I0|B7Z1I0_HUMAN Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=2 SV=1;>tr|B7Z418|B7Z418_HUMAN Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=2 0.17 -0.18 -0.28 -0.04 1.17 0.74 0.50 0.40 + 1.546912843 -0.784961485 "aging;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological adhesion;biological regulation;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;cell adhesion;cell aging;cell cycle arrest;cell cycle process;cell junction assembly;cell junction organization;cell morphogenesis;cell morphogenesis involved in differentiation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;developmental process;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;establishment or maintenance of epithelial cell apical/basal polarity;extracellular matrix organization;extracellular structure organization;fibril organization;integrin-mediated signaling pathway;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;myelin assembly;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cardiac muscle cell apoptosis;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of kinase activity;negative regulation of locomotion;negative regulation of molecular function;negative regulation of muscle cell apoptosis;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of smooth muscle cell migration;negative regulation of smooth muscle cell proliferation;negative regulation of striated muscle cell apoptosis;negative regulation of transferase activity;neuron projection morphogenesis;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of BMP signaling pathway;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of dendrite morphogenesis;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of gene expression;positive regulation of growth;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of muscle cell differentiation;positive regulation of myoblast differentiation;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of osteoblast differentiation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein serine/threonine kinase activity;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;positive regulation of Wnt receptor signaling pathway;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein metabolic process;protein modification process;protein oligomerization;protein phosphorylation;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of biosynthetic process;regulation of BMP signaling pathway;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac muscle cell apoptosis;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of gene expression;regulation of growth;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell apoptosis;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of myoblast differentiation;regulation of nervous system development;regulation of neurogenesis;regulation of neuron apoptosis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of smooth muscle cell migration;regulation of smooth muscle cell proliferation;regulation of striated muscle cell apoptosis;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of Wnt receptor signaling pathway;response to stimulus;signal transduction;substrate adhesion-dependent cell spreading;tissue morphogenesis;tube morphogenesis" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;axon part;cell body;cell junction;cell part;cell projection;cell projection part;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;costamere;cytoplasmic part;cytosol;dendritic shaft;focal adhesion;intracellular part;lamellipodium;macromolecular complex;membrane;neuronal cell body;organelle part;plasma membrane;protein complex;sarcomere;synapse part;terminal button Bacterial invasion of epithelial cells;Endometrial cancer;Focal adhesion;PPAR signaling pathway 1.28E-50 5 11 11 25.4

Q93052;C9JUT4;C9JXK9;C9JE51;C9J2R5;C9JIY7;C9JT42;C9J3U9;C9J1K7;C9J5C8;C9J4E3 Lipoma-preferred partner LPP ">sp|Q93052|LPP_HUMAN Lipoma-preferred partner OS=Homo sapiens GN=LPP PE=1 SV=1;>tr|C9JUT4|C9JUT4_HUMAN LIM domain containing preferred translocation partner in lipoma, isoform CRA_e OS=Homo sapiens GN=LPP PE=2 SV=1;>tr|C9JXK9|C9JXK9_HUMAN Lipoma-preferred" -0.53 -0.23 -0.07 -0.10 0.69 0.60 0.36 0.28 + 1.831147996 -0.718123812 biological adhesion;cell adhesion;cellular process binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;focal adhesion;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 8.64E-82 11 11 11 22.9

Q8TAT6;Q8TAT6-2;B4DG89;I3L4U9 Nuclear protein localization protein 4 homolog NPLOC4 >sp|Q8TAT6|NPL4_HUMAN Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4 PE=1 SV=3;>sp|Q8TAT6-2|NPL4_HUMAN Isoform 2 of Nuclear protein localization protein 4 homolog OS=Homo sapiens GN=NPLOC4;>tr|B4DG89|B4DG89_HUMAN Nuclear protein l 0.23 0.06 -0.16 -0.15 0.52 0.66 0.47 0.53 + 1.90838076 -0.550445813 catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular process;ER-associated protein catabolic process;Golgi organization;macromolecule catabolic process;macromolecule metabolic process;membrane fusion;membrane organization;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;organelle organization;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane part;membrane-bounded organelle;nuclear outer membrane-endoplasmic reticulum membrane network;nucleus;organelle Protein processing in endoplasmic reticulum 2.75E-104 4 11 11 24.2

P29728-2;P29728;F8W1C5;P29728-3 2-5-oligoadenylate synthase 2OAS2 >sp|P29728-2|OAS2_HUMAN Isoform p69 of 2-5-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2;>sp|P29728|OAS2_HUMAN 2-5-oligoadenylate synthase 2 OS=Homo sapiens GN=OAS2 PE=1 SV=30.13 0.10 0.06 0.14 -2.64 -1.78 -1.15 -0.66 + 1.527324812 1.667721296 biological regulation;biosynthetic process;carbohydrate metabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;glycosylation;heterocycle biosynthetic process;heterocycle metabolic process;immune effector process;immune response;immune system process;interferon-gamma-mediated signaling pathway;macromolecule catabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;protein acylation;protein glycosylation;protein lipidation;protein metabolic process;protein modification process;protein myristoylation;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of cellular process;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;RNA catabolic process;RNA metabolic process;signal transduction;small molecule metabolic process;type I interferon-mediated signaling pathway "2'-5'-oligoadenylate synthetase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;adenylyltransferase activity;ATP binding;binding;catalytic activity;cation binding;double-stranded RNA binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;nucleotidyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;nucleus;organelle;perinuclear region of cytoplasm Hepatitis C;Measles 2.51E-117 4 11 11 19.2

O15460-2;O15460;C9JCP0;C9JX45;A8MXE0;E7ERI1;E7ENX0;E7EPI9;C9JN43;C9JIG4 Prolyl 4-hydroxylase subunit alpha-2 P4HA2 >sp|O15460-2|P4HA2_HUMAN Isoform IIa of Prolyl 4-hydroxylase subunit alpha-2 OS=Homo sapiens GN=P4HA2;>sp|O15460|P4HA2_HUMAN Prolyl 4-hydroxylase subunit alpha-2 OS=Homo sapiens GN=P4HA2 PE=1 SV=1 -0.43 -0.42 -0.40 -0.08 1.14 1.10 0.38 0.88 + 2.06831817 -1.20796442 4-hydroxyproline metabolic process;amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;heterocycle metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-proline hydroxylation;peptidyl-proline hydroxylation to 4-hydroxy-L-proline;peptidyl-proline modification;primary metabolic process;protein metabolic process;protein modification process;small molecule metabolic process "binding;carboxylic acid binding;catalytic activity;cation binding;dioxygenase activity;electron carrier activity;ion binding;iron ion binding;L-ascorbic acid binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptidyl-proline 4-dioxygenase activity;peptidyl-proline dioxygenase activity;procollagen-proline 4-dioxygenase activity;procollagen-proline dioxygenase activity;transition metal ion binding;vitamin binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part Arginine and proline metabolism 3.18E-90 10 11 11 31

P62906 60S ribosomal protein L10a RPL10A >sp|P62906|RL10A_HUMAN 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 0.02 -0.02 0.38 -0.01 -0.25 -0.50 -0.29 -0.26 + 1.465824744 0.417333579 "anatomical structure morphogenesis;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome 2.25E-63 1 11 11 42.4

P61254;J3QRI7;J3QQQ9;J3QQV1;J3KTJ8;E5RIT6;J3QRC4;Q9UNX3;J3KSS0;E5RHH1;J3KS10;H7C1F9;Q2PPJ7-3;Q2PPJ7-2;Q2PPJ7 60S ribosomal protein L26;60S ribosomal protein L26-like 1 RPL26;KRBA2;RPL26L1 >sp|P61254|RL26_HUMAN 60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1;>tr|J3QRI7|J3QRI7_HUMAN 60S ribosomal protein L26 (Fragment) OS=Homo sapiens GN=RPL26 PE=4 SV=1;>tr|J3QQQ9|J3QQQ9_HUMAN KRAB-A domain-containing protein 2 OS=Homo sapiens GN 0.01 0.00 0.19 -0.07 -0.20 -0.47 -0.16 -0.30 + 1.425228467 0.314634081 "activation of Ral GTPase activity;activation of Ras GTPase activity;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular signal transduction;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;membrane organization;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Ral GTPase activity;positive regulation of Ras GTPase activity;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;Ral protein signal transduction;Ras protein signal transduction;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of exocyst localization;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of purine nucleotide catabolic process;regulation of Ral GTPase activity;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;reproductive process;response to stimulus;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;signal transduction;small GTPase mediated signal transduction;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleic acid binding;nucleoside-triphosphatase regulator activity;protein binding;protein dimerization activity;protein heterodimerization activity;Ral GTPase activator activity;Ras GTPase activator activity;RNA binding;small GTPase regulator activity;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosol;cytosolic large ribosomal subunit;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex Ribosome 3.85E-41 15 11 11 46.9

Q14669-4;Q14669;Q14669-2;Q14669-3;H7C2Y1 E3 ubiquitin-protein ligase TRIP12 TRIP12 >sp|Q14669-4|TRIPC_HUMAN Isoform 4 of E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12;>sp|Q14669|TRIPC_HUMAN E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1;>sp|Q14669-2|TRIPC_HUMAN Isoform 2 of E3 ubiquitin-protein liga 0.16 0.25 0.14 0.21 -0.23 -0.26 -0.32 0.03 + 1.730624967 0.383101042 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;DNA repair;embryo development;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA repair;negative regulation of double-strand break repair;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of double-strand break repair;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;response to DNA damage stimulus;response to stimulus;response to stress "acid-amino acid ligase activity;binding;catalytic activity;hormone receptor binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;nuclear hormone receptor binding;protein binding;receptor binding;small conjugating protein ligase activity;thyroid hormone receptor binding;transcription factor binding;ubiquitin-protein ligase activity" cell part;cytoplasm;intracellular;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part Ubiquitin mediated proteolysis 5.58E-87 5 11 11 8.3

O75691 Small subunit processome component 20 homolog UTP20 >sp|O75691|UTP20_HUMAN Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3 0.27 0.39 0.27 0.29 -0.51 -0.74 -0.78 -0.16 + 1.999038906 0.848888233 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cleavage involved in rRNA processing;endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage involved in rRNA processing;endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA);macromolecule metabolic process;metabolic process;ncRNA 5'-end processing;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;RNA 5'-end processing;RNA metabolic process;RNA processing;rRNA 5'-end processing" "90S preribosome;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;preribosome;preribosome, small subunit precursor;ribonucleoprotein complex;small-subunit processome" 4.12E-59 1 11 11 4.6

Q5JSH3-2;Q5JSH3;Q5JSH3-4;H7BY83;Q5JSH3-3 WD repeat-containing protein 44 WDR44 >sp|Q5JSH3-2|WDR44_HUMAN Isoform 2 of WD repeat-containing protein 44 OS=Homo sapiens GN=WDR44;>sp|Q5JSH3|WDR44_HUMAN WD repeat-containing protein 44 OS=Homo sapiens GN=WDR44 PE=1 SV=1;>sp|Q5JSH3-4|WDR44_HUMAN Isoform 4 of WD repeat-containing protein 44 O 0.02 0.01 -0.21 -0.13 0.09 0.28 0.52 0.34 + 1.457590985 -0.386826611 cell part;cytoplasmic part;cytosol;endosomal part;endosome membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm 5.99E-48 5 11 11 15.5

P52597 "Heterogeneous nuclear ribonucleoprotein F;Heterogeneous nuclear ribonucleoprotein F, N-terminally processed" HNRNPF >sp|P52597|HNRPF_HUMAN Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 0.06 0.09 -0.06 0.17 -0.33 -0.76 -0.42 -0.53 + 1.940065786 0.573356004 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding;single-stranded RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex 1.24E-181 1 13 11 42.2

P67809;H0Y449;C9J5V9;Q9Y2T7 Nuclease-sensitive element-binding protein 1 YBX1 >sp|P67809|YBOX1_HUMAN Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3;>tr|H0Y449|H0Y449_HUMAN Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens GN=YBX1 PE=4 SV=1 0.09 0.14 -0.10 0.13 -0.15 -0.38 -0.42 -0.57 + 1.628460268 0.44144666 "anatomical structure development;biological regulation;biosynthetic process;cell development;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;chordate embryonic development;CRD-mediated mRNA stabilization;developmental process;developmental process involved in reproduction;embryo development;embryo development ending in birth or egg hatching;gamete generation;germ cell development;in utero embryonic development;macromolecule biosynthetic process;macromolecule metabolic process;male gamete generation;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;multicellular organismal process;multicellular organismal reproductive process;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of muscle cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of RNA metabolic process;negative regulation of striated muscle cell differentiation;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oocyte development;positive regulation of biological process;positive regulation of cell division;positive regulation of cellular process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cell division;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mRNA stability;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of striated muscle cell differentiation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization;spermatid development;spermatogenesis;transcription from RNA polymerase II promoter;transcription, DNA-dependent;translational attenuation" binding;chromatin binding;DNA binding;double-stranded DNA binding;lipid binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;ribonucleoprotein binding;RNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;translation regulator activity cell part;CRD-mediated mRNA stability complex;cytoplasm;cytoplasmic part;extracellular region;histone pre-mRNA 3'end processing complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;polysome;protein complex;ribonucleoprotein complex;RNA granule;spliceosomal complex;stress granule;U12-type spliceosomal complex 0 4 15 11 53.1

P31150;G5E9U5 Rab GDP dissociation inhibitor alpha GDI1 >sp|P31150|GDIA_HUMAN Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 0.20 -0.06 -0.33 -0.04 0.63 0.78 0.48 0.35 + 1.639665277 -0.616795416 biological regulation;cellular process;cellular response to stimulus;establishment of localization;establishment of protein localization;intracellular signal transduction;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neurogenesis;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;protein transport;regulation of anatomical structure morphogenesis;regulation of axonogenesis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport enzyme activator activity;enzyme regulator activity;GDP-dissociation inhibitor activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Rab GDP-dissociation inhibitor activity;small GTPase regulator activity cell part;cell projection;cytoplasmic part;cytosol;intracellular part;macromolecular complex;midbody;neuron projection;protein complex 1.56E-254 2 20 11 51.2

P04792;C9J3N8 Heat shock protein beta-1 HSPB1 >sp|P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 -0.52 -0.03 -0.39 -0.03 0.30 1.00 0.88 0.55 + 1.708045996 -0.924835178 biological regulation;cell death;cell surface receptor linked signaling pathway;cellular component movement;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to vascular endothelial growth factor stimulus;death;enzyme linked receptor protein signaling pathway;gene expression;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;metabolic process;mRNA metabolic process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of angiogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of blood vessel endothelial cell migration;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine biosynthetic process;positive regulation of cytokine production;positive regulation of developmental process;positive regulation of endothelial cell migration;positive regulation of interleukin-1 beta production;positive regulation of interleukin-1 production;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of protein metabolic process;positive regulation of tumor necrosis factor biosynthetic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of blood vessel endothelial cell migration;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of developmental process;regulation of endothelial cell migration;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of interleukin-1 beta production;regulation of interleukin-1 production;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of translation;regulation of translational initiation;regulation of tumor necrosis factor biosynthetic process;regulation of tumor necrosis factor production;response to biotic stimulus;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;response to virus;RNA metabolic process;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;vascular endothelial growth factor receptor signaling pathway;vascular endothelial growth factor receptor signaling pathway involved in endothelial cell chemotaxis binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;kinase binding;kinase inhibitor activity;kinase regulator activity;protein binding;protein kinase binding;protein kinase C binding;protein kinase C inhibitor activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity;small conjugating protein binding;ubiquitin binding cell part;cell surface;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;proteasome complex;protein complex;spindle;Z disc Amoebiasis;MAPK signaling pathway;VEGF signaling pathway 8.91E-285 2 20 11 90.7

P67936;K7EMU5;K7EPV9;K7EPB9;Q2TAC2-2;Q2TAC2 Tropomyosin alpha-4 chain TPM4 >sp|P67936|TPM4_HUMAN Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 -0.01 -0.05 -0.10 0.06 0.46 0.44 0.23 0.33 + 2.069257557 -0.387707911 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;cellular component movement;cellular process;muscle filament sliding;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress binding;calcium ion binding;cation binding;ion binding;metal ion binding;structural constituent of muscle;structural molecule activity actin filament bundle;actomyosin;cell cortex part;cell part;contractile fiber part;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;muscle thin filament tropomyosin;non-membrane-bounded organelle;organelle;organelle part;podosome;protein complex;stress fiber Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM) 0 6 42 11 87.1

Q9BZZ5-2;G3V1C3;Q9BZZ5;Q9BZZ5-3;Q9BZZ5-5;B4E283;Q9BZZ5-1;H0YER7;E9PQK6 Apoptosis inhibitor 5 API5 >sp|Q9BZZ5-2|API5_HUMAN Isoform 2 of Apoptosis inhibitor 5 OS=Homo sapiens GN=API5;>tr|G3V1C3|G3V1C3_HUMAN Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=2 SV=1;>sp|Q9BZZ5|API5_HUMAN Apoptosis inhibitor 5 OS=Homo sapiens GN=API5 PE=1 SV=3;>sp|Q9BZZ5-3|AP 0.02 0.11 0.11 0.24 -0.18 -0.50 -0.61 -0.52 + 1.905398589 0.574111296 apoptosis;biological regulation;cell death;cellular process;death;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex 2.52E-148 9 12 12 29

Q6DD88;F5H6I7;C9JUU1;F5GWF8 Atlastin-3ATL3 >sp|Q6DD88|ATLA3_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1;>tr|F5H6I7|F5H6I7_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=2 SV=1;>tr|C9JUU1|C9JUU1_HUMAN Atlastin-3 OS=Homo sapiens GN=ATL3 PE=2 SV=1 0.01 0.00 -0.12 -0.08 0.69 0.92 0.21 0.46 + 1.532757118 -0.616549991 catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;endoplasmic reticulum organization;Golgi organization;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 1.13E-150 4 12 12 38.4

P04040 Catalase CAT >sp|P04040|CATA_HUMAN Catalase OS=Homo sapiens GN=CAT PE=1 SV=3 -0.17 -0.29 -0.24 0.00 0.47 0.59 0.65 0.22 + 1.984264388 -0.656819157 "acylglycerol metabolic process;aerobic respiration;alcohol metabolic process;anatomical structure development;biological regulation;catabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular respiration;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to hydrogen peroxide;cellular response to organic substance;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cholesterol metabolic process;development of secondary female sexual characteristics;development of secondary sexual characteristics;developmental process;developmental process involved in reproduction;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;glycerol ether metabolic process;glycerolipid metabolic process;hemoglobin metabolic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;menopause;menstrual cycle phase;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of programmed cell death;negative regulation of sequence-specific DNA binding transcription factor activity;neutral lipid metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organic ether metabolic process;ovulation cycle process;oxidation-reduction process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell division;positive regulation of cellular process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;purine base metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell division;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphatidylinositol 3-kinase cascade;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to hydrogen peroxide;response to hyperoxia;response to hypoxia;response to inorganic substance;response to light stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to oxygen levels;response to radiation;response to reactive oxygen species;response to stimulus;response to stress;response to UV;response to vitamin;response to vitamin E;rhythmic process;small molecule metabolic process;steroid metabolic process;sterol metabolic process;system development;triglyceride metabolic process;UV protection""aminoacylase activity;antioxidant activity;binding;catalase activity;catalytic activity;cation binding;coenzyme binding;cofactor binding;heme binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;identical protein binding;ion binding;iron ion binding;metal ion binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;protein binding;protein dimerization activity;protein homodimerization activity;tetrapyrrole binding;transition metal ion binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosome;lytic vacuole;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrial intermembrane space;mitochondrial part;organelle;organelle envelope lumen;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part;plasma membrane;vacuole Amyotrophic lateral sclerosis (ALS);Methane metabolism;Peroxisome;Tryptophan metabolism 3.78E-71 1 12 12 35.3

P26196 Probable ATP-dependent RNA helicase DDX6 DDX6 >sp|P26196|DDX6_HUMAN Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 0.05 0.10 -0.04 0.11 0.01 -0.26 -0.24 -0.28 + 1.304225581 0.248494163 "catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoplasmic mRNA processing body assembly;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;gene expression;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA catabolic process;RNA metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity" cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;RNA granule;RNAi effector complex;RNA-induced silencing complex;stress granule RNA degradation 2.42E-153 1 12 12 36.2

Q13409-3;B7ZA04;Q13409-2;Q13409;F8W8S0;Q13409-6;Q13409-5;E7EQL5;E7EQU2;E7ESD3;E7EMU4;E7EV09;E9PGG1;E7EUM4;E7ERR6;E7ERH4;E7ET01;E7ETL8;E7EU01 Cytoplasmic dynein 1 intermediate chain 2 DYNC1I2 >sp|Q13409-3|DC1I2_HUMAN Isoform 2C of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2;>tr|B7ZA04|B7ZA04_HUMAN Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1;>sp|Q13409-2|DC1I2_HUMAN Isoform 2B of Cytopl 0.04 0.02 -0.14 -0.10 0.11 0.20 0.24 0.19 + 1.662041392 -0.228424456 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cell cycle process;cellular component movement;cellular process;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;interaction with host;interspecies interaction between organisms;microtubule-based movement;microtubule-based process;multi-organism process;reproductive process;transport;viral reproductive process;virus-host interaction "catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;pyrophosphatase activity" cell part;centrosome;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle Phagosome;Vasopressin-regulated water reabsorption 1.66E-156 19 12 12 26.1

Q04446;E9PGM4 "1,4-alpha-glucan-branching enzyme" GBE1 ">sp|Q04446|GLGB_HUMAN 1,4-alpha-glucan-branching enzyme OS=Homo sapiens GN=GBE1 PE=1 SV=3;>tr|E9PGM4|E9PGM4_HUMAN 1,4-alpha-glucan-branching enzyme OS=Homo sapiens GN=GBE1 PE=2 SV=1" -0.02 -0.14 -0.27 -0.09 0.77 0.72 0.59 0.14 + 1.679466976 -0.684763392 alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan biosynthetic process;glucan metabolic process;glucose metabolic process;glycogen biosynthetic process;glycogen metabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;oxidation-reduction process;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process;small molecule metabolic process "1,4-alpha-glucan branching enzyme activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;ion binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;cytosol;intracellular part Starch and sucrose metabolism 1.54E-52 2 12 12 26.1

P08648;H0YIV7 Integrin alpha-5;Integrin alpha-5 heavy chain;Integrin alpha-5 light chain ITGA5 >sp|P08648|ITA5_HUMAN Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2 -0.10 -0.15 -0.46 0.03 1.51 1.27 0.27 0.58 + 1.404565477 -1.077846619 "anatomical structure formation involved in morphogenesis;angiogenesis;axon guidance;behavior;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell adhesion mediated by integrin;cell junction assembly;cell junction organization;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell adhesion mediated by integrin;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;chemotaxis;coagulation;cognition;developmental process;extracellular matrix organization;extracellular structure organization;hemostasis;heterophilic cell-cell adhesion;immune system process;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;learning or memory;leukocyte cell-cell adhesion;leukocyte migration;locomotion;memory;multicellular organismal process;multi-organism process;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;neurological system process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of vascular endothelial growth factor receptor signaling pathway;regulation of anoikis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell communication;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to growth factor stimulus;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of vascular endothelial growth factor receptor signaling pathway;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;system process;taxis;viral reproductive process;virus-host interaction;wound healing, spreading of cells;wound healing, spreading of epidermal cells"binding;cation binding;cytokine receptor binding;growth factor receptor binding;ion binding;metal ion binding;platelet-derived growth factor receptor binding;protein binding;receptor binding;vascular endothelial growth factor receptor 2 binding;vascular endothelial growth factor receptor binding alphav-beta3 integrin-vitronectin complex;cell part;cell projection;external side of plasma membrane;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex;ruffle;synapse Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Phagosome;Regulation of actin cytoskeleton;Shigellosis 1.70E-97 2 12 12 17.1

Q9UNF1;Q9UNF1-2;H7BXW3;Q5H909;Q5H907;G5E999;B1AKF1;G5E9N2;Q12816-2;Q9Y5V3;Q9Y5V3-2;F5GY27;B1AKE9;Q12816 Melanoma-associated antigen D2 MAGED2 >sp|Q9UNF1|MAGD2_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2;>sp|Q9UNF1-2|MAGD2_HUMAN Isoform 2 of Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2;>tr|H7BXW3|H7BXW3_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens -0.06 -0.05 -0.36 -0.08 0.60 0.56 0.44 0.43 + 2.316286886 -0.65009642 "biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular process;cellular response to stimulus;embryo implantation;enzyme linked receptor protein signaling pathway;homophilic cell adhesion;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of epithelial cell proliferation;negative regulation of gene expression;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nerve growth factor receptor signaling pathway;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of branching involved in ureteric bud morphogenesis;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of kinase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of branching involved in ureteric bud morphogenesis;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of epithelial cell proliferation;regulation of gene expression;regulation of growth;regulation of kidney development;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;reproductive process;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway"protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;cytoplasm;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane;plasma membrane part;protein complex Neurotrophin signaling pathway 2.56E-34 14 12 12 26.1

P08621;P08621-2;P08621-3;M0QYR1;P08621-4;M0QX04U1 small nuclear ribonucleoprotein 70 kDa SNRNP70 >sp|P08621|RU17_HUMAN U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2;>sp|P08621-2|RU17_HUMAN Isoform 2 of U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70;>sp|P08621-3|RU17_HUMAN Isoform 3 of U1 small nuc 0.15 0.16 0.09 0.18 -0.12 -0.56 -0.71 -0.73 + 1.735433642 0.674913103 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 2.93E-78 6 12 12 33.6

O43399;O43399-5;O43399-7;O43399-2;O43399-4;O43399-3;O43399-6 Tumor protein D54 TPD52L2 >sp|O43399|TPD54_HUMAN Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2;>sp|O43399-5|TPD54_HUMAN Isoform 5 of Tumor protein D54 OS=Homo sapiens GN=TPD52L2;>sp|O43399-7|TPD54_HUMAN Isoform 7 of Tumor protein D54 OS=Homo sapiens GN=TPD52L2;>sp|O43399-2 -0.22 -0.10 -0.05 0.00 0.36 0.37 0.42 0.23 + 2.214172006 -0.437318704 biological regulation;regulation of biological process;regulation of cell proliferation;regulation of cellular process binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity cell part;cytoplasmic part;intracellular part;perinuclear region of cytoplasm 6.95E-178 7 12 12 78.2

Q14694;Q14694-3;Q14694-2;J3KT19;H3BQP1;H3BNS8;H3BQC6;H3BNA1;H3BVF1 Ubiquitin carboxyl-terminal hydrolase 10 USP10 >sp|Q14694|UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2;>sp|Q14694-3|UBP10_HUMAN Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10;>sp|Q14694-2|UBP10_HUMAN Isoform 2 of Ubiquitin carbo 0.03 0.13 -0.02 -0.03 -0.17 -0.26 -0.24 -0.16 + 1.897833508 0.237240963 "autophagy;biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA damage response, signal transduction by p53 class mediator;DNA metabolic process;DNA repair;intracellular signal transduction;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of autophagy;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;ubiquitin-dependent protein catabolic process" "binding;catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion channel binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" cell part;cytoplasmic part;cytoskeleton;early endosome;endosome;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 7.96E-55 9 12 12 23.1

Q9HAV4;H0Y9I3;E2QRM3;H0Y3W3 Exportin-5 XPO5 >sp|Q9HAV4|XPO5_HUMAN Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1 0.24 0.05 0.07 -0.01 -0.31 -0.49 -0.16 -0.47 + 1.743868334 0.445852862 biological regulation;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;gene expression;gene silencing;gene silencing by RNA;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;nuclear export;nuclear transport;nucleocytoplasmic transport;protein export from nucleus;protein targeting;protein transport;regulation of biological process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;transport binding;nucleic acid binding;protein transporter activity;RNA binding;substrate-specific transporter activity;transporter activity;tRNA binding cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;nuclear part;nuclear pore;nucleoplasm;nucleus;organelle;organelle part;pore complex;protein complex RNA transport3.33E-140 4 12 12 12.8

Q9Y6M1-1;Q9Y6M1;F8W930;Q9Y6M1-5;Q9Y6M1-6;Q9Y6M1-3;Q9Y6M1-4 Insulin-like growth factor 2 mRNA-binding protein 2 IGF2BP2 >sp|Q9Y6M1-1|IF2B2_HUMAN Isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2;>sp|Q9Y6M1|IF2B2_HUMAN Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2;>tr|F8W930|F8W930_HUMAN Ins 0.04 0.14 0.17 0.08 0.05 -0.33 -0.49 -0.31 + 1.304182647 0.375825834 anatomical structure morphogenesis;biological regulation;developmental process;gene expression;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation binding;mRNA 3'-UTR binding;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;translation regulator activity cell part;cytoplasmic part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 5.82E-148 7 14 12 32.7

P29508;P29508-2 Serpin B3 SERPINB3 >sp|P29508|SPB3_HUMAN Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2;>sp|P29508-2|SPB3_HUMAN Isoform 2 of Serpin B3 OS=Homo sapiens GN=SERPINB3 -0.38 0.42 0.17 0.01 1.41 1.93 1.28 0.44 + 1.387686414 -1.213749665 biological regulation;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;receptor activity;serine-type endopeptidase inhibitor activity;viral receptor activity cell part;cytoplasm;extracellular membrane-bounded organelle;extracellular organelle;extracellular region;extracellular region part;extracellular vesicular exosome;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;organelle;vesicle Amoebiasis 6.58E-240 2 28 12 64.4

P37268;E9PNM1;B4DJE5;B3KQ95;B4DT56;B7Z1J3;E9PJG4;E9PS69 Squalene synthase FDFT1 >sp|P37268|FDFT_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1;>tr|E9PNM1|E9PNM1_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1;>tr|B4DJE5|B4DJE5_HUMAN Squalene synthase OS=Homo sapiens GN=FDFT1 PE=2 SV=1;>tr|B3KQ95|B3KQ95_HUMAN Squ 0.07 -0.01 -0.01 0.12 -0.51 -0.65 -0.32 -0.29 + 1.918938057 0.485383175 alcohol metabolic process;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;farnesyl diphosphate metabolic process;isoprenoid biosynthetic process;isoprenoid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;organophosphate metabolic process;phospholipid metabolic process;prenol metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "catalytic activity;farnesyl-diphosphate farnesyltransferase activity;farnesyltranstransferase activity;oxidoreductase activity;prenyltransferase activity;squalene synthase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Steroid biosynthesis 2.23E-132 8 13 13 35.7

Q9UJ70;Q9UJ70-2;H7C3G9;C9JEV6;H7C1L7;H0YEB7;E9PPU6;H0YC94;H0YF44 N-acetyl-D-glucosamine kinase NAGK >sp|Q9UJ70|NAGK_HUMAN N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK PE=1 SV=4;>sp|Q9UJ70-2|NAGK_HUMAN Isoform 2 of N-acetyl-D-glucosamine kinase OS=Homo sapiens GN=NAGK;>tr|H7C3G9|H7C3G9_HUMAN N-acetyl-D-glucosamine kinase (Fragment) OS=Homo sapien -0.30 -0.27 0.14 -0.02 0.76 0.60 0.66 0.51 + 2.110241902 -0.744667051 alcohol catabolic process;alcohol metabolic process;amino sugar catabolic process;amino sugar metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;glucosamine metabolic process;mannosamine metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;N-acetylglucosamine metabolic process;N-acetylmannosamine metabolic process;N-acetylneuraminate catabolic process;N-acetylneuraminate metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate kinase activity;catalytic activity;kinase activity;N-acetylglucosamine kinase activity;N-acylmannosamine kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" Amino sugar and nucleotide sugar metabolism 2.29E-102 9 13 13 47.4

Q05209;Q05209-2;E9PBR5;H0YC15;C9J1X8;F8WB51;C9JJC1;H3BM04 Tyrosine-protein phosphatase non-receptor type 12 PTPN12 >sp|Q05209|PTN12_HUMAN Tyrosine-protein phosphatase non-receptor type 12 OS=Homo sapiens GN=PTPN12 PE=1 SV=3;>sp|Q05209-2|PTN12_HUMAN Isoform 2 of Tyrosine-protein phosphatase non-receptor type 12 OS=Homo sapiens GN=PTPN12;>tr|E9PBR5|E9PBR5_HUMAN Tyrosine- -0.08 -0.05 -0.03 -0.22 0.66 0.69 0.43 0.49 + 2.484815196 -0.662622498 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;dephosphorylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;non-membrane spanning protein tyrosine phosphatase activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein tyrosine phosphatase activity" cell junction;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;podosome;protein complex 9.97E-102 8 13 13 23.8

D6RFM5;P31040;E9PBJ5;H0Y8X1 "Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial" SDHA ">tr|D6RFM5|D6RFM5_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=2 SV=1;>sp|P31040|DHSA_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 S" 0.03 0.01 0.14 0.08 -0.18 -0.43 -0.79 -0.58 + 1.624822473 0.559978368 acetyl-CoA catabolic process;acetyl-CoA metabolic process;anatomical structure development;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental process;dicarboxylic acid metabolic process;electron transport chain;generation of precursor metabolites and energy;metabolic process;nervous system development;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;respiratory electron transport chain;small molecule metabolic process;succinate metabolic process;system development;tricarboxylic acid cycle "binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor;succinate dehydrogenase (ubiquinone) activity;succinate dehydrogenase activity" cell part;cytoplasmic part;fumarate reductase complex;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex II;organelle part;protein complex;succinate dehydrogenase complex;succinate dehydrogenase complex (ubiquinone) Alzheimer's disease;Citrate cycle (TCA cycle);Huntington's disease;Oxidative phosphorylation;Parkinson's disease 6.01E-92 4 13 13 29.3

Q53FA7;Q53FA7-2;H7BZH6 Quinone oxidoreductase PIG3 TP53I3 >sp|Q53FA7|QORX_HUMAN Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2;>sp|Q53FA7-2|QORX_HUMAN Isoform 2 of Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3;>tr|H7BZH6|H7BZH6_HUMAN Quinone oxidoreductase PIG3 (Fragment) OS=Homo sapiens 0.27 0.03 -0.18 -0.38 0.91 1.57 1.12 1.29 + 2.122408433 -1.285161044 biological regulation;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;heterocycle metabolic process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of apoptosis by oxidative stress;induction of programmed cell death;metabolic process;NADP metabolic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;oxidoreduction coenzyme metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;small molecule metabolic process "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;ion binding;metal ion binding;NADP binding;NADPH binding;NADPH:quinone reductase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;quinone binding;transition metal ion binding;zinc ion binding" p53 signaling pathway 2.51E-90 3 13 13 50.3

O95361;B3KP96;H0Y626;O95361-2;J3KPT5;K7ENN8;Q309B1;I3L3K9;I3L2F3;J3QKY5;K7EL43;I3L1X9;J3QL38 Tripartite motif-containing protein 16 TRIM16;TRIM16L >sp|O95361|TRI16_HUMAN Tripartite motif-containing protein 16 OS=Homo sapiens GN=TRIM16 PE=1 SV=3;>tr|B3KP96|B3KP96_HUMAN Tripartite motif-containing protein 16 OS=Homo sapiens GN=TRIM16 PE=2 SV=1;>tr|H0Y626|H0Y626_HUMAN Uncharacterized protein OS=Homo sap -0.06 -0.14 0.08 0.05 0.40 0.85 0.82 0.16 + 1.325828711 -0.575100799 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic

process;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;histone acetylation;histone H3 acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine
acetylation;internal protein amino acid acetylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular
biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of cytokine secretion;positive regulation of developmental
process;positive regulation of epidermal cell differentiation;positive regulation of epidermis development;positive regulation of epithelial cell differentiation;positive regulation of gene expression;positive regulation of
interleukin-1 beta production;positive regulation of interleukin-1 beta secretion;positive regulation of interleukin-1 production;positive regulation of interleukin-1 secretion;positive regulation of keratinocyte
differentiation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal
process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein secretion;positive regulation of protein
transport;positive regulation of response to stimulus;positive regulation of retinoic acid receptor signaling pathway;positive regulation of RNA metabolic process;positive regulation of secretion;positive regulation of signal
transduction;positive regulation of signaling;positive regulation of transcription, DNA-dependent;positive regulation of transport;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein
modification process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular
localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of cytokine secretion;regulation of
developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of establishment of protein localization;regulation of gene
expression;regulation of interleukin-1 beta production;regulation of interleukin-1 beta secretion;regulation of interleukin-1 production;regulation of interleukin-1 secretion;regulation of keratinocyte differentiation;regulation of
localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular
organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of
protein secretion;regulation of protein transport;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of RNA metabolic process;regulation of secretion;regulation of signal
transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular
stimulus;response to growth hormone stimulus;response to hormone stimulus;response to insecticide;response to nutrient;response to nutrient levels;response to organic substance;response to organophosphorus;response to
peptide hormone stimulus;response to retinoic acid;response to stimulus;response to toxin;response to vitamin;response to vitamin A" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid
binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear body;nuclear part;nucleoplasm part;organelle part;PML body 8.21E-41 13 13 13 31.6
P12532;P12532-2;F8WCN3;C9JSQ1;E9PCP8;J3KQ93;C9J8F6;C9JJX8;C9J995;C9J6W7;C9JT96;P17540;H3BNI9;D6RHV3;D6R998 "Creatine kinase U-type, mitochondrial" CKMT1A;CKMT1B
">sp|P12532|KCRU_HUMAN Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1;>sp|P12532-2|KCRU_HUMAN Isoform 2 of Creatine kinase U-type, mitochondrial OS=Homo sapiens
GN=CKMT1A;>tr|F8WCN3|F8WCN3_HUMAN Creatine kinase U-type, mitochondri" -0.02 0.03 0.23 0.18 -1.12 -0.64 -0.41 -0.49 + 1.699452858 0.772071179 amine metabolic process;biological
regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic
process;cellular nitrogen compound metabolic process;cellular process;creatine metabolic process;metabolic process;multicellular organismal process;muscle contraction;muscle system process;nitrogen compound metabolic
process;organic acid metabolic process;oxoacid metabolic process;phosphagen metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic
process;regulation of biological process;regulation of cell cycle;regulation of cellular process;small molecule metabolic process;system process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP
binding;binding;catalytic activity;creatine kinase activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;phosphotransferase activity, nitrogenous group as acceptor;protein kinase
activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring
phosphorus-containing groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial
inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part Arginine and proline metabolism 1.04E-158 15 14 13 35.7
J3QR09;J3KTE4;P84098;J3QL15 Ribosomal protein L19;60S ribosomal protein L19 RPL19 >tr|J3QR09|J3QR09_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=3
SV=1;>tr|J3KTE4|J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=3 SV=1;>sp|P84098|RL19_HUMAN 60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 -0.03 0.04
0.16 0.12 -0.05 -0.32 -0.42 -0.44 + 1.510695633 0.380933513 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular
component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular
level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule
metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic
process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic
reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic
process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic
process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex
disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA
catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription"
binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded
organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome
Ribosome 2.75E-132 4 14 13 44.6
Q13177;H7C1X3;O75914-2;O75914;O75914-4;O75914-3;B1AKS5 Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-2p34 PAK2 >sp|Q13177|PAK2_HUMAN Serine/threonine-protein kinase PAK 2 OS=Homo
sapiens GN=PAK2 PE=1 SV=3 -0.02 -0.04 -0.16 0.02 0.33 0.23 0.31 0.02 + 1.3543467 -0.272358218 activation of immune response;anatomical structure development;anatomical structure
morphogenesis;antigen receptor-mediated signaling pathway;axon guidance;axonogenesis;biological regulation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked
signaling pathway;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component
organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule
metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chemotaxis;dendrite development;dendritic spine morphogenesis;dendritic spine
organization;developmental process;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling
pathway;immune response-regulating signaling pathway;immune system process;interaction with host;interspecies interaction between organisms;locomotion;lymphocyte costimulation;macromolecule metabolic
process;macromolecule modification;metabolic process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell
death;negative regulation of cellular process;negative regulation of kinase activity;negative regulation of molecular function;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative
regulation of transferase activity;neuron projection development;neuron projection morphogenesis;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound
metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cellular process;positive regulation of immune
response;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of response to stimulus;positive regulation of T cell
activation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of actin cytoskeleton organization;regulation of actin filament
length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of apoptosis;regulation of
biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell activation;regulation of cell death;regulation of cellular component biogenesis;regulation of cellular component
organization;regulation of cellular component size;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of
defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of growth;regulation of immune effector process;regulation of immune response;regulation of immune system
process;regulation of kinase activity;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular

function;regulation of multi-organism process;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of T cell activation;regulation of transferase activity;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;synapse organization;T cell costimulation;T cell receptor signaling pathway;taxis;viral reproduction;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;ion binding;kinase activator activity;kinase activity;kinase regulator activity;MAP kinase kinase activity;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activator activity;protein kinase activity;protein kinase regulator activity;protein serine/threonine kinase activity;protein serine/threonine/tyrosine kinase activity;protein tyrosine kinase activator activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane Axon guidance;ErbB signaling pathway;Focal adhesion;MAPK signaling pathway;Regulation of actin cytoskeleton;Renal cell carcinoma;T cell receptor signaling pathway 5.49E-224 7 16 13 41.8

P62701;A6NH36;C9JQ55 "40S ribosomal protein S4, X isoform" RPS4X ">sp|P62701|RS4X_HUMAN 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2" -0.03 -0.03 0.06 0.05 -0.36 -0.64 -0.16 -0.33 + 1.477832116 0.38359512 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;multicellular organismal development;multicellular organismal process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;polysome;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 5.11E-245 3 26 13 72.6

Q07960;H0YE29;E9PNR6 Rho GTPase-activating protein 1 ARHGAP1 >sp|Q07960|RHG01_HUMAN Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1;>tr|H0YE29|H0YE29_HUMAN Rho GTPase-activating protein 1 (Fragment) OS=Homo sapiens GN=ARHGAP1 PE=4 SV=1 -0.05 -0.14 0.07 -0.06 0.25 0.30 0.48 0.05 + 1.313538981 -0.317171376 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;Ras protein signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction "binding;binding, bridging;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;protein binding, bridging;Rac GTPase activator activity;Ras GTPase activator activity;Rho GTPase activator activity;SH3/SH2 adaptor activity;signaling adaptor activity;small GTPase regulator activity" cell part;cell projection;cytoplasmic part;cytosol;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle;plasma membrane;ruffle 3.84E-128 3 14 14 44.4

O43852;O43852-3;O43852-2;O43852-4;O43852-5;O43852-6;O43852-10;O43852-9;O43852-13;O43852-14;O43852-15;O43852-11;H0Y875;O43852-8;O43852-12;O43852-7 Calumenin CALU >sp|O43852|CALU_HUMAN Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2;>sp|O43852-3|CALU_HUMAN Isoform 3 of Calumenin OS=Homo sapiens GN=CALU;>sp|O43852-2|CALU_HUMAN Isoform 2 of Calumenin OS=Homo sapiens GN=CALU;>sp|O43852-4|CALU_HUMAN Isoform 4 of Calumenin O -0.16 -0.17 -0.42 -0.26 1.35 1.01 0.55 0.53 + 1.897432445 -1.111790743 cell activation;cellular process;establishment of localization;establishment of localization in cell;exocytosis;platelet activation;platelet degranulation;secretion;secretion by cell;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular region;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;sarcoplasmic reticulum lumen;vesicle 8.62E-68 16 14 14 54

O43252 Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1;Sulfate adenylyltransferase;Adenylyl-sulfate kinasePAPSS1 >sp|O43252|PAPS1_HUMAN Bifunctional 3-phosphoadenosine 5-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2 -0.03 -0.22 0.04 -0.02 0.20 0.06 0.20 0.28 + 1.362787206 -0.24544527 3'-phosphoadenosine 5'-phosphosulfate biosynthetic process;3'-phosphoadenosine 5'-phosphosulfate metabolic process;anatomical structure development;biosynthetic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;developmental process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate biosynthetic process;nucleoside bisphosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;purine nucleoside bisphosphate biosynthetic process;purine nucleoside bisphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside bisphosphate biosynthetic process;purine ribonucleoside bisphosphate metabolic process;purine-containing compound metabolic process;ribonucleoside bisphosphate biosynthetic process;ribonucleoside bisphosphate metabolic process;skeletal system development;small molecule metabolic process;sulfate assimilation;sulfur compound metabolic process;system development;xenobiotic metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;adenylylsulfate kinase activity;adenylyltransferase activity;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;nucleotidyltransferase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;sulfate adenylyltransferase (ATP) activity;sulfate adenylyltransferase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part Purine metabolism;Selenocompound metabolism;Sulfur metabolism 6.74E-77 1 14 14 26.8

P15880;H0YEN5;E9PQD7;E9PMM9;E9PPT0;I3L404;E9PM36;H3BNG3;H0YE27 40S ribosomal protein S2 RPS2 >sp|P15880|RS2_HUMAN 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2;>tr|H0YEN5|H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=2 SV=1;>tr|E9PQD7|E9PQD7_HUMAN 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=2 SV=1 0.00 0.01 -0.09 0.04 -0.16 -0.40 -0.19 -0.34 + 1.575962274 0.261707425 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 2.32E-135 9 14 14 46.1

M0R0F0;P46782;M0R0R2;M0QZN2;Q9NWB6-2;Q9NWB6;REV__Q96SI9-2;REV__Q96SI9 "40S ribosomal protein S5;40S ribosomal protein S5, N-terminally processed" RPS5 >tr|M0R0F0|M0R0F0_HUMAN 40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=3 SV=1;>sp|P46782|RS5_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4;>tr|M0R0R2|M0R0R2_HUMAN 40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=3 SV=1 0.09 0.03 0.01 0.07 -0.31 -0.51 -0.18 -0.15 + 1.563962504 0.340085709 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational elongation;regulation of translational fidelity;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;transcription, DNA-dependent;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome 1.71E-128 8 14 14 55

P46781;B5MCT8;C9JM19;F2Z3C0;A8MXK4 40S ribosomal protein S9 RPS9 >sp|P46781|RS9_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3;>tr|B5MCT8|B5MCT8_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=2 SV=1;>tr|C9JM19|C9JM19_HUMAN 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=2 SV=1 0.04 0.00 0.08 0.01 -0.10 -0.35 -0.19 -0.30 + 1.716377765 0.269346238 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cell proliferation;regulation of cellular process;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity;translation regulator activity cell part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome 2.81E-63 5 14 14 60.8

Q6XPR3 Repetin RPTN >sp|Q6XPR3|RPTN_HUMAN Repetin OS=Homo sapiens GN=RPTN PE=1 SV=1 -0.63 0.72 -1.11 -0.56 2.09 3.20 1.42 1.68 + 1.687676826 -2.488543257 binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cornified envelope;cytoskeleton;extracellular matrix;extracellular region part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle;proteinaceous extracellular matrix 4.00E-122 1 14 14 33.4

Q9Y696;P12273 Chloride intracellular channel protein 4 CLIC4 >sp|Q9Y696|CLIC4_HUMAN Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 -0.36 -0.36 -0.27 -0.15 0.84 0.91 0.83 0.97 + 3.546044861 -1.1721013 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological regulation;branching morphogenesis of a tube;cation homeostasis;cell differentiation;cell morphogenesis;cell morphogenesis involved in differentiation;cellular cation homeostasis;cellular chemical homeostasis;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular monovalent inorganic cation homeostasis;cellular process;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;chemical homeostasis;developmental process;endothelial cell morphogenesis;epidermal cell differentiation;epithelial cell differentiation;epithelial cell morphogenesis;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;fertilization;growth;homeostatic process;intracellular pH reduction;ion homeostasis;keratinocyte differentiation;monovalent inorganic cation homeostasis;morphogenesis of a branching structure;multicellular organism growth;multicellular organismal process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;pH reduction;regulation of biological process;regulation of biological quality;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular pH;regulation of cellular process;regulation of cytoskeleton organization;regulation of intracellular pH;regulation of localization;regulation of locomotion;regulation of organelle organization;regulation of pH;reproductive process;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;retina vasculature morphogenesis in camera-type eye;tube morphogenesis;vacuolar acidification actin binding;anion channel activity;anion transmembrane transporter activity;binding;channel activity;chloride channel activity;cytoskeletal protein binding;gated channel activity;ion channel activity;ion transmembrane transporter activity;passive transmembrane transporter activity;protein binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated chloride channel activity;voltage-gated ion channel activity actin cytoskeleton;apical part of cell;apical plasma membrane;cell junction;cell part;cell projection;cell surface;cell-cell junction;centrosome;chloride channel complex;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule organizing center;microvillus;midbody;mitochondrion;non-membrane-bounded organelle;nuclear matrix;nuclear part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;vacuole;vesicle membrane 1.07E-170 2 15 14 71.9

Q07955;J3KTL2;Q07955-3;Q07955-2;J3KSR8;J3QQV5;J3KSW7 Serine/arginine-rich splicing factor 1 SRSF1 >sp|Q07955|SRSF1_HUMAN Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2;>tr|J3KTL2|J3KTL2_HUMAN Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=4 SV=1;>sp|Q07955-3|SRSF1_HUMAN Isoform ASF-3 of Serine/arginine-ric 0.02 0.15 0.16 0.15 -0.07 -0.54 -0.85 -0.49 + 1.466801638 0.609347096 "biosynthetic process;cardiac muscle contraction;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;establishment of localization;establishment of localization in cell;establishment of RNA localization;in utero embryonic development;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA splice site selection;mRNA transport;multicellular organismal process;muscle contraction;muscle system process;nitrogen compound metabolic process;nuclear export;nuclear mRNA 5'-splice site recognition;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA transport;striated muscle contraction;system process;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 3.89E-67 7 15 14 52.8

P23528;E9PP50;E9PK25;G3V1A4;E9PS23;E9PQB7;E9PLJ3 Cofilin-1 CFL1 >sp|P23528|COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3;>tr|E9PP50|E9PP50_HUMAN Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=2 SV=1;>tr|E9PK25|E9PK25_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=2 SV=1;>tr|G3V1A4|G3V1A4_HUMAN Cofilin 1 (Non-musc -0.05 -0.10 -0.28 -0.08 -0.01 0.22 0.50 0.29 + 1.306467115 -0.376155297 actin cytoskeleton organization;actin filament depolymerization;actin filament organization;actin filament-based process;actin polymerization or depolymerization;ameboidal cell migration;anatomical structure morphogenesis;axon guidance;biological regulation;cell activation;cell migration;cell motility;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;chemotaxis;cytokinesis;cytoskeleton organization;defense response;developmental process;embryonic morphogenesis;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment or maintenance of cell polarity;exocytosis;immune response;immune system process;innate immune response;intracellular signal transduction;locomotion;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of an epithelial fold;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;neural crest cell migration;neural fold formation;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;platelet degranulation;positive regulation of actin filament depolymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex disassembly;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein depolymerization;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cell morphogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of organelle organization;regulation of programmed cell death;regulation of protein complex disassembly;response to acid;response to amine stimulus;response to amino acid stimulus;response to biotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to organic nitrogen;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;Rho protein signal transduction;secretion;secretion by cell;signal transduction;small GTPase mediated signal transduction;taxis;tissue morphogenesis;transport;vesicle-mediated transport actin cytoskeleton;cell cortex part;cell part;cell projection membrane;cell projection part;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium membrane;leading edge membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear matrix;nuclear part;nucleus;organelle;organelle part;plasma membrane part;ruffle membrane Axon guidance;Fc gamma R-mediated phagocytosis;Regulation of actin cytoskeleton 2.65E-218 7 18 14 72.3

P38919;I3L3H2 Eukaryotic initiation factor 4A-III EIF4A3 >sp|P38919|IF4A3_HUMAN Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 -0.02 0.35 0.18 0.42 -0.18 -0.33 -0.78 -0.10 + 1.308674915 0.578997638 "biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of RNA localization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;mRNA transport;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;rRNA metabolic process;rRNA processing;signal transduction;transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mRNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;single-stranded RNA binding" catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;exon-exon junction complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport;Spliceosome 2.70E-85 2 18 14 48.4

P17858;P17858-2 "6-phosphofructokinase, liver type" PFKL ">sp|P17858|K6PL_HUMAN 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6;>sp|P17858-2|K6PL_HUMAN Isoform 2 of 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL" 0.17 -0.15 -0.24 -0.27 0.48 0.15 0.54 0.59 + 1.541116955 -0.561541457 "alcohol catabolic process;alcohol metabolic process;biological regulation;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular process;fructose 1,6-bisphosphate metabolic process;fructose 6-phosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;negative regulation of biological process;negative regulation of cellular process;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of secretion;negative regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;response to carbohydrate stimulus;response to chemical stimulus;response to glucose stimulus;response to hexose stimulus;response to monosaccharide stimulus;response to organic substance;response to stimulus;small molecule catabolic process;small molecule metabolic process" "6-phosphofructokinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate binding;carbohydrate kinase activity;catalytic activity;cation binding;fructose binding;fructose-6-phosphate binding;ion binding;kinase activity;metal ion binding;monosaccharide binding;nucleotide binding;phosphofructokinase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;sugar binding;transferase activity;transferase activity, transferring phosphorus-containing groups" 6-phosphofructokinase complex;cell part;cytoplasmic part;cytosolic part;intracellular part;macromolecular complex;protein complex Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Methane metabolism;Pentose phosphate pathway 2.37E-185 2 19 14 33.7

P42765;K7EME0;K7ER88;K7EJB1;K7EJ68 "3-ketoacyl-CoA thiolase, mitochondrial" ACAA2 ">sp|P42765|THIM_HUMAN 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2;>tr|K7EME0|K7EME0_HUMAN 3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=3 SV=1" -1.51 -1.06 -0.33 0.06 1.46 1.13 0.77 0.71 + 1.660404841 -1.72796151 alcohol metabolic process;biological regulation;biosynthetic process;carboxylic acid metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "acetyl-CoA C-acyltransferase activity;C-acyltransferase activity;catalytic activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part "Benzoate degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Valine, leucine and isoleucine degradation" 3.43E-134 5 15 15 50.9

Q29RF7;H0Y9L6;Q29RF7-3;Q9NTI5-3 Sister chromatid cohesion protein PDS5 homolog A PDS5A >sp|Q29RF7|PDS5A_HUMAN Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1 0.12 0.19 0.12 0.00 -0.06 -0.33 -0.77 -0.67 + 1.368217925 0.567026189 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular process;cytokinesis;M phase;M phase of mitotic cell cycle;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;S phase;S phase of mitotic cell cycle "cell part;chromatin;chromosomal part;chromosome, centromeric region;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;membrane;nuclear part;nucleoplasm;organelle part;plasma membrane" 5.61E-193 4 16 15 18.5

P37802;C9J5W6 Transgelin-2 TAGLN2 >sp|P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3 0.29 -0.02 -0.10 -0.20 0.30 0.28 0.53 0.41 + 1.322776967 -0.391777613 "anatomical structure development;biological regulation;developmental process;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;organ development;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 0 2 16 15 74.4

O00425;O00425-2;F8WD15 Insulin-like growth factor 2 mRNA-binding protein 3 IGF2BP3 >sp|O00425|IF2B3_HUMAN Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2 -0.07 0.03 0.10 0.04 -0.21 -0.26 -0.35 -0.22 + 2.076953219 0.284501228 anatomical structure morphogenesis;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;translation binding;mRNA 3'-UTR binding;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;translation regulator activity cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 7.72E-195 3 18 15 36.6

Q06830 Peroxiredoxin-1 PRDX1 >sp|Q06830|PRDX1_HUMAN Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1 0.13 -0.02 -0.27 -0.14 0.33 0.26 0.48 0.13 + 1.34145122 -0.373513104 anatomical structure development;biological regulation;catabolic process;cell killing;cell proliferation;cellular catabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to oxygen radical;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cellular response to superoxide;defense response;developmental process;erythrocyte homeostasis;homeostasis of number of cells;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;leukocyte mediated cytotoxicity;leukocyte mediated immunity;lymphocyte mediated immunity;metabolic process;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular localization;regulation of cellular process;regulation of cellular response to stress;regulation of establishment of protein localization;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of MAPKKK cascade;regulation of NF-kappaB import into nucleus;regulation of nucleocytoplasmic transport;regulation of programmed cell death;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of transcription factor import into nucleus;regulation of transmembrane transport;regulation of transport;removal of superoxide radicals;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to oxygen radical;response to reactive oxygen species;response to stimulus;response to stress;response to superoxide;skeletal system development;superoxide metabolic process;system development "antioxidant activity;binding;catalytic activity;cation binding;heme binding;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;peroxiredoxin activity;tetrapyrrole binding;thioredoxin peroxidase activity;transition metal ion binding" cell part;chromatin;chromosomal part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;euchromatin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microbody lumen;microbody part;mitochondrial matrix;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleolus;nucleus;organelle;organelle lumen;organelle part;peroxisomal matrix;peroxisomal part;pigment granule;vesicle Peroxisome 9.54E-101 1 19 15 70.9

Q9Y2D5-6;Q9Y2D5;Q9Y2D5-5;Q9Y2D5-4;Q9Y2D5-7;C9JVY5;O75781-2;C9JA33;Q8IXS6;O75781;Q8IXS6-2;D3YTA4;B1ALY0 A-kinase anchor protein 2 AKAP2 >sp|Q9Y2D5-6|AKAP2_HUMAN Isoform 4 of A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2;>sp|Q9Y2D5|AKAP2_HUMAN A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 PE=1 SV=3;>sp|Q9Y2D5-5|AKAP2_HUMAN Isoform 3 of A-kinase anchor protein 2 OS=Homo sapiens GN= 0.08 0.05 -0.24 -0.12 0.74 0.65 0.30 0.52 + 1.823555848 -0.611284249 biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to abiotic stimulus;cellular response to electrical stimulus;cellular response to stimulus;cytoskeleton organization;developmental maturation;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;intracellular protein transport;intracellular transport;negative regulation of adenylate cyclase activity;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cellular process;negative regulation of cyclase activity;negative regulation of dopamine receptor signaling pathway;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of lyase activity;negative regulation of molecular function;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle organization;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of dendritic spine development;positive regulation of developmental process;positive regulation of filopodium assembly;protein targeting;protein targeting to plasma membrane;protein transport;regulation of adenylate cyclase activity;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell shape;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of dendrite development;regulation of dendritic spine development;regulation of developmental process;regulation of dopamine receptor signaling pathway;regulation of filopodium assembly;regulation of G-protein coupled receptor protein signaling pathway;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to abiotic stimulus;response to electrical stimulus;response to stimulus;synapse maturation;synapse organization;transportbinding;enzyme binding;protein binding apicolateral plasma membrane;axon;basolateral plasma membrane;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;dendrite membrane;dendritic spine membrane;filopodium membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;leading edge membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuron projection;neuron projection membrane;organelle;plasma membrane;plasma membrane part;vesicle 1.84E-74 13 16 16 21.7

Q8TEQ6 Gem-associated protein 5 GEMIN5 >sp|Q8TEQ6|GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens GN=GEMIN5 PE=1 SV=3 0.14 0.06 0.09 -0.10 -0.31 -0.50 -0.07 -0.41 + 1.407730221 0.369930025 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;spliceosomal snRNP assemblybinding;nucleic acid binding;RNA binding;snRNA binding Cajal body;cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex RNA transport 3.65E-155 1 16 16 14.4

Q14847;Q14847-2;C9J9W2;B4DGQ0;F6S2S5;K7ESD6;O76041-2 LIM and SH3 domain protein 1 LASP1 >sp|Q14847|LASP1_HUMAN LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2;>sp|Q14847-2|LASP1_HUMAN Isoform 2 of LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1;>tr|C9J9W2|C9J9W2_HUMAN LIM and SH3 domain protein 1 (Fragment) OS=Homo sapie 0.00 -0.15 -0.13 -0.15 0.70 0.42 0.48 0.35 + 2.248181951 -0.597988589 "binding;binding, bridging;cation binding;ion binding;ion transmembrane transporter activity;metal ion binding;protein binding;protein binding, bridging;SH3/SH2 adaptor activity;signaling adaptor activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transition metal ion binding;transmembrane transporter activity;transporter activity;zinc ion binding" adherens junction;anchoring junction;cell cortex part;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part 2.31E-146 7 16 16 44.8

Q9UHX1-6;Q9UHX1-4;Q9UHX1-5;Q9UHX1-2;Q9UHX1-3;Q9UHX1;E9PQ56;H0YEM1;E9PMU7;E9PN18;H0YCP8;E9PL19Poly(U)-binding-splicing factor PUF60 PUF60 >sp|Q9UHX1-6|PUF60_HUMAN Isoform 6 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60;>sp|Q9UHX1-4|PUF60_HUMAN Isoform 4 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60;>sp|Q9UHX1-5|PUF60_HUMAN Isoform 5 of Poly(U)-binding- 0.16 0.09 -0.05 -0.02 -0.10 -0.49 -0.42 -0.58 + 1.513453922 0.445089256 "apoptosis;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex Spliceosome 1.14E-191 12 16 16 42.1

P05455;E7ERC4;E9PGX9;E9PFL9 Lupus La protein SSB >sp|P05455|LA_HUMAN Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2;>tr|E7ERC4|E7ERC4_HUMAN Lupus La protein (Fragment) OS=Homo sapiens GN=SSB PE=2 SV=1 0.05 0.01 0.08 0.05 0.01 -0.47 -0.47 -0.58 + 1.311300328 0.425745888 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;histone mRNA metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA modification;RNA processing;tRNA metabolic process;tRNA modification;tRNA processing binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;tRNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex Systemic lupus erythematosus 8.41E-62 4 16 16 39.7

Q9NYL9;H0YKU1;H0YNJ8;H0YNU8;Q5T7W3;G5EA42;Q9NZR1;P28289;Q15911-2;Q15911 Tropomodulin-3 TMOD3 >sp|Q9NYL9|TMOD3_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=1 SV=1;>tr|H0YKU1|H0YKU1_HUMAN Tropomodulin-3 (Fragment) OS=Homo sapiens GN=TMOD3 PE=4 SV=1;>tr|H0YNJ8|H0YNJ8_HUMAN Tropomodulin-3 OS=Homo sapiens GN=TMOD3 PE=2 SV=1 0.25 0.16 -0.04 0.13 -0.65 -0.55 -0.26 -0.65 + 2.023924281 0.650849185 "actin cytoskeleton organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;actomyosin structure organization;adult behavior;adult locomotory behavior;anatomical structure development;anatomical structure formation involved in morphogenesis;behavior;biological regulation;cell communication;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cognition;cytoskeleton organization;developmental process;learning or memory;locomotory behavior;multicellular organismal process;muscle filament sliding;muscle organ development;muscle structure development;myofibril assembly;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of muscle cell differentiation;negative regulation of myoblast differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nervous system development;neurological system process;neuron-neuron synaptic transmission;organ development;organelle organization;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of G-protein coupled receptor protein signaling pathway;positive regulation of muscle cell differentiation;positive regulation of myoblast differentiation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of G-protein coupled receptor protein signaling pathway;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of myoblast differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;signaling;synaptic transmission;system development;system process" binding;cation binding;cytoskeletal protein binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific distal enhancer binding RNA polymerase II transcription factor activity;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription regulatory region DNA binding;transition metal ion binding;tropomyosin binding;zinc ion binding	cell cortex part;cell part;cell projection part;contractile fiber;contractile fiber part;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;growth cone;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;myofibril;non-membrane-bounded organelle;nuclear part;nucleoplasm part;organelle;organelle part;protein complex;site of polarized growth;striated muscle thin filament;transcription factor complex		1.39E-104	10	16	16	56.2

P19525;P19525-2;C9JZT2;F8WBH4	"Interferon-induced, double-stranded RNA-activated protein kinase"	EIF2AK2">sp|P19525|E2AK2_HUMAN Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens GN=EIF2AK2 PE=1 SV=2;>sp|P19525-2|E2AK2_HUMAN Isoform 2 of Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens GN=EIF2AK2"	0.30 0.30 0.06 0.03 -0.97 -0.78	-0.44	-0.69	+	2.16783872	0.892148637	apoptosis;avoidance of defenses of other organism involved in symbiotic interaction;avoidance of host defenses;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cellular response to topologically incorrect protein;cellular response to unfolded protein;death;defense response;defense response to virus;endoplasmic reticulum unfolded protein response;ER-nucleus signaling pathway;evasion by virus of host immune response;evasion of host defenses by virus;evasion or tolerance of defense response of other organism involved in symbiotic interaction;evasion or tolerance of defenses of other organism involved in symbiotic interaction;evasion or tolerance of host defense response;evasion or tolerance of host defenses;evasion or tolerance of host immune response;evasion or tolerance of immune response of other organism involved in symbiotic interaction;immune effector process;immune system process;interaction with host;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification by symbiont of host morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by symbiont of host cellular process;modulation by virus of host cellular process;multi-organism process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of osteoblast proliferation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;programmed cell death;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biological quality;regulation of cell proliferation;regulation of cellular process;regulation of osteoblast proliferation;reproductive process;response to biotic stimulus;response to chemical stimulus;response to defenses of other organism involved in symbiotic interaction;response to endoplasmic reticulum stress;response to host;response to host defenses;response to host immune response;response to immune response of other organism involved in symbiotic interaction;response to organic substance;response to other organism;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;response to virus;signal transduction;translation;viral infectious cycle;viral reproductive process;virus-host interaction;virus-infected cell apoptosis	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;double-stranded RNA binding;enzyme regulator activity;eukaryotic translation initiation factor 2alpha kinase activity;kinase activity;non-membrane spanning protein tyrosine kinase activity;nucleic acid binding;nucleotide binding;phosphatase regulator activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups"cell part;cytoplasmic part;cytosol;intracellular part	Hepatitis C;Measles;Protein processing in endoplasmic reticulum	3.68E-111	4	17	17	31.8

B4DVY1;O15371;B0QYA5;B0QYA4;B0QYA3;B0QYA6;B0QYA7;B0QYA8	Eukaryotic translation initiation factor 3 subunit D	EIF3D	>tr|B4DVY1|B4DVY1_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=2 SV=1;>sp|O15371|EIF3D_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	0.16 0.06 0.06 0.02 -0.08	-0.20 -0.05	-0.33	+	1.359135911	0.23989087	cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;formation of translation initiation complex;macromolecular complex assembly;macromolecular complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity"	cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex	RNA transport2.28E-149	8	17	17	46.3

P43490;Q5SYT8;F5H246;C9JG65;C9JF35	Nicotinamide phosphoribosyltransferase	NAMPT;NAMPTL >sp|P43490|NAMPT_HUMAN Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1;>tr|Q5SYT8|Q5SYT8_HUMAN Protein NAMPTL (Fragment) OS=Homo sapiens GN=NAMPTL PE=2 SV=1	-0.01	-0.19	0.09 0.03 0.20 0.23 0.44 0.17 +	1.340124358	-0.27844656	"alkaloid metabolic process;biological regulation;biosynthetic process;cell communication;cell-cell signaling;cellular amide metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;NAD biosynthetic process;NAD metabolic process;nicotinamide metabolic process;nicotinamide nucleotide biosynthetic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidoreduction coenzyme metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitric-oxide synthase biosynthetic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;pyridine nucleotide biosynthetic process;pyridine nucleotide metabolic process;pyridine-containing compound biosynthetic process;pyridine-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitric-oxide synthase biosynthetic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;signal transduction;signaling;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process" "binding;catalytic activity;cytokine activity;nicotinamide phosphoribosyltransferase activity;nicotinate phosphoribosyltransferase activity;nicotinate-nucleotide diphosphorylase (carboxylating) activity;protein binding;receptor binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups"	cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part	Nicotinate and nicotinamide metabolism	1.39E-260	5	17	17	48.3

O14776-2;O14776;G3V220;Q5VWI1	Transcription elongation regulator 1	TCERG1 >sp|O14776-2|TCRG1_HUMAN Isoform 2 of Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1;>sp|O14776|TCRG1_HUMAN Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=2;>tr|G3V220|G3V220_HUMAN Transcription elongation regulator	0.06 0.02 0.23 0.04 -0.05 -0.48	-0.65	-0.60	+	1.455308087	0.53030737		protein binding transcription factor activity;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription corepressor activity;RNA polymerase II transcription factor binding transcription factor activity;RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Spliceosome 9.82E-48 4 17 17 16.7

Q9BZQ8;H0Y7M9 Protein Niban FAM129A >sp|Q9BZQ8|NIBAN_HUMAN Protein Niban OS=Homo sapiens GN=FAM129A PE=1 SV=1 0.41 0.02 0.44 0.09 -0.77 -1.37 -0.99 -0.96 + 2.332958615 1.261678152 biological regulation;cellular process;cellular response to stimulus;cellular response to stress;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of translation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of translation;response to endoplasmic reticulum stress;response to stimulus;response to stress cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 4.98E-144 2 18 17 27.6

O15042-2;O15042;E7ET15;O15042-3;C9JB80;E7EW00;H0Y8D9;C9JDJ7;C9J5L1;H7C4V2 U2 snRNP-associated SURP motif-containing protein U2SURP >sp|O15042-2|SR140_HUMAN Isoform 2 of U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP;>sp|O15042|SR140_HUMAN U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=2;>tr|E7ET15|E7ET15_HUMAN U2 snRNP- -0.13 0.33 0.00 0.31 -0.30 -0.40 -0.97 -0.54 + 1.449526447 0.682602941 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Spliceosome 1.23E-80 10 18 17 20.9

Q13596;Q13596-2;Q13596-3;A6NKH4;H0YK42;H0YK43;J3KPH4;H0YKD5;H0YKL5;H0YK58 Sorting nexin-1 SNX1 >sp|Q13596|SNX1_HUMAN Sorting nexin-1 OS=Homo sapiens GN=SNX1 PE=1 SV=3;>sp|Q13596-2|SNX1_HUMAN Isoform 1A of Sorting nexin-1 OS=Homo sapiens GN=SNX1;>sp|Q13596-3|SNX1_HUMAN Isoform 3 of Sorting nexin-1 OS=Homo sapiens GN=SNX1;>tr|A6NKH4|A6NKH4_HUMAN Sorti -0.08 -0.18 -0.15 -0.21 0.22 0.15 0.58 0.17 + 1.601431121 -0.432892228 "biological regulation;cell communication;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;early endosome to Golgi transport;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular protein transport;intracellular transport;membrane invagination;membrane organization;positive regulation of biological process;positive regulation of catabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;protein transport;regulation of biological process;regulation of catabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;retrograde transport, endosome to Golgi;transport;vesicle-mediated transport" binding;lipid binding;phosphatidylinositol binding;phospholipid binding;protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;early endosome membrane;endosomal part;endosome;endosome membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part 7.91E-139 10 19 17 42.1

Q06210-2;Q06210 Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 GFPT1 >sp|Q06210-2|GFPT1_HUMAN Isoform 2 of Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1;>sp|Q06210|GFPT1_HUMAN Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 -0.04 -0.19 -0.07 -0.13 0.36 0.25 0.55 0.30 + 2.107683824 -0.471355791 activation of signaling protein activity involved in unfolded protein response;alcohol biosynthetic process;alcohol metabolic process;amine metabolic process;amino sugar biosynthetic process;amino sugar metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;dolichol-linked oligosaccharide biosynthetic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;fructose 6-phosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;glucosamine biosynthetic process;glucosamine metabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;glycosylation;hexose metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;N-acetylglucosamine biosynthetic process;N-acetylglucosamine metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of carbohydrate metabolic process;negative regulation of cellular biosynthetic process;negative regulation of cellular carbohydrate metabolic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of glycogen biosynthetic process;negative regulation of glycogen metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;post-translational protein modification;primary metabolic process;protein complex assembly;protein complex subunit organization;protein glycosylation;protein homooligomerization;protein homotetramerization;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein oligomerization;protein tetramerization;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular carbohydrate metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen biosynthetic process;regulation of glycogen metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to carbohydrate stimulus;response to chemical stimulus;response to disaccharide stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to sucrose stimulus;small molecule biosynthetic process;small molecule metabolic process;UDP-N-acetylglucosamine biosynthetic process;UDP-N-acetylglucosamine metabolic process "amine binding;amino acid binding;binding;carbohydrate binding;carboxylic acid binding;catalytic activity;glutamine-fructose-6-phosphate transaminase (isomerizing) activity;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups" cell part;cytoplasmic part;cytosol;intracellular part "Alanine, aspartate and glutamate metabolism;Amino sugar and nucleotide sugar metabolism" 4.00E-141 2 22 17 42

Q16666-3;Q16666-2;Q16666;Q16666-7;Q16666-6;E7EPR3;H3BM18;H3BVE6;Q6K0P9-6;Q6K0P9-5;Q6K0P9-4;Q6K0P9-3;Q6K0P9-2;Q6K0P9;H3BR65;H3BR88 Gamma-interferon-inducible protein 16 IFI16 >sp|Q16666-3|IF16_HUMAN Isoform 3 of Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16;>sp|Q16666-2|IF16_HUMAN Isoform 2 of Gamma-interferon-inducible protein 16 OS=Homo sapiens GN=IFI16;>sp|Q16666|IF16_HUMAN Gamma-interferon-inducible protein -0.04 0.12 -0.21 -0.05 -0.48 -0.85 -0.94 -0.43 + 1.649333979 0.628013197 "activation of immune response;activation of innate immune response;autophagy;biological regulation;biosynthetic process;catabolic process;cell communication;cell cycle;cell differentiation;cell proliferation;cellular biosynthetic process;cellular catabolic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular

process;cellular response to abiotic stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to ionizing radiation;cellular response to
nutrient levels;cellular response to radiation;cellular response to starvation;cellular response to stimulus;cellular response to stress;defense response;defense response to virus;developmental process;DNA damage response, signal
transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;immune
effector process;immune response;immune system process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;inflammatory response;innate immune response;intracellular
signal transduction;leukocyte differentiation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monocyte differentiation;multi-organism process;myeloid cell differentiation;myeloid
leukocyte differentiation;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cellular biosynthetic
process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cysteine-type endopeptidase
activity;negative regulation of defense response;negative regulation of DNA binding;negative regulation of endopeptidase activity;negative regulation of gene expression;negative regulation of hydrolase activity;negative
regulation of immune response;negative regulation of immune system process;negative regulation of innate immune response;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule
metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound
metabolic process;negative regulation of peptidase activity;negative regulation of reproductive process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of
transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic
process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation
of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of defense
response;positive regulation of gene expression;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of interleukin-1 beta
production;positive regulation of interleukin-1 production;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive
regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell
death;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive
regulation of type I interferon production;primary metabolic process;regulation of apoptosis;regulation of autophagy;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of catabolic
process;regulation of catalytic activity;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular
metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cytokine production;regulation of defense response;regulation of DNA binding;regulation of endopeptidase
activity;regulation of gene expression;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interleukin-1 beta
production;regulation of interleukin-1 production;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of
multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic
process;regulation of programmed cell death;regulation of reproductive process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription from RNA
polymerase II promoter;regulation of transcription, DNA-dependent;regulation of type I interferon production;regulation of viral genome replication;regulation of viral reproduction;response to abiotic stimulus;response to biotic
stimulus;response to DNA damage stimulus;response to external stimulus;response to extracellular stimulus;response to ionizing radiation;response to nutrient levels;response to other organism;response to radiation;response to
starvation;response to stimulus;response to stress;response to virus;response to wounding;RNA biosynthetic process;RNA metabolic process;signal transduction;signal transduction by p53 class mediator;signal transduction by
p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;transcription, DNA-dependent" binding;DNA binding;double-stranded DNA binding;nucleic acid binding;protein
binding;structure-specific DNA binding;transcription factor binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular
part;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part 7.43E-80 16 18 18 31.2
Q5JRX3;Q5JRX3-2;C9JSL2;Q5JRX3-3;H0Y7L7;B1APQ0;B1APQ1"Presequence protease, mitochondrial" PITRM1 ">sp|Q5JRX3|PREP_HUMAN Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1
SV=3;>sp|Q5JRX3-2|PREP_HUMAN Isoform 2 of Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1;>tr|C9JSL2|C9JSL2_HUMAN Uncharacterized protein OS=Homo sapiens"-0.60 -0.60 0.02
0.08 0.41 0.48 0.46 0.29 + 1.422601192 -0.686190275 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "binding;catalytic activity;cation
binding;endopeptidase activity;enzyme activator activity;enzyme regulator activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity,
acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded
organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part 4.97E-98 7 18 18 23.3
O60664-4;O60664-3;O60664;K7ERZ3;K7EL96;O60664-2;K7ER39;K7EJD0 Perilipin-3 PLIN3 >sp|O60664-4|PLIN3_HUMAN Isoform 4 of Perilipin-3 OS=Homo sapiens GN=PLIN3;>sp|O60664-3|PLIN3_HUMAN
Isoform 3 of Perilipin-3 OS=Homo sapiens GN=PLIN3;>sp|O60664|PLIN3_HUMAN Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3;>tr|K7ERZ3|K7ERZ3_HUMAN Perilipin-3 0.11 -0.19 0.07 -0.09 0.68
0.39 0.44 0.17 + 1.41134209 -0.444619877 cellular process;establishment of localization;transport;vesicle-mediated transport cell part;cytoplasmic part;endosomal part;endosome;endosome membrane;Golgi
apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part
4.01E-293 8 18 18 55.9
Q99536;B4DPX4;K7ERT7;B0AZP7;K7ESA3;K7ENX2;K7EM19;K7EJM4;K7ER81;Q9NQW1-5;Q9NQW1 Synaptic vesicle membrane protein VAT-1 homolog VAT1 >sp|Q99536|VAT1_HUMAN Synaptic vesicle
membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2;>tr|B4DPX4|B4DPX4_HUMAN Chromaffin granule amine transporter OS=Homo sapiens GN=VAT1 PE=2
SV=1;>tr|K7ERT7|K7ERT7_HUMAN Chromaffin granule amine transpor -0.38 0.01 -0.73 0.02 0.25 0.65 0.47 0.54 + 1.484878492 -0.74825368 biological regulation;cellular process;establishment of
localization;establishment of protein localization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental
process;negative regulation of mitochondrial fusion;negative regulation of mitochondrion organization;negative regulation of organelle organization;protein transport;regulation of anatomical structure morphogenesis;regulation
of biological process;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of mitochondrial fusion;regulation of mitochondrion organization;regulation of
organelle organization;transport;vesicle-mediated transport binding;catalytic activity;cation binding;ion binding;metal ion binding;oxidoreductase activity;transition metal ion binding;zinc ion binding cell part;coated vesicle
membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum membrane;endoplasmic reticulum part;ER to Golgi transport vesicle membrane;integral to membrane;intracellular
organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer
membrane;transport vesicle membrane;vesicle membrane Protein processing in endoplasmic reticulum 1.50E-109 11 18 18 56.2
P63010;P63010-2;Q7Z451;K7EJT8;K7EN71;K7ERB2 AP-2 complex subunit beta AP2B1 >sp|P63010|AP2B1_HUMAN AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1;>sp|P63010-
2|AP2B1_HUMAN Isoform 2 of AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1;>tr|Q7Z451|Q7Z451_HUMAN AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=2 SV= -0.18 -0.06 -0.16
0.08 0.25 0.21 0.05 0.16 + 1.372956224 -0.250907156 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen
processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and
presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component assembly;cellular
component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular
level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to stimulus;chemotaxis;clathrin coat assembly;enzyme
linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;immune system
process;intracellular protein transport;intracellular transport;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;negative regulation of biological process;negative regulation of cell
communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative
regulation of signaling;nerve growth factor receptor signaling pathway;organelle organization;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cell
communication;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of epidermal growth factor receptor signaling
pathway;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to
stress;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;synaptic transmission;taxis;transmembrane receptor

protein tyrosine kinase signaling pathway;transport;vesicle coating;vesicle organization;vesicle-mediated transport;viral reproduction protein transporter activity;substrate-specific transporter activity;transporter activity AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;clathrin coated vesicle membrane;clathrin-coated endocytic vesicle membrane;coated pit;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endocytic vesicle membrane;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;plasma membrane;protein complex;trans-Golgi network;vesicle membrane Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease 3.34E-259 6 33 18 38.6

Q9UQB8-3;Q9UQB8-5;Q9UQB8-4;Q9UQB8-6;Q9UQB8-2;Q9UQB8;I3L4C2;F8W878;B4DWA1;I3L327;I3L2M4;I3L3C6;I3L125;I3L0M4;I3L1C8;I3L526;I3L0Y9;I3L3J7;I3L113;I3L3C5;I3L2J6;I3L4A3 Brain-specific angiogenesis inhibitor 1-associated protein 2 BAIAP2 >sp|Q9UQB8-3|BAIP2_HUMAN Isoform 3 of Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2;>sp|Q9UQB8-5|BAIP2_HUMAN Isoform 5 of Brain-specific angiogenesis inhibitor 1-associated protein 2 OS=Homo sapiens GN=BAIAP2;>sp|Q9 0.22 0.19 0.33 0.08 -1.30 -0.92 -0.42 -0.93 + 2.001926947 1.099750798 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;anatomical structure development;anatomical structure morphogenesis;axonogenesis;biological regulation;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytoskeleton organization;defense response;dendrite development;developmental process;enzyme linked receptor protein signaling pathway;filopodium assembly;immune response;immune system process;innate immune response;insulin receptor signaling pathway;microspike assembly;multi-organism process;neuron projection development;neuron projection morphogenesis;organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of multicellular organismal process;regulation of neurological system process;regulation of organelle organization;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to other organism;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway "binding;binding, bridging;cytoskeletal adaptor activity;cytoskeletal protein binding;proline-rich region binding;protein binding;protein binding, bridging;protein C-terminus binding"cell junction;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;filopodium;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nucleus;organelle;plasma membrane;ruffle Adherens junction;Regulation of actin cytoskeleton 3.86E-199 22 19 19 51.6

P26006;P26006-1;B4DDT0;K7EMU3;H0YA32;D6R9X8;H0YA49 Integrin alpha-3;Integrin alpha-3 heavy chain;Integrin alpha-3 light chain ITGA3 >sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5;>sp|P26006-1|ITA3_HUMAN Isoform 2 of Integrin alpha-3 OS=Homo sapiens GN=ITGA3 -0.11 0.01 -0.25 0.08 -1.02 -0.87 -0.29 -0.64 + 1.456676153 0.63875034 behavior;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular process;cellular response to stimulus;coagulation;cognition;hemostasis;immune system process;integrin-mediated signaling pathway;learning or memory;leukocyte migration;locomotion;memory;multicellular organismal process;neurological system process;neuron migration;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;response to stimulus;signal transduction;system process binding;cation binding;ion binding;metal ion binding basolateral plasma membrane;cell part;cell surface;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex;synapse Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer 2.61E-144 7 19 19 21.3

P06756-3;P06756;P06756-2 Integrin alpha-V;Integrin alpha-V heavy chain;Integrin alpha-V light chain ITGAV >sp|P06756-3|ITAV_HUMAN Isoform 3 of Integrin alpha-V OS=Homo sapiens GN=ITGAV;>sp|P06756|ITAV_HUMAN Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2;>sp|P06756-2|ITAV_HUMAN Isoform 2 of Integrin alpha-V OS=Homo sapiens GN=ITGAV -0.73 -0.58 -0.09 0.08 0.14 0.58 0.68 0.84 + 1.44659532 -0.892231243 "anatomical structure formation involved in morphogenesis;angiogenesis;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptotic cell clearance;axon guidance;biological adhesion;biological regulation;blood coagulation;cell adhesion;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;coagulation;developmental process;endocytosis;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of organism into cell of other organism by promotion of phagocytosis in other organism involved in symbiotic interaction;entry of symbiont into host cell by promotion of host phagocytosis;entry of virus into host cell;ERK1 and ERK2 cascade;establishment of localization;extracellular matrix organization;extracellular structure organization;hemostasis;immune system process;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;leukocyte migration;locomotion;MAPKKK cascade;membrane invagination;membrane organization;modification by symbiont of host morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by symbiont of host cellular process;modulation by symbiont of host phagocytosis;modulation of phagocytosis in other organism involved in symbiotic interaction;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multicellular organismal process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of entry of bacterium into host cell;negative regulation of lipid storage;negative regulation of lipid transport;negative regulation of lipoprotein metabolic process;negative regulation of locomotion;negative regulation of low-density lipoprotein particle receptor biosynthetic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of macrophage derived foam cell differentiation;negative regulation of metabolic process;negative regulation of multi-organism process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of receptor biosynthetic process;negative regulation of transport;phagocytosis;positive regulation by organism of phagocytosis in other organism involved in symbiotic interaction;positive regulation by symbiont of host phagocytosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of locomotion;positive regulation of osteoblast proliferation;positive regulation of phagocytosis;positive regulation of transport;regulation of apoptosis;regulation of apoptotic cell clearance;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell adhesion;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of endocytosis;regulation of entry of bacterium into host cell;regulation of lipid storage;regulation of lipid transport;regulation of lipoprotein metabolic process;regulation of localization;regulation of locomotion;regulation of low-density lipoprotein particle receptor biosynthetic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of macrophage derived foam cell differentiation;regulation of metabolic process;regulation of multi-organism process;regulation of osteoblast proliferation;regulation of phagocytosis;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of receptor biosynthetic process;regulation of symbiosis, encompassing mutualism through parasitism;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis;transport;vesicle-mediated transport" binding;calcium channel activity;cation binding;cation channel activity;cation transmembrane transporter activity;channel activity;cytokine binding;gated channel activity;growth factor binding;ion binding;ion channel activity;ion transmembrane transporter activity;metal ion binding;passive transmembrane transporter activity;protein binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transforming growth factor beta binding;transmembrane transporter activity;transporter activity;voltage-gated calcium channel activity;voltage-gated cation channel activity;voltage-gated channel activity;voltage-gated ion channel activity alphav-beta3 integrin-IGF-1-IGF1R complex;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;external side of plasma membrane;integrin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;phagocytic vesicle;plasma membrane part;protein complex;receptor complex;vesicle Arrhythmogenic right ventricular cardiomyopathy (ARVC);Cell

adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Small cell lung cancer
1.17E-105 3 19 19 25
Q8NC51;Q8NC51-3;Q8NC51-2;Q8NC51-4 Plasminogen activator inhibitor 1 RNA-binding protein SERBP1 >sp|Q8NC51|PAIRB_HUMAN Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2;>sp|Q8NC51-3|PAIRB_HUMAN Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1;>sp|Q8NC51-2|PAIRB_HUMAN -0.06 -0.01 0.05 0.07 -0.27 -0.60 -0.22 -0.56 + 1.583485786 0.422787549 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;RNA metabolic processbinding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;RNA binding cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane
0 4 19 19 51.2
P55265-5;P55265;P55265-4;E7ENU4;P55265-3;H0YCK3;P55265-2 Double-stranded RNA-specific adenosine deaminase ADAR >sp|P55265-5|DSRAD_HUMAN Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR;>sp|P55265|DSRAD_HUMAN Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4;>sp|P55265-4|DSRAD_HUMAN Isoform 4 of D 0.24 0.09 0.11 0.15 -0.48 -0.44 -0.67 -0.24 + 2.124909165 0.605925675 adenosine to inosine editing;base conversion or substitution editing;biological regulation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;establishment of localization;establishment of localization in cell;establishment of protein localization;gene expression;gene silencing;gene silencing by RNA;immune effector process;immune system process;intracellular protein transport;intracellular transport;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA metabolic process;mRNA modification;mRNA processing;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;nitrogen compound metabolic process;nuclear export;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;positive regulation of biological process;positive regulation of reproductive process;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;protein export from nucleus;protein import;protein import into nucleus;protein targeting;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-alpha;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;RNA metabolic process;RNA modification;RNA processing;signal transduction;transport;type I interferon-mediated signaling pathway "adenosine deaminase activity;binding;catalytic activity;cation binding;deaminase activity;DNA binding;double-stranded RNA adenosine deaminase activity;double-stranded RNA binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;ion binding;metal ion binding;nucleic acid binding;RNA binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part Cytosolic DNA-sensing pathway;Measles 6.60E-140 7 20 20 27.1
P11717 Cation-independent mannose-6-phosphate receptor IGF2R >sp|P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3 -0.09 -0.10 -0.28 -0.18 0.40 0.24 0.19 0.23 + 2.151617153 -0.429411488 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;membrane invagination;membrane organization;receptor-mediated endocytosis;transport;vesicle-mediated transport "binding;carbohydrate binding;catalytic activity;glycoprotein binding;insulin-like growth factor-activated receptor activity;kinase activity;mannose binding;molecular transducer activity;monosaccharide binding;phosphoprotein binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein tyrosine kinase activity;receptor activity;signal transducer activity;signaling receptor activity;sugar binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity;transporter activity" cell part;cell surface;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;endosome;Golgi apparatus part;Golgi-associated vesicle;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;nuclear envelope lumen;nuclear part;organelle;organelle envelope lumen;organelle membrane;organelle part;plasma membrane part;trans-Golgi network transport vesicle;transport vesicle;vacuolar membrane;vacuolar part;vesicle Lysosome 1.87E-62 1 20 20 9
P18669;P15259;Q8N0Y7 Phosphoglycerate mutase 1 PGAM1 >sp|P18669|PGAM1_HUMAN Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2 -0.03 -0.07 -0.20 -0.01 0.17 0.22 0.36 0.14 + 1.732085696 -0.303448273 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;gamete generation;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;male gamete generation;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multicellular organismal process;multicellular organismal reproductive process;muscle contraction;muscle system process;primary metabolic process;regulation of biological process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of cellular amide metabolic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of generation of precursor metabolites and energy;regulation of glucose metabolic process;regulation of glycolysis;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide metabolic process;regulation of pentose-phosphate shunt;regulation of primary metabolic process;regulation of secondary metabolic process;reproductive process;respiratory burst;response to chemical stimulus;response to inorganic substance;response to mercury ion;response to metal ion;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;spermatogenesis;striated muscle contraction;system process "2,3-bisphosphoglycerate-dependent phosphoglycerate mutase activity;binding;bisphosphoglycerate 2-phosphatase activity;bisphosphoglycerate mutase activity;bisphosphoglycerate phosphatase activity;catalytic activity;cofactor binding;hydrolase activity;hydrolase activity, acting on ester bonds;intramolecular transferase activity;intramolecular transferase activity, phosphotransferases;isomerase activity;phosphatase activity;phosphoglycerate mutase activity;phosphoric ester hydrolase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Glycolysis / Gluconeogenesis;Methane metabolism 4.65E-261 3 20 20 78.3
P26373;P26373-2;J3QSB4;H3BTH3;J3KS98;H3BUK8 60S ribosomal protein L13 RPL13 >sp|P26373|RL13_HUMAN 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4;>sp|P26373-2|RL13_HUMAN Isoform 2 of 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13;>tr|J3QSB4|J3QSB4_HUMAN 60S ribosomal protein L13 (Fragment) OS=Homo sapiens GN=RPL13 0.02 0.00 0.12 0.04 -0.07 -0.44 -0.35 -0.38 + 1.568222348 0.35554699 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA

binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.23E-143 6 20 20 60.2

Q9Y230;B3KQ59;M0R0Y3;M0QXI6;M0R0Z0;M0QXZ7 RuvB-like 2 RUVBL2 >sp|Q9Y230|RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3;>tr|B3KQ59|B3KQ59_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=2 SV=1;>tr|M0R0Y3|M0R0Y3_HUMAN RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=4 SV=1 0.11 0.02 0.15 0.02 -0.22 -0.57 -0.03 -0.44 + 1.296363428 0.392331501 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to light stimulus;cellular response to radiation;cellular response to stimulus;cellular response to stress;cellular response to UV;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA recombination;DNA repair;histone acetylation;histone H2A acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein folding;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "5'-3' DNA helicase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent 5'-3' DNA helicase activity;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;damaged DNA binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;unfolded protein binding" cell part;chromatin remodeling complex;chromosomal part;cytoplasm;DNA helicase complex;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;histone methyltransferase complex;Ino80 complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;methyltransferase complex;MLL1 complex;NuA4 histone acetyltransferase complex;nuclear chromosome part;nuclear matrix;nuclear part;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex 1.23E-247 6 20 20 48.8

O60701;O60701-2;O60701-3;E7ER83;E7ETF4;E7EV97;E7ER95;D6RHF4;E9PBD2 UDP-glucose 6-dehydrogenase UGDH >sp|O60701|UGDH_HUMAN UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1;>sp|O60701-2|UGDH_HUMAN Isoform 2 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH;>sp|O60701-3|UGDH_HUMAN Isoform 3 of UDP-glucose 6-dehydrogenase OS=Homo sapiens GN -0.24 -0.38 -0.63 -0.31 1.30 0.67 0.74 0.32 + 1.869040814 -1.147604823 alcohol metabolic process;amine metabolic process;aminoglycan biosynthetic process;aminoglycan metabolic process;anatomical structure morphogenesis;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;embryonic morphogenesis;gastrulation;gastrulation with mouth forming second;glucose metabolic process;glucuronate biosynthetic process;glucuronate metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan metabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;UDP-glucose metabolic process;UDP-glucuronate biosynthetic process;UDP-glucuronate metabolic process;uronic acid metabolic process;xenobiotic metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;electron carrier activity;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;UDP-glucose 6-dehydrogenase activity" cell part;cytoplasmic part;cytosol;intracellular part Amino sugar and nucleotide sugar metabolism;Ascorbate and aldarate metabolism;Pentose and glucuronate interconversions;Starch and sucrose metabolism 9.14E-185 9 20 20 53.4

P09525;Q6P452;B4DDF9 Annexin A4;Annexin ANXA4 >sp|P09525|ANXA4_HUMAN Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4;>tr|Q6P452|Q6P452_HUMAN Annexin OS=Homo sapiens GN=ANXA4 PE=2 SV=1;>tr|B4DDF9|B4DDF9_HUMAN Annexin OS=Homo sapiens GN=ANXA4 PE=2 SV=1 -0.10 -0.22 -0.08 -0.12 0.17 0.46 0.71 0.50 + 1.851172609 -0.591824839 biological regulation;cellular process;cellular response to stimulus;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of coagulation;negative regulation of multicellular organismal process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of coagulation;regulation of multicellular organismal process;regulation of programmed cell death;response to stimulus;signal transduction binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phospholipase inhibitor activity;phospholipid binding cell part;cytoplasm;intracellular part 0 3 22 20 58

Q13464;C9JFJ0 Rho-associated protein kinase 1 ROCK1 >sp|Q13464|ROCK1_HUMAN Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1 0.01 -0.15 0.01 -0.14 0.33 0.39 0.41 0.04 + 1.465774778 -0.358883741 actin cytoskeleton organization;actin filament-based process;actin-mediated cell contraction;apical constriction;axon guidance;biological adhesion;biological regulation;bleb assembly;cell adhesion;cell projection assembly;cell projection organization;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;intracellular signal transduction;leukocyte cell-cell adhesion;leukocyte tethering or rolling;locomotion;membrane docking;membrane to membrane docking;multicellular organismal process;muscle contraction;muscle system process;negative regulation of angiogenesis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;organelle organization;Ras protein signal transduction;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of cell adhesion;regulation of cell death;regulation of cell differentiation;regulation of cell motility;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of establishment of cell polarity;regulation of establishment or maintenance of cell polarity;regulation of focal adhesion assembly;regulation of keratinocyte differentiation;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of neuron apoptosis;regulation of organelle organization;regulation of programmed cell death;regulation of stress fiber assembly;response to chemical stimulus;response to external stimulus;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction;smooth muscle contraction;system process;taxis "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;lipid binding;metal ion binding;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" bleb;cell part;cell projection;centriole;cytoplasmic part;cytoskeletal part;cytosol;Golgi apparatus part;Golgi membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;microtubule organizing center part;non-membrane-bounded organelle;organelle;organelle membrane;organelle part Axon guidance;Chemokine signaling pathway;Focal adhesion;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis;TGF-beta signaling pathway;Vascular smooth muscle contraction;Wnt signaling pathway 2.86E-119 2 24 20 22.1

C9J2Y9;P30876;C9J4M6 DNA-directed RNA polymerase;DNA-directed RNA polymerase II subunit RPB2 POLR2B >tr|C9J2Y9|C9J2Y9_HUMAN DNA-directed RNA polymerase OS=Homo sapiens GN=POLR2B PE=2 SV=2;>sp|P30876|RPB2_HUMAN DNA-directed RNA polymerase II subunit RPB2 OS=Homo sapiens GN=POLR2B PE=1 SV=1;>tr|C9J4M6|C9J4M6_HUMAN DNA-directed RNA polymerase OS=Homo sapien 0.08 0.35 -0.09 0.13 -0.24 -0.27 -0.12 -0.25 + 1.3966362 0.333936865 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA capping;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA capping;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent;transcription-coupled nucleotide-excision repair;viral reproductive process" "binding;catalytic activity;cation binding;chromatin binding;DNA binding;DNA-directed RNA polymerase activity;ion binding;metal ion binding;nucleic acid binding;nucleoside binding;nucleotidyltransferase activity;ribonucleoside binding;RNA polymerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" "cell part;DNA-directed RNA polymerase complex;DNA-directed RNA polymerase II, core complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear DNA-directed RNA polymerase complex;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;RNA polymerase complex" Huntington's disease;Purine metabolism;Pyrimidine metabolism;RNA polymerase 1.79E-100 3 21 21 24.9

Q9Y265;Q9Y265-2;E7ETR0;H7C4G5;J3QLR1;H7C4I3 RuvB-like 1 RUVBL1 >sp|Q9Y265|RUVB1_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1;>sp|Q9Y265-2|RUVB1_HUMAN Isoform 2 of RuvB-like 1 OS=Homo sapiens GN=RUVBL1;>tr|E7ETR0|E7ETR0_HUMAN RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=2 SV=1 0.09 0.00 0.08 0.02 -0.28 -0.52 -0.03 -0.44 + 1.341001482 0.363730015 "ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell division;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;covalent chromatin modification;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA recombination;DNA repair;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;gamete generation;histone acetylation;histone exchange;histone H2A acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;mitosis;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle fission;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;spermatogenesis;transcription, DNA-dependent" "5'-3' DNA helicase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent 5'-3' DNA helicase activity;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromatin remodeling complex;chromosomal part;cytoplasmic part;cytoskeletal part;DNA helicase complex;Golgi apparatus;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;histone methyltransferase complex;Ino80 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;methyltransferase complex;microtubule organizing center;MLL1 complex;NuA4 histone acetyltransferase complex;nuclear chromosome part;nuclear matrix;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex Wnt signaling pathway 1.01E-231 6 21 21 66.4

Q93008-1;Q93008;O00507;O00507-2;E9PFG1;H7C2M9 Probable ubiquitin carboxyl-terminal hydrolase FAF-X USP9X >sp|Q93008-1|USP9X_HUMAN Isoform 2 of Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X;>sp|Q93008|USP9X_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3 0.15 -0.10 -0.09 -0.22 0.40 0.34 0.61 0.10 + 1.33310072 -0.424455091 "biological regulation;biosynthetic process;BMP signaling pathway;catabolic process;cell cycle phase;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromosome segregation;enzyme linked receptor protein signaling pathway;female gamete generation;gamete generation;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;mitosis;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle fission;organelle organization;primary metabolic process;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;spermatogenesis;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;ubiquitin-dependent protein catabolic process" "binding;catalytic activity;co-SMAD binding;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;SMAD binding;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" apical part of cell;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part 1.34E-85 6 21 21 10.7

Q08J23-2;Q08J23;G3V1R4;D6RAS3 tRNA (cytosine(34)-C(5))-methyltransferase NSUN2 >sp|Q08J23-2|NSUN2_HUMAN Isoform 2 of tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2;>sp|Q08J23|NSUN2_HUMAN tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2;>tr|G3V1R4|G3V1R4_HUMAN NOL1/NOP2/Sun domain fami 0.27 0.06 0.12 0.04 -0.48 -0.49 -0.23 -0.32 + 2.04957808 0.500906098 cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;mitosis;nuclear division;organelle fission;organelle organization "binding;catalytic activity;methyltransferase activity;nucleic acid binding;RNA binding;RNA methyltransferase activity;S-adenosylmethionine-dependent methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups;tRNA (cytosine) methyltransferase activity;tRNA (cytosine-5-)-methyltransferase activity;tRNA binding;tRNA methyltransferase activity" cell part;cytoplasm;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;spindle 2.18E-188 4 22 21 38.5

P47895;H0Y2X5;H0YKF9;H0YNQ3;O94788-4;H0YMG7;O94788-3;O94788;H0YLT1 Aldehyde dehydrogenase family 1 member A3 ALDH1A3 ">sp|P47895|AL1A3_HUMAN Aldehyde dehydrogenase family 1 member A3 OS=Homo sapiens GN=ALDH1A3 PE=1 SV=2;>tr|H0Y2X5|H0Y2X5_HUMAN Aldehyde dehydrogenase 1 family, member A3, isoform CRA_b OS=Homo sapiens GN=ALDH1A3 PE=2 SV=1" -0.73 -0.75 -0.98 -0.49 0.70 1.44 1.73 1.98 + 2.308896896 -2.201345176 9-cis-retinoic acid biosynthetic process;9-cis-retinoic acid metabolic process;anatomical structure development;anatomical structure maturation;anatomical structure morphogenesis;anterior/posterior pattern specification;apocarotenoid metabolic process;appendage morphogenesis;biological regulation;biosynthetic process;blood vessel development;camera-type eye development;carboxylic acid metabolic process;cardiac muscle tissue development;cell communication;cell development;cell differentiation;cellular aldehyde metabolic process;cellular biosynthetic process;cellular developmental process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;determination of bilateral symmetry;developmental maturation;developmental process;digestive tract development;diterpenoid metabolic process;embryonic appendage morphogenesis;embryonic camera-type eye development;embryonic digestive tract development;embryonic eye morphogenesis;embryonic forelimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic organ development;embryonic organ morphogenesis;eye development;eye morphogenesis;face development;fat-soluble vitamin biosynthetic process;fat-soluble vitamin metabolic process;forelimb morphogenesis;gland development;heart morphogenesis;hindbrain development;hormone metabolic process;intracellular receptor mediated signaling pathway;isoprenoid biosynthetic process;isoprenoid metabolic process;kidney development;limb morphogenesis;lipid biosynthetic process;lipid metabolic process;liver development;lung development;mesenchymal cell development;metabolic process;midgut development;monocarboxylic acid metabolic process;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;muscle tissue development;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;neural crest cell development;neural nucleus development;neural tube development;neuron differentiation;nucleus accumbens development;olfactory pit development;optic cup morphogenesis involved in camera-type eye development;organ development;organ maturation;organ morphogenesis;organic acid metabolic process;oxoacid metabolic process;pancreas development;pattern specification process;pituitary gland development;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of programmed cell death;primary metabolic process;proximal/distal pattern formation;regionalization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of gene expression;regulation of hormone levels;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of programmed cell death;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to retinoic acid;response to steroid hormone stimulus;response to stimulus;response to vitamin;response to vitamin A;retinal metabolic process;retinoic acid biosynthetic process;retinoic acid metabolic process;retinoic acid receptor signaling pathway;retinoid metabolic process;retinol metabolic process;sensory organ development;signal transduction;small molecule biosynthetic process;small molecule metabolic process;specification of symmetry;striated muscle tissue development;terpenoid metabolic process;tissue development;tissue morphogenesis;ureter maturation;vitamin A biosynthetic process;vitamin A metabolic process;vitamin biosynthetic process;vitamin metabolic process "3-chloroallyl aldehyde dehydrogenase activity;aldehyde dehydrogenase (NAD) activity;aldehyde dehydrogenase [NAD(P)+] activity;binding;catalytic activity;coenzyme binding;cofactor binding;hormone binding;identical protein binding;isoprenoid binding;lipid binding;NAD binding;NAD+ binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;protein binding;protein dimerization activity;protein homodimerization activity;retinal binding;retinal dehydrogenase activity;retinoid binding;thyroid hormone binding;vitamin binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm beta-Alanine metabolism;Drug metabolism - cytochrome P450;Glycolysis / Gluconeogenesis;Histidine metabolism;Metabolism of xenobiotics by cytochrome P450;Phenylalanine metabolism;Retinol metabolism;Tyrosine metabolism 4.14E-195 9 24 21 48.6

Q9UQ80;F8VR77;F8W0A3;H0YIN7;F8VZ69 Proliferation-associated protein 2G4 PA2G4 >sp|Q9UQ80|PA2G4_HUMAN Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3;>tr|F8VR77|F8VR77_HUMAN Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=2 SV=1 0.14 0.04 0.02 0.00 -0.39 -0.68 -0.24 -0.44 + 1.835530422 0.492823569 "biological regulation;biosynthetic process;cell cycle arrest;cell cycle process;cell proliferation;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;RNA biosynthetic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;transcription, DNA-dependent" binding;catalytic activity;DNA binding;hydrolase activity;nucleic acid binding;nucleic acid binding transcription factor activity;RNA binding;sequence-specific DNA binding transcription factor activity cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex 5.04E-228 5 22 22 55.1

O00469-2;E7ETU9;O00469;B3KWS3;C9JXZ0;F8WEW3 "Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2" PLOD2 ">sp|O00469-2|PLOD2_HUMAN Isoform 2 of Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2;>tr|E7ETU9|E7ETU9_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2 PE=2 SV=1;>sp|O00469|PLOD2_HUMAN Procollagen" -1.28 -0.97 -1.25 -0.30 2.13 2.57 1.02 1.78 + 2.242437194 -2.826530613 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification process;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress "binding;carboxylic acid binding;catalytic activity;cation binding;dioxygenase activity;ion binding;iron ion binding;L-ascorbic acid binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptidyl-lysine 5-dioxygenase activity;procollagen-lysine 5-dioxygenase activity;transition metal ion binding;vitamin binding" cell part;collagen;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular matrix part;extracellular region part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;rough endoplasmic reticulum membrane Lysine degradation 9.37E-150 6 22 22 34.8

P50454;E9PPV6;E9PR70;E9PK86;E9PMI5;E9PKH2;E9PNX1;E9PJH8;E9PIG2;E9PRS3;E9PQ34;E9PLA6;H0YEP8 Serpin H1 SERPINH1 >sp|P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2;>tr|E9PPV6|E9PPV6_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=2 SV=1;>tr|E9PR70|E9PR70_HUMAN Serpin H1 (Fragment) OS=Homo sapiens GN=SERPINH1 PE=2 SV=1;>tr|E9PK86|E9PK86_HUMAN Serpin -0.34 -0.41 -0.51 -0.19 1.01 0.37 0.79 0.46 + 2.074610646 -1.017582029 biological regulation;biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen biosynthetic process;collagen fibril organization;collagen metabolic process;extracellular matrix organization;extracellular structure organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;primary metabolic process;protein maturation;protein metabolic process;regulation of biological process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein binding;collagen binding;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;protein binding;serine-type endopeptidase inhibitor activity cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part 1.98E-237 13 22 22 60

P05556;P05556-2;P05556-5;P05556-4;P05556-3;H7C4N8;E7EQW5;C9JPK5;Q5T3E6;E9PLR6;E7EUI6;E7ERX5 Integrin beta-1 ITGB1 >sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2;>sp|P05556-2|ITB1_HUMAN Isoform Beta-1B of Integrin beta-1 OS=Homo sapiens GN=ITGB1;>sp|P05556-5|ITB1_HUMAN Isoform Beta-1D of Integrin beta-1 OS=Homo sapiens GN=ITGB1;>sp|P05556-4|IT -0.04 -0.02 -0.10 0.00 -0.23 -0.35 -0.22 -0.15 + 1.591185974 0.196856157 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;anatomical structure homeostasis;axon guidance;B cell activation;B cell differentiation;biological adhesion;biological regulation;blood coagulation;blood vessel endothelial cell migration;calcium ion homeostasis;calcium-independent cell-matrix adhesion;cardiac cell differentiation;cardiac muscle cell differentiation;cation homeostasis;cell activation;cell adhesion;cell adhesion mediated by integrin;cell communication;cell cycle process;cell differentiation;cell fate specification;cell junction assembly;cell junction organization;cell migration;cell migration involved in sprouting angiogenesis;cell motility;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell adhesion mediated by integrin;cell-cell junction assembly;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular defense response;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular membrane organization;cellular metal ion homeostasis;cellular process;cellular process involved in reproduction;cellular response to abiotic stimulus;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to ionizing radiation;cellular response to mechanical stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to radiation;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin D;chemical homeostasis;chemotaxis;chordate embryonic development;coagulation;cytoskeleton organization;defense response;developmental process;divalent inorganic cation homeostasis;embryo development;embryo development ending in birth or egg hatching;endothelial cell migration;establishment of localization;establishment of localization in cell;establishment of protein localization;extracellular matrix organization;extracellular structure organization;G1/S transition of mitotic cell cycle;germ cell migration;hemostasis;homeostatic process;homophilic cell adhesion;immune system process;in utero embryonic development;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;ion homeostasis;leukocyte activation;leukocyte cell-cell adhesion;leukocyte differentiation;leukocyte migration;locomotion;lymphocyte activation;lymphocyte differentiation;maternal process involved in female pregnancy;membrane organization;metal ion homeostasis;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell differentiation;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neuron differentiation;negative regulation of programmed cell death;neuron projection development;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cell-substrate adhesion;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of endocytosis;positive regulation of intracellular protein kinase cascade;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of neuron differentiation;positive regulation of neuron projection development;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transport;protein transport;protein transport within lipid bilayer;regulation of anoikis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cell-substrate adhesion;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of endocytosis;regulation of G-protein coupled receptor protein signaling pathway;regulation of immune response;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to abiotic stimulus;response to activity;response to chemical stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to gonadotropin stimulus;response to growth factor stimulus;response to hormone stimulus;response to ionizing radiation;response to mechanical stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to radiation;response to stimulus;response to stress;response to transforming growth factor beta stimulus;response to vitamin;response to vitamin D;sarcomere organization;signal transduction;striated muscle cell differentiation;taxis;tight junction assembly;tissue homeostasis;transport;viral reproductive process;virus-host interaction actin binding;binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;peptide binding;protein binding;protein dimerization activity;protein heterodimerization activity;receptor activity acrosomal vesicle;adherens junction;alpha3-beta1 integrin complex;alpha8-beta1 integrin complex;alpha9-beta1 integrin complex;anchoring junction;basement membrane;cell division site part;cell junction;cell part;cell projection;cell surface;cell-cell contact zone;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cleavage furrow;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;external side of plasma membrane;extracellular matrix part;extracellular region part;filopodium;focal adhesion;hemidesmosome;integrin complex;intercalated disc;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;myelin sheath abaxonal region;neuromuscular junction;organelle;pigment granule;plasma membrane;plasma membrane part;protein complex;receptor complex;ruffle;sarcolemma;stored secretory granule;synapse;vesicle Arrhythmogenic right ventricular cardiomyopathy (ARVC);Axon guidance;Bacterial invasion of epithelial cells;Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leishmaniasis;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Shigellosis;Small cell lung cancer;Toxoplasmosis 6.34E-208 12 23 22 31.1

H0Y4R1;P12268;E7ETK5 Inosine-5-monophosphate dehydrogenase 2 IMPDH2 >tr|H0Y4R1|H0Y4R1_HUMAN Inosine-5-monophosphate dehydrogenase 2 (Fragment) OS=Homo sapiens GN=IMPDH2 PE=3 SV=1;>sp|P12268|IMDH2_HUMAN Inosine-5-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2 0.27 0.01 0.24 0.10 -0.33 -0.64 -0.15 -0.73 + 1.603873642 0.618086896 anatomical structure development;biosynthetic process;cell activation;cell proliferation;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;developmental process;GMP biosynthetic process;GMP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;immune system process;leukocyte activation;leukocyte proliferation;lymphocyte activation;lymphocyte proliferation;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;mononuclear cell proliferation;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;retina development in camera-type eye;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;DNA binding;IMP dehydrogenase activity;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;RNA binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microbody;microbody membrane;microbody part;nucleus;organelle;organelle membrane;organelle part;peroxisomal membrane;peroxisomal part Drug metabolism - other enzymes;Purine metabolism 1.01E-255 3 24 22 53.6

F5H365;Q15436;F5H6C4;B3KXI2;G3V4V1;G3V1W4;G3V3G5;G3V2R6;G3V5X8;G3V4Q2;G3V5K1 Protein transport protein Sec23A SEC23A >tr|F5H365|F5H365_HUMAN Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=2 SV=1;>sp|Q15436|SC23A_HUMAN Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2;>tr|F5H6C4|F5H6C4_HUMAN Protein transport protein Sec23A OS=Homo sapien 0.00 -0.15 -0.14 -0.09 0.91 0.75 0.36 0.44 + 1.874485753 -0.711384096 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;small molecule metabolic process;transport;vesicle coating;vesicle organization;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;coated vesicle membrane;COPII vesicle coat;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;ER to Golgi transport vesicle membrane;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;smooth endoplasmic reticulum membrane;transport vesicle membrane;vesicle coat;vesicle membrane Protein processing in endoplasmic reticulum 7.68E-235 11 25 22 39.9

O14617;O14617-5;O14617-4;O14617-3;E7EMM2;O14617-2;G5E988;K7ELX8;K7ERW8 AP-3 complex subunit delta-1 AP3D1 >sp|O14617|AP3D1_HUMAN AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1 PE=1 SV=1;>sp|O14617-5|AP3D1_HUMAN Isoform 5 of AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1;>sp|O14617-4|AP3D1_HUMAN Isoform 4 of AP-3 complex subunit delta-1 OS=Homo sa 0.03 -0.09 -0.28 -0.40 0.37 0.19 0.56 0.13 + 1.449053484 -0.497463941 "anterograde axon cargo transport;anterograde synaptic vesicle transport;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of lipid antigen via MHC class Ib;antigen processing and presentation via MHC class Ib;antigen processing and presentation, exogenous lipid antigen via MHC class Ib;axon cargo transport;biological regulation;biosynthetic process;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cytoskeleton-dependent intracellular transport;establishment of localization;establishment of localization in cell;establishment of protein localization;eye pigment biosynthetic process;eye pigment metabolic process;immune system process;intracellular protein transport;intracellular transport;localization;macromolecule localization;membrane organization;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;pigment biosynthetic process;pigment metabolic process;pigment metabolic process involved in developmental pigmentation;pigment metabolic process involved in pigmentation;positive regulation of alpha-beta T cell activation;positive regulation of alpha-beta T cell differentiation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of NK T cell differentiation;positive regulation of T cell activation;positive regulation of T cell differentiation;protein localization;protein localization to organelle;protein transport;regulation of alpha-beta T cell activation;regulation of alpha-beta T cell differentiation;regulation of biological process;regulation of cell activation;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of homeostatic process;regulation of immune system process;regulation of ion homeostasis;regulation of leukocyte activation;regulation of localization;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of NK T cell differentiation;regulation of sequestering of zinc ion;regulation of T cell activation;regulation of T cell differentiation;synaptic vesicle membrane organization;synaptic vesicle transport;transport;vesicle-mediated transport" protein transporter activity;substrate-specific transporter activity;transporter activity axon part;cell part;cell projection part;cytoplasmic part;endosomal part;endosome membrane;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex;synapse part;terminal button Lysosome 1.05E-127 9 23 23 25.1

F5H897;Q12931;I3L0K7;I3L239;I3L2D5;I3L253 "Heat shock protein 75 kDa, mitochondrial" TRAP1 ">tr|F5H897|F5H897_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=2 SV=1;>sp|Q12931|TRAP1_HUMAN Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3;>tr|I3L0K7|I3L0K7_HUMAN Heat shock protein 75 kDa, mitoch" 0.11 0.06 0.19 0.05 -0.32 -0.72 -0.50 -0.79 + 2.074791778 0.685381338 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cytokine receptor binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;tumor necrosis factor receptor binding;tumor necrosis factor receptor superfamily binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 5.77E-293 6 24 23 49.3

P02786;G3V0E5;F5H6B1;H7C3V5;F8WBE5 "Transferrin receptor protein 1;Transferrin receptor protein 1, serum form"TFRC ">sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2;>tr|G3V0E5|G3V0E5_HUMAN Transferrin receptor (P90, CD71), isoform CRA_c OS=Homo sapiens GN=TFRC PE=2 SV=1;>tr|F5H6B1|F5H6B1_HUMAN Transferrin receptor protein 1, serum f" 0.21 0.19 -1.12 -0.61 0.79 0.73 0.72 0.80 + 1.35515269 -1.091328815 biological regulation;cation homeostasis;cation transport;cell differentiation;cellular cation homeostasis;cellular chemical homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;chemical homeostasis;developmental process;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;leukocyte differentiation;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;multi-organism process;myeloid cell differentiation;myeloid leukocyte differentiation;osteoclast differentiation;positive regulation of biological process;positive regulation of bone remodeling;positive regulation of bone resorption;positive regulation of homeostatic process;positive regulation of multicellular organismal process;positive regulation of tissue remodeling;primary metabolic process;protein metabolic process;protein transport;proteolysis;regulation of biological process;regulation of biological quality;regulation of bone remodeling;regulation of bone resorption;regulation of homeostatic process;regulation of multicellular organismal process;regulation of tissue remodeling;reproductive process;transferrin transport;transition metal ion transport;transmembrane transport;transport;viral reproductive process;virus-host interaction cargo receptor activity;catalytic activity;hydrolase activity;peptidase activity;receptor activity;transferrin receptor activity cell part;coated pit;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endosome;external side of plasma membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region;extracellular region part;extracellular vesicular exosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;perinuclear region of cytoplasm;pigment granule;plasma membrane part;vesicle Endocytosis;Hematopoietic cell lineage;Phagosome 1.69E-186 5 24 24 38.2

Q9UMD9-2;Q9UMD9;A2A2Y8 Collagen alpha-1(XVII) chain;120 kDa linear IgA disease antigen;97 kDa linear IgA disease antigen COL17A1 >sp|Q9UMD9-2|COHA1_HUMAN Isoform 2 of Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1;>sp|Q9UMD9|COHA1_HUMAN Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL17A1 PE=1 SV=3;>tr|A2A2Y8|A2A2Y8_HUMAN Collagen alpha-1(XVII) chain OS=Homo sapiens GN=C -0.34 0.11 -0.06 0.15 -1.82 -1.06 -0.51 -0.81 + 1.366902804 1.018288672 anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;developmental process;epidermis development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;tissue development basement membrane;cell junction;cell part;cell-cell junction;cell-substrate junction;collagen;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region;extracellular region part;hemidesmosome;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane part Protein digestion and absorption 5.58E-115 3 25 24 17.7

O43143;B0V0F8 Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15DHX15 >sp|O43143|DHX15_HUMAN Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 0.27 0.24 0.07 0.17 -0.02 -0.23 -0.54 -0.40 + 1.568612649 0.486302513 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA helicase activity" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complexSpliceosome 1.12E-124 2 25 24 37

P23396;P23396-2;E9PL09;E9PPU1;F2Z2S8;H0YCJ7;E9PL45;H0YF32;H0YEU2;E9PQ96;E9PJH4;E9PK82;E9PSF4;E9PQX2;H0YES8 40S ribosomal protein S3 RPS3 >sp|P23396|RS3_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2;>sp|P23396-2|RS3_HUMAN Isoform 2 of 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3;>tr|E9PL09|E9PL09_HUMAN 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=2 SV=1;>tr|E9PP 0.02 0.04 -0.03 -0.01 -0.27 -0.52 -0.19 -0.30 + 1.687243835 0.325578284 "activation of caspase activity;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;induction of apoptosis;induction of programmed cell death;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA repair;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of sequence-specific DNA binding transcription factor activity;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;positive regulation of programmed cell death;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of DNA metabolic process;regulation of DNA repair;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" "binding;carbon-oxygen lyase activity;catalytic activity;damaged DNA binding;DNA binding;DNA-(apurinic or apyrimidinic site) lyase activity;endonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;iron-sulfur cluster binding;lyase activity;metal cluster binding;mRNA binding;nuclease activity;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity" cell part;cell projection membrane;cell projection part;cytoplasm;cytoplasmic part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part;ribonucleoprotein complex;ribosome;ruffle membrane;small ribosomal subunit Ribosome 5.92E-291 15 25 24 81.5

P18124;A8MUD9;C9JIJ5;C9JZ88;H0Y4W2;Q9Y4A5-2;F2Z2U4;Q9Y4A5 60S ribosomal protein L7 RPL7 >sp|P18124|RL7_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1;>tr|A8MUD9|A8MUD9_HUMAN 60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=2 SV=1 -0.03 -0.01 0.22 0.06 -0.04 -0.46 -0.30 -0.42 + 1.355706922 0.364498386 "biological regulation;biosynthetic process;catabolic process;cell cycle checkpoint;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;cotranslational protein targeting to membrane;covalent chromatin modification;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;histone acetylation;histone deubiquitination;histone H2A acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic cell cycle checkpoint;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein complex disassembly;protein complex subunit organization;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;transcription, DNA-dependent;translational elongation;translational initiation;translational termination;transport;viral transcription" "binding;catalytic activity;DNA binding;mRNA binding;nucleic acid binding;phosphotransferase activity, alcohol group as acceptor;protein binding transcription factor activity;RNA binding;structural constituent of ribosome;structural molecule activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytosolic large ribosomal subunit;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;NuA4 histone acetyltransferase complex;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;PCAF complex;protein complex;ribonucleoprotein complex;SAGA-type complex;STAGA complex;transcription factor complex;transcription factor TFTC complex Ribosome 1.52E-162 8 25 25 63.3

P50570-2;P50570-5;P50570;P50570-3;P50570-4;F5H4R9;E5RHK8;Q9UQ16-2;Q9UQ16-3;Q9UQ16;Q9UQ16-4;Q6P2G1;E5RIK2;K7ELR1;K7EPK9 Dynamin-2 DNM2 >sp|P50570-2|DYN2_HUMAN Isoform 2 of Dynamin-2 OS=Homo sapiens GN=DNM2;>sp|P50570-5|DYN2_HUMAN Isoform 5 of Dynamin-2 OS=Homo sapiens GN=DNM2;>sp|P50570|DYN2_HUMAN Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2;>sp|P50570-3|DYN2_HUMAN Isoform 3 of Dynamin-2 O -0.03 -0.07 0.07 -0.06 0.42 0.38 0.24 0.11 + 1.557780237 -0.31145865 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;catabolic process;cation transport;cell cycle process;cell projection assembly;cell projection organization;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;ferric iron transport;filopodium assembly;G2/M transition of mitotic cell cycle;Golgi vesicle transport;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;immune system process;intracellular transport;ion transport;iron ion transport;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;metal ion transport;microspike assembly;nitric oxide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;post-Golgi vesicle-mediated transport;primary metabolic process;protein transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oxidoreductase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;synapse assembly;synapse organization;synaptic vesicle transport;transferrin transport;transition metal ion transport;transport;vesicle-mediated transport"	"binding;catalytic activity;cytoskeletal protein binding;enzyme binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;microtubule binding;nucleoside-triphosphatase activity;nucleotide binding;phospholipid binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;tubulin binding"	cell junction;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endocytic vesicle membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule;midbody;mitochondrion;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;postsynaptic density;postsynaptic membrane;protein complex;synapse part;synaptic membrane;vesicle membrane	Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Fc gamma R-mediated phagocytosis	2.43E-164	15	34	25	43.8

Q15942;H0Y2Y8;B4DQX7;B4DQR8;C9IZ41;H7C3D3;H7C3R3;C9JJK5	Zyxin	ZYX	>sp|Q15942|ZYX_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1;>tr|H0Y2Y8|H0Y2Y8_HUMAN Zyxin (Fragment) OS=Homo sapiens GN=ZYX PE=2 SV=1;>tr|B4DQX7|B4DQX7_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=2 SV=1;>tr|B4DQR8|B4DQR8_HUMAN Zyxin OS=Homo sapiens GN=ZYX PE=2 S	-0.49	-0.29	0.11	-0.06	0.50	0.32	0.24	0.20	+	1.362998916	-0.494258984	biological adhesion;biological regulation;cell adhesion;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;interaction with host;interspecies interaction between organisms;multi-organism process;regulation of biological process;regulation of cellular process;reproductive process;response to stimulus;signal transduction;signaling;viral reproductive process;virus-host interaction	binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding	actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeletal part;focal adhesion;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part;stress fiber	Focal adhesion	1.33E-295	8	26	26	60.8

P08758;D6RBL5;E9PHT9;D6RBE9;D6RCN3	Annexin A5;Annexin	ANXA5	>sp|P08758|ANXA5_HUMAN Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2;>tr|D6RBL5|D6RBL5_HUMAN Annexin OS=Homo sapiens GN=ANXA5 PE=2 SV=1;>tr|E9PHT9|E9PHT9_HUMAN Annexin OS=Homo sapiens GN=ANXA5 PE=2 SV=1;>tr|D6RBE9|D6RBE9_HUMAN Annexin OS=Homo sapiens GN=AN	-0.05	-0.35	0.01	-0.07	0.86	0.54	0.54	0.24	+	1.667884125	-0.655832265	biological regulation;blood coagulation;cellular process;cellular response to stimulus;coagulation;hemostasis;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of coagulation;negative regulation of multicellular organismal process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell death;regulation of cellular process;regulation of coagulation;regulation of multicellular organismal process;regulation of programmed cell death;response to chemical stimulus;response to organic substance;response to stimulus;signal transduction	binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;cell surface binding;enzyme inhibitor activity;enzyme regulator activity;eukaryotic cell surface binding;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phospholipase inhibitor activity;phospholipid binding	blood microparticle;cell part;cytoplasm;endothelial microparticle;external side of plasma membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular part;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane part;vesicle
0	5	28	26	73.8

P21399;Q9HBB2;Q5VZA6;F5H2R8;F5H143;F5H3Z7;Q6ZMR1;E9PEF1;O00408-4;F6W5Z0;O00408	Cytoplasmic aconitate hydratase	ACO1;IRP1	>sp|P21399|ACOC_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3;>tr|Q9HBB2|Q9HBB2_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=IRP1 PE=2 SV=1	-0.37	-0.23	-0.59	0.05	0.62	0.67	0.64	0.16	+	1.693063332	-0.809523065	"acetyl-CoA catabolic process;acetyl-CoA metabolic process;anatomical structure development;biological regulation;blood coagulation;cAMP catabolic process;cAMP metabolic process;cAMP-mediated signaling;carboxylic acid metabolic process;catabolic process;cation homeostasis;cell development;cell differentiation;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to cGMP;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to drug;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to granulocyte macrophage colony-stimulating factor stimulus;cellular response to growth factor stimulus;cellular response to macrophage colony-stimulating factor stimulus;cellular response to mechanical stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to transforming growth factor beta stimulus;cGMP catabolic process;cGMP metabolic process;cGMP-mediated signaling;chemical homeostasis;circulatory system process;citrate metabolic process;coagulation;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;cyclic nucleotide catabolic process;cyclic nucleotide metabolic process;cyclic-nucleotide-mediated signaling;developmental process;digestive system process;endothelial cell development;epithelial cell development;establishment of endothelial barrier;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;hemostasis;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;intestinal absorption;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;iron ion homeostasis;leukocyte differentiation;metabolic process;metal ion homeostasis;mitochondrial transport;monocyte differentiation;multicellular organismal process;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cAMP biosynthetic process;negative regulation of cAMP metabolic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cyclic nucleotide biosynthetic process;negative regulation of cyclic nucleotide metabolic process;negative regulation of gene expression;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleotide biosynthetic process;negative regulation of nucleotide metabolic process;negative regulation of protein import into nucleus, translocation;negative regulation of protein transport;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transport;negative regulation of vascular permeability;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate catabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of defense response;positive regulation of inflammatory response;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of vascular permeability;post-embryonic development;posttranscriptional regulation of gene expression;primary metabolic process;protein import;protein targeting;protein targeting to mitochondrion;protein transport;purine nucleotide catabolic process;purine nucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of defense response;regulation of establishment of protein localization;regulation of gene expression;regulation of inflammatory response;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of transmembrane transport;regulation of transport;regulation of vascular permeability;response to abiotic stimulus;response to cGMP;response to chemical stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to granulocyte macrophage colony-stimulating factor stimulus;response to growth factor stimulus;response to inorganic substance;response to iron ion;response to iron(II) ion;response to macrophage colony-stimulating factor stimulus;response to mechanical stimulus;response to metal ion;response to organic substance;response to stimulus;response to transforming growth factor beta stimulus;second-messenger-mediated signaling;signal transduction;small molecule metabolic process;system process;transport;tricarboxylic acid cycle;tricarboxylic acid metabolic process;vascular process in circulatory system" "3',5'-cyclic-nucleotide phosphodiesterase activity;4 iron, 4 sulfur cluster binding;aconitate hydratase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;AMP binding;binding;calcium channel activity;cAMP binding;carbon-oxygen lyase activity;catalytic activity;cation binding;cation channel activity;cation transmembrane transporter activity;cGMP binding;cGMP-stimulated cyclic-nucleotide phosphodiesterase activity;channel activity;citrate hydro-lyase (cis-aconitate-forming) activity;cyclic nucleotide binding;cyclic-nucleotide phosphodiesterase activity;drug binding;GMP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on ester bonds;hydro-lyase activity;ion binding;ion channel activity;ion transmembrane transporter activity;iron-responsive element binding;iron-sulfur cluster binding;isocitrate hydro-lyase (cis-aconitate-forming) activity;lyase activity;metal cluster binding;metal ion binding;mRNA binding;nucleic acid binding;nucleotide binding;passive transmembrane transporter activity;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" axon;cell part;cell projection;cytoplasmic part;cytosol;dendrite;endoplasmic reticulum;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;neuron projection;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane;presynaptic membrane;synapse part;synaptic membrane Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism;Purine metabolism 2.79E-226 11 27 27 43.2

P78347-2;P78347-4;P78347-3;P78347;Q86U51;C9J6M0;H7BYM4;G8JLD9;Q86UP8-3;Q86UP8;Q6EKJ0 General transcription factor II-I GTF2I >sp|P78347-2|GTF2I_HUMAN Isoform 2 of General transcription factor II-I OS=Homo sapiens GN=GTF2I;>sp|P78347-4|GTF2I_HUMAN Isoform 4 of General transcription factor II-I OS=Homo sapiens GN=GTF2I;>sp|P78347-3|GTF2I_HUMAN Isoform 3 of General transcription fa 0.05 0.30 0.02 0.20 -0.37 -0.48 -0.74 -0.41 + 2.053093429 0.643708416 "biological regulation;biosynthetic process;calcium ion homeostasis;cation homeostasis;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chemical homeostasis;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;embryo development;homeostatic process;ion homeostasis;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;metal ion homeostasis;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of developmental process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;reduction of cytosolic calcium ion concentration;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity cell body;cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;neuronal cell body;nucleus;organelle Basal transcription factors 5.08E-175 11 27 27 38.9

Q92614-4;Q92614;J3KNX9;Q92614-3;Q92614-2;Q92614-5;H0YEV9 Unconventional myosin-XVIIIa MYO18A >sp|Q92614-4|MY18A_HUMAN Isoform 4 of Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A;>sp|Q92614|MY18A_HUMAN Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3;>tr|J3KNX9|J3KNX9_HUMAN Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO 0.00 0.55 0.30 0.51 -0.57 0.02 -0.45 -0.09 + 1.323660533 0.611640353 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;biological regulation;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoskeleton organization;DNA metabolic process;locomotion;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;DNA binding;DNA-dependent ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actomyosin;cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;myosin complex;organelle;organelle part;protein complex 3.72E-128 7 27 27 18.4

P61247;F5H4F9;E9PFI5;H0Y9Y4;D6RG13;D6RAT0;H0Y8L7;D6RB09;D6R9B6;D6RAS7;D6RI02;D6RED7;D6RGE0 40S ribosomal protein S3a RPS3A >sp|P61247|RS3A_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2;>tr|F5H4F9|F5H4F9_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=2 SV=1;>tr|E9PFI5|E9PFI5_HUMAN 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=2 SV=1;>tr -0.13 -0.02 0.09 0.02 -0.38 -0.68 -0.26 -0.38 + 1.606530513 0.417918929 "biological regulation;biosynthetic process;catabolic process;cell differentiation;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;induction of apoptosis;induction of programmed cell death;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 1.64E-195 13 27 27 72.3

O75083;O75083-3;D6RD66 WD repeat-containing protein 1 WDR1 >sp|O75083|WDR1_HUMAN WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4;>sp|O75083-3|WDR1_HUMAN Isoform 2 of WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1;>tr|D6RD66|D6RD66_HUMAN WD repeat-containing protein 1 (Fragment) OS=Homo sap0.03 -0.10 -0.37 -0.15 0.58 0.56 0.66 0.32 + 2.061350869 -0.680063903 cell activation;cellular process;establishment of localization;establishment of localization in cell;exocytosis;multicellular organismal process;neurological system process;platelet activation;platelet degranulation;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;system process;transport;vesicle-mediated transport cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 2.42E-278 3 27 27 59.9

Q9Y4K1;B4DU04;Q96QW7 Absent in melanoma 1 protein AIM1 >sp|Q9Y4K1|AIM1_HUMAN Absent in melanoma 1 protein OS=Homo sapiens GN=AIM1 PE=1 SV=3 -0.12 0.19 0.20 0.39 -0.29 -0.41 -0.49 -0.45 + 1.816703839 0.574009178 1.19E-226 3 28 28 24.1

P56192;A6NC17;B3KVK7;H0YIP0;H0YHV5;H0YIC2;H0YI94;F5H2V6;F8VPL7;F8VS26;H0YHL6;F8W0M7;F8W0S4;F8VZZ9;H0YI27;Q96PB7-6;Q96PB7-4;Q96PB7-2;REV__Q0VDD8;REV__Q0VDD8-4 "Methionine--tRNA ligase, cytoplasmic" MARS ">sp|P56192|SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2;>tr|A6NC17|A6NC17_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=2 SV=3;>tr|B3KVK7|B3KVK7_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo" 0.08 -0.04 0.12 0.01 -0.22 -0.44 -0.13 -0.50 + 1.510378565 0.364965697 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;methionyl-tRNA aminoacylation;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;methionine-tRNA ligase activity;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Aminoacyl-tRNA biosynthesis;Selenocompound metabolism 2.61E-273 20 28 28 41.3

Q9Y6K5;F8VWK9;F8VS35;F8VW22;H0YHL3 2-5-oligoadenylate synthase 3OAS3 >sp|Q9Y6K5|OAS3_HUMAN 2-5-oligoadenylate synthase 3 OS=Homo sapiens GN=OAS3 PE=1 SV=3 0.52 0.38 0.13 -0.05 -2.21 -1.58 -0.72 -0.82 + 1.618788137 1.576929277 biological regulation;cell surface receptor linked signaling pathway;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;immune effector process;immune response;immune system process;interferon-gamma-mediated signaling pathway;metabolic process;multi-organism process;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular process;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of reproductive process;regulation of ribonuclease activity;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;signal transduction;type I interferon-mediated signaling pathway "2'-5'-oligoadenylate synthetase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;adenylyltransferase activity;ATP binding;binding;catalytic activity;cation binding;double-stranded RNA binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;nucleotidyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Hepatitis C;Measles 1.40E-109 5 28 28 26.4

Q7L014;D6RJA6;H0Y9U3 Probable ATP-dependent RNA helicase DDX46 DDX46 >sp|Q7L014|DDX46_HUMAN Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2 0.18 0.06 0.05 -0.05 -0.05 -0.33 -0.48 -0.57 + 1.37508558 0.417377915 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding" Cajal body;cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part Spliceosome 1.27E-122 3 29 28 28.3

P45974-2;P45974;F5H571;REV__Q9UPY3-2;REV__Q9UPY3 Ubiquitin carboxyl-terminal hydrolase 5 USP5 >sp|P45974-2|UBP5_HUMAN Isoform Short of Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5;>sp|P45974|UBP5_HUMAN Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2 0.04 -0.05 0.00 0.00 0.18 0.44 0.54 0.22 + 1.543815654 -0.346566794 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of proteolysis;primary metabolic process;protein deubiquitination;protein K48-linked deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of proteolysis;ubiquitin-dependent protein catabolic process "binding;catalytic activity;cation binding;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;exopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;omega peptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;thiolester hydrolase activity;transition metal ion binding;ubiquitin thiolesterase activity;zinc ion binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane-bounded organelle;organelle;vacuole 2.33E-262 5 30 28 44.1

O60763;O60763-2;F5H4X1;F5GYR8;F5GZ76;H0Y7C0 General vesicular transport factor p115 USO1 >sp|O60763|USO1_HUMAN General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2;>sp|O60763-2|USO1_HUMAN Isoform 2 of General vesicular transport factor p115 OS=Homo sapiens GN=USO1;>tr|F5H4X1|F5H4X1_HUMAN General vesicular transport factor 0.04 -0.05 -0.06 -0.12 0.25 0.16 0.28 0.08 + 1.605766058 -0.241410651 cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;M phase;M phase of mitotic cell cycle;membrane fusion;membrane organization;mitotic prophase;organelle fusion;organelle organization;prophase;protein transport;transcytosis;transport;vesicle fusion;vesicle fusion with Golgi apparatus;vesicle organization;vesicle-mediated transport protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;perinuclear region of cytoplasm 0 6 29 29 38.9

P49748-3;P49748;P49748-2;G3V1M7;K7EQP4;J3QRJ8;K7EJW8;J3KSR4;J3QKU9;J3KS89;K7EMF8 "Very long-chain specific acyl-CoA dehydrogenase, mitochondrial" ACADVL ">sp|P49748-3|ACADV_HUMAN Isoform 3 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL;>sp|P49748|ACADV_HUMAN Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1;>sp|P49" -0.41 -0.06 -0.12 0.07 0.69 0.75 0.21 0.17 + 1.301260879 -0.585979344 activation of signaling protein activity involved in unfolded protein response;biological regulation;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;energy derivation by oxidation of organic compounds;fatty acid beta-oxidation;fatty acid beta-oxidation using acyl-CoA dehydrogenase;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;generation of precursor metabolites and energy;homeostatic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;macromolecule metabolic process;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;multicellular organismal homeostasis;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of fatty acid biosynthetic process;negative regulation of fatty acid metabolic process;negative regulation of fatty acid oxidation;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cholesterol metabolic process;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of fatty acid oxidation;regulation of hydrolase activity;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of steroid metabolic process;regulation of transferase activity;small molecule catabolic process;small molecule metabolic process;temperature homeostasis "acyl-CoA dehydrogenase activity;binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;long-chain-acyl-CoA dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors" cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle part Fatty acid metabolism 1.68E-206 11 30 30 49.7

Q15046;Q15046-2;H3BVA8;J3KRL2;H3BPV7;H3BRC9;REV__E5RGG2;REV__A8MWU7;REV__Q8N1C3;REV__P18507;REV__P18507-2;REV__P18507-3;Q5JR59;J3KQA9;Q8IWU2 Lysine--tRNA ligase KARS >sp|Q15046|SYK_HUMAN Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3;>sp|Q15046-2|SYK_HUMAN Isoform Mitochondrial of Lysine--tRNA ligase OS=Homo sapiens GN=KARS 0.06 0.00 0.10 -0.04 -0.23 -0.47 -0.10 -0.39 + 1.45918476 0.324838863 amine metabolic process;amino acid activation;biosynthetic process;bis(5'-nucleosidyl) oligophosphate biosynthetic process;bis(5'-nucleosidyl) oligophosphate metabolic process;carboxylic acid metabolic process;cation transport;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;diadenosine polyphosphate biosynthetic process;diadenosine polyphosphate metabolic process;diadenosine tetraphosphate biosynthetic process;diadenosine tetraphosphate metabolic process;early endosome to late endosome transport;endocytic recycling;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;ferric iron transport;heterocycle biosynthetic process;heterocycle metabolic process;interaction with host;interspecies interaction between organisms;intracellular transport;ion transport;iron ion transport;lysyl-tRNA aminoacylation;macromolecule metabolic process;macromolecule modification;metabolic process;metal ion transport;multi-organism process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;organic acid metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;peptidyl-threonine modification;peptidyl-threonine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;protein transport;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;receptor metabolic process;receptor recycling;reproductive process;ribonucleoside biosynthetic process;ribonucleoside metabolic process;RNA metabolic process;RNA processing;small molecule metabolic process;transferrin transport;transition metal ion transport;transport;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tRNA processing;vesicle-mediated transport;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic acid binding;catalytic activity;cation binding;cytoskeletal protein binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;kinase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;lysine-tRNA ligase activity;metal ion binding;microtubule binding;nucleic acid binding;nucleotide binding;phosphatase inhibitor activity;phosphatase regulator activity;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein phosphatase inhibitor activity;protein phosphatase regulator activity;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups;tRNA binding;tubulin binding"aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;early endosome;endosome;extracellular region;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;microtubule;microtubule cytoskeleton;mitochondrial matrix;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex;recycling endosome Aminoacyl-tRNA biosynthesis 5.30E-179 15 30 30 47.9

P36578;H3BM89;H3BTP7;H3BU31 60S ribosomal protein L4 RPL4 >sp|P36578|RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5;>tr|H3BM89|H3BM89_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=2 SV=1 -0.16 0.05 0.06 0.06 -0.15 -0.59 -0.41 -0.51 + 1.486964817 0.417596301 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.01E-160 4 33 33 56

O94979;D6REX3;O94979-3;O94979-9;O94979-2;O94979-8;O94979-4;O94979-6;B7ZL00;D6RHZ5;O94979-7;H7BXG7;O94979-5;H0YAB3;H0Y9T9;H0Y9K1;H0Y8V7;H0Y8W8;H0YAF5;D6RE64;D6RCQ9;H0Y9V3;D6RBT0;D6RHE8;REV__A8MVM7 Protein transport protein Sec31A SEC31A >sp|O94979|SC31A_HUMAN Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=3;>tr|D6REX3|D6REX3_HUMAN Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=2 SV=1;>sp|O94979-3|SC31A_HUMAN Isoform 3 of Protein transport protein Sec31A -0.13 -0.21 -0.11 -0.17 0.89 0.70 0.53 0.05 + 1.508579971 -0.699511609 activation of signaling protein activity involved in unfolded protein response;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;establishment of localization;establishment of protein localization;glycosylation;immune system process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;transport;vesicle coating;vesicle organization cell part;COPII vesicle coat;cytoplasm;cytoplasmic part;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;vesicle coat Protein processing in endoplasmic reticulum 1.64E-187 25 35 35 29.6

O75643;O75643-2;C9JAQ9;B4E0P5 U5 small nuclear ribonucleoprotein 200 kDa helicase SNRNP200 >sp|O75643|U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 0.16 0.39 0.02 0.29 -0.04 -0.41 -0.90 -0.47 + 1.3906195 0.66866773 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cis assembly of pre-catalytic spliceosome;macromolecular complex assembly;macromolecular complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA helicase activity;RNA-dependent ATPase activity" catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U5 snRNP Spliceosome 0 4 35 35 23.9

O60716-21;O60716-19;O60716-13;O60716-11;O60716-5;O60716-3;O60716-18;O60716-17;O60716-10;O60716-9;C9JZR2;O60716-2;O60716;O60716-24;O60716-23;O60716-16;O60716-15;O60716-8;O60716-7;O60716-22;O60716-20;O60716-14;O60716-12;O60716-6;O60716-4;O60716-29;O60716-27;O60716-26;O60716-25;O60716-32;O60716-31;O60716-30;O60716-28;E9PRE2;H0YC95;E9PKY0;E9PKL1;D6R9A8;B4DRK2;E9PHB5;E7EPC8;Q99569-2;Q9UQB3-2;Q99569;Q9UQB3 Catenin delta-1 CTNND1>sp|O60716-21|CTND1_HUMAN Isoform 3A of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716-19|CTND1_HUMAN Isoform 3AC of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O60716-13|CTND1_HUMAN Isoform 2A of Catenin delta-1 OS=Homo sapiens GN=CTNND1;>sp|O6071 -0.12 0.03 0.30 0.20 -0.77 -0.41 -0.25 -0.25 + 1.373673749 0.522840609 "adherens junction organization;anatomical structure morphogenesis;behavior;biological adhesion;biological regulation;biosynthetic process;cell adhesion;cell communication;cell differentiation;cell differentiation involved in salivary gland development;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cell-cell signaling;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cognition;developmental process;epidermal cell differentiation;epithelial cell differentiation;epithelial cell differentiation involved in salivary gland development;gland morphogenesis;keratinocyte differentiation;learning;learning or memory;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;morphogenesis of a branching structure;morphogenesis of a polarized epithelium;morphogenesis of an epithelium;multicellular organismal development;multicellular organismal process;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;neurological system process;neuron cell-cell adhesion;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle cytokinesis;positive regulation of cell cycle process;positive regulation of cell division;positive regulation of cellular process;positive regulation of cytokinesis;positive regulation of gene expression;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell cycle cytokinesis;regulation of cell cycle process;regulation of cell division;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokinesis;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription, DNA-dependent;regulation of transmission of nerve impulse;regulation of Wnt receptor signaling pathway;response to stimulus;RNA biosynthetic process;RNA metabolic process;salivary gland morphogenesis;signal transduction;signaling;system process;tissue morphogenesis;transcription, DNA-dependent;Wnt receptor signaling pathway" adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;desmosome;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane part;membrane-bounded organelle;midbody;mitotic spindle;non-membrane-bounded organelle;nucleus;organelle;organelle part;perikaryon;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;spindle;spindle midzone;spindle pole Adherens junction;Leukocyte transendothelial migration 0 45 37 37 52.6

Q9BSJ8;Q9BSJ8-2;F8VZB1 Extended synaptotagmin-1 ESYT1 >sp|Q9BSJ8|ESYT1_HUMAN Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1;>sp|Q9BSJ8-2|ESYT1_HUMAN Isoform 2 of Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 -0.20 -0.20 -0.09 0.04 0.12 0.46 0.35 0.50 + 1.698135354 -0.469707171 cell part;integral to membrane;intrinsic to membrane;membrane part 0 3 37 37 40.5

E9PLK3;P55786;B7Z463;E5RJ24;E7EWZ2;A6NEC2;F5GZY4;H0YAQ6;E9PP11;A6NEC2-2;H0YDG0;H0YCQ5;E9PJY4;E9PJ74;E9PPD4;A6NEC2-3;L7N488;E9PRQ5;E9PI82;E9PJF9;E9PPZ2 Puromycin-sensitive aminopeptidase NPEPPS >tr|E9PLK3|E9PLK3_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=2 SV=1;>sp|P55786|PSA_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2;>tr|B7Z463|B7Z463_HUMAN Puromycin-sensitive aminopeptidase OS=Homo sa 0.03 -0.03 -0.11 -0.01 0.27 0.66 0.53 0.22 + 1.577901586 -0.444781196 antigen processing and presentation;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;cellular macromolecule metabolic process;cellular metabolic process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hypoxia;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;immune system process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 5.37E-260 21 38 38 48.4

Q9BQG0;Q9BQG0-2;I3L1L3;I3L2H8;A6NLJ0;Q8NCU7;REV__Q9H972-2;REV__Q9H972;O75161 Myb-binding protein 1A MYBBP1A >sp|Q9BQG0|MBB1A_HUMAN Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2;>sp|Q9BQG0-2|MBB1A_HUMAN Isoform 2 of Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A;>tr|I3L1L3|I3L1L3_HUMAN Myb-binding protein 1A (Fragment) OS=Homo sapiens

GN=MYBBP1A -0.20 0.24 0.24 0.32 -0.42 -0.43 -1.30 -0.45 + 1.314071971 0.798989531 "actin cytoskeleton organization;actin filament-based process;anatomical structure development;behavior;biological adhesion;biological regulation;biosynthetic process;cell adhesion;cell communication;cell-cell adhesion;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;cytoskeleton organization;developmental process;electron transport chain;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;hippo signaling cascade;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;organelle organization;oxidation-reduction process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;respiratory electron transport chain;response to abiotic stimulus;response to external stimulus;response to extracellular stimulus;response to light stimulus;response to nutrient levels;response to radiation;response to starvation;response to stimulus;response to stress;retina development in camera-type eye;RNA biosynthetic process;RNA metabolic process;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;transcription, DNA-dependent;transport;visual behavior" "binding;catalytic activity;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;nucleic acid binding;nucleotidyltransferase activity;protein binding;sequence-specific DNA binding;structural molecule activity;transcription factor binding;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection part;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;cilium;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule basal body;microtubule organizing center;NLS-dependent protein nuclear import complex;non-membrane-bounded organelle;nuclear part;nucleocytoplasmic shuttling complex;nucleolus;nucleus;occluding junction;organelle;organelle part;protein complex;tight junction 0 9 39 39 33.6

P12956;B1AHC8;B1AHC9;F5H1I8 X-ray repair cross-complementing protein 6 XRCC6 ">sp|P12956|XRCC6_HUMAN X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2;>tr|B1AHC8|B1AHC8_HUMAN X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_b OS=Homo sapiens GN=XR" 0.05 0.00 0.10 0.12 -0.08 -0.45 -0.45 -0.55 + 1.605927333 0.447986123 "anatomical structure homeostasis;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;DNA ligation;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via nonhomologous end joining;homeostatic process;immune system process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to DNA damage stimulus;response to ionizing radiation;response to radiation;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;telomere maintenance;telomere organization;transcription, DNA-dependent;V(D)J recombination" "5'-deoxyribose-5-phosphate lyase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;carbon-oxygen lyase activity;catalytic activity;damaged DNA binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;double-stranded DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lyase activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;sequence-specific DNA binding;structure-specific DNA binding;telomeric DNA binding;transcription regulatory region DNA binding" cell part;chromosomal part;cytoplasm;intracellular organelle part;intracellular part;Ku70:Ku80 complex;macromolecular complex;membrane;nonhomologous end joining complex;nuclear chromosome part;nuclear part;nuclear telomere cap complex;nucleoplasm part;organelle part;protein complex;protein-DNA complex;telomere cap complex;transcription factor complex Non-homologous end-joining 0 4 41 41 61.2

P13010;C9JZ81;H7C0H9 X-ray repair cross-complementing protein 5 XRCC5 >sp|P13010|XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 0.07 0.01 0.07 0.08 -0.05 -0.42 -0.41 -0.42 + 1.571891449 0.379162962 "anatomical structure homeostasis;biological regulation;biosynthetic process;cell differentiation;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;developmental process;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via nonhomologous end joining;hemopoietic stem cell differentiation;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of neurogenesis;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;stem cell differentiation;telomere maintenance;telomere organization;transcription, DNA-dependent"	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;damaged DNA binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;double-stranded DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;sequence-specific DNA binding;structure-specific DNA binding;telomeric DNA binding;transcription regulatory region DNA binding"	cell part;chromosomal part;cytoplasm;intracellular organelle part;intracellular part;Ku70:Ku80 complex;macromolecular complex;nonhomologous end joining complex;nuclear chromosome part;nuclear part;nuclear telomere cap complex;nucleoplasm;organelle part;protein complex;protein-DNA complex;telomere cap complex	Non-homologous end-joining	0	3	43	42	66.4

P38646;D6RJI2;H0YBG6;D6RA73;H0Y8S0;D6RDH7;D6RCD7;H0Y8K0	"Stress-70 protein, mitochondrial"	HSPA9	">sp|P38646|GRP75_HUMAN Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2"	-0.08	0.04	0.05	0.06	-0.11	-0.13	-0.31	-0.18	+	1.444094603	0.200661381	biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nuclear export;nuclear transport;nucleocytoplasmic transport;primary metabolic process;protein export from nucleus;protein folding;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;transport	adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein bindingcell part;cell surface;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleoid;nucleolus;organelle;organelle part	ko05152;RNA degradation	0	8	44	43	62.7

P46821;D6RA32;D6RA40;D6RCL2;D6RGJ3;P78559;P78559-2;J3KPX8;E9PGC8	Microtubule-associated protein 1B;MAP1B heavy chain;MAP1 light chain LC1	MAP1B	>sp|P46821|MAP1B_HUMAN Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2	-0.94	-0.20	-0.81	-0.30	2.41	2.27	0.04	0.77	+	1.299574527	-1.93128536	"anatomical structure development;anatomical structure morphogenesis;axonogenesis;biological regulation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;dendrite development;developmental process;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of mitochondrion localization;establishment of mitochondrion localization, microtubule-mediated;establishment of monopolar cell polarity;establishment of organelle localization;establishment or maintenance of cell polarity;establishment or maintenance of monopolar cell polarity;intracellular transport;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrion transport along microtubule;multicellular organismal process;negative regulation of biological process;negative regulation of intracellular transport;negative regulation of transport;neurological system process;neuron projection development;neuron projection morphogenesis;organelle organization;organelle transport along microtubule;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of neurogenesis;regulation of anatomical structure morphogenesis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of intracellular transport;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of transport;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;system process;transport"	catalytic activity;hydrolase activity;structural molecule activity	cell junction;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;dendritic spine;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule associated complex;neuron projection;neuron spine;organelle part;plasma membrane;protein complex;synapse		0	9	44	44	28.9

Q05682-5;E7EX44;Q05682-3;E9PGZ1;Q05682-4;F5H1Z9;Q05682-6;Q05682-2;Q05682;C9J813;C9JEK3;C9JE79;F8WE61;REV__H0YH95;REV__H0YEF9;REV__E9PJZ7;REV__H0YHK3;REV__O75334-6;REV__O75334-5;REV__Q13136-2;REV__Q13136;REV__O75334-2;REV__J3KNM3;REV__O75334-4;REV__G3V200;REV__O75334-3;REV__O75334	Caldesmon	CALD1	>sp|Q05682-5|CALD1_HUMAN Isoform 5 of Caldesmon OS=Homo sapiens GN=CALD1;>tr|E7EX44|E7EX44_HUMAN Caldesmon OS=Homo sapiens GN=CALD1 PE=2 SV=1;>sp|Q05682-3|CALD1_HUMAN Isoform 3 of Caldesmon OS=Homo sapiens GN=CALD1;>tr|E9PGZ1|E9PGZ1_HUMAN Caldesmon OS=Homo	-0.52	-0.26	-0.10	0.08	0.15	0.39	0.43	0.63	+	1.470852461	-0.601154685	cellular component movement;cellular process;multicellular organismal process;muscle contraction;muscle system process;system process	actin binding;binding;calmodulin binding;cytoskeletal protein binding;protein binding;tropomyosin binding	actin cap;actin cytoskeleton;cell cortex part;cell part;contractile fiber;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;myofibril;non-membrane-bounded organelle;organelle;organelle part;plasma membrane	Vascular smooth muscle contraction	0	27	45	44	71.6

P20591;F8W8T1;P20591-2;H9KVC7;H9KVC9;H9KVD0;H9KVC4;P20592;H9KVD3;B7Z5D3;H9KVC3;C9JEL4;C9JS04;C9JZQ9;Q5JVD6;Q7Z7A1-3;Q8WX70;Q7Z7A1-2;Q7Z7A1-5;Q7Z7A1	"Interferon-induced GTP-binding protein Mx1;Interferon-induced GTP-binding protein Mx1, N-terminally processed"	MX1	">sp|P20591|MX1_HUMAN Interferon-induced GTP-binding protein Mx1 OS=Homo sapiens GN=MX1 PE=1 SV=4;>tr|F8W8T1|F8W8T1_HUMAN Interferon-induced GTP-binding protein Mx1, N-terminally processed OS=Homo sapiens GN=MX1 PE=2 SV=1;>sp|P20591-2|MX1_HUMAN Isoform 2 of"	0.53	0.32	0.22	0.00	-3.85	-2.74	-1.12	-1.13	+	1.457271427	2.47843029	biological regulation;catabolic process;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;establishment of localization;establishment of protein localization;establishment of RNA localization;G2/M transition of mitotic cell cycle;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;immune effector process;immune system process;induction of apoptosis;induction of programmed cell death;metabolic process;mRNA transport;multi-organism process;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic process;nucleic acid transport;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell death;regulation of cellular localization;regulation of cellular process;regulation of intracellular transport;regulation of localization;regulation of nucleocytoplasmic transport;regulation of programmed cell death;regulation of reproductive process;regulation of transport;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;RNA transport;signal transduction;small molecule metabolic process;transport;type I interferon-mediated signaling pathway	"binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;pore complex;protein complex Measles 0 20 46 46 69.2

P07237;H7BZ94;F5H8J2;I3L312;H0Y3Z3;I3L398;I3L4M2;I3NI03;I3L0S0;I3L3U6;I3L3P5;I3L514;I3L1Y5Protein disulfide-isomerase P4HB >sp|P07237|PDIA1_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3;>tr|H7BZ94|H7BZ94_HUMAN Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=2 SV=2;>tr|F5H8J2|F5H8J2_HUMAN Uncharacterized protein OS=Homo sapiens GN=P4HB PE=2 SV=1 -0.04 -0.15 -0.29 -0.17 0.73 0.38 0.47 0.16 + 1.71972063 -0.593917643 4-hydroxyproline metabolic process;amine metabolic process;biological regulation;carboxylic acid metabolic process;cell redox homeostasis;cellular amine metabolic process;cellular amino acid metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;extracellular matrix organization;extracellular structure organization;glycerol ether metabolic process;heterocycle metabolic process;homeostatic process;lipid metabolic process;lipoprotein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid metabolic process;organic ether metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-proline hydroxylation;peptidyl-proline hydroxylation to 4-hydroxy-L-proline;peptidyl-proline modification;primary metabolic process;protein metabolic process;protein modification process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;peptidyl-proline 4-dioxygenase activity;peptidyl-proline dioxygenase activity;procollagen-proline 4-dioxygenase activity;procollagen-proline dioxygenase activity;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;plasma membrane;vesicle Protein processing in endoplasmic reticulum 0 13 46 46 77.8

Q14203-3;E7EX90;Q14203-4;Q14203-6;Q14203;Q14203-5;Q14203-2;Q6AWB1;E7EWF7;C9JJD0;C9JZA4;C9JTE5;C9JJN7;C9JKG6;E9PCY0;C9J1B7;C9JUI8 Dynactin subunit 1 DCTN1;DKFZp686E0752 >sp|Q14203-3|DCTN1_HUMAN Isoform 3 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1;>tr|E7EX90|E7EX90_HUMAN Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=2 SV=1;>sp|Q14203-4|DCTN1_HUMAN Isoform 4 of Dynactin subunit 1 OS=Homo sapiens GN=DCTN1;>sp|Q14203-6|D -0.03 -0.11 0.05 -0.09 0.43 0.42 0.38 0.03 + 1.429076573 -0.359879623 activation of signaling protein activity involved in unfolded protein response;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;cell cycle phase;cell cycle process;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;developmental process;establishment of localization;G2/M transition of mitotic cell cycle;immune system process;macromolecule metabolic process;metabolic process;mitosis;nervous system development;nuclear division;organelle fission;organelle organization;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;system development;transport "catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;pyrophosphatase activity" cell leading edge;cell part;centrosome;chromosomal part;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;spindle pole Huntington's disease;Vasopressin-regulated water reabsorption 0 17 47 46 51.1

Q9NYU2-2;Q9NYU2;H7BZG0;Q9NYU1;REV__G3V0I7;REV__F8WCP1;REV__G5E9N5;REV__Q60I27 UDP-glucose:glycoprotein glucosyltransferase 1 UGGT1 >sp|Q9NYU2-2|UGGG1_HUMAN Isoform 2 of UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1;>sp|Q9NYU2|UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3 -0.04 -0.11 -0.07 -0.17 0.61 0.35 0.57 0.08 + 1.540135931 -0.497780803 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine "binding;catalytic activity;glucosyltransferase activity;protein binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;UDP-glucose:glycoprotein glucosyltransferase activity;UDP-glucosyltransferase activity;UDP-glycosyltransferase activity;unfolded protein binding" cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part Protein processing in endoplasmic reticulum 0 8 48 48 43.8

P22314;Q5JRR6;Q5JRR9;Q5JRS0;Q5JRS1;Q5JRS3;Q5JRS2 Ubiquitin-like modifier-activating enzyme 1 UBA1 >sp|P22314|UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3 -0.11 -0.12 -0.11 0.02 0.49 0.64 0.46 0.21 + 1.944636768 -0.529563012 cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small protein activating enzyme activity Parkinson's disease;Ubiquitin mediated proteolysis 0 7 50 50 51.7

P10809;E7EXB4;E7ESH4;B7Z712;C9JL25;C9JCQ4;C9JL19;C9J0S9 "60 kDa heat shock protein, mitochondrial" HSPD1 ">sp|P10809|CH60_HUMAN 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2" 0.01 0.13 -0.03 0.08 -0.05 -0.23 -0.53 -0.39 + 1.303717148 0.346613856 activation of caspase activity;activation of immune response;activation of innate immune response;adaptive immune response;adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;B cell activation;B cell activation involved in immune response;B cell cytokine production;B cell mediated immunity;B cell proliferation;biological regulation;cell activation;cell activation involved in immune response;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;chaperone-mediated protein complex assembly;cytokine production;cytokine production involved in immune response;'de novo' protein folding;DNA metabolic process;DNA recombination;immune effector process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response-activating signal transduction;interaction with host;interspecies interaction between organisms;isotype switching;isotype switching to IgG isotypes;leukocyte activation;leukocyte activation involved in immune response;leukocyte mediated immunity;leukocyte proliferation;lymphocyte activation;lymphocyte activation involved in immune response;lymphocyte mediated immunity;lymphocyte proliferation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mononuclear cell proliferation;multicellular organismal process;multi-organism process;MyD88-dependent toll-like receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;pattern recognition receptor signaling pathway;positive regulation of adaptive immune response;positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell death;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of hydrolase activity;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune response to tumor cell;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of interferon-alpha production;positive regulation of interferon-gamma production;positive regulation of interleukin-10 production;positive regulation of interleukin-12 production;positive regulation of interleukin-6 production;positive regulation of leukocyte activation;positive regulation of leukocyte mediated immunity;positive regulation of lymphocyte activation;positive regulation of lymphocyte mediated immunity;positive regulation of macrophage activation;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of response to biotic stimulus;positive regulation of response to stimulus;positive regulation of response to tumor cell;positive regulation of T cell activation;positive regulation of T cell mediated immune response to tumor cell;positive regulation of T cell mediated immunity;positive regulation of type I interferon production;posttranscriptional regulation of gene expression;primary metabolic process;production of molecular mediator of immune response;protein complex assembly;protein complex subunit organization;protein folding;protein maturation;protein metabolic process;protein refolding;protein stabilization;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell activation;regulation of cell death;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of immune effector process;regulation of immune response;regulation of immune response to tumor cell;regulation of immune system process;regulation of innate immune response;regulation of interferon-alpha production;regulation of interferon-gamma production;regulation of interleukin-10 production;regulation of interleukin-12 production;regulation of interleukin-6 production;regulation of leukocyte activation;regulation of leukocyte mediated immunity;regulation of lymphocyte activation;regulation of lymphocyte mediated immunity;regulation of macromolecule metabolic process;regulation of macrophage activation;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of peptidase activity;regulation of programmed cell death;regulation of protein stability;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of response to tumor cell;regulation of T cell activation;regulation of T cell mediated immune response to tumor cell;regulation of T cell mediated immunity;regulation of type I interferon production;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;signal transduction;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response;T cell activation;toll-like receptor signaling pathway;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cell surface binding;DNA binding;DNA replication origin binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipopolysaccharide binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;sequence-specific DNA binding;single-stranded DNA binding;structure-specific DNA binding;unfolded protein binding" cell part;cell surface;coated pit;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;early endosome;endosome;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lipopolysaccharide receptor complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane part;protein complex;receptor complex;stored secretory granule;vesicleko05152;RNA degradation;Type I diabetes mellitus 0 8 51 51 80.1

P26038 Moesin MSN >sp|P26038|MOES_HUMAN Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 -0.03 -0.19 -0.02 -0.09 0.27 0.42 0.69 0.18 + 1.54925793 -0.46949807 biological adhesion;biological regulation;cell adhesion;cell migration;cell motility;cell-cell adhesion;cellular component movement;cellular process;immune system process;leukocyte cell-cell adhesion;leukocyte migration;locomotion;membrane docking;membrane to membrane docking;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of immune system process;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of lymphocyte migration structural constituent of cytoskeleton;structural molecule activity apical part of cell;apical plasma membrane;basolateral plasma membrane;cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;extrinsic to membrane;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microvillus;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;plasma membrane part;uropod;vesicle Leukocyte transendothelial migration;Measles;Regulation of actin cytoskeleton 0 1 75 57 87.7

Q14764;H3BQK6;H3BRL2;H3BUK7;H3BNF6;H3BP76;H3BPZ2;H3BNF2;H3BUP3;H3BQE7;I3L155 Major vault protein MVP >sp|Q14764|MVP_HUMAN Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 -0.26 -0.07 -0.20 0.04 0.58 0.87 0.22 0.67 + 1.734286989 -0.710450857 biological regulation;establishment of localization;establishment of protein localization;establishment of RNA localization;mRNA transport;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of kinase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein autophosphorylation;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of protein tyrosine kinase activity;negative regulation of signaling;negative regulation of transferase activity;nucleic acid transport;nucleobase-containing compound transport;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein autophosphorylation;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein tyrosine kinase activity;regulation of signaling;regulation of transferase activity;RNA transport;transport binding;enzyme binding;phosphatase binding;protein binding;protein phosphatase binding cell part;cytoplasmic part;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleus;organelle;organelle part;perinuclear region of cytoplasm;pore complex;protein complex;ribonucleoprotein complex;vesicle 0 11 58 58 69.4

P02751-3;P02751;P02751-5;P02751-17;P02751-7;P02751-15;P02751-6;F8W7G7;P02751-14;P02751-8;P02751-10;P02751-9;P02751-11;P02751-13;P02751-4;P02751-12;H0Y7Z1;P02751-16;P02751-2;H0Y4K8 Fibronectin;Anastellin;Ugl-Y1;Ugl-Y2;Ugl-Y3 FN1 >sp|P02751-3|FINC_HUMAN Isoform 3 of Fibronectin OS=Homo sapiens GN=FN1;>sp|P02751|FINC_HUMAN Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4;>sp|P02751-5|FINC_HUMAN Isoform 5 of Fibronectin OS=Homo sapiens GN=FN1;>sp|P02751-17|FINC_HUMAN Isoform 17 of Fibron -2.10 -1.34 -1.44 -0.87 2.87 3.21 0.48 3.59 + 1.88948768 -3.973259643 acute inflammatory response;acute-phase response;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological adhesion;biological regulation;calcium-independent cell-matrix adhesion;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;defense response;developmental process;establishment of localization;establishment of localization in cell;exocytosis;extracellular matrix organization;extracellular structure organization;immune system process;inflammatory response;leukocyte migration;locomotion;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;platelet activation;platelet degranulation;primary metabolic process;protein metabolic process;protein modification process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to stimulus;response to stress;response to wounding;secretion;secretion by cell;substrate adhesion-dependent cell spreading;transport;vesicle-mediated transport binding;carbohydrate binding;collagen binding;enzyme activator activity;enzyme regulator activity;extracellular matrix structural constituent;glycosaminoglycan binding;heparin binding;pattern binding;peptidase activator activity;peptidase regulator activity;polysaccharide binding;protein binding;structural molecule activity apical plasma membrane;basement membrane;cell part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;endoplasmic reticulum-Golgi intermediate compartment;extracellular matrix;extracellular matrix part;extracellular region;extracellular region part;fibrinogen complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane part;platelet alpha granule lumen;protein complex;proteinaceous extracellular matrix;secretory granule lumen;vesicle lumen Amoebiasis;Bacterial invasion of epithelial cells;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer 0 20 61 61 36.9

Q7KZF4;H7C597;Q5W0U4-2;Q5W0U4 Staphylococcal nuclease domain-containing protein 1 SND1 >sp|Q7KZF4|SND1_HUMAN Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1 0.07 -0.11 -0.07 -0.09 0.26 0.10 0.40 0.14 + 1.391708742 -0.27633694 "biological regulation;biosynthetic process;calcium ion transport;cation transport;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;gene silencing;gene silencing by RNA;interaction with host;interspecies interaction between organisms;ion transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;metal ion transport;multi-organism process;negative regulation of biological process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;transport;viral reproductive process;virus-host interaction" "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nuclease activity;nucleic acid binding;protein binding transcription factor activity;transcription cofactor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding" adherens junction;anchoring junction;cell junction;cell leading edge;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;focal adhesion;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;nucleus;organelle;perinuclear region of cytoplasm;pigment granule;ribonucleoprotein complex;RNAi effector complex;RNA-induced silencing complex;vesicle 0 4 64 64 69

P18206-2;P18206;Q5JQ13;B4DTM7;P18206-3 Vinculin VCL >sp|P18206-2|VINC_HUMAN Isoform 1 of Vinculin OS=Homo sapiens GN=VCL;>sp|P18206|VINC_HUMAN Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4;>tr|Q5JQ13|Q5JQ13_HUMAN Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=2 SV=1 -0.12 -0.26 -0.01 -0.04 0.43 0.52 0.79 0.31 + 1.902545721 -0.619204298 adherens junction assembly;adherens junction organization;anatomical structure morphogenesis;apical junction assembly;biological adhesion;biological regulation;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell projection assembly;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;developmental process;epithelial cell-cell adhesion;establishment of localization;establishment of localization in cell;exocytosis;lamellipodium assembly;localization;macromolecule localization;morphogenesis of an epithelium;multicellular organismal process;muscle contraction;muscle system process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;platelet activation;platelet degranulation;protein localization;protein localization at cell surface;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of locomotion;secretion;secretion by cell;system process;tissue morphogenesis;transport;vesicle-mediated transport actin binding;beta-catenin binding;binding;cadherin binding;cell adhesion molecule binding;cytoskeletal protein binding;protein binding;structural molecule activity actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;costamere;cytoplasmic part;cytoskeleton;cytosol;extracellular region;fascia adherens;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;sarcolemma;Z disc Adherens junction;Amoebiasis;Bacterial invasion of epithelial cells;Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Shigellosis 0 5 66 66 64.9

P55072;C9IZA5;C9JUP7;E5RJB6;E5RK93;K7EM02;Q8TDX6-3;Q8N6G5-2;K7EIJ8;Q96A70-3;Q96A70-4;Q96A70;Q8IYT4-2;Q96A70-2;Q8TDX6;Q8IYT4;Q8N6G5;E7EQM8 Transitional endoplasmic reticulum ATPase VCP >sp|P55072|TERA_HUMAN Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 -0.04 0.01 -0.11 -0.06 0.06 0.20 0.27 0.18 + 1.685296498 -0.22958777 "activation of caspase activity;aggresome assembly;agmatine biosynthetic process;alcohol metabolic process;amine biosynthetic process;amine metabolic process;amino sugar metabolic process;aminoglycan biosynthetic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;cartilage development;catabolic process;cell proliferation;cell recognition;cellular amine metabolic process;cellular amino acid metabolic process;cellular biogenic amine biosynthetic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cellular response to topologically incorrect protein;cellular response to unfolded protein;chondroitin sulfate biosynthetic process;chondroitin sulfate metabolic process;chondroitin sulfate proteoglycan biosynthetic process;chondroitin sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process;chondroitin sulfate proteoglycan metabolic process;dermatan sulfate proteoglycan biosynthetic process;dermatan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process;dermatan sulfate proteoglycan metabolic process;developmental process;DNA biosynthetic process;DNA metabolic process;DNA repair;double-strand break repair;endochondral ossification;endoplasmic reticulum unfolded protein response;ER to Golgi vesicle-mediated transport;ER-associated protein catabolic process;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;extracellular matrix organization;extracellular structure organization;gamete generation;glucuronate metabolic process;glycoprotein biosynthetic process;glycoprotein metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan metabolic process;glycosylation;Golgi vesicle transport;heparan sulfate proteoglycan biosynthetic process, polysaccharide chain biosynthetic process;heparin biosynthetic process;heparin metabolic process;inclusion body assembly;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;multicellular organismal process;multicellular organismal reproductive process;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;organic acid metabolic process;ornithine metabolic process;ossification;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;polyamine biosynthetic process;polyamine metabolic process;polysaccharide biosynthetic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cellular catabolic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of peptidase activity;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein complex assembly;positive regulation of protein metabolic process;positive regulation of proteolysis;postreplication repair;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex assembly;protein complex subunit organization;protein glycosylation;protein homooligomerization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein oligomerization;protein transport;protein ubiquitination;proteoglycan biosynthetic process;proteoglycan metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein metabolic process;regulation of proteolysis;reproductive process;response to chemical stimulus;response to DNA damage stimulus;response to endoplasmic reticulum stress;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;retrograde protein transport, ER to cytosol;signal transduction;small molecule metabolic process;spermatogenesis;sulfur compound biosynthetic process;sulfur compound metabolic process;system development;tissue development;translesion synthesis;transport;ubiquitin-dependent protein catabolic process;UDP-glucuronate metabolic process;UDP-N-acetylgalactosamine metabolic process;uronic acid metabolic process;vesicle-mediated transport" "acetylgalactosaminyltransferase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;arginine decarboxylase activity;ATP binding;ATPase activity;ATPase activity, coupled;binding;carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-acetylgalactosaminyltransferase activity;glucuronosyltransferase activity;glucuronylgalactosylproteoglycan 4-beta-N-acetylgalactosaminyltransferase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;lipid binding;lyase activity;metal ion binding;microtubule-severing ATPase activity;nucleoside-triphosphatase activity;nucleotide binding;ornithine decarboxylase activator activity;ornithine decarboxylase regulator activity;peptidoglycan glycosyltransferase activity;polyubiquitin binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;small conjugating protein binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;ubiquitin binding;UDP-glycosyltransferase activity" cell part;chromosomal part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;endoplasmic reticulum;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;integral to Golgi membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to Golgi membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;mitochondrion;nucleus;organelle;organelle membrane;organelle part;proteasome complex;protein complex;site of double-strand break Arginine and proline metabolism;Glycosaminoglycan biosynthesis - chondroitin sulfate;Protein processing in endoplasmic reticulum 0 18 72 72 78.9

Q00610-2;Q00610;J3KS13;K7EJJ5;J3KSQ2;J3KRF5;J3QL20;F5H5N6 Clathrin heavy chain 1 CLTC >sp|Q00610-2|CLH1_HUMAN Isoform 2 of Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC;>sp|Q00610|CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 -0.08 -0.01 -0.14 -0.08 0.19 0.29 0.20 0.06 + 1.780739039 -0.264078494 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cation transport;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;ferric iron transport;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;ion transport;iron ion transport;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;metal ion transport;mitosis;nuclear division;organelle fission;organelle organization;post-Golgi vesicle-mediated transport;protein transport;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;transferrin transport;transition metal ion transport;transport;vesicle-mediated transport structural molecule activity cell part;clathrin coat;clathrin coat of coated pit;clathrin coat of trans-Golgi network vesicle;clathrin coated vesicle membrane;clathrin vesicle coat;clathrin-coated endocytic vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endocytic vesicle membrane;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane coat;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;protein complex;spindle;trans-Golgi network membrane;vesicle;vesicle coat;vesicle membrane Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease;Lysosome 0 8 95 74 61.3

Q9NZM1-6;Q9NZM1;F8W8J4;Q9NZM1-3;C9JCN0;Q9NZM1-2;Q9NZM1-5;H0YD14;Q9NZM1-7;Q9NZM1-8;Q9NZM1-4;REV__J3KTL3;REV__E9PFL1;REV__B4DDR8;REV__F5H5K2;REV__F8W9R9;REV__F5H0K1;REV__O75448-2;REV__O75448;REV__F5GY88 Myoferlin MYOF >sp|Q9NZM1-6|MYOF_HUMAN Isoform 6 of Myoferlin OS=Homo sapiens GN=MYOF;>sp|Q9NZM1|MYOF_HUMAN Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1;>tr|F8W8J4|F8W8J4_HUMAN Myoferlin OS=Homo sapiens GN=MYOF PE=2 SV=1;>sp|Q9NZM1-3|MYOF_HUMAN Isoform 3 of Myoferlin OS=H -0.10 0.00 -0.45 -0.22 0.08 0.11 0.37 0.36 + 1.352268548 -0.418974804 biological regulation;blood circulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;circulatory system process;membrane organization;multicellular organismal process;muscle contraction;muscle system process;plasma membrane organization;plasma membrane repair;regulation of biological process;regulation of cellular process;regulation of cellular response to growth factor stimulus;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of vascular endothelial growth factor receptor signaling pathway;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus;system process binding;lipid binding;phospholipid binding caveola;cell part;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;envelope;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;nuclear envelope;nuclear membrane;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;plasma membrane;plasma membrane part;vesicle;vesicle membrane 0 20 83 82 47.6

Q9Y490;Q5TCU6 Talin-1 TLN1 >sp|Q9Y490|TLN1_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3;>tr|Q5TCU6|Q5TCU6_HUMAN Talin-1 OS=Homo sapiens GN=TLN1 PE=2 SV=1 -0.17 -0.33 -0.37 -0.23 1.46 0.90 0.61 0.13 + 1.470958678 -1.049826846 actin cytoskeleton organization;actin filament-based process;activation of signaling protein activity involved in unfolded protein response;axon guidance;biological adhesion;biological regulation;cell activation;cell adhesion;cell junction assembly;cell junction organization;cell-cell junction assembly;cell-cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;locomotion;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;metabolic process;multicellular organismal process;muscle contraction;muscle system process;organelle organization;platelet activation;platelet degranulation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to chemical stimulus;response to external stimulus;secretion;secretion by cell;system process;taxis;transport;vesicle-mediated transport structural constituent of cytoskeleton;structural molecule activity actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;plasma membrane part;ruffle;ruffle membrane;vesicle Focal adhesion 0 2 111 100 53.5

P46940;H0YLE8;H0YKA5;Q13576-2;J3KR91;F5H7S7;E9PDT6;REV__Q29RF7 Ras GTPase-activating-like protein IQGAP1 IQGAP1 >sp|P46940|IQGA1_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1;>tr|H0YLE8|H0YLE8_HUMAN Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=2 SV=1 -0.01 0.00 0.01 -0.06 0.14 0.09 0.32 0.14 + 1.446102335 -0.188136615 anatomical structure development;biological regulation;cell development;cellular developmental process;cellular metabolic process;cellular process;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;developmental process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;epithelial cell development;generation of precursor metabolites and energy;glomerular epithelial cell development;glomerular visceral epithelial cell development;intracellular signal transduction;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of dephosphorylation;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;oxidation-reduction process;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of Ras GTPase activity;positive regulation of transferase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of dephosphorylation;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of secretion;regulation of signaling;regulation of transferase activity;regulation of transport;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process binding;calcium ion binding;calmodulin binding;cation binding;enzyme activator activity;enzyme inhibitor activity;enzyme regulator activity;GTPase activator activity;GTPase inhibitor activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;protein binding;Ras GTPase activator activity;small GTPase regulator activity actin filament;cell junction;cell leading edge;cell part;cell projection;cell-cell junction;cytoplasm;cytoskeletal part;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;midbody;neuron projection;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ribonucleoprotein complex Regulation of actin cytoskeleton 0 8 105 101 62.5

P02538;CON__P02538 "Keratin, type II cytoskeletal 6A" KRT6A ">sp|P02538|K2C6A_HUMAN Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3;>P02538 SWISS-PROT:P02538 Tax_Id=9606 Gene_Symbol=KRT6A Keratin, type II cytoskeletal 6A" -0.37 1.13 -0.32 1.06 -0.50 0.88 -0.50 0.84 0.121955389 0.195049897 anatomical structure development;biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;ectoderm development;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;tissue development structural constituent of cytoskeleton;structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex 0 2 75 5 73.8

Q04695;CON__Q04695;K7EPJ9;K7ESE1;K7ELP7;J3QR55 "Keratin, type I cytoskeletal 17" KRT17 ">sp|Q04695|K1C17_HUMAN Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2;>Q04695 SWISS-PROT:Q04695 Tax_Id=9606 Gene_Symbol=KRT17 Keratin, type I cytoskeletal 17" -0.30 1.11 0.02 1.10 -0.79 0.57 -0.58 0.75 0.372089434 0.494326685 anatomical structure development;anatomical structure morphogenesis;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;epidermis development;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;keratinization;morphogenesis of an epithelium;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell growth;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of epidermis development;positive regulation of growth;positive regulation of hair follicle development;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of epidermis development;regulation of gene expression;regulation of growth;regulation of hair cycle;regulation of hair follicle development;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;tissue development;tissue morphogenesis MHC class II receptor activity;molecular transducer activity;receptor activity;signal transducer activity;signaling receptor activity;structural constituent of cytoskeleton;structural molecule activity;transmembrane signaling receptor activity cell part;cell periphery;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex 0 6 70 6 97.2

P13647;CON__P13647;H0YI76;F8W0C6;H0YIN9;F8VV57;F8VU69 "Keratin, type II cytoskeletal 5" KRT5 ">sp|P13647|K2C5_HUMAN Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3;>P13647 SWISS-PROT:P13647 Tax_Id=9606 Gene_Symbol=KRT5 Keratin, type II cytoskeletal 5" -0.33 1.14 -0.25 1.29 -1.18 0.27 -0.99 0.45 0.575627341 0.826145075 anatomical structure development;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;hemidesmosome assembly;tissue development structural constituent of cytoskeleton;structural molecule activity cell part;cytoplasmic part;cytoskeletal part;cytosol;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;organelle;organelle part;plasma membrane;protein complex 0 7 77 13 70

P02533;CON__P02533;P35900;CON__P35900;K7ENV3;E5RIJ0;REV__H7BZT2;H0YBJ0;Q8N1A0-2;Q8N1A0;CON__Q8N1A0;P06746;Q14525;CON__Q14525;Q15323;CON__Q9UE12;CON__Q15323;O76013-2;Q14532;CON__Q14532;O76014;CON__A2AB72;O76015;CON__O76015;O76013;CON__O76013;Q7Z3Y9;CON__Q7Z3Y9;CON__O76014;CON__REFSEQ:XP_986630;Q2M2I5;CON__Q2M2I5;G3V186;REV__Q5SZL2;REV__Q5SZL2-4;Q9ULK0 "Keratin, type I cytoskeletal 14" KRT14 ">sp|P02533|K1C14_HUMAN Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4;>P02533 SWISS-PROT:P02533 Tax_Id=9606 Gene_Symbol=KRT14 Keratin, type I cytoskeletal 14" -0.28 1.11 -0.09 1.31 -1.26 0.31 -0.91 0.59 0.574198998 0.829985313 anatomical structure development;apoptosis;base-excision repair;biological regulation;biosynthetic process;cell death;cell differentiation;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cell-substrate junction assembly;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;cytoskeleton organization;death;developmental process;DNA metabolic process;DNA repair;DNA replication;DNA-dependent DNA replication;epidermis development;epithelial cell differentiation;glutamate signaling pathway;hemidesmosome assembly;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;ionotropic glutamate receptor signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;programmed cell death;pyrimidine dimer repair;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell differentiation;regulation of cellular localization;regulation of cellular process;regulation of developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of establishment of protein localization;regulation of keratinocyte differentiation;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of programmed cell death;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of secretion;regulation of transport;response to abiotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to ethanol;response to inorganic substance;response to ionizing radiation;response to metal ion;response to organic substance;response to radiation;response to stimulus;response to stress;response to zinc ion;signal transduction;tissue development "binding;catalytic activity;cation binding;channel activity;cytoskeletal protein binding;damaged DNA binding;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;excitatory extracellular ligand-gated ion channel activity;extracellular ligand-gated ion channel activity;extracellular-glutamate-gated ion channel activity;gated channel activity;glutamate receptor activity;ion binding;ion channel activity;ion transmembrane transporter activity;ionotropic glutamate receptor activity;ligand-gated channel activity;ligand-gated ion channel activity;lyase activity;metal ion binding;microtubule binding;molecular transducer activity;nucleic acid binding;nucleotidyltransferase activity;passive transmembrane transporter activity;protein binding;receptor activity;signal transducer activity;signaling receptor activity;structural constituent of cytoskeleton;structural constituent of epidermis;structural molecule activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane signaling receptor activity;transmembrane transporter activity;transporter activity;tubulin binding"cell junction;cell part;cell periphery;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;external encapsulating structure part;integral to membrane;intermediate filament;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;keratin filament;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;outer membrane-bounded periplasmic space;periplasmic space;plasma membrane;postsynaptic membrane;protein complex;spindle microtubule;synapse part;synaptic membrane Base excision repair;Neuroactive ligand-receptor interaction 0 36 71 18 83.9

Q6RW13-2;Q6RW13 Type-1 angiotensin II receptor-associated protein AGTRAP >sp|Q6RW13-2|ATRAP_HUMAN Isoform 2 of Type-1 angiotensin II receptor-associated protein OS=Homo sapiens GN=AGTRAP;>sp|Q6RW13|ATRAP_HUMAN Type-1 angiotensin II receptor-associated protein OS=Homo sapiens GN=AGTRAP PE=1 SV=1 0.12 0.25 -0.11 0.26 -2.30 -2.10 -0.85 -0.22

1.227415323 1.500373317 biological regulation;regulation of biological quality;regulation of blood pressure;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress "angiotensin receptor activity;angiotensin type II receptor activity;binding;G-protein coupled receptor activity;molecular transducer activity;peptide binding;peptide receptor activity;peptide receptor activity, G-protein coupled;receptor activity;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity" cell cortex;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;vesicle membrane 1.76E-43 2 1 1 14.5

Q8WYA1-4;Q8WYA1-5;Q8WYA1-2;Q8WYA1 Aryl hydrocarbon receptor nuclear translocator-like protein 2 ARNTL2 >sp|Q8WYA1-4|BMAL2_HUMAN Isoform 4 of Aryl hydrocarbon receptor nuclear translocator-like protein 2 OS=Homo sapiens GN=ARNTL2;>sp|Q8WYA1-5|BMAL2_HUMAN Isoform 5 of Aryl hydrocarbon receptor nuclear translocator-like protein 2 OS=Homo sapiens GN=ARNTL2;>sp| -0.32 1.16 -0.25 1.32 -1.31 0.28 -1.05 0.70 0.517397526 0.819369704 "biological regulation;circadian rhythm;entrainment of circadian clock;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of circadian rhythm;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to external stimulus;response to stimulus;rhythmic process" binding;DNA binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;signal transducer activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;transcription factor complex 0.0019634 4 1 1 2

Q96MW1;Q86WV7 Coiled-coil domain-containing protein 43 CCDC43 >sp|Q96MW1|CCD43_HUMAN Coiled-coil domain-containing protein 43 OS=Homo sapiens GN=CCDC43 PE=1 SV=2;>tr|Q86WV7|Q86WV7_HUMAN CCDC43 protein OS=Homo sapiens GN=CCDC43 PE=2 SV=1 0.26 -0.08 0.30 -0.09 -0.25 -0.23 0.35 0.10 0.231475358 0.10815903 6.03E-24 2 1 1 4.9

E9PNW4;P13987;E9PR17 CD59 glycoprotein CD59 >tr|E9PNW4|E9PNW4_HUMAN CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=2 SV=1;>sp|P13987|CD59_HUMAN CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1;>tr|E9PR17|E9PR17_HUMAN CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=2 SV=1 -0.37 0.56 -1.44 1.51 -0.05 0.74 -0.97 0.08 0.055190894 0.117993766 biological regulation;blood coagulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;coagulation;hemostasis;multicellular organismal process;negative regulation of activation of membrane attack complex;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of complement activation;negative regulation of humoral immune response;negative regulation of immune effector process;negative regulation of immune response;negative regulation of immune system process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;negative regulation of protein activation cascade;negative regulation of protein metabolic process;negative regulation of protein processing;negative regulation of response to stimulus;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of leukocyte proliferation;positive regulation of lymphocyte activation;positive regulation of lymphocyte proliferation;positive regulation of mononuclear cell proliferation;positive regulation of T cell activation;positive regulation of T cell proliferation;regulation of activation of membrane attack complex;regulation of acute inflammatory response;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell activation;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of complement activation;regulation of defense response;regulation of gene expression;regulation of humoral immune response;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mononuclear cell proliferation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein activation cascade;regulation of protein metabolic process;regulation of protein processing;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of T cell activation;regulation of T cell proliferation;response to stimulus;signal transduction anchored to external side of plasma membrane;anchored to membrane;anchored to plasma membrane;cell part;compact myelin;extracellular region part;extracellular space;intrinsic to external side of plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane;plasma membrane part;sarcolemma Complement and coagulation cascades;Hematopoietic cell lineage 7.11E-06 3 1 1 7.4

F8VNT9;F8VV56;P08962-3;P08962-2;F8W022;F8VWK8;C9JV86;P08962 CD63 antigen CD63 >tr|F8VNT9|F8VNT9_HUMAN CD63 antigen (Fragment) OS=Homo sapiens GN=CD63 PE=2 SV=1;>tr|F8VV56|F8VV56_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=2 SV=1;>sp|P08962-3|CD63_HUMAN Isoform 3 of CD63 antigen OS=Homo sapiens GN=CD63;>sp|P08962-2|CD63_HUMAN Isofo 0.09 -0.10 -0.43 -0.17 1.29 -0.17 -0.32 0.04 0.382744741 -0.361539296 biological regulation;cell activation;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;establishment of localization;establishment of localization in cell;exocytosis;localization;macromolecule localization;platelet activation;platelet degranulation;protein localization;regulation of biological process;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of rubidium ion transport;regulation of transport;secretion;secretion by cell;transport;vesicle-mediated transport cell part;cell surface;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endosomal part;endosome;endosome membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome;late endosome membrane;lysosomal membrane;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part;platelet dense granule membrane;secretory granule membrane;vacuolar membrane;vacuolar part;vacuole;vesicle membrane Lysosome 3.13E-07 8 1 1 7.5

Q9Y4W2-3;Q9Y4W2-2;Q9Y4W2 Ribosomal biogenesis protein LAS1L LAS1L >sp|Q9Y4W2-3|LAS1L_HUMAN Isoform 3 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L;>sp|Q9Y4W2-2|LAS1L_HUMAN Isoform 2 of Ribosomal biogenesis protein LAS1L OS=Homo sapiens GN=LAS1L;>sp|Q9Y4W2|LAS1L_HUMAN Ribosomal biogenesis protein LAS1L OS -0.12 0.90 0.46 0.83 -0.52 0.15 -1.09 0.69 0.667310396 0.709626231 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;cytoplasm;histone methyltransferase complex;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL1 complex;nuclear part;nucleoplasm part;organelle part;protein complex 4.74E-05 3 1 1 3.6

D6RIZ4;D6RA47;Q14728;D6RE79 Major facilitator superfamily domain-containing protein 10 MFSD10 >tr|D6RIZ4|D6RIZ4_HUMAN Major facilitator superfamily domain-containing protein 10 OS=Homo sapiens GN=MFSD10 PE=2 SV=1;>tr|D6RA47|D6RA47_HUMAN Major facilitator superfamily domain-containing protein 10 OS=Homo sapiens GN=MFSD10 PE=2 SV=1;>sp|Q14728|MFS10_H -1.17 0.20 0.05 -0.56 -2.47 0.03 -2.12 -0.57 0.565000036 0.910779386 apoptosis;cell death;cellular process;death;establishment of localization;programmed cell death;transmembrane transport;transport antibiotic transporter activity;drug transmembrane transporter activity;tetracycline transporter activity;transmembrane transporter activity;transporter activity cell part;integral to membrane;intrinsic to membrane;membrane part 9.97E-05 4 1 1 3.7

K7EM62;O95427 GPI ethanolamine phosphate transferase 1 PIGN >tr|K7EM62|K7EM62_HUMAN GPI ethanolamine phosphate transferase 1 (Fragment) OS=Homo sapiens GN=PIGN PE=4 SV=1;>sp|O95427|PIGN_HUMAN GPI ethanolamine phosphate transferase 1 OS=Homo sapiens GN=PIGN PE=1 SV=1 -0.05 0.04 -0.08 0.03 0.11 0.22 -0.65 0.30 0.011346153 -0.007786073 biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;C-terminal protein amino acid modification;C-terminal protein lipidation;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;GPI anchor biosynthetic process;GPI anchor metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;organophosphate metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;post-translational protein modification;preassembly of GPI anchor in ER membrane;primary metabolic process;protein lipidation;protein metabolic process;protein modification process "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;sulfuric ester hydrolase activity;transferase activity"cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Glycosylphosphatidylinositol(GPI)-anchor biosynthesis 0.001875 2 1 1 6.2

E7EUI7;E7EMN6;Q6NXS1;P41236 Putative protein phosphatase inhibitor 2-like protein 3;Protein phosphatase inhibitor 2 PPP1R2;PPP1R2P3 >tr|E7EUI7|E7EUI7_HUMAN Protein phosphatase inhibitor 2 OS=Homo sapiens GN=PPP1R2 PE=2 SV=1;>tr|E7EMN6|E7EMN6_HUMAN Protein phosphatase inhibitor 2 (Fragment) OS=Homo sapiens GN=PPP1R2 PE=2 SV=1;>sp|Q6NXS1|IPP2M_HUMAN Putative protein phosphatase inhibitor 0.22 -0.04 0.23 0.17 0.43 0.10 0.29 0.05 0.261572368 -0.073576951 biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan metabolic process;glycogen metabolic process;macromolecule metabolic process;metabolic process;oxidation-reduction process;polysaccharide metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling enzyme inhibitor activity;enzyme regulator activity;phosphatase inhibitor activity;phosphatase regulator activity;protein phosphatase inhibitor activity;protein phosphatase regulator activity;protein serine/threonine phosphatase inhibitor activity 5.50E-10 4 1 1 18.8

O60216 Double-strand-break repair protein rad21 homolog RAD21 >sp|O60216|RAD21_HUMAN Double-strand-break repair protein rad21 homolog OS=Homo sapiens GN=RAD21 PE=1 SV=2 0.55 0.44 0.37 0.43 -0.06 0.58 -1.16 0.65 0.433980231 0.445392614 "anaphase;apoptosis;biological regulation;cell cycle phase;cell cycle process;cell death;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular response to stimulus;cellular response to stress;chromosome segregation;cytokinesis;death;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;localization;M phase;M phase of mitotic cell cycle;macromolecule localization;macromolecule metabolic process;metabolic process;mitotic anaphase;mitotic prometaphase;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;protein localization;protein localization to chromatin;protein localization to chromosome;protein localization to organelle;reciprocal DNA recombination;reciprocal meiotic recombination;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle" "cell part;chromosomal part;chromosome, centromeric region;cohesin complex;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;meiotic cohesin complex;nuclear chromosome part;nuclear cohesin complex;nuclear meiotic cohesin complex;nuclear part;nucleoplasm;organelle part;protein complex" Cell cycle;Cell cycle - yeast 4.53E-07 1 1 1 2.1

Q9UHV5-2;F5H2D5;Q9UHV5-3;Q9UHV5 Rap guanine nucleotide exchange factor-like 1 RAPGEFL1 >sp|Q9UHV5-2|RPGFL_HUMAN Isoform 2 of Rap guanine nucleotide exchange factor-like 1 OS=Homo sapiens GN=RAPGEFL1;>tr|F5H2D5|F5H2D5_HUMAN Rap guanine nucleotide exchange factor-like 1 OS=Homo sapiens GN=RAPGEFL1 PE=2 SV=1;>sp|Q9UHV5-3|RPGFL_HUMAN Isoform 3 o -0.19 1.02 0.26 1.10 1.53 0.80 -0.40 0.80 0.094584526 -0.137073185 anatomical structure development;biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;developmental process;G-protein coupled receptor protein signaling pathway;intracellular signal transduction;nervous system development;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;system development enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity cell part;intracellular;membrane 0.0012706 4 1 1 2.2

Q5T093;Q5T092;Q5T091;O15258 Protein RER1 RER1 >tr|Q5T093|Q5T093_HUMAN Protein RER1 OS=Homo sapiens GN=RER1 PE=2 SV=1;>tr|Q5T092|Q5T092_HUMAN Protein RER1 (Fragment) OS=Homo sapiens GN=RER1 PE=2 SV=1;>tr|Q5T091|Q5T091_HUMAN Protein RER1 OS=Homo sapiens GN=RER1 PE=2 SV=1;>sp|O15258|RER1_HUMAN Protein RE -0.16 0.39 -0.14 -0.03 -0.44 -0.33 -1.26 -0.76 1.218805294 0.714214699 "cellular process;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle-mediated transport" cell part;cytoplasmic part;Golgi apparatus part;integral to Golgi membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to Golgi membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane part;organelle part 5.96E-05 4 1 1 16.2

Q15427 Splicing factor 3B subunit 4 SF3B4 >sp|Q15427|SF3B4_HUMAN Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1 -0.29 0.49 -0.12 0.36 0.28 0.02 -1.12 -0.22 0.426838791 0.372333881 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome 2.59E-15 1 1 1 3.3

Q8NBK3-2;Q8NBK3-5;Q8NBK3;Q8NBK3-3;F5GXA0 Sulfatase-modifying factor 1 SUMF1 >sp|Q8NBK3-2|SUMF1_HUMAN Isoform 2 of Sulfatase-modifying factor 1 OS=Homo sapiens GN=SUMF1;>sp|Q8NBK3-5|SUMF1_HUMAN Isoform 5 of Sulfatase-modifying factor 1 OS=Homo sapiens GN=SUMF1;>sp|Q8NBK3|SUMF1_HUMAN Sulfatase-modifying factor 1 OS=Homo sapiens GN=S 0.04 -0.13 -0.34 -0.06 0.23 -0.02 0.41 0.19 1.136151097 -0.32271706 cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycolipid metabolic process;glycosphingolipid metabolic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;membrane lipid metabolic process;metabolic process;post-translational protein modification;primary metabolic process;protein metabolic process;protein modification process;small molecule metabolic process;sphingolipid metabolic process binding;catalytic activity;cation binding;ion binding;metal ion binding;oxidoreductase activity cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Lysosome 0.0001846 5 1 1 4.6

P61956-2;Q6EEV6;P61956;H7BZT4;P55854;A8MUA9;B4DUW4;A8MU27 Small ubiquitin-related modifier 4;Small ubiquitin-related modifier 2;Small ubiquitin-related modifier 3 SUMO4;SUMO2;SUMO3 >sp|P61956-2|SUMO2_HUMAN Isoform 2 of Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2;>sp|Q6EEV6|SUMO4_HUMAN Small ubiquitin-related modifier 4 OS=Homo sapiens GN=SUMO4 PE=1 SV=2;>sp|P61956|SUMO2_HUMAN Small ubiquitin-related modifier 2 OS=Homo 0.69 0.30 -1.28 -0.57 1.46 0.89 0.21 0.55 0.824362892 -0.99402618 "biological regulation;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;localization;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catabolic process;positive regulation of cellular biosynthetic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;positive regulation of proteolysis;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein localization;protein localization to nucleus;protein localization to organelle;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein sumoylation;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of proteolysis;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent" "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;SUMO ligase activity" cell part;chromosomal part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;PML body;protein complex RNA transport 3.19E-13 8 1 1 16.9

Q8NF91-8;Q8NF91-2;E7ENN3;Q8NF91-4;E9PEL9;Q8NF91 Nesprin-1SYNE1 >sp|Q8NF91-8|SYNE1_HUMAN Isoform 8 of Nesprin-1 OS=Homo sapiens GN=SYNE1;>sp|Q8NF91-2|SYNE1_HUMAN Isoform 2 of Nesprin-1 OS=Homo sapiens GN=SYNE1;>tr|E7ENN3|E7ENN3_HUMAN Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=2 SV=1;>sp|Q8NF91-4|SYNE1_HUMAN Isoform 4 of Nes -0.08 0.37 0.03 0.48 -0.16 -0.06 -0.88 -0.28 1.016923429 0.543998277 biological regulation;cell death;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeletal anchoring at nuclear membrane;cytoskeleton organization;death;developmental process;Golgi organization;maintenance of location;maintenance of location in cell;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;maintenance of protein location in nucleus;muscle cell differentiation;nuclear matrix anchoring at nuclear membrane;nuclear matrix organization;nucleus organization;organelle organization;regulation of biological quality actin binding;binding;cytoskeletal protein binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity cell part;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeleton;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear membrane;nuclear outer membrane;nuclear part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;postsynaptic membrane;protein complex;sarcomere;SUN-KASH complex;synapse part;synaptic membrane 0.00043684 6 1 1 0.3

C9JYN0;Q16563-2;Q16563 Synaptophysin-like protein 1 SYPL1 >tr|C9JYN0|C9JYN0_HUMAN Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=2 SV=1;>sp|Q16563-2|SYPL1_HUMAN Isoform 2 of Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1;>sp|Q16563|SYPL1_HUMAN Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 -0.23 -0.20 0.06 -0.17 0.62 0.49 -0.04 0.11 1.065662468 -0.42888497 cell communication;cell-cell signaling;cellular process;signaling;synaptic transmission transporter activity cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;stored secretory granule;synapse part;synaptic vesicle;vesicle;vesicle membrane 3.42E-06 3 1 1 4.9

Q96C24;F8W9B9 Synaptotagmin-like protein 4 SYTL4 >sp|Q96C24|SYTL4_HUMAN Synaptotagmin-like protein 4 OS=Homo sapiens GN=SYTL4 PE=1 SV=2;>tr|F8W9B9|F8W9B9_HUMAN Synaptotagmin-like protein 4 OS=Homo sapiens GN=SYTL4 PE=2 SV=1 -0.30 1.05 0.18 1.07 -0.60 0.79 -0.62 0.84 0.29308302 0.398549739 biological regulation;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;intracellular protein transport;intracellular transport;multivesicular body sorting pathway;negative regulation of biological process;negative regulation of cellular process;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of secretion;negative regulation of transport;positive regulation of biological process;positive regulation of cellular process;positive regulation of exocytosis;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of secretion;positive regulation of transport;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of exocytosis;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of secretion;regulation of signaling;regulation of transport;regulation of vesicle-mediated transport;secretion;secretion by cell;transport;vesicle-mediated transport binding;cation binding;ion binding;lipid binding;metal ion binding;neurexin family protein binding;phospholipid binding;protein binding;transition metal ion binding;transporter activity;zinc ion binding cell part;centrosome;clathrin-coated vesicle;coated vesicle;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;endosome;extrinsic to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;plasma membrane;stored secretory granule;synapse part;synaptic vesicle;transport vesicle membrane;vesicle;vesicle membrane 0.0015219 2 1 1 1.8

Q86TJ2-3;Q86TJ2-2;Q86TJ2 Transcriptional adapter 2-beta TADA2B >sp|Q86TJ2-3|TAD2B_HUMAN Isoform 3 of Transcriptional adapter 2-beta OS=Homo sapiens GN=TADA2B;>sp|Q86TJ2-2|TAD2B_HUMAN Isoform 2 of Transcriptional adapter 2-beta OS=Homo sapiens GN=TADA2B;>sp|Q86TJ2|TAD2B_HUMAN Transcriptional adapter 2-beta OS=Homo sapi -0.41 1.14 0.10 1.34 -1.18 0.17 -0.93 0.54 0.642532483 0.892188907 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cation binding;chromatin binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding cell part;histone acetyltransferase complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm part;organelle part;protein complex;SAGA-type complex;STAGA complex 3.33E-05 3 1 1 2.1

E9PF19;Q9Y4P3 Transducin beta-like protein 2 TBL2 >tr|E9PF19|E9PF19_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=2 SV=1;>sp|Q9Y4P3|TBL2_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1 0.04 0.33 -0.11 -0.08 0.57 0.16 -0.60 0.08 0.009865291 -0.008035514 7.09E-47 2 1 1 3.2

C9JAP5;C9JEN3;C9IYT2;F8WDY4;C9IZ27;C9JW19;C9JWV9;B4DUD2;Q969X1 Protein lifeguard 3 TMBIM1 >tr|C9JAP5|C9JAP5_HUMAN Protein lifeguard 3 (Fragment) OS=Homo sapiens GN=TMBIM1 PE=2 SV=1;>tr|C9JEN3|C9JEN3_HUMAN Protein lifeguard 3 (Fragment) OS=Homo sapiens GN=TMBIM1 PE=2 SV=1;>tr|C9IYT2|C9IYT2_HUMAN Protein lifeguard 3 (Fragment) OS=Homo sapiens GN= 0.16 0.46 -0.33 0.13 -0.03 -0.89 -0.44 0.10 0.640190387 0.417471082 cell part;cytoplasmic part;endosomal part;endosome membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal membrane;membrane;membrane part;organelle membrane;organelle part;vacuolar membrane;vacuolar part 3.13E-11 9 1 1 15.2

H3BRL3;O14562 Ubiquitin domain-containing protein UBFD1 UBFD1 >tr|H3BRL3|H3BRL3_HUMAN Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens GN=UBFD1 PE=2 SV=1;>sp|O14562|UBFD1_HUMAN Ubiquitin domain-containing protein UBFD1 OS=Homo sapiens GN=UBFD1 PE=1 SV=2 0.47 0.03 0.26 0.08 0.53 0.55 0.62 1.44 1.019377559 -0.577529149 2.55E-05 2 1 1 4

C4AMC7;Q6VEQ5;A8K0Z3;H3BV49;A8MWX3 Putative WAS protein family homolog 3;WAS protein family homolog 2;WAS protein family homolog 1 WASH3P;WASH2P;WASH1 >sp|C4AMC7|WASH3_HUMAN Putative WAS protein family homolog 3 OS=Homo sapiens GN=WASH3P PE=2 SV=2;>sp|Q6VEQ5|WASH2_HUMAN WAS protein family homolog 2 OS=Homo sapiens GN=WASH2P PE=2 SV=2;>sp|A8K0Z3|WASH1_HUMAN WAS protein family homolog 1 OS=Homo sapiens GN= 0.09 -0.16 0.06 -0.18 -0.16 0.06 0.05 -0.22 0.067327091 0.019831593 "actin cytoskeleton organization;actin filament organization;actin filament-based process;actin nucleation;Arp2/3 complex-mediated actin nucleation;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;endosome transport;establishment of localization;establishment of localization in cell;intracellular transport;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;retrograde transport, endosome to Golgi;transport;vesicle-mediated transport" alpha-tubulin binding;binding;cytoskeletal protein binding;protein binding;tubulin binding cell part;cell projection;cytoplasmic part;early endosome;early endosome membrane;endosomal part;endosome;endosome membrane;filopodium;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex;recycling endosome;recycling endosome membrane;WASH complex 1.11E-27 5 3 1 8.4

C9IZY8;Q96PY5;Q96PY5-3 Formin-like protein 2 FMNL2 >tr|C9IZY8|C9IZY8_HUMAN Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=2 SV=1;>sp|Q96PY5|FMNL2_HUMAN Formin-like protein 2 OS=Homo sapiens GN=FMNL2 PE=1 SV=3;>sp|Q96PY5-3|FMNL2_HUMAN Isoform 2 of Formin-like protein 2 OS=Homo sapiens GN=FMNL2 0.02 0.34 0.02 0.09 0.83 0.34 -0.39 -0.15 0.043313489 -0.036551727 actin cytoskeleton organization;actin filament-based process;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;organelle organization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of cell morphogenesis;regulation of cellular component organization;regulation of cellular process;regulation of developmental process cell part;cytoplasm;intracellular part 3.42E-09 3 4 1 10.6

E9PM17;B3KNX7;Q13153;Q13153-2;H0YCG5;H0YCM0 Serine/threonine-protein kinase PAK 1 PAK1 >tr|E9PM17|E9PM17_HUMAN Serine/threonine-protein kinase PAK 1 OS=Homo sapiens GN=PAK1 PE=2 SV=1;>tr|B3KNX7|B3KNX7_HUMAN Serine/threonine-protein kinase PAK 1 OS=Homo sapiens GN=PAK1 PE=2 SV=1;>sp|Q13153|PAK1_HUMAN Serine/threonine-protein kinase PAK 1 OS=H -0.05 0.03 0.68 0.25 0.52 0.04 0.47 -0.15 0.007580086 0.005413533 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;activation of immune response;anatomical structure development;anatomical structure morphogenesis;antigen receptor-mediated signaling pathway;apoptosis;axon guidance;biological regulation;branching morphogenesis of a tube;cell death;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chemotaxis;cytoskeleton organization;death;defense response;dendrite development;developmental process;establishment of localization;establishment of localization in cell;exocytosis;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;innate immune response;localization;locomotion;lymphocyte costimulation;macromolecule localization;macromolecule metabolic process;macromolecule modification;membrane organization;metabolic process;morphogenesis of a branching structure;multicellular organismal process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cell proliferation involved in contact inhibition;negative regulation of cellular process;neuromuscular junction development;neuron projection development;neuron projection morphogenesis;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of actin filament bundle assembly;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytoskeleton organization;positive regulation of estrogen receptor signaling pathway;positive regulation of immune response;positive regulation of immune system process;positive regulation of JUN kinase activity;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of peptidyl-serine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of steroid hormone receptor signaling pathway;positive regulation of stress fiber assembly;positive regulation of T cell activation;positive regulation of transferase activity;primary metabolic process;programmed cell death;protein autophosphorylation;protein localization;protein localization in membrane;protein metabolic process;protein modification process;protein phosphorylation;receptor clustering;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of biological process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cytoskeleton organization;regulation of estrogen receptor signaling pathway;regulation of immune response;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of organelle organization;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of stress fiber assembly;regulation of stress-activated protein kinase signaling cascade;regulation of T cell activation;regulation of transferase activity;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to hormone stimulus;response to hypoxia;response to insulin stimulus;response to organic substance;response to oxygen levels;response to peptide hormone stimulus;response to stimulus;response to stress;response to wounding;secretion;secretion by cell;signal transduction;synapse organization;T cell costimulation;T cell receptor signaling pathway;taxis;transport;tube morphogenesis;vesicle-mediated transport;wound healing "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;axon;cell junction;cell part;cell projection;cell projection part;cell-cell contact zone;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasmic part;cytosol;dendrite;focal adhesion;Golgi apparatus;growth cone;intercalated disc;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;neuron projection;nuclear membrane;nuclear part;organelle;organelle membrane;organelle part;plasma membrane;protein complex;ruffle;site of polarized growth;Z disc Axon guidance;Chemokine signaling pathway;Epithelial cell signaling in Helicobacter pylori infection;ErbB signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;MAPK signaling pathway;MAPK signaling pathway - yeast;Natural killer cell mediated cytotoxicity;Regulation of actin cytoskeleton;Renal cell carcinoma;T cell receptor signaling pathway 8.07E-133 6 4 1 12.3

H0YEF7;H0YEH1;H0YE97;H0YEY8;H0YD48 PICALM >tr|H0YEF7|H0YEF7_HUMAN Phosphatidylinositol-binding clathrin assembly protein (Fragment) OS=Homo sapiens GN=PICALM PE=4 SV=1;>tr|H0YEH1|H0YEH1_HUMAN Phosphatidylinositol-binding clathrin assembly protein (Fragment) OS=Homo sapiens GN=PICALM PE=4 SV=1;>tr| -0.12 0.00 -0.18 0.16 0.07 0.29 -0.19 0.09 0.33631736 -0.103348533 cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle 2.50E-33 5 4 1 24.5

P63096;P63096-2;C9JPP4 Guanine nucleotide-binding protein G(i) subunit alpha-1 GNAI1 >sp|P63096|GNAI1_HUMAN Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 PE=1 SV=2;>sp|P63096-2|GNAI1_HUMAN Isoform 2 of Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Homo sapiens GN=GNAI1 -0.09 0.28 -1.12 0.29 -2.03 -0.17 -0.78 -0.51 0.573641877 0.713673644 "biological regulation;cAMP-mediated signaling;cell activation;cell communication;cell cycle;cell division;cell surface receptor linked signaling pathway;cell-cell signaling;cellular process;cellular response to stimulus;cyclic-nucleotide-mediated signaling;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;negative regulation of adenylate cyclase activity;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of molecular function;platelet activation;regulation of adenylate cyclase activity;regulation of biological process;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;second-messenger-mediated signaling;signal transduction;signaling;synaptic transmission" "binding;catalytic activity;cation binding;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metabotropic serotonin receptor binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity" cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;microtubule organizing center;midbody;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part;protein complex Axon guidance;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Gap junction;Gastric acid secretion;Leukocyte transendothelial migration;Long-term depression;Melanogenesis;Progesterone-mediated oocyte maturation;Tight junction;Toxoplasmosis 6.99E-21 3 5 1 16.7

P08754 Guanine nucleotide-binding protein G(k) subunit alpha GNAI3 >sp|P08754|GNAI3_HUMAN Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 0.05 0.16

0.26 0.28 -0.23 -0.05 -0.55 -0.01 1.218076626 0.394408358 "biological regulation;cAMP-mediated signaling;cell activation;cell communication;cell cycle;cell division;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;cellular response to stimulus;cyclic-nucleotide-mediated signaling;establishment of localization;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;membrane fusion;membrane organization;negative regulation of adenylate cyclase activity;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of molecular function;organelle fusion;organelle organization;platelet activation;regulation of adenylate cyclase activity;regulation of biological process;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;response to stimulus;second-messenger-mediated signaling;signal transduction;signaling;synaptic transmission;transport;vesicle fusion;vesicle organization" "binding;catalytic activity;cation binding;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metabotropic serotonin receptor binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity" cell part;centrosome;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus;heterotrimeric G-protein complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;midbody;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;protein complex;stored secretory granule;vesicle;zymogen granule Axon guidance;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Gap junction;Gastric acid secretion;Leukocyte transendothelial migration;Long-term depression;Melanogenesis;Progesterone-mediated oocyte maturation;Tight junction;Toxoplasmosis 1.69E-29 1 5 1 16.7

Q5RHS7 S100A2 >tr|Q5RHS7|Q5RHS7_HUMAN Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=2 SV=2 -0.25 -0.18 -0.89 -0.09 -1.86 -1.08 0.64 0.22 0.098781714 0.17027027 binding;calcium ion binding;cation binding;ion binding;metal ion binding 4.52E-49 1 5 1 41.1

O00273-2;K7ERT1 >sp|O00273-2|DFFA_HUMAN Isoform DFF35 of DNA fragmentation factor subunit alpha OS=Homo sapiens GN=DFFA 0.34 -0.06 0.38 0.04 -1.27 -1.07 0.05 -0.16 0.969210301 0.783065869 apoptosis;biological regulation;cell death;cellular process;cellular response to stimulus;death;programmed cell death;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction cell part;intracellular 4.12E-65 2 6 1 32.1

P29590;P29590-11;P29590-4;P29590-2;P29590-9;P29590-3;P29590-8;P29590-14;P29590-10;H3BT57;P29590-13;H3BT29;H3BVD2 Protein PML PML >sp|P29590|PML_HUMAN Protein PML OS=Homo sapiens GN=PML PE=1 SV=3;>sp|P29590-11|PML_HUMAN Isoform PML-11 of Protein PML OS=Homo sapiens GN=PML;>sp|P29590-4|PML_HUMAN Isoform PML-6 of Protein PML OS=Homo sapiens GN=PML;>sp|P29590-2|PML_HUMAN Isoform PML-5 o -0.23 -0.07 0.17 0.22 -0.02 -0.05 -0.74 0.29 0.241956759 0.151963922 "activation of caspase activity;aging;anatomical structure morphogenesis;biological regulation;biosynthetic process;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a tube;calcium ion homeostasis;catabolic process;cation homeostasis;cell aging;cell cycle arrest;cell cycle process;cell differentiation;cell fate commitment;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;cellular senescence;chemical homeostasis;common-partner SMAD protein phosphorylation;cytokine-mediated signaling pathway;defense response;defense response to virus;developmental process;divalent inorganic cation homeostasis;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;endoplasmic reticulum calcium ion homeostasis;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;homeostatic process;immune effector process;immune system process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;ion homeostasis;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;maintenance of location;maintenance of location in cell;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;maintenance of protein location in nucleus;metabolic process;metal ion homeostasis;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;multi-organism process;myeloid cell differentiation;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of gene expression;negative regulation of growth;negative regulation of homeostatic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitotic cell cycle;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;negative regulation of RNA metabolic process;negative regulation of telomerase activity;negative regulation of telomere maintenance;negative regulation of telomere maintenance via telomerase;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of translation;negative regulation of translation in response to oxidative stress;negative regulation of translation in response to stress;nitrogen compound metabolic process;nuclear body organization;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;nucleus organization;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;PML body organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of defense response to virus by host;positive regulation of histone deacetylation;positive regulation of histone modification;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of protein deacetylation;positive regulation of protein metabolic process;positive regulation of protein modification process;posttranscriptional regulation of gene expression;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex assembly;protein complex subunit organization;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein phosphorylation;protein stabilization;protein targeting;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome organization;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by host;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA repair;regulation of DNA replication;regulation of double-strand break repair;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of histone deacetylation;regulation of histone modification;regulation of homeostatic process;regulation of hydrolase activity;regulation of immune effector process;regulation of immune system process;regulation of ion homeostasis;regulation of ion transport;regulation of

localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of MHC class I biosynthetic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein deacetylation;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein ubiquitination;regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of proteolysis;regulation of response to biotic stimulus;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of telomerase activity;regulation of telomere maintenance;regulation of telomere maintenance via telomerase;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of translation in response to oxidative stress;regulation of translation in response to stress;regulation of transport;reproductive process;response to abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to gamma radiation;response to hypoxia;response to interferon-gamma;response to ionizing radiation;response to light stimulus;response to organic substance;response to other organism;response to oxidative stress;response to oxygen levels;response to radiation;response to stimulus;response to stress;response to UV;response to virus;retinoic acid receptor signaling pathway;RNA biosynthetic process;RNA metabolic process;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;SMAD protein import into nucleus;tissue morphogenesis;transcription, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;transport;tube morphogenesis;ubiquitin-dependent protein catabolic process;viral reproductive process;virus-host interaction"
binding;cation binding;cobalt ion binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein heterodimerization activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;cytoplasmic part;cytosol;early endosome membrane;endoplasmic reticulum part;endosomal part;endosome membrane;extrinsic to endoplasmic reticulum membrane;extrinsic to membrane;extrinsic to organelle membrane;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear membrane;nuclear part;nucleolus;nucleoplasm part;nucleus;organelle;organelle membrane;organelle part;PML body Acute myeloid leukemia;Endocytosis;Pathways in cancer;Ubiquitin mediated proteolysis 1.66E-38 13 7 1 13

P26232-2;P26232-5;P26232;P26232-3;C9J144;C9IZ88 Catenin alpha-2 CTNNA2>sp|P26232-2|CTNA2_HUMAN Isoform 2 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232-5|CTNA2_HUMAN Isoform 5 of Catenin alpha-2 OS=Homo sapiens GN=CTNNA2;>sp|P26232|CTNA2_HUMAN Catenin alpha-2 OS=Homo sapiens GN=CTNNA2 PE=1 SV=5;>sp|P26232-3|CTNA2_HU -0.04 0.14 0.10 0.16 -0.99 -0.35 -0.27 -0.01 0.980624815 0.490300329 anatomical structure morphogenesis;axonogenesis;biological adhesion;biological regulation;brain morphogenesis;cell adhesion;cell differentiation;cell migration;cell migration in hindbrain;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;dendrite morphogenesis;developmental process;hindbrain radial glia guided cell migration;locomotion;muscle cell differentiation;negative regulation of biological process;negative regulation of response to external stimulus;negative regulation of response to stimulus;neuron projection morphogenesis;organ morphogenesis;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle cell differentiation;prepulse inhibition;radial glia guided migration of Purkinje cell;regulation of biological process;regulation of cell differentiation;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of muscle cell differentiation;regulation of response to external stimulus;regulation of response to stimulus;regulation of synapse organization;regulation of synapse structural plasticity structural constituent of cytoskeleton;structural molecule activity actin cytoskeleton;adherens junction;anchoring junction;axon;basolateral plasma membrane;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane part;neuron projection;non-membrane-bounded organelle;organelle;plasma membrane part Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Endometrial cancer;Leukocyte transendothelial migration;Pathways in cancer;Tight junction 1.78E-158 6 8 1 10.6

H7BZJ3 Thioredoxin PDIA3 >tr|H7BZJ3|H7BZJ3_HUMAN Thioredoxin (Fragment) OS=Homo sapiens GN=PDIA3 PE=2 SV=1 0.25 -0.22 -0.37 -0.28 0.08 -0.22 0.59 -0.06 0.470417306 -0.2525022 biological regulation;cell redox homeostasis;cellular homeostasis;cellular process;glycerol ether metabolic process;homeostatic process;metabolic process;organic ether metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide oxidoreductase activity" 7.63E-175 1 8 1 58.5

O00560;B4DHN5;E9PBU7;O00560-3 Syntenin-1 SDCBP >sp|O00560|SDCB1_HUMAN Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1;>tr|B4DHN5|B4DHN5_HUMAN Syntenin-1 OS=Homo sapiens GN=SDCBP PE=2 SV=1;>tr|E9PBU7|E9PBU7_HUMAN Syntenin-1 OS=Homo sapiens GN=SDCBP PE=2 SV=1;>sp|O00560-3|SDCB1_HUMAN Isoform 3 of Syntenin- -0.13 0.11 -0.51 0.07 0.79 0.49 -0.05 0.15 0.842894214 -0.459353073 "actin cytoskeleton organization;actin filament-based process;axon guidance;biological regulation;cell communication;cell projection assembly;cell projection organization;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotion;organelle organization;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of JNK cascade;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;protein targeting;protein targeting to membrane;protein transport;Ras protein signal transduction;regulation of biological process;regulation of cell communication;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of MAPKKK cascade;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;small GTPase mediated signal transduction;substrate-dependent cell migration, cell extension;synaptic transmission;taxis;transport"
"binding;binding, bridging;cytokine receptor binding;cytoskeletal adaptor activity;cytoskeletal protein binding;growth factor receptor binding;interleukin-5 receptor binding;protein binding;protein binding, bridging;receptor binding;syndecan binding" adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;focal adhesion;interleukin-5 receptor complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;pigment granule;plasma membrane part;protein complex;receptor complex;vesicle 1.34E-119 4 8 1 37.2

P10316;P01892;A9R9N7;A9R9N8;P01891;H0Y842;P30511-2;E9PGX5;P30511;P30511-3 "HLA class I histocompatibility antigen, A-69 alpha chain;HLA class I histocompatibility antigen, A-2 alpha chain;HLA class I histocompatibility antigen, A-68 alpha chain" HLA-A ">sp|P10316|1A69_HUMAN HLA class I histocompatibility antigen, A-69 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=2;>sp|P01892|1A02_HUMAN HLA class I histocompatibility antigen, A-2 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1;>tr|A9R9N7|A9R9N7_HUMAN HLA c" -0.50 -0.03 -0.51 0.09 0.94 0.46 0.46 -0.52 0.712201957 -0.573568686 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;immune response;immune system process;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;multi-organism process;regulation of biological process;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;response to type I interferon;signal transduction;type I interferon-mediated signaling pathway;viral reproduction;viral reproductive process;virus-host interaction" cell part;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome membrane;endocytic vesicle membrane;endoplasmic reticulum part;endosomal part;endosome membrane;ER to Golgi transport vesicle membrane;Golgi apparatus part;Golgi membrane;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane;membrane part;MHC class I protein complex;MHC protein complex;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;plasma membrane part;protein complex;transport vesicle membrane;vesicle membrane Allograft rejection;Antigen processing and presentation;Autoimmune thyroid disease;Cell adhesion molecules (CAMs);Endocytosis;Graft-versus-host disease;Natural killer cell mediated cytotoxicity;Phagosome;Type I diabetes mellitus;Viral myocarditis 3.95E-127 10 9 1 36.4

O60812 Heterogeneous nuclear ribonucleoprotein C-like 1 HNRNPCL1 >sp|O60812|HNRCL_HUMAN Heterogeneous nuclear ribonucleoprotein C-like 1 OS=Homo sapiens GN=HNRNPCL1 PE=1 SV=1 -0.24 1.30 -0.03 1.41 -0.33 0.48 -1.58 0.17 0.628078868 0.928081653 binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex 2.54E-53 1 9 1 21.2

P67775;P67775-2;H0YC23;E5RHC1;H0YBN9;E5RFI3;E5RHP4;E7ESG8;E5RI56 Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform PPP2CA >sp|P67775|PP2AA_HUMAN Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1;>sp|P67775-2|PP2AA_HUMAN Isoform 2 of Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens 0.19 0.09 -0.13 -0.04 0.14 0.09 0.17 0.06 0.492467879 -0.089389688 "anaphase;anatomical structure development;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;ceramide metabolic process;dephosphorylation;developmental process;enzyme linked receptor protein signaling pathway;fibroblast growth factor receptor signaling pathway;inactivation of MAPK activity;induction of apoptosis;induction of programmed cell death;intracellular signal transduction;lipid metabolic process;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;meiosis;membrane lipid metabolic process;membrane organization;mesoderm development;metabolic process;mitotic anaphase;mitotic nuclear envelope reassembly;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell morphogenesis involved in differentiation;negative regulation of cellular component organization;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of epithelial to mesenchymal transition;negative regulation of growth;negative regulation of intracellular protein kinase cascade;negative regulation of JAK-STAT cascade;negative regulation of kinase activity;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidyl-tyrosine phosphorylation;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of protein serine/threonine kinase activity;negative regulation of Ras protein signal transduction;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of small GTPase mediated signal transduction;negative regulation of transferase activity;negative regulation of tyrosine phosphorylation of STAT protein;negative regulation of tyrosine phosphorylation of Stat3 protein;nitrogen compound metabolic process;nuclear envelope organization;nuclear envelope reassembly;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex assembly;protein complex subunit organization;protein dephosphorylation;protein heterooligomerization;protein heterotrimerization;protein metabolic process;protein modification process;protein oligomerization;protein trimerization;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of epithelial to mesenchymal transition;regulation of gene expression;regulation of growth;regulation of intracellular protein kinase cascade;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein autophosphorylation;regulation of protein catabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of Ras protein signal transduction;regulation of receptor activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat3 protein;regulation of Wnt receptor signaling pathway;response to antibiotic;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hydrogen peroxide;response to inorganic substance;response to organic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;second-messenger-mediated signaling;signal transduction;sphingoid metabolic process;sphingolipid metabolic process;tissue development;transmembrane receptor protein tyrosine kinase signaling pathway;ubiquitin-dependent protein catabolic process" "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity" "cell part;chromosomal part;chromosome, centromeric region;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule cytoskeleton;mitochondrion;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex;spindle pole" Cell cycle - yeast;Chagas disease (American trypanosomiasis);Hepatitis C;Long-term depression;Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;TGF-beta signaling pathway;Tight junction;Wnt signaling pathway 1.23E-84 9 9 1 37.5

P0CW22;P08708;H0YK46;H0YN73;REV__F8WFC6;H3BLW3;H3BNC9;REV__H7BXY5;REV__Q0ZGT2-4;REV__Q0ZGT2-3;REV__Q9H089;REV__Q0ZGT2-2;REV__Q0ZGT2;REV__Q96JM4-2;REV__Q96JM4 40S ribosomal protein S17-like;40S ribosomal protein S17 RPS17L;RPS17 >sp|P0CW22|RS17L_HUMAN 40S ribosomal protein S17-like OS=Homo sapiens GN=RPS17L PE=1 SV=1;>sp|P08708|RS17_HUMAN 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2;>tr|H0YK46|H0YK46_HUMAN 40S ribosomal protein S17 (Fragment) OS=Homo sapiens GN=RPS 0.05 0.06 0.34 0.17 -0.98 -0.76 -0.15 0.02 1.059315148 0.621461029 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;erythrocyte homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;homeostasis of number of cells;homeostatic process;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA

catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological quality;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;nucleotide binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit
Ribosome 4.99E-132 15 9 1 65.2

Q5JTV8;H0YD16;H0Y4R4;Q5JTV8-2;H0YDU3Torsin-1A-interacting protein 1 TOR1AIP1 >sp|Q5JTV8|TOIP1_HUMAN Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2;>tr|H0YD16|H0YD16_HUMAN Torsin-1A-interacting protein 1 (Fragment) OS=Homo sapiens GN=TOR1AIP1 PE=4 SV=1 0.05 0.23 0.26 0.33 0.19 0.06 -1.00 -0.08 0.654238006 0.424693918 cellular component organization;cellular component organization or biogenesis;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;localization;macromolecule localization;membrane organization;nuclear membrane organization;protein localization;protein localization to nucleus;protein localization to organelle cell part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;nuclear inner membrane;nuclear membrane;nuclear part;organelle inner membrane;organelle membrane;organelle part
2.52E-83 5 9 1 21.8

P16989-2 >sp|P16989-2|YBOX3_HUMAN Isoform 2 of Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 -0.48 0.06 0.11 0.15 -0.31 -0.51 -0.35 -0.59 1.056816329 0.405239409
1.78E-143 1 9 1 59.7

Q562R1 Beta-actin-like protein 2 ACTBL2 >sp|Q562R1|ACTBL_HUMAN Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 -0.27 0.55 -1.09 0.90 -1.03 0.33 -0.28 0.78 0.040515757 0.071991742 adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 1.74E-122 1
11 1 20.2

Q71TU5;D6REM4;E7ETM0 CSNK1A1 ">tr|Q71TU5|Q71TU5_HUMAN Casein kinase 1, alpha 1, isoform CRA_g OS=Homo sapiens GN=CSNK1A1 PE=2 SV=1;>tr|D6REM4|D6REM4_HUMAN Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=2 SV=1;>tr|E7ETM0|E7ETM0_HUMAN Casein kinase I isoform alpha OS=Homo sa" -0.12 0.66 0.11 0.63 -0.75 -0.03 -0.73 0.17 0.911375782 0.652775933 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" Hedgehog signaling pathway;Wnt signaling pathway 7.03E-91 3 11 1 39.7

Q14978-3 >sp|Q14978-3|NOLC1_HUMAN Isoform 3 of Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 -0.31 1.19 0.16 1.28 -0.76 -0.15 -1.48 0.17
0.906359304 1.133439071 8.50E-93 1 13 1 19.6

Q9UJU6-2;Q9UJU6-3;B4DDD6;B4DDP6;C9J7P1;F8WBG8;F8WC20;F8WBB2;F8WFE1;F2Z2V3;F8WB73;F8WCK3;F2Z3E3;H7C111 DBNL >sp|Q9UJU6-2|DBNL_HUMAN Isoform 2 of Drebrin-like protein OS=Homo sapiens GN=DBNL;>sp|Q9UJU6-3|DBNL_HUMAN Isoform 3 of Drebrin-like protein OS=Homo sapiens GN=DBNL;>tr|B4DDD6|B4DDD6_HUMAN Drebrin-like protein OS=Homo sapiens GN=DBNL PE=2 SV=1;>tr|B4DDP6|B4 0.04 -0.08 -0.01 -0.02 0.24 0.12 0.25 -0.21 0.44250717 -0.118131424 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;Rac protein signal transduction;Ras protein signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction cell cortex;cell part;cell projection;cytoplasmic part;cytoskeletal part;intracellular;intracellular organelle part;intracellular part;lamellipodium;organelle part;postsynaptic density;ruffle;synapse part 3.65E-231 14 14 1
42.5

Q5T9A4;Q5T9A4-3 ATPase family AAA domain-containing protein 3B ATAD3B>sp|Q5T9A4|ATD3B_HUMAN ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1;>sp|Q5T9A4-3|ATD3B_HUMAN Isoform 3 of ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B 0.07 1.21 0.21 0.90 -0.49 0.36 -1.22 0.72 0.622336049 0.755640039 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part
2.46E-124 2 17 1 27.8

O15231-3;H0Y704;O15231-5;O15231-2;J3KNL4;H7C3U6;H7BZT5 ZNF185 >sp|O15231-3|ZN185_HUMAN Isoform 3 of Zinc finger protein 185 OS=Homo sapiens GN=ZNF185;>tr|H0Y704|H0Y704_HUMAN Zinc finger protein 185 (Fragment) OS=Homo sapiens GN=ZNF185 PE=4 SV=1;>sp|O15231-5|ZN185_HUMAN Isoform 5 of Zinc finger protein 185 OS=Homo sap 0.56 1.11 0.52 0.45 0.30 1.31 -0.89 -0.33
0.467818783 0.559287421 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding 1.58E-135 7 20 1 43.3

P09651 Heterogeneous nuclear ribonucleoprotein A1 HNRNPA1 >sp|P09651|ROA1_HUMAN Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 -0.21 0.79 -0.03 0.81 -0.02 0.09 -1.39 -0.06 0.662895119 0.686461011 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear export;nuclear import;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;reproductive process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;transport;viral reproductive process;virus-host interaction" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;single-stranded DNA binding;single-stranded RNA binding;structure-specific DNA binding catalytic step 2 spliceosome;cell part;cytoplasm;cytoskeleton;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 5.44E-230 1 21 1
59.7

Q5VT79;Q5VT79-2;E7EVD9 Annexin A8-like protein 2;Annexin ANXA8L2 >sp|Q5VT79|AXA82_HUMAN Annexin A8-like protein 2 OS=Homo sapiens GN=ANXA8L2 PE=2 SV=1;>sp|Q5VT79-2|AXA82_HUMAN Isoform 2 of Annexin A8-like protein 2 OS=Homo sapiens GN=ANXA8L2;>tr|E7EVD9|E7EVD9_HUMAN Annexin OS=Homo sapiens GN=ANXA8L2 PE=2 SV=2 0.29 0.25 -0.04 -0.38 -0.70 -0.15 0.71 0.36 0.023904072 -0.02499856 binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;ion binding;lipid binding;metal ion binding;phospholipid binding
1.07E-303 3 22 1 62.7

P31946-2 >sp|P31946-2|1433B_HUMAN Isoform Short of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB -0.28 -0.07 -0.18 0.01 0.02 0.05 0.15 -0.14 0.738038947 -0.150999598
0 1 22 1 68.4

Q02218;E9PCR7;Q02218-2;E9PDF2;E9PFG7;Q02218-3;Q9ULD0;Q9ULD0-3;Q9ULD0-2;C9J4G7 "2-oxoglutarate dehydrogenase, mitochondrial" OGDH ">sp|Q02218|ODO1_HUMAN 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3;>tr|E9PCR7|E9PCR7_HUMAN 2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=2 SV=1;>sp|Q02218-2|ODO1_HUMAN Isoform 2 of 2-oxoglutarate de" -0.36 0.22 0.04 0.33 0.27 0.57 -1.04 0.04 0.08936225 0.097566023 2-oxoglutarate metabolic process;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol catabolic process;alcohol metabolic process;amine catabolic process;amine metabolic process;anatomical structure development;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell development;cell migration;cell motility;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular component movement;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;central nervous system neuron development;cerebellar cortex development;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental process;dicarboxylic acid metabolic process;forebrain cell migration;forebrain neuron development;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;hippocampus development;locomotion;lysine catabolic process;lysine metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;NAD metabolic process;NADH metabolic process;neuron development;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;olfactory bulb mitral cell layer development;organic acid catabolic process;organic acid metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;pyramidal neuron development;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule catabolic process;small molecule metabolic process;striatum development;succinyl-CoA metabolic process;tangential migration from the subventricular zone to the olfactory bulb;telencephalon cell migration;thalamus development;tricarboxylic acid cycle "binding;catalytic activity;coenzyme binding;cofactor binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxoglutarate dehydrogenase (NAD+) activity;oxoglutarate dehydrogenase (succinyl-transferring) activity;thiamine pyrophosphate binding;vitamin binding"cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;oxoglutarate dehydrogenase complex;protein complex Citrate cycle (TCA cycle);Lysine degradation;Tryptophan metabolism 2.98E-165 10 26 1 36.4

P61978-3;Q5T6W5;Q5T6W2 HNRNPK >sp|P61978-3|HNRPK_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK;>tr|Q5T6W5|Q5T6W5_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=2 SV=1;>tr|Q5T6W2|Q5T6W2_HUMAN Heterogeneous nuclear ri -0.12 0.37 -0.05 0.44 -0.04 -0.17 -0.96 -0.22 0.867102674 0.509575912 binding;nucleic acid binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 0 3 29 1 62.7

P08195-2;F5H0E2;F5H867 >sp|P08195-2|4F2_HUMAN Isoform 2 of 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 -0.15 -0.13 -0.20 -0.06 -0.99 -0.70 0.04 -0.21 0.595614618 0.331936941 amine transport;amino acid import;amino acid transport;branched-chain aliphatic amino acid transport;carbohydrate metabolic process;carboxylic acid transport;establishment of localization;leucine import;leucine transport;metabolic process;neutral amino acid transport;nitrogen compound transport;organic acid transport;organic substance transport;primary metabolic process;transport active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;binding;carboxylic acid transmembrane transporter activity;catalytic activity;cation binding;ion binding;neutral amino acid transmembrane transporter activity;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity 0 3 29 1 56.9

Q5JPE7-2;P69849;Q5JPE7;J3KN36;Q4G177;F5H826;I3L0Q6;H3BTW1;H3BPS9 Nodal modulator 3;Nodal modulator 2 NOMO3;NOMO2 >sp|Q5JPE7-2|NOMO2_HUMAN Isoform 2 of Nodal modulator 2 OS=Homo sapiens GN=NOMO2;>sp|P69849|NOMO3_HUMAN Nodal modulator 3 OS=Homo sapiens GN=NOMO3 PE=2 SV=2;>sp|Q5JPE7|NOMO2_HUMAN Nodal modulator 2 OS=Homo sapiens GN=NOMO2 PE=1 SV=1;>tr|J3KN36|J3KN36_HUMAN 0.10 0.03 -0.16 -0.22 0.63 0.46 0.10 0.06 1.002056109 -0.372744325 binding;carbohydrate binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part 4.00E-204 9 30 1 36.7

B7Z468;E7EN75;D6RGF7;D6RBR1 CAST >tr|B7Z468|B7Z468_HUMAN DNA-directed RNA polymerase I subunit RPA34 OS=Homo sapiens GN=CAST PE=2 SV=1 0.02 0.20 -0.11 -0.14 -0.08 0.50 0.38 0.42 0.896479186 -0.318080684 1.35E-286 4 32 1 57

Q13045;Q13045-3;J3QQQ2;J3QLR6;J3QQU5;J3KT47 Protein flightless-1 homolog FLII >sp|Q13045|FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens GN=FLII PE=1 SV=2;>sp|Q13045-3|FLII_HUMAN Isoform 3 of Protein flightless-1 homolog OS=Homo sapiens GN=FLII 0.25 0.02 -0.14 -0.12 -0.05 0.02 0.29 -0.09 0.114780328 -0.039851818 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;muscle contraction;muscle system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;system process;transcription, DNA-dependent" actin binding;binding;cytoskeletal protein binding;protein binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part 3.93E-270 6 33 1 35.1

Q14247-3;Q14247-2 >sp|Q14247-3|SRC8_HUMAN Isoform 3 of Src substrate cortactin OS=Homo sapiens GN=CTTN;>sp|Q14247-2|SRC8_HUMAN Isoform 2 of Src substrate cortactin OS=Homo sapiens GN=CTTN -0.24 0.08 0.26 -0.13 0.04 0.35 0.51 0.95 0.913909796 -0.467607345 0 2 34 1 60.6

O00429;O00429-3;O00429-6;O00429-5;B4DGC9;F8VZ52;B4DPZ9;F8W1W3;B4DDQ3;F8VUJ9;F8VR28;F8VYL3;H0YHY4;H0YI79 Dynamin-1-like protein DNM1L >sp|O00429|DNM1L_HUMAN Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2;>sp|O00429-3|DNM1L_HUMAN Isoform 2 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L;>sp|O00429-6|DNM1L_HUMAN Isoform 6 of Dynamin-1-like protein OS=Homo sapiens GN=DNM1L;>sp 0.21 0.08 -0.03 -0.06 -0.48 -0.23 0.24 0.07 0.358320611 0.153012383 anatomical structure morphogenesis;apoptotic mitochondrial changes;biological regulation;catabolic process;cell part morphogenesis;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;developmental process;dynamin polymerization involved in membrane fission;dynamin polymerization involved in mitochondrial fission;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;membrane fission;membrane fission involved in mitochondrial fission;membrane organization;metabolic process;mitochondrial fission;mitochondrial fragmentation involved in apoptosis;mitochondrion morphogenesis;mitochondrion organization;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle fission;organelle organization;peroxisome fission;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of mitochondrial fission;positive regulation of mitochondrion organization;positive regulation of organelle organization;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of release of cytochrome c from mitochondria;positive regulation of secretion;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein polymerization;protein tetramerization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of developmental process;regulation of establishment of protein localization;regulation of localization;regulation of mitochondrial fission;regulation of mitochondrion organization;regulation of organelle organization;regulation of programmed cell death;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of release of cytochrome c from mitochondria;regulation of secretion;regulation of transport;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytoskeletal part;cytosol;endomembrane system;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microbody;microtubule;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;perinuclear region of cytoplasm;peroxisome;protein complex Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Fc gamma R-mediated phagocytosis 0 14 36 1 64.7

Q9UHD8 Septin-9 09-Sep >sp|Q9UHD8|SEPT9_HUMAN Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 -0.15 0.03 0.06 0.14 0.19 0.08 -0.36 -0.01 0.117852327 0.044539404 cell cycle;cell division;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin filament bundle;actomyosin;cell part;cytoplasmic part;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;microtubule;organelle part;perinuclear region of cytoplasm;protein complex;stress fiber 2.56E-244 1 37 1 67.4

F8VQE1;Q9UHB6-2;Q9UHB6;F8VS07;Q9UHB6-3;F8VRN8;J3QQM5;Q9BT23 LIM domain and actin-binding protein 1 LIMA1 >tr|F8VQE1|F8VQE1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=2 SV=1;>sp|Q9UHB6-2|LIMA1_HUMAN Isoform Alpha of LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1;>sp|Q9UHB6|LIMA1_HUMAN LIM domain and actin-binding -0.07 1.15 -0.27 0.97 -1.05 0.54 -0.76 0.96 0.3435459 0.521334901 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;biological regulation;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;negative regulation of actin filament depolymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex disassembly;organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex disassembly;ruffle organization actin binding;actin filament binding;actin monomer binding;binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding;transition metal ion binding;zinc ion binding actin cytoskeleton;actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeletal part;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;stress fiber 5.34E-264 8 37 1 67.9

Q14697;F5H6X6 Neutral alpha-glucosidase AB GANAB >sp|Q14697|GANAB_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3;>tr|F5H6X6|F5H6X6_HUMAN Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=2 SV=1 -0.01 -0.16 0.08 -0.02 0.63 0.21 0.23 -0.16 0.635660554 -0.252654586 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine "alpha-glucosidase activity;binding;carbohydrate binding;catalytic activity;glucan 1,3-alpha-glucosidase activity;glucosidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum lumen;endoplasmic reticulum part;glucosidase II complex;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;protein complex;vesicle N-Glycan biosynthesis;Protein processing in endoplasmic reticulum 0 2 45 1 54.2

F8W9J4;Q03001;E7ERU2;E9PEB9;E7ERU0;E9PHM6;F6QMI7;E7ETB9;Q03001-13;Q5T0V7 Dystonin DST >tr|F8W9J4|F8W9J4_HUMAN Dystonin OS=Homo sapiens GN=DST PE=2 SV=1;>sp|Q03001|DYST_HUMAN Dystonin OS=Homo sapiens GN=DST PE=1 SV=4;>tr|E7ERU2|E7ERU2_HUMAN Dystonin OS=Homo sapiens GN=DST PE=2 SV=2;>tr|E9PEB9|E9PEB9_HUMAN Dystonin OS=Homo sapiens GN=DST PE=2 0.22 0.64 0.00 -0.14 1.04 0.51 -0.35 0.58 0.309684807 -0.264564977 anatomical structure morphogenesis;axon cargo transport;axonogenesis;biological adhesion;biological regulation;cell adhesion;cell cycle arrest;cell cycle process;cell junction assembly;cell junction organization;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;cytoplasmic microtubule organization;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;establishment of localization;establishment of localization in cell;establishment or maintenance of cell polarity;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;integrin-mediated signaling pathway;intermediate filament cytoskeleton organization;intermediate filament-based process;intracellular transport;locomotion;maintenance of cell polarity;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;neuron projection morphogenesis;organelle organization;regulation of biological process;regulation of cell cycle;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of organelle organization;response to stimulus;response to stress;response to wounding;retrograde axon cargo transport;signal transduction;transport "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of substances;binding;calcium ion binding;catalytic activity;cation binding;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;ion binding;metal ion binding;microtubule binding;microtubule plus-end binding;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transmembrane transporter activity;transporter activity;tubulin binding" actin cytoskeleton;axon;axon part;basal plasma membrane;basement membrane;cell cortex;cell junction;cell leading edge;cell part;cell projection;cell projection part;cell-substrate junction;contractile fiber part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;extracellular matrix part;extracellular region part;H zone;hemidesmosome;integral to membrane;intermediate filament;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microtubule cytoskeleton;microtubule plus end;neurofilament cytoskeleton;neuron projection;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleus;organelle;organelle envelope;organelle membrane;organelle part;plasma membrane part;protein complex;vesicle;Z disc 0 10 52 1 9.6

Q01082-3;Q01082-2;F8W6C1;Q86UT5-3;E9PPZ1;Q86UT5-2;Q86UT5 ">sp|Q01082-3|SPTB2_HUMAN Isoform 2 of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1;>sp|Q01082-2|SPTB2_HUMAN Isoform Short of Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1" -0.25 0.31 0.26 0.14 -0.95 -0.30 -0.09 -0.15 0.880937457 0.484975401 biological regulation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cGMP-mediated signaling;common-partner SMAD protein phosphorylation;cyclic-nucleotide-mediated signaling;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;fluid transport;intracellular protein transport;intracellular signal transduction;intracellular transport;ion transport;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cGMP biosynthetic process;negative regulation of cGMP metabolic process;negative regulation of cyclic nucleotide biosynthetic process;negative regulation of cyclic nucleotide metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleotide biosynthetic process;negative regulation of nucleotide metabolic process;nuclear import;nuclear transport;nucleocytoplasmic transport;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein targeting to plasma membrane;protein transport;receptor guanylyl cyclase signaling pathway;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cGMP biosynthetic process;regulation of cGMP metabolic process;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;response to chemical stimulus;response to stimulus;response to toxin;second-messenger-mediated signaling;signal transduction;SMAD protein import into nucleus;transport;water transport channel inhibitor activity;channel regulator activity;cyclase inhibitor activity;cyclase regulator activity;enzyme inhibitor activity;enzyme regulator activity;guanylate cyclase inhibitor activity;guanylate cyclase regulator activity;ion channel inhibitor activity apical part of cell;brush border;cell cortex part;cell part;cell projection;contractile fiber part;cuticular plate;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;M band;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;subapical complex 0 7 105 1 59.3

Q15149-3;H0YDN1;E9PKG0;E9PIA2;E9PQ28;REV__Q2KJ03-2;REV__Q2KJ03;Q8WTU0;REV__Q8IWV8-3;Q9ULE0-2;F5H1E4;Q8IZF5-2;Q8IY63-2;Q8IY63;Q8IZF5-3;Q8N283;Q8IZF5;Q66GS9;REV__Q9Y4H2;REV__Q8IWV8-4;REV__Q8IWV8 >sp|Q15149-3|PLEC_HUMAN Isoform 3 of Plectin OS=Homo sapiens GN=PLEC 0.12 0.14 0.06 0.02 -0.02 0.32 0.23 0.19 0.50699299 -0.094251777 biological regulation;cell cycle process;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;centriole replication;centriole-centriole cohesion;centrosome organization;establishment of cell polarity;establishment of cell polarity involved in ameboidal cell migration;establishment or maintenance of cell polarity;G2/M transition of mitotic cell cycle;G-protein coupled receptor protein signaling pathway;hippo signaling cascade;intracellular signal transduction;macromolecule metabolic process;metabolic process;microtubule organizing center organization;microtubule-based process;neuropeptide signaling pathway;organelle organization;positive regulation of biological process;positive regulation of blood vessel endothelial cell migration;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of endothelial cell migration;positive regulation of locomotion;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of blood vessel endothelial cell migration;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of endothelial cell migration;regulation of localization;regulation of locomotion;response to stimulus;signal transduction;Wnt receptor signaling pathway "aspartic-type endopeptidase activity;aspartic-type peptidase activity;binding;catalytic activity;endopeptidase activity;G-protein coupled receptor activity;hydrolase activity;identical protein binding;molecular transducer activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;receptor activity;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity" apical plasma membrane;cell junction;cell part;cell projection;cell-cell junction;centriole;contractile fiber;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lamellipodium;membrane;membrane part;microtubule organizing center part;non-membrane-bounded organelle;occluding junction;organelle;organelle part;plasma membrane;plasma membrane part;tight junction;vesicle Tight junction 0 21 460 1 77.6

B7Z9S8;A6NGH2;P05026-2;P05026 Sodium/potassium-transporting ATPase subunit beta-1ATP1B1 >tr|B7Z9S8|B7Z9S8_HUMAN Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=2 SV=1;>tr|A6NGH2|A6NGH2_HUMAN Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=2 SV=3;>sp|P05026-2|AT1B1_HUMAN Isoform 0.11 0.20 -0.08 -0.10 -1.53 -1.01 -0.12 -0.22 0.938199016 0.754464082 biological adhesion;biological regulation;blood coagulation;cation transport;cell adhesion;cell migration;cell motility;cellular component movement;cellular process;coagulation;establishment of localization;hemostasis;immune system process;ion transport;leukocyte migration;locomotion;metal ion transport;monovalent inorganic cation transport;multicellular organismal process;potassium ion transport;regulation of biological quality;regulation of body fluid levels;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;sodium ion transport;transport "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;potassium ion transmembrane transporter activity;potassium-transporting ATPase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;pyrophosphatase activity;sodium ion transmembrane transporter activity;sodium:potassium-exchanging ATPase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" apical plasma membrane;basolateral plasma membrane;caveola;cell part;macromolecular complex;membrane part;membrane raft;plasma membrane part;protein complex;sodium:potassium-exchanging ATPase complexAldosterone-regulated sodium reabsorption;Bile secretion;Carbohydrate digestion and absorption;Cardiac muscle contraction;Endocrine and other factor-regulated calcium reabsorption;Gastric acid secretion;Mineral absorption;Pancreatic secretion;Protein digestion and absorption;Proximal tubule bicarbonate reclamation;Salivary secretion 4.73E-17 4 2 2 10.1

Q9H3H3;Q9H3H3-2;Q9H3H3-3 UPF0696 protein C11orf68 C11orf68 >sp|Q9H3H3|CK068_HUMAN UPF0696 protein C11orf68 OS=Homo sapiens GN=C11orf68 PE=1 SV=2;>sp|Q9H3H3-2|CK068_HUMAN Isoform 2 of UPF0696 protein C11orf68 OS=Homo sapiens GN=C11orf68;>sp|Q9H3H3-3|CK068_HUMAN Isoform 3 of UPF0696 protein C11orf68 OS=Homo sapiens 0.07 -0.14 0.20 -0.17 1.46 0.95 0.22 0.36 1.069371739 -0.759251092 1.47E-07 3 2 2 9.6

F8VYN8;Q9Y592-2;Q9Y592;J3KNW7;REV__Q9UHB4-3;REV__D3YTG6;REV__Q9UHB4;REV__Q9UHB4-2 Coiled-coil domain-containing protein 41 CCDC41 >tr|F8VYN8|F8VYN8_HUMAN Centrosomal protein of 83 kDa OS=Homo sapiens GN=CCDC41 PE=2 SV=1;>sp|Q9Y592-2|CEP83_HUMAN Isoform 2 of Centrosomal protein of 83 kDa OS=Homo sapiens GN=CCDC41;>sp|Q9Y592|CEP83_HUMAN Centrosomal protein of 83 kDa OS=Homo sapiens GN= -0.29 1.19 0.07 1.24 -0.44 0.00 -1.61 0.14 0.795284858 1.031990099 9.60E-05 8 2 2 4

Q5ZPR3-3;Q5ZPR3-4;Q5ZPR3 CD276 antigen CD276 >sp|Q5ZPR3-3|CD276_HUMAN Isoform 3 of CD276 antigen OS=Homo sapiens GN=CD276;>sp|Q5ZPR3-4|CD276_HUMAN Isoform 4 of CD276 antigen OS=Homo sapiens GN=CD276;>sp|Q5ZPR3|CD276_HUMAN CD276 antigen OS=Homo sapiens GN=CD276 PE=1 SV=1 -0.17 -0.05 -0.33 -0.20 -0.03 0.22 0.72 1.55 0.96956823 -0.802165044 biological regulation;cell activation;cell proliferation;cellular process;immune response;immune system process;leukocyte activation;lymphocyte activation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell activation;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine biosynthetic process;negative regulation of defense response;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of interferon-gamma biosynthetic process;negative regulation of interleukin-2 biosynthetic process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mononuclear cell proliferation;negative regulation of protein metabolic process;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of T cell activation;negative regulation of T cell proliferation;positive regulation of biological process;positive regulation of biomineral tissue development;positive regulation of biosynthetic process;positive regulation of bone mineralization;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine biosynthetic process;positive regulation of developmental process;positive regulation of immune system process;positive regulation of interferon-gamma biosynthetic process;positive regulation of leukocyte activation;positive regulation of leukocyte proliferation;positive regulation of lymphocyte activation;positive regulation of lymphocyte proliferation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mononuclear cell proliferation;positive regulation of multicellular organismal process;positive regulation of ossification;positive regulation of osteoblast differentiation;positive regulation of protein metabolic process;positive regulation of T cell activation;positive regulation of T cell proliferation;regulation of biological process;regulation of biomineral tissue development;regulation of biosynthetic process;regulation of bone mineralization;regulation of cell activation;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of defense response;regulation of developmental process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of interferon-gamma biosynthetic process;regulation of interferon-gamma production;regulation of interleukin-2 biosynthetic process;regulation of interleukin-2 production;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of ossification;regulation of osteoblast differentiation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of T cell activation;regulation of T cell proliferation;response to stimulus;T cell activation binding;protein binding;receptor binding cell part;external side of plasma membrane;integral to membrane;intrinsic to membrane;membrane part;plasma membrane part Cell adhesion molecules (CAMs) 1.28E-12 3 2 2 8.9

Q9UQC9 "Calcium-activated chloride channel regulator 2;Calcium-activated chloride channel regulator 2, 109 kDa form;Calcium-activated chloride channel regulator 2, 35 kDa form" CLCA2 >sp|Q9UQC9|CLCA2_HUMAN Calcium-activated chloride channel regulator 2 OS=Homo sapiens GN=CLCA2 PE=1 SV=2 -0.77 0.04 -0.65 -0.07 -0.48 0.94 0.66 0.88 0.946400818 -0.862428186 biological adhesion;cell adhesion;cellular process anion channel activity;anion transmembrane transporter activity;channel activity;chloride channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;ligand-gated channel activity;ligand-gated ion channel activity;passive transmembrane transporter activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity basal plasma membrane;cell junction;cell part;extracellular region;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Olfactory transduction;Pancreatic secretion 1.82E-16 1 2 2 3.3

H0YFF5;F5GX99;B4DXW4;Q9H078-3;Q9H078-4;Q9H078-2;Q9H078;H0YGM0;F5H392;F5H7A5;Q7Z777 Caseinolytic peptidase B protein homolog CLPB >tr|H0YFF5|H0YFF5_HUMAN Caseinolytic peptidase B protein homolog (Fragment) OS=Homo sapiens GN=CLPB PE=4 SV=1;>tr|F5GX99|F5GX99_HUMAN Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=2 SV=1;>tr|B4DXW4|B4DXW4_HUMAN Caseinolytic peptidase -0.04 -0.01 0.27 0.19 0.47 0.04 -0.13 -0.36 0.191289998 0.098481118 cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 1.99E-05 11 2 2 9.5

Q9UP83;Q9UP83-2;Q9UP83-3 Conserved oligomeric Golgi complex subunit 5 COG5 >sp|Q9UP83|COG5_HUMAN Conserved oligomeric Golgi complex subunit 5 OS=Homo sapiens GN=COG5 PE=1 SV=3;>sp|Q9UP83-2|COG5_HUMAN Isoform 2 of Conserved oligomeric Golgi complex subunit 5 OS=Homo sapiens GN=COG5;>sp|Q9UP83-3|COG5_HUMAN Isoform 3 of Conserved ol 0.11 -0.01 0.14 -0.08 -0.25 -0.17 -0.12 0.00 0.990422804 0.17262633 cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;intra-Golgi vesicle-mediated transport;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;cytosol;Golgi apparatus part;Golgi membrane;Golgi transport complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;protein complex 1.26E-13 3 2 2 3

P50416-2;P50416 "Carnitine O-palmitoyltransferase 1, liver isoform" CPT1A ">sp|P50416-2|CPT1A_HUMAN Isoform 2 of Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A;>sp|P50416|CPT1A_HUMAN Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2" -0.41 -0.87 0.12 0.12 1.00 1.39 0.61 -0.14 1.021326277 -0.976582123 acylglycerol metabolic process;alcohol metabolic process;amine metabolic process;amine transport;amino acid transmembrane transport;amino acid transport;behavior;betaine metabolic process;betaine transport;biological regulation;carbohydrate metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;carboxylic acid transport;carnitine metabolic process;carnitine shuttle;carnitine transport;catabolic process;cation transport;cellular amine metabolic process;cellular amino acid metabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;eating behavior;establishment of localization;establishment of localization in cell;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;fatty acid transport;feeding behavior;glucose metabolic process;glycerol ether metabolic process;glycerolipid metabolic process;hexose metabolic process;intracellular lipid transport;intracellular transport;ion transport;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;lipid transport;long-chain fatty acid metabolic process;long-chain fatty acid transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;mitochondrial transport;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;monosaccharide metabolic process;neutral lipid metabolic process;nitrogen compound metabolic process;nitrogen compound transport;organic acid catabolic process;organic acid metabolic process;organic acid transport;organic cation transport;organic ether metabolic process;organic substance transport;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of fatty acid beta-oxidation;positive regulation of fatty acid metabolic process;positive regulation of fatty acid oxidation;positive regulation of lipid catabolic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;quaternary ammonium group transport;regulation of biological process;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of fatty acid beta-oxidation;regulation of fatty acid metabolic process;regulation of fatty acid oxidation;regulation of hormone secretion;regulation of insulin secretion;regulation of lipid catabolic process;regulation of lipid metabolic process;regulation of localization;regulation of metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of primary metabolic process;regulation of secretion;regulation of signaling;regulation of transport;response to chemical stimulus;response to drug;response to organic cyclic compound;response to organic substance;response to stimulus;small molecule catabolic process;small molecule metabolic process;transmembrane transport;transport;triglyceride metabolic process "carnitine O-acyltransferase activity;carnitine O-palmitoyltransferase activity;catalytic activity;O-acyltransferase activity;O-palmitoyltransferase activity;palmitoyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;integral to membrane;integral to mitochondrial membrane;integral to mitochondrial outer membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to mitochondrial outer membrane;intrinsic to organelle membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Adipocytokine signaling pathway;Fatty acid metabolism;PPAR signaling pathway 6.95E-06 2 2 2 3.7

F5H895;F5GXX5;P61803 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 DAD1 >tr|F5H895|F5H895_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=2 SV=1;>tr|F5GXX5|F5GXX5_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD -1.53 0.16 0.68 1.16 -2.59 -1.16 -0.81 -0.39 0.765967709 1.353015915 anatomical structure development;apoptosis;biological regulation;blastocyst development;carbohydrate metabolic process;cell death;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;developmental process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;programmed cell death;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to chemical stimulus;response to drug;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to stimulus "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;oligosaccharyltransferase complex;organelle part;protein complex N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis 4.07E-15 3 2 2 33.8

Q15125;C9J719;C9JJ78 "3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase" EBP ">sp|Q15125|EBP_HUMAN 3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase OS=Homo sapiens GN=EBP PE=1 SV=3;>tr|C9J719|C9J719_HUMAN 3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase (Fragment) OS=Homo sapiens GN=EBP PE=2 SV=1;>tr|C9JJ78|C9JJ78_HUMAN 3-beta-hyd" -1.37 0.05 0.78 0.02 -2.98 -1.39 -2.33 -0.98 1.173033813 1.789741122 alcohol metabolic process;anatomical structure development;biosynthetic process;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;hemopoiesis;hemopoietic or lymphoid organ development;lipid biosynthetic process;lipid metabolic process;metabolic process;organ development;primary metabolic process;skeletal system development;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;system development "C-8 sterol isomerase activity;catalytic activity;cholestenol delta-isomerase activity;drug transmembrane transporter activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, transposing C=C bonds;isomerase activity;molecular transducer activity;receptor activity;signal transducer activity;signaling receptor activity;steroid delta-isomerase activity;transmembrane signaling receptor activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part Steroid biosynthesis 1.09E-10 3 2 2 12.2

Q9BW60-2;Q9BW60 Elongation of very long chain fatty acids protein 1 ELOVL1 >sp|Q9BW60-2|ELOV1_HUMAN Isoform 2 of Elongation of very long chain fatty acids protein 1 OS=Homo sapiens GN=ELOVL1;>sp|Q9BW60|ELOV1_HUMAN Elongation of very long chain fatty acids protein 1 OS=Homo sapiens GN=ELOVL1 PE=1 SV=1 -0.14 0.29 -0.24 0.12 -1.51 -0.93 -1.10 0.11 1.006980984 0.864228407 "acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;fatty acid biosynthetic process;fatty acid elongation;fatty acid elongation, monounsaturated fatty acid;fatty acid elongation, saturated fatty acid;fatty acid elongation, unsaturated fatty acid;fatty acid metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;membrane lipid biosynthetic process;membrane lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic ether metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process;thioester biosynthetic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process;very long-chain fatty acid biosynthetic process;very long-chain fatty acid metabolic process" "catalytic activity;fatty acid elongase activity;fatty acid synthase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane part;organelle part 2.18E-16 2 2 2 9.9

Q8IYI6 Exocyst complex component 8 EXOC8 >sp|Q8IYI6|EXOC8_HUMAN Exocyst complex component 8 OS=Homo sapiens GN=EXOC8 PE=1 SV=2 0.01 0.17 0.17 0.09 -0.17 0.19 0.27 0.16 6.57E-06 -2.14E-06 cellular component organization;cellular component organization or biogenesis;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;localization;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;primary metabolic process;protein localization;protein metabolic process;protein transport;secretion;secretion by cell;transport;vesicle-mediated transport binding;lipid binding;phospholipid binding cell cortex part;cell part;cell projection part;cytoplasm;cytoplasmic part;exocyst;growth cone;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane;protein complex;site of polarized growth 1.11E-06 1 2 2 4.7

A3KFL4;Q13868;A3KFL1;A3KFL5;B4DKK6;A3KFL2 Exosome complex component RRP4 EXOSC2 >tr|A3KFL4|A3KFL4_HUMAN Exosome complex component RRP4 OS=Homo sapiens GN=EXOSC2 PE=2 SV=1;>sp|Q13868|EXOS2_HUMAN Exosome complex component RRP4 OS=Homo sapiens GN=EXOSC2 PE=1 SV=2;>tr|A3KFL1|A3KFL1_HUMAN Exosome complex component RRP4 (Fragment) OS=Homo s -0.13 0.29 0.28 0.47 0.05 -0.54 -1.08 -0.89 1.238407598 0.838103565 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;primary metabolic process;regulation of biological process;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing" "3'-5' exonuclease activity;3'-5'-exoribonuclease activity;7S RNA binding;binding;catalytic activity;exonuclease activity;exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;exoribonuclease activity;exoribonuclease activity, producing 5'-phosphomonoesters;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding;ribonuclease activity;RNA binding" cell part;cytoplasmic part;cytosol;exosome (RNase complex);intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;protein complex RNA degradation 5.45E-11 6 2 2 10.3

F5H4E4;Q9HA64;I3L378;I3L2G3;I3L139 Ketosamine-3-kinase FN3KRP >tr|F5H4E4|F5H4E4_HUMAN Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=2 SV=1;>sp|Q9HA64|KT3K_HUMAN Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2;>tr|I3L378|I3L378_HUMAN Ketosamine-3-kinase (Fragment) OS=Homo sapiens GN=FN3KRP PE=2 SV=1;>tr|I3L -0.70 -0.57 0.20 0.18 -0.46 0.23 -0.65 -0.09 0.019975997 0.018877681 "catalytic activity;kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" 3.14E-06 5 2 2 13.5

Q9H4A6 Golgi phosphoprotein 3 GOLPH3 >sp|Q9H4A6|GOLP3_HUMAN Golgi phosphoprotein 3 OS=Homo sapiens GN=GOLPH3 PE=1 SV=1 -0.09 0.25 -0.21 0.21 0.49 0.46 0.14 -0.33 0.257229497 -0.14822552 biological regulation;cell proliferation;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of TOR signaling cascade;regulation of biological process;regulation of cell communication;regulation of cellular component organization;regulation of cellular process;regulation of mitochondrion organization;regulation of organelle organization;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of TOR signaling cascade binding;lipid binding cell part;cytoplasmic part;cytosol;endosome;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial intermembrane space;mitochondrial part;mitochondrion;nuclear membrane;nuclear part;organelle;organelle envelope lumen;organelle membrane;organelle part;plasma membrane;trans-Golgi network 3.31E-28 1 2 2 9.4

P49841;P49841-2 Glycogen synthase kinase-3 beta GSK3B >sp|P49841|GSK3B_HUMAN Glycogen synthase kinase-3 beta OS=Homo sapiens GN=GSK3B PE=1 SV=2;>sp|P49841-2|GSK3B_HUMAN Isoform 2 of Glycogen synthase kinase-3 beta OS=Homo sapiens GN=GSK3B 0.07 -0.10 -0.22 0.25 -0.81 -0.16 0.45 -0.05 0.187708941 0.141127635 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;axon guidance;biological regulation;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling pathway involved in positive regulation of apoptosis;carbohydrate metabolic process;cell cycle process;cell differentiation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell surface receptor linked signaling pathway;cellular carbohydrate metabolic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular glucan metabolic process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular polysaccharide metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;chemotaxis;circadian rhythm;defense response;developmental process;DNA hypermethylation;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epithelial to mesenchymal transition;ER overload response;ER-nucleus signaling pathway;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment or maintenance of cell polarity;fat cell differentiation;fibroblast growth factor receptor signaling pathway;generation of precursor metabolites and energy;genetic imprinting;glucan metabolic process;glycogen metabolic process;hippocampus development;hypermethylation of CpG island;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;intracellular protein transport;intracellular signal transduction;intracellular transport;localization;locomotion;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;myoblast fusion;negative regulation of apoptosis;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of carbohydrate metabolic process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular biosynthetic process;negative regulation of cellular carbohydrate metabolic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of dendrite morphogenesis;negative regulation of developmental process;negative regulation of gene expression;negative regulation of glycogen (starch) synthase activity;negative regulation of glycogen biosynthetic process;negative regulation of glycogen metabolic process;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of neurogenesis;negative regulation of NFAT protein import into nucleus;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of programmed cell death;negative regulation of protein binding;negative regulation of protein complex assembly;negative regulation of protein import into nucleus;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of protein transport;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription factor import into nucleus;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of transmembrane transport;negative regulation of transport;negative regulation of type B pancreatic cell development;negative regulation of Wnt receptor signaling pathway;nerve growth factor receptor signaling pathway;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;organ morphogenesis;oxidation-reduction process;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;polysaccharide metabolic process;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell differentiation;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of peptidyl-serine phosphorylation;positive regulation of peptidyl-threonine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein binding;positive regulation of protein catabolic process;positive regulation of protein complex assembly;positive regulation of protein export from nucleus;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein transport;positive regulation of Rac GTPase activity;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;positive regulation of RNA metabolic process;positive regulation of stem cell differentiation;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transport;primary metabolic process;protein export from nucleus;protein localization;protein localization to microtubule;protein localization to organelle;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein transport;re-entry into mitotic cell cycle;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of carbohydrate biosynthetic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cellular biosynthetic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA methylation;regulation of establishment of protein localization;regulation of gene expression;regulation of gene expression by genetic imprinting;regulation of gene expression, epigenetic;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen (starch) synthase activity;regulation of glycogen biosynthetic process;regulation of glycogen metabolic process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of microtubule-based process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of NFAT protein import into nucleus;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of peptidyl-serine phosphorylation;regulation of peptidyl-threonine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein binding;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stem cell differentiation;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmembrane transport;regulation of transmission of nerve impulse;regulation of transport;regulation of type B pancreatic cell development;regulation of Wnt receptor signaling pathway;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to endoplasmic reticulum stress;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to inorganic substance;response to lithium ion;response to metal ion;response to organic substance;response to stimulus;response to stress;rhythmic process;signal transduction;superior temporal gyrus development;syncytium formation;syncytium formation by plasma membrane fusion;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;Wnt receptor signaling pathway"	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;p53 binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;tau-protein kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups"	beta-catenin destruction complex;cell body;cell part;cell projection;cell projection part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;dendritic shaft;dendritic spine;growth cone;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;microtubule organizing center;neuron projection;neuron spine;neuronal cell body;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex;ribonucleoprotein complex;site of polarized growth	Alzheimer's disease;Axon guidance;B cell receptor signaling pathway;Basal cell carcinoma;Cell cycle;Chemokine signaling pathway;Circadian rhythm - fly;Colorectal cancer;Endometrial cancer;ErbB signaling pathway;Focal adhesion;Hedgehog signaling pathway;Hepatitis C;Insulin signaling pathway;Measles;Melanogenesis;Neurotrophin signaling pathway;Pathways in cancer;Prostate cancer;T cell receptor signaling pathway;Wnt signaling pathway	5.49E-08 2	2	2	7.9

O14929-2;O14929	Histone acetyltransferase type B catalytic subunit HAT1	>sp|O14929-2|HAT1_HUMAN Isoform B of Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1;>sp|O14929|HAT1_HUMAN Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1	0.47 0.11 -0.12	0.01 -0.18	-0.75	-0.33	0.02	0.881157632 0.426393631	"biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin silencing;chromatin silencing at telomere;DNA conformation change;DNA metabolic process;DNA packaging;gene silencing;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of gene expression, epigenetic;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to stimulus"	"acetyltransferase activity;catalytic activity;histone acetyltransferase activity;lysine N-acetyltransferase activity;N-acetyltransferase activity;N-acyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups"	cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear matrix;nuclear part;nucleoplasm;nucleus;organelle;organelle part	6.12E-33 2	2	2	9.3

C9JAW5;Q9Y241;C9JNU6;Q9Y241-2 "HIG1 domain family member 1A, mitochondrial"	HIGD1A ">tr|C9JAW5|C9JAW5_HUMAN HIG1 domain family member 1A, mitochondrial OS=Homo sapiens GN=HIGD1A PE=2 SV=1;>sp|Q9Y241|HIG1A_HUMAN HIG1 domain family member 1A, mitochondrial OS=Homo sapiens GN=HIGD1A PE=1 SV=1;>tr|C9JNU6|C9JNU6_HUMAN HIG1 domain family member"0.23 0.61 -0.45 0.81 0.24 0.30 -1.03	0.16	0.364371671	0.38102749	biological regulation;cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;oxidation-reduction process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to stimulus;response to stress		cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex;respiratory chain		1.58E-80 4	2	2	48.2

Q9NSC5-5;Q9NSC5-2;Q9NSC5;M0R2T8;Q9NSC5-4;Q9NSC5-3;M0QZN1;M0QYF9;M0R2U7	Homer protein homolog 3	HOMER3	>sp|Q9NSC5-5|HOME3_HUMAN Isoform 5 of Homer protein homolog 3 OS=Homo sapiens GN=HOMER3;>sp|Q9NSC5-2|HOME3_HUMAN Isoform 2 of Homer protein homolog 3 OS=Homo sapiens GN=HOMER3;>sp|Q9NSC5|HOME3_HUMAN Homer protein homolog 3 OS=Homo sapiens

GN=HOMER3 PE=1 SV -0.01 0.21 -0.33 0.06 -0.44 0.00 -0.09 0.22 0.11889622 0.059254573 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;glutamate signaling pathway;G-protein coupled receptor protein signaling pathway;intracellular protein transport;intracellular transport;metabotropic glutamate receptor signaling pathway;protein targeting;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;transport basal part of cell;cell junction;cell part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;membrane;organelle part;plasma membrane;postsynaptic density;postsynaptic membrane;synapse part;synaptic membrane 4.47E-13 9 2 2 8.9

O15397;F5H2I3 Importin-8 IPO8 >sp|O15397|IPO8_HUMAN Importin-8 OS=Homo sapiens GN=IPO8 PE=1 SV=2;>tr|F5H2I3|F5H2I3_HUMAN Importin-8 (Fragment) OS=Homo sapiens GN=IPO8 PE=2 SV=1 0.26 0.08 -0.39 -0.02 0.05 0.11 0.19 -0.38 0.016140758 -0.009305562 biological regulation;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;transport binding;enzyme binding;GTPase binding;protein binding;protein transporter activity;Ran GTPase binding;Ras GTPase binding;small GTPase binding;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;organelle part;pore complex;protein complex 1.05E-18 2 2 2 2.1

Q14739;C9JXK0 Lamin-B receptor LBR>sp|Q14739|LBR_HUMAN Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2;>tr|C9JXK0|C9JXK0_HUMAN Lamin-B receptor (Fragment) OS=Homo sapiens GN=LBR PE=2 SV=1 -0.57 0.48 -0.99 -0.80 1.06 0.05 -0.04 -0.44 0.572788768 -0.62218287 alcohol metabolic process;biosynthetic process;cholesterol biosynthetic process;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "binding;catalytic activity;DNA binding;lamin binding;nucleic acid binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;protein binding" cell part;cytoplasmic part;integral to membrane;integral to nuclear inner membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to nuclear inner membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;nuclear membrane;nuclear membrane part;nuclear part;organelle;organelle membrane;organelle part 8.10E-25 2 2 2 5.5

P38571-2;P38571;Q5T073 Lysosomal acid lipase/cholesteryl ester hydrolase LIPA >sp|P38571-2|LICH_HUMAN Isoform 2 of Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA;>sp|P38571|LICH_HUMAN Lysosomal acid lipase/cholesteryl ester hydrolase OS=Homo sapiens GN=LIPA PE=1 SV=2;>tr|Q5T073|Q5T073_HUMAN Lysosomal acid -0.35 -0.35 -0.30 -0.13 -0.18 -0.58 0.46 -0.01 0.369806948 -0.203135409 anatomical structure development;anatomical structure homeostasis;anatomical structure morphogenesis;biological regulation;catabolic process;cell morphogenesis;cell proliferation;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;cytokine production;defense response;developmental process;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;inflammatory response;lipid catabolic process;lipid metabolic process;lung development;metabolic process;multicellular organismal process;organ development;primary metabolic process;regulation of biological quality;response to stimulus;response to stress;response to wounding;tissue homeostasis;tissue remodeling "carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;sterol esterase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane-bounded organelle;organelle;vacuole Lysosome;Steroid biosynthesis 3.98E-06 3 2 2 7.9

P20645;H0YGT2;H0YF90 Cation-dependent mannose-6-phosphate receptor M6PR >sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1;>tr|H0YGT2|H0YGT2_HUMAN Cation-dependent mannose-6-phosphate receptor (Fragment) OS=Homo sapiens GN=M6PR PE=4 SV=1;>tr|H0YF90|H0YF90_HUMAN Cation-dependen 0.07 -0.01 0.02 -0.01 0.36 -0.09 -0.11 -0.37 0.152050951 0.063803002 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;endosome to lysosome transport;endosome transport;establishment of localization;establishment of localization in cell;intracellular transport;lysosomal transport;membrane invagination;membrane organization;receptor-mediated endocytosis;transport;vacuolar transport;vesicle-mediated transport binding;carbohydrate binding;carbohydrate transmembrane transporter activity;hexose transmembrane transporter activity;mannose binding;mannose transmembrane transporter activity;molecular transducer activity;monosaccharide binding;monosaccharide transmembrane transporter activity;receptor activity;signal transducer activity;signaling receptor activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;sugar binding;sugar transmembrane transporter activity;transmembrane signaling receptor activity;transmembrane transporter activity;transporter activity cell part;cell surface;cytoplasmic part;endosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome;lysosomal membrane;lytic vacuole;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part;vacuolar membrane;vacuolar part;vacuole Lysosome;Phagosome 9.35E-08 3 2 2 12.6

F5GXS7;P53582;H0Y955 Methionine aminopeptidase;Methionine aminopeptidase 1 METAP1 >tr|F5GXS7|F5GXS7_HUMAN Methionine aminopeptidase OS=Homo sapiens GN=METAP1 PE=2 SV=1;>sp|P53582|MAP11_HUMAN Methionine aminopeptidase 1 OS=Homo sapiens GN=METAP1 PE=1 SV=2;>tr|H0Y955|H0Y955_HUMAN Methionine aminopeptidase 1 (Fragment) OS=Homo sapiens GN=M 0.26 -0.06 0.08 0.27 -0.28 -0.49 0.13 -0.26 1.016641109 0.361819018 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;N-terminal protein amino acid modification;peptidyl-amino acid modification;peptidyl-methionine modification;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;protein modification process;proteolysis;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasm;intracellular part 8.90E-13 3 2 2 6.5

B8ZZG1;Q9NZW5;C9J4Q3 MAGUK p55 subfamily member 6 MPP6 >tr|B8ZZG1|B8ZZG1_HUMAN MAGUK p55 subfamily member 6 OS=Homo sapiens GN=MPP6 PE=2 SV=1;>sp|Q9NZW5|MPP6_HUMAN MAGUK p55 subfamily member 6 OS=Homo sapiens GN=MPP6 PE=1 SV=2;>tr|C9J4Q3|C9J4Q3_HUMAN MAGUK p55 subfamily member 6 (Fragment) OS=Homo sapiens GN=M -0.36 0.13 -0.17 0.48 -0.20 -0.62 -0.54 -0.71 1.05994305 0.539314363 cellular component assembly;cellular component organization;cellular component organization or biogenesis;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization cell part;membrane;plasma membrane 4.97E-07 3 2 2 6.5

Q9BYD1;H0YAX3;E5RFI2;E5RJI7 "39S ribosomal protein L13, mitochondrial" MRPL13 ">sp|Q9BYD1|RM13_HUMAN 39S ribosomal protein L13, mitochondrial OS=Homo sapiens GN=MRPL13 PE=1 SV=1;>tr|H0YAX3|H0YAX3_HUMAN 39S ribosomal protein L13, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL13 PE=2 SV=1;>tr|E5RFI2|E5RFI2_HUMAN 39S ribosomal protein" -0.11 0.18 -0.16 -0.18 0.28 -0.16 -0.92 -0.45 0.366348448 0.241734017 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;mitochondrial large ribosomal subunit;mitochondrial part;mitochondrion;non-membrane-bounded organelle;organellar large ribosomal subunit;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 9.40E-07 4 2 2 11.2

Q15800-2;Q15800 Methylsterol monooxygenase 1 MSMO1 >sp|Q15800-2|MSMO1_HUMAN Isoform 2 of Methylsterol monooxygenase 1 OS=Homo sapiens GN=MSMO1;>sp|Q15800|MSMO1_HUMAN Methylsterol monooxygenase 1 OS=Homo sapiens GN=MSMO1 PE=1 SV=1 0.03 -0.02 0.01 0.21 -0.47 0.03 -0.71 0.03 0.759781755 0.340693415 alcohol metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;fatty acid biosynthetic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "binding;C-4 methylsterol oxidase activity;catalytic activity;cation binding;ion binding;iron ion binding;metal ion binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;transition metal ion binding" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part;plasma membrane Steroid biosynthesis 4.72E-54 2 2 2 9.3

Q9UGV2-3;Q9UGV2-2;Q9UGV2;Q5TH30;B7Z341;F8WBF9 Protein NDRG3 NDRG3 >sp|Q9UGV2-3|NDRG3_HUMAN Isoform 3 of Protein NDRG3 OS=Homo sapiens GN=NDRG3;>sp|Q9UGV2-2|NDRG3_HUMAN Isoform 2 of Protein NDRG3 OS=Homo sapiens GN=NDRG3;>sp|Q9UGV2|NDRG3_HUMAN Protein NDRG3 OS=Homo sapiens GN=NDRG3 PE=1 SV=2;>tr|Q5TH30|Q5TH30_HUMAN NDRG f 0.06 -0.01 -0.13

-0.22 0.16 0.10 0.59 0.10 1.003203076 -0.312409138 biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;gamete generation;male gamete generation;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cell growth;negative regulation of cellular process;negative regulation of growth;regulation of biological process;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;reproductive process;spermatogenesis cell part;cytoplasm;intracellular part 9.96E-10 6 2 2 10.1

P53384-2;P53384;I3L531 Cytosolic Fe-S cluster assembly factor NUBP1 NUBP1 >sp|P53384-2|NUBP1_HUMAN Isoform 2 of Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1;>sp|P53384|NUBP1_HUMAN Cytosolic Fe-S cluster assembly factor NUBP1 OS=Homo sapiens GN=NUBP1 PE=1 SV=2;>tr|I3L531|I3L531_HUMAN Cytosolic Fe-S cluste -0.31 -0.01 -0.59 0.35 0.00 0.14 -0.15 -0.10 0.206457062 -0.116168349 biological regulation;biosynthetic process;cation homeostasis;cell growth;cellular biosynthetic process;cellular cation homeostasis;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular process;chemical homeostasis;cofactor biosynthetic process;cofactor metabolic process;growth;homeostatic process;ion homeostasis;iron ion homeostasis;iron-sulfur cluster assembly;metabolic process;metal ion homeostasis;metallo-sulfur cluster assembly;regulation of biological quality;small molecule metabolic process "4 iron, 4 sulfur cluster binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane 9.40E-18 3 2 2 8.7

Q9NZJ9-2;Q9NZJ9-3;Q9NZJ9 Diphosphoinositol polyphosphate phosphohydrolase 2 NUDT4 >sp|Q9NZJ9-2|NUDT4_HUMAN Isoform 2 of Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Homo sapiens GN=NUDT4;>sp|Q9NZJ9-3|NUDT4_HUMAN Isoform 3 of Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Homo sapiens GN=NUDT4;>sp|Q9NZJ9|NUDT4_HUMAN Dipho 0.16 0.19 -0.50 -0.16 0.40 0.18 0.24 -0.09 0.573931193 -0.259454809 biological regulation;calcium-mediated signaling;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cyclic nucleotide metabolic process;cyclic-nucleotide-mediated signaling;establishment of localization;establishment of localization in cell;inositol phosphate metabolic process;intracellular signal transduction;intracellular transport;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organophosphate metabolic process;primary metabolic process;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of intracellular transport;regulation of localization;regulation of nucleobase-containing compound transport;regulation of nucleocytoplasmic transport;regulation of RNA export from nucleus;regulation of transport;response to stimulus;second-messenger-mediated signaling;signal transduction;small molecule metabolic process;transport "binding;catalytic activity;cation binding;diphosphoinositol-polyphosphate diphosphatase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;pyrophosphatase activity;RNA binding;snoRNA binding" cell part;cytoplasmic part;cytosol;intracellular part 8.38E-07 3 2 2 14.4

Q01804-3;Q01804;G3V0I6 OTU domain-containing protein 4 OTUD4 ">sp|Q01804-3|OTUD4_HUMAN Isoform 3 of OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4;>sp|Q01804|OTUD4_HUMAN OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=3;>tr|G3V0I6|G3V0I6_HUMAN OTU domain containing 4, isoform CRA_f OS=Homo" 0.15 -0.17 0.33 -0.02 -0.21 0.06 0.35 0.17 0.042544275 -0.020174136 3.23E-11 3 2 2 3.8

Q86U42-2;Q86U42;H0YJH9;B4DEH8;G3V4T2;Q92843-2Polyadenylate-binding protein 2 PABPN1 >sp|Q86U42-2|PABP2_HUMAN Isoform 2 of Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1;>sp|Q86U42|PABP2_HUMAN Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABPN1 PE=1 SV=3;>tr|H0YJH9|H0YJH9_HUMAN Polyadenylate-binding protein 2 (Fragment) OS -0.02 0.35 0.14 0.35 0.00 -0.53 -1.40 -0.70 1.190824929 0.863103622 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;macromolecule metabolic process;metabolic process;modification by symbiont of host morphology or physiology;modification by virus of host mRNA processing;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by symbiont of host cellular process;modulation by virus of host cellular process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;multicellular organismal process;multi-organism process;muscle contraction;muscle system process;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;poly(A)+ mRNA export from nucleus;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;reproductive process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;system process;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport;viral infectious cycle;viral reproductive process;virus-host interaction" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex mRNA surveillance pathway 3.49E-14 6 2 2 9.1

D6RJF2;Q9H074-3;D6RD97;D6RJ02;D6REB4;Q9H074-2;Q9H074 Polyadenylate-binding protein-interacting protein 1 PAIP1 >tr|D6RJF2|D6RJF2_HUMAN Polyadenylate-binding protein-interacting protein 1 (Fragment) OS=Homo sapiens GN=PAIP1 PE=2 SV=1;>sp|Q9H074-3|PAIP1_HUMAN Isoform 3 of Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens GN=PAIP1;>tr|D6RD97|D6RD97_H -0.11 -0.02 -0.28 0.19 -0.10 0.00 0.19 0.30 0.471202877 -0.151484935 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;RNA stabilization;translational initiation "binding;DNA binding;nucleic acid binding;RNA binding;translation activator activity;translation regulator activity;translation regulator activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;intracellular part RNA transport 6.67E-06 7 2 2 11.5

Q9H2J4 Phosducin-like protein 3 PDCL3 >sp|Q9H2J4|PDCL3_HUMAN Phosducin-like protein 3 OS=Homo sapiens GN=PDCL3 PE=1 SV=1 0.22 0.11 -0.02 0.05 -0.27 -0.25 0.39 -0.29 0.466625568 0.193916027 apoptosis;cell death;cellular process;death;interaction with host;interspecies interaction between organisms;multi-organism process;programmed cell death;reproductive process;viral reproductive process;virus-host interaction cell part;cytoplasm;intracellular part 1.12E-14 1 2 2 9.6

Q15165-3;J3QT77;Q15165-1;Q15165;G3V1K3;G3XAK4 Serum paraoxonase/arylesterase 2 PON2 >sp|Q15165-3|PON2_HUMAN Isoform 3 of Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2;>tr|J3QT77|J3QT77_HUMAN Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2 PE=4 SV=1;>sp|Q15165-1|PON2_HUMAN Isoform 1 of Serum paraoxonase/arylesterase 2 O -0.38 -0.21 0.17 0.29 0.12 0.51 0.35 0.44 0.936440309 -0.389056074 aromatic compound catabolic process;catabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular metabolic process;cellular process;metabolic process;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress "arylesterase activity;binding;carboxylic ester hydrolase activity;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;identical protein binding;ion binding;metal ion binding;protein binding"cell part;cytoplasmic part;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane;membrane-bounded organelle;mitochondrion;nucleus;organelle;plasma membrane;vacuole Aminobenzoate degradation;Bisphenol degradation 2.82E-37 6 2 2 10.2

P50897;E9PSE5;E9PP28;E9PK48;P50897-2;E9PMG2 Palmitoyl-protein thioesterase 1 PPT1 >sp|P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1;>tr|E9PSE5|E9PSE5_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=2 SV=1;>tr|E9PP28|E9PP28_HUMAN Palmitoyl-protein thioesterase 1 (Fragment) OS=Homo -0.05 -0.10 -0.86 0.05 -0.48 0.03 -0.03 -0.43 0.016973795 -0.012913771 "adult behavior;adult locomotory behavior;anatomical structure development;associative learning;behavior;biological regulation;brain development;catabolic process;cation homeostasis;cell development;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular monovalent inorganic cation homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular protein catabolic process;cellular protein metabolic process;chemical homeostasis;cofactor metabolic process;cofactor transport;cognition;developmental process;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;grooming behavior;homeostatic process;intracellular pH reduction;ion homeostasis;learning;learning or memory;lipid catabolic process;lipid metabolic process;lipoprotein catabolic process;lipoprotein metabolic process;locomotory behavior;lysosomal lumen acidification;lysosome organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane lipid catabolic process;membrane lipid metabolic process;membrane organization;membrane raft organization;metabolic process;monovalent inorganic cation homeostasis;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell growth;negative regulation of cellular process;negative regulation of growth;negative regulation of neuron apoptosis;negative regulation of programmed cell death;neurological system process;neuron development;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;organ development;organelle organization;pH reduction;pinocytosis;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of pinocytosis;positive regulation of receptor-mediated endocytosis;positive regulation of transport;primary metabolic process;protein catabolic process;protein deacylation;protein depalmitoylation;protein metabolic process;protein modification process;protein transport;receptor-mediated endocytosis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular component organization;regulation of cellular pH;regulation of cellular process;regulation of endocytosis;regulation of growth;regulation of hydrolase activity;regulation of intracellular pH;regulation of lipase activity;regulation of localization;regulation of lysosomal lumen pH;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of neurotransmitter levels;regulation of pH;regulation of phospholipase A2 activity;regulation of phospholipase activity;regulation of pinocytosis;regulation of programmed cell death;regulation of receptor-mediated endocytosis;regulation of synapse structure and activity;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;secretion;secretion by cell;sensory perception;sensory perception of light stimulus;signal release;sphingolipid catabolic process;sphingolipid metabolic process;system process;transport;vacuole organization;vesicle-mediated transport;visual perception" "acyl-CoA thioesterase activity;catalytic activity;CoA hydrolase activity;hydrolase activity;hydrolase activity, acting on ester bonds;palmitoyl-(protein) hydrolase activity;palmitoyl-CoA hydrolase activity;thiolester hydrolase activity" axon;cell body;cell part;cell projection;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;dendrite;extracellular region;extracellular region part;extracellular space;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;neuron projection;neuronal cell body;nucleus;organelle;synapse part;synaptic vesicle;vacuole;vesicle Fatty acid elongation in mitochondria;Lysosome 5.42E-69 6 2 2 10.8

B7Z7Q6;P42785;P42785-2;E9PLY4;E9PNF7;E9PQB5;E9PL85;E9PNJ1;E9PQN3;E9PKN6;E9PIG4 Lysosomal Pro-X carboxypeptidase PRCP >tr|B7Z7Q6|B7Z7Q6_HUMAN Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=2 SV=1;>sp|P42785|PCP_HUMAN Lysosomal Pro-X carboxypeptidase OS=Homo sapiens GN=PRCP PE=1 SV=1;>sp|P42785-2|PCP_HUMAN Isoform 2 of Lysosomal Pro-X carboxypeptidase OS=Homo 0.04 -0.39 -0.15 0.19 1.33 0.99 0.21 -0.34 0.672959338 -0.625088902 "blood coagulation, intrinsic pathway;macromolecule metabolic process;metabolic process;primary metabolic process;protein activation cascade;protein metabolic process;proteolysis;response to stimulus""carboxypeptidase activity;catalytic activity;exopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type carboxypeptidase activity;serine-type exopeptidase activity;serine-type peptidase activity"cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane;membrane-bounded organelle;organelle;plasma membrane;vacuole Protein digestion and absorption 2.19E-09 11 2 2 7.9

O75475;O75475-3;O75475-2 PC4 and SFRS1-interacting protein PSIP1 >sp|O75475|PSIP1_HUMAN PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1;>sp|O75475-3|PSIP1_HUMAN Isoform 3 of PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1;>sp|O75475-2|PSIP1_HUMAN Isoform 2 of PC4 and SFRS1-interacting pro -0.04 0.04 -0.10 0.11 0.05 -0.09 0.15 -0.39 0.211960679 0.070888632 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA splice site selection;nitrogen compound metabolic process;nuclear mRNA 5'-splice site recognition;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to chemical stimulus;response to heat;response to oxidative stress;response to stimulus;response to stress;response to temperature stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" activating transcription factor binding;binding;chromatin binding;DNA binding;nucleic acid binding;protein binding;protein binding transcription factor activity;RNA polymerase II transcription coactivator activity;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;RNA polymerase II transcription factor binding transcription factor activity involved in positive regulation of transcription;structure-specific DNA binding;supercoiled DNA binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity cell part;chromatin;chromosomal part;cytoplasmic part;cytosol;heterochromatin;intracellular organelle part;intracellular part;nuclear chromatin;nuclear chromosome part;nuclear heterochromatin;nuclear part;nuclear periphery;nucleoplasm;organelle part;transcriptionally active chromatin 6.72E-07 3 2 2 4.7

F8WBH5;Q14997 Proteasome activator complex subunit 4 PSME4 >tr|F8WBH5|F8WBH5_HUMAN Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=2 SV=1;>sp|Q14997|PSME4_HUMAN Proteasome activator complex subunit 4 OS=Homo sapiens GN=PSME4 PE=1 SV=2 0.43 -0.03 0.22 -0.24 -0.03 -0.28 0.43 -0.01 0.112589207 0.066094652 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cell differentiation;cellular catabolic process;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;gamete generation;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;spermatogenesis;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;proteasome complex;protein complex Proteasome 7.65E-07 2 2

2 4.9

P20962;F5H7R9;F5GXR3 Parathymosin PTMS >sp|P20962|PTMS_HUMAN Parathymosin OS=Homo sapiens GN=PTMS PE=1 SV=2;>tr|F5H7R9|F5H7R9_HUMAN Parathymosin (Fragment) OS=Homo sapiens GN=PTMS PE=2 SV=1;>tr|F5GXR3|F5GXR3_HUMAN Parathymosin OS=Homo sapiens GN=PTMS PE=2 SV=1 -0.42 -0.42 0.18 0.22 0.71 0.11 0.21 -0.18 0.520654519 -0.321310781 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA metabolic process;DNA replication;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 7.70E-31 3 2 2 22.5

Q15223-3;Q15223-2;Q15223 Poliovirus receptor-related protein 1 PVRL1 >sp|Q15223-3|PVRL1_HUMAN Isoform Gamma of Poliovirus receptor-related protein 1 OS=Homo sapiens GN=PVRL1;>sp|Q15223-2|PVRL1_HUMAN Isoform Alpha of Poliovirus receptor-related protein 1 OS=Homo sapiens GN=PVRL1;>sp|Q15223|PVRL1_HUMAN Poliovirus receptor-rel -0.66 -0.24 0.56 0.32 -1.15 -1.84 -0.71 -0.96 1.29163953 1.158268932 adherens junction organization;anatomical structure development;anatomical structure morphogenesis;biological adhesion;biomineral tissue development;cation transport;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;enamel mineralization;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of virus into host cell;establishment of localization;heterophilic cell-cell adhesion;homophilic cell adhesion;immune response;immune system process;interaction with host;interspecies interaction between organisms;ion transport;iron ion transport;lens morphogenesis in camera-type eye;locomotion;metal ion transport;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multi-organism process;response to stimulus;retina development in camera-type eye;tissue development;tooth mineralization;transition metal ion transport;transport binding;coreceptor activity;identical protein binding;molecular transducer activity;protein binding;protein dimerization activity;protein homodimerization activity;receptor activity;signal transducer activity;signaling receptor activity adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;extracellular region;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Adherens junction;Cell adhesion molecules (CAMs) 8.76E-06 3 2 2 7.1

H3BPG5;H3BV80;H3BMS0;Q15287-3;Q15287-2;H3BMM9;H3BTC0;Q15287 RNA-binding protein with serine-rich domain 1 RNPS1 ">tr|H3BPG5|H3BPG5_HUMAN RNA binding protein S1, serine-rich domain, isoform CRA_c OS=Homo sapiens GN=RNPS1 PE=2 SV=1;>tr|H3BV80|H3BV80_HUMAN RNA-binding protein with serine-rich domain 1 OS=Homo sapiens GN=RNPS1 PE=2 SV=2;>tr|H3BMS0|H3BMS0_HUMAN RNA-bindin" -0.26 0.76 0.11 0.88 -0.23 -0.19 -1.58 -0.01 0.829937059 0.875314143 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part mRNA surveillance pathway;RNA transport 1.59E-24 8 2 2 18

Q9BVL4 Selenoprotein O SELO >sp|Q9BVL4|SELO_HUMAN Selenoprotein O OS=Homo sapiens GN=SELO PE=2 SV=3 0.29 -0.22 0.23 0.15 -0.16 0.27 0.29 0.16 0.051745278 -0.023822494 2.02E-11 1 2 2 4.8

F8VUY8;Q96QD8 Sodium-coupled neutral amino acid transporter 2 SLC38A2 >tr|F8VUY8|F8VUY8_HUMAN Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=2 SV=1;>sp|Q96QD8|S38A2_HUMAN Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2 0.51 0.54 -0.42 -0.32 -0.30 -0.02 -0.18 0.16 0.219803379 0.161821974 biological regulation;cation transport;cellular process;establishment of localization;establishment of localization in cell;glutamate secretion;ion transport;metal ion transport;monovalent inorganic cation transport;neurotransmitter secretion;neurotransmitter transport;regulation of biological quality;regulation of neurotransmitter levels;secretion;secretion by cell;signal release;sodium ion transport;transmembrane transport;transport active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;carboxylic acid transmembrane transporter activity;organic acid transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Protein digestion and absorption 1.34E-103 2 2 2 25

P84022-3;P84022-2;P84022;B7Z5N5;Q15796-2;Q15796;H0YMP2;H0YL71;H3BP09;H3BVD1;K7EJX0;P84022-4;O15198-2;O15198 Mothers against decapentaplegic homolog 3;Mothers against decapentaplegic homolog 2;Mothers against decapentaplegic homolog 9 SMAD3;SMAD2;SMAD9 >sp|P84022-3|SMAD3_HUMAN Isoform 3 of Mothers against decapentaplegic homolog 3 OS=Homo sapiens GN=SMAD3;>sp|P84022-2|SMAD3_HUMAN Isoform 2 of Mothers against decapentaplegic homolog 3 OS=Homo sapiens GN=SMAD3;>sp|P84022|SMAD3_HUMAN Mothers against decapen 0.23 0.16 -0.05 0.10 -0.03 -0.46 0.18 -0.21 0.672647256 0.237107874 "activation of caspase activity;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;anatomical structure regression;anterior/posterior pattern specification;apoptotic mitochondrial changes;avoidance of defenses of other organism involved in symbiotic interaction;avoidance of host defenses;axis specification;biological regulation;biosynthetic process;BMP signaling pathway;bone development;cartilage development;cell activation;cell cycle arrest;cell cycle process;cell development;cell differentiation;cell fate commitment;cell junction organization;cell surface receptor linked signaling pathway;cell-cell junction organization;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;chordate embryonic development;common-partner SMAD protein phosphorylation;developmental growth;developmental process;developmental process involved in reproduction;dorsal/ventral axis specification;embryo development;embryo development ending in birth or egg hatching;embryonic axis specification;embryonic cranial skeleton morphogenesis;embryonic foregut morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;embryonic pattern specification;embryonic skeletal system morphogenesis;endoderm development;enzyme linked receptor protein signaling pathway;epithelium development;establishment of localization;establishment of localization in cell;evasion of host defenses by virus;evasion or tolerance of defenses of other organism involved in symbiotic interaction;evasion or tolerance of host defenses;formation of primary germ layer;gland development;growth;heart looping;hindbrain development;hormone secretion;hormone transport;immune response;immune system development;immune system process;in utero embryonic development;induction of apoptosis;induction of programmed cell death;insulin secretion;interaction with host;interspecies interaction between organisms;intracellular signal transduction;lens fiber cell differentiation;leukocyte activation;liver development;lung development;lymphocyte activation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;mesoderm formation;mesoderm morphogenesis;metabolic process;midbrain development;mitochondrion organization;Mullerian duct regression;multi-organism process;ncRNA metabolic process;ncRNA processing;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catabolic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of defense response;negative regulation of developmental process;negative regulation of gene expression;negative regulation of growth;negative regulation of inflammatory response;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitotic cell cycle;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of osteoblast differentiation;negative regulation of osteoblast proliferation;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of programmed cell death;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of wound healing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organ growth;organ morphogenesis;organelle organization;osteoblast development;palate development;pancreas development;paraxial mesoderm morphogenesis;pattern specification process;peptide hormone secretion;peptide secretion;peptide transport;pericardium development;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of actin filament bundle assembly;positive regulation of alkaline phosphatase activity;positive regulation of apoptosis;positive regulation of behavior;positive regulation of biological process;positive regulation of biomineral tissue development;positive regulation of biosynthetic process;positive regulation of BMP signaling pathway;positive regulation of bone mineralization;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of catenin import into nucleus;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell morphogenesis involved in differentiation;positive regulation of cell motility;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of chondrocyte differentiation;positive regulation of cytokine production;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of epithelial to mesenchymal transition;positive regulation of focal adhesion assembly;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of interleukin-1 beta production;positive regulation of interleukin-1 production;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of organelle organization;positive regulation of ossification;positive regulation of peptidase activity;positive regulation of phosphatase activity;positive regulation of positive chemotaxis;positive regulation of programmed cell death;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress fiber assembly;positive regulation of transcription factor import into nucleus;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transforming growth factor beta production;positive regulation of transforming growth factor beta3 production;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of Wnt receptor signaling pathway;post-embryonic development;posttranscriptional regulation of gene expression;primary metabolic process;primary miRNA processing;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification process;protein phosphorylation;protein stabilization;regionalization;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of alkaline phosphatase activity;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of behavior;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biomineral tissue development;regulation of biosynthetic process;regulation of BMP signaling pathway;regulation of bone mineralization;regulation of canonical Wnt receptor signaling pathway;regulation of cartilage development;regulation of catabolic process;regulation of catalytic activity;regulation of catenin import into nucleus;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell proliferation;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of chondrocyte differentiation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of cytoskeleton organization;regulation of defense response;regulation of dephosphorylation;regulation of developmental process;regulation of endopeptidase activity;regulation of epithelial cell proliferation;regulation of epithelial to mesenchymal transition;regulation of establishment of protein localization;regulation of focal adhesion assembly;regulation of gene expression;regulation of growth;regulation of hormone levels;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of interleukin-1 beta production;regulation of interleukin-1 production;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoblast proliferation;regulation of peptidase activity;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of positive chemotaxis;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stress fiber assembly;regulation of striated muscle tissue development;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transforming growth factor beta production;regulation of transforming growth factor beta receptor signaling pathway;regulation of transforming growth factor beta2 production;regulation of transforming growth factor beta3 production;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmembrane transport;regulation of transport;regulation of Wnt receptor signaling pathway;regulation of wound healing;release of cytochrome c from mitochondria;reproductive process;response to biotic stimulus;response to carbohydrate stimulus;response to chemical stimulus;response to cholesterol;response to defenses of other organism involved in symbiotic interaction;response to glucose stimulus;response to hexose stimulus;response to host;response to host defenses;response to hypoxia;response to lipid;response to monosaccharide stimulus;response to organic cyclic compound;response to organic substance;response to other organism;response to oxygen levels;response to stimulus;response to stress;response to wounding;RNA biosynthetic process;RNA metabolic process;RNA processing;secretion;secretion by cell;segmentation;signal release;signal transduction;skeletal system morphogenesis;SMAD protein complex assembly;somitogenesis;system development;T cell activation;thyroid gland development;tissue development;tissue morphogenesis;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent;transdifferentiation;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;transport;tube development;tube morphogenesis;ureteric bud development;viral reproductive process;virus-host interaction;wound healing;zygotic specification of dorsal/ventral axis" "binding;cation binding;chromatin binding;chromatin DNA binding;core promoter proximal region DNA binding;core promoter proximal region sequence-specific DNA binding;DNA binding;double-stranded DNA binding;ion binding;metal ion binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;receptor signaling protein activity;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;signal transducer activity;small conjugating protein binding;structure-specific DNA binding;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding;transforming growth factor beta receptor, cytoplasmic mediator activity;transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity;transition metal ion binding;ubiquitin binding;zinc ion binding" activin responsive factor complex;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane;nuclear inner membrane;nuclear membrane;nuclear part;nucleoplasm;nucleoplasm part;organelle inner membrane;organelle membrane;organelle part;plasma membrane;protein complex;receptor complex;SMAD protein complex;transcription factor complex Adherens junction;Cell cycle;Chagas disease (American trypanosomiasis);Colorectal cancer;Endocytosis;Pancreatic cancer;Pathways in cancer;TGF-beta signaling pathway;Wnt signaling pathway 1.35E-06 14 2 2 12.8

J3QLI9;P62314 Small nuclear ribonucleoprotein Sm D1SNRPD1 >tr|J3QLI9|J3QLI9_HUMAN Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD1 PE=4 SV=1;>sp|P62314|SMD1_HUMAN Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 -1.39 0.23 0.03 1.17 -0.70 -0.56 -1.97 -0.07 0.52251114 0.831891898 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;spliceosomal snRNP assembly;spliceosome assembly binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome;Systemic lupus erythematosus 5.55E-44 2 2 2 44

Q96L92-3;Q96L92;Q96L92-2 Sorting nexin-27 SNX27 >sp|Q96L92-3|SNX27_HUMAN Isoform 2 of Sorting nexin-27 OS=Homo sapiens GN=SNX27;>sp|Q96L92|SNX27_HUMAN Sorting nexin-27 OS=Homo sapiens GN=SNX27 PE=1 SV=2;>sp|Q96L92-2|SNX27_HUMAN Isoform 3 of Sorting nexin-27 OS=Homo sapiens GN=SNX27 0.06 0.00 -0.35 -0.01 -0.19 -0.24 -0.23 -0.39 0.788701374 0.18955388 biological regulation;cellular process;cellular response to stimulus;endosome to lysosome transport;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;lysosomal transport;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;transport;vacuolar transport;vesicle-mediated transport binding;lipid binding;phosphatidylinositol binding;phospholipid binding cell part;cytoplasm;cytoplasmic part;cytosol;early endosome;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.59E-07 3 2 2 7.2

O95219;F8WDD4;F8W9T3;B4DQV4 Sorting nexin-4 SNX4 >sp|O95219|SNX4_HUMAN Sorting nexin-4 OS=Homo sapiens GN=SNX4 PE=1 SV=1;>tr|F8WDD4|F8WDD4_HUMAN Sorting nexin-4 OS=Homo sapiens GN=SNX4 PE=2 SV=1;>tr|F8W9T3|F8W9T3_HUMAN Sorting nexin-4 (Fragment) OS=Homo sapiens GN=SNX4 PE=2 SV=1;>tr|B4DQV4|B4DQV4_HUMAN S 0.20 -0.15 0.02 -0.17 -0.03 0.10 0.26 0.09 0.526998879 -0.131487146 cell communication;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytic recycling;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;membrane invagination;membrane organization;protein transport;transport;vesicle-mediated transport binding;lipid binding;phosphatidylinositol binding;phospholipid binding cell part;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;dynein complex;early endosome membrane;endosomal part;endosome membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule associated complex;organelle membrane;organelle part;protein complex 1.07E-06 4 2 2 7.1

Q9HC07;D6RBL0;D6RD79;B4DHW1 Transmembrane protein 165 TMEM165 >sp|Q9HC07|TM165_HUMAN Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=1 SV=1;>tr|D6RBL0|D6RBL0_HUMAN Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=2 SV=1;>tr|D6RD79|D6RD79_HUMAN Transmembrane protein 165 OS=Homo sapiens GN=TMEM165 PE=2 S -0.43 0.08 -0.17 -0.10 -0.08 -0.34 -0.87 0.00 0.301856028 0.170634247 cell part;cytoplasmic part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle 4.85E-09 4 2 2 13.9

O43156 TELO2-interacting protein 1 homolog TTI1 >sp|O43156|TTI1_HUMAN TELO2-interacting protein 1 homolog OS=Homo sapiens GN=TTI1 PE=1 SV=3 0.35 0.02 0.40 0.05 -0.08 -0.33 -0.20 -0.74 1.278877442 0.545383444 biological regulation;regulation of biological process;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of TOR signaling cascade cell part;cytoplasm;intracellular part;macromolecular complex;protein complex;TORC1 complex;TORC2 complex 9.51E-23 1 2 2 3

Q96CW5-3;Q96CW5-2;Q96CW5 Gamma-tubulin complex component 3 TUBGCP3 >sp|Q96CW5-3|GCP3_HUMAN Isoform 3 of Gamma-tubulin complex component 3 OS=Homo sapiens GN=TUBGCP3;>sp|Q96CW5-2|GCP3_HUMAN Isoform 2 of Gamma-tubulin complex component 3 OS=Homo sapiens GN=TUBGCP3;>sp|Q96CW5|GCP3_HUMAN Gamma-tubulin complex component 3 OS=H 0.44 0.00 0.27 -0.10 0.09 -0.44 0.11 -0.29 0.652489089 0.283856456 cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;fertilization;G2/M transition of mitotic cell cycle;microtubule cytoskeleton organization;microtubule nucleation;microtubule-based process;organelle organization;reproductive process;single fertilization binding;cytoskeletal protein binding;gamma-tubulin binding;protein binding;structural constituent of cytoskeleton;structural molecule activity;tubulin binding cell part;centriole;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule organizing center part;non-membrane-bounded organelle;organelle;organelle part;polar microtubule;protein complex;spindle microtubule 7.81E-05 3 2 2 7.4

H0Y614;P61960 Ubiquitin-fold modifier 1 UFM1 >tr|H0Y614|H0Y614_HUMAN Ubiquitin-fold modifier 1 (Fragment) OS=Homo sapiens GN=UFM1 PE=4 SV=1;>sp|P61960|UFM1_HUMAN Ubiquitin-fold modifier 1 OS=Homo sapiens GN=UFM1 PE=1 SV=1 -0.21 0.40 -0.24 0.57 0.14 0.44 -0.42 -0.04 0.13423229 0.102296582 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ufmylation cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 7.61E-07 2 2 2 28.4

B4DXK8;Q8TED0;D6RF65;B4DU75;H0Y8P4 U3 small nucleolar RNA-associated protein 15 homolog UTP15 >tr|B4DXK8|B4DXK8_HUMAN U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens GN=UTP15 PE=2 SV=1;>sp|Q8TED0|UTP15_HUMAN U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens GN=UTP15 PE=1 SV=3;>tr|D6RF65|D6RF65_HUMAN U3 small 0.07 1.12 -0.07 0.89 -0.23 0.09 -0.96 0.25 0.768168159 0.713115033 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes 9.69E-10 5 2 2 5.4

P56181-2 ">sp|P56181-2|NDUV3_HUMAN Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial OS=Homo sapiens GN=NDUFV3" -0.36 1.20 -0.05 0.71 0.28 0.50 -1.15 0.43 0.265090907 0.362214824 5.84E-30 1 2 2 6.8

Q9BY43;Q14D22;E9PQI5;E9PQ80;E9PSI1;CON__ENSEMBL:ENSBTAP00000032840 Charged multivesicular body protein 4a CHMP4A;TM9SF1>sp|Q9BY43|CHM4A_HUMAN Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A PE=1 SV=3;>tr|Q14D22|Q14D22_HUMAN Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A PE=2 SV=1;>tr|E9PQI5|E9PQI5_HUMAN Charged multivesicular body protein -0.05 -0.05 0.27 0.04 -0.24 -0.45 0.17 -0.19 0.652438765 0.2300625 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;membrane organization;protein transport;transport;vesicle-mediated transport binding;lipid binding cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endosomal part;endosome membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;late endosome membrane;membrane;membrane part;organelle membrane;organelle part;vesicle membrane Endocytosis 1.02E-34 6 3 2 16.7

Q9H1H9-3;Q9H1H9-4;Q9H1H9-2;E9PDX3;Q9H1H9;H0Y925;H0Y9Z7;H0Y307 Kinesin-like protein KIF13A KIF13A >sp|Q9H1H9-3|KI13A_HUMAN Isoform 3 of Kinesin-like protein KIF13A OS=Homo sapiens GN=KIF13A;>sp|Q9H1H9-4|KI13A_HUMAN Isoform 4 of Kinesin-like protein KIF13A OS=Homo sapiens GN=KIF13A;>sp|Q9H1H9-2|KI13A_HUMAN Isoform 2 of Kinesin-like protein KIF13A OS=Hom 0.06 0.17 0.00 -0.10 -0.02 0.20 0.39 0.14 0.590884133 -0.143599698 cargo loading into vesicle;cell cycle;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytokinesis;cytoskeleton-dependent intracellular transport;endosome to lysosome transport;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;intracellular protein transport;intracellular transport;localization;lysosomal transport;macromolecular complex assembly;macromolecular complex subunit organization;melanosome organization;microtubule-based movement;microtubule-based process;microtubule-based transport;organelle localization;organelle organization;organelle transport along microtubule;pigment granule organization;plus-end-directed organelle transport along microtubule;plus-end-directed vesicle transport along microtubule;post-Golgi vesicle-mediated transport;protein complex assembly;protein complex subunit organization;protein transport;transport;vacuolar transport;vesicle localization;vesicle organization;vesicle transport along microtubule;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;centrosome;cytoplasmic part;cytoskeletal part;endosomal part;endosome membrane;Golgi apparatus part;Golgi membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule associated complex;microtubule organizing center;midbody;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex;trans-Golgi network membrane 9.13E-14 8 3 2 2.3

P02795;P80297;P13640-2;P13640;H3BSF1;Q8N339;CON__P67983;P80294;P04731;H3BSP9 Metallothionein-2;Metallothionein-1X;Metallothionein-1G MT2A;MT1X;MT1G >sp|P02795|MT2_HUMAN Metallothionein-2 OS=Homo sapiens GN=MT2A PE=1 SV=1;>sp|P80297|MT1X_HUMAN Metallothionein-1X OS=Homo sapiens GN=MT1X PE=1 SV=1;>sp|P13640-2|MT1G_HUMAN Isoform 2 of Metallothionein-1G OS=Homo sapiens GN=MT1G;>sp|P13640|MT1G_HUMAN Metall 0.40 -0.22 -0.29 -0.30 1.56 -0.08 0.37 0.27 0.683190779 -0.631447809 biological regulation;cation homeostasis;cell activation;cell differentiation;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular copper ion homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular process;cellular response to cadmium ion;cellular response to chemical stimulus;cellular response to copper ion;cellular response to cytokine stimulus;cellular response to drug;cellular response to growth factor stimulus;cellular response to inorganic substance;cellular response to interferon-gamma;cellular response to metal ion;cellular response to organic substance;cellular response to stimulus;cellular response to vascular

endothelial growth factor stimulus;cellular response to zinc ion;chemical homeostasis;copper ion homeostasis;cytokine-mediated signaling pathway;developmental process;homeostatic process;immune system process;interferon-gamma-mediated signaling pathway;ion homeostasis;leukocyte activation;leukocyte differentiation;monocyte activation;monocyte differentiation;myeloid cell differentiation;myeloid leukocyte activation;myeloid leukocyte differentiation;negative regulation of biological process;negative regulation of growth;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of growth;response to cadmium ion;response to chemical stimulus;response to copper ion;response to cytokine stimulus;response to drug;response to growth factor stimulus;response to inorganic substance;response to interferon-gamma;response to metal ion;response to organic substance;response to stimulus;response to zinc ion;signal transduction binding;cadmium ion binding;cation binding;copper ion binding;drug binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm
Mineral absorption 2.57E-33 10 3 2 65.6

A6NIZ0;Q9GZM8-3;Q9GZM8;Q9GZM8-2;J3QRZ1;J3KT16;I3L2R3;J3KRK9;J3QL85;I3L522;J3QSD2 Nuclear distribution protein nudE-like 1 NDEL1 >tr|A6NIZ0|A6NIZ0_HUMAN Nuclear distribution protein nudE-like 1 OS=Homo sapiens GN=NDEL1 PE=2 SV=4;>sp|Q9GZM8-3|NDEL1_HUMAN Isoform 3 of Nuclear distribution protein nudE-like 1 OS=Homo sapiens GN=NDEL1;>sp|Q9GZM8|NDEL1_HUMAN Nuclear distribution protein 0.26 0.28 0.32 0.30 0.42 0.42 -1.14 -0.38 0.511440549 0.459128067 activation of Cdc42 GTPase activity;activation of Ras GTPase activity;activation of Rho GTPase activity;anaphase;anatomical structure morphogenesis;axon cargo transport;axonogenesis;biological regulation;cell cycle phase;cell cycle process;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell proliferation;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular membrane organization;cellular process;central nervous system neuron axonogenesis;centrosome localization;cerebral cortex cell migration;cerebral cortex radially oriented cell migration;chromosome segregation;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;establishment of localization;establishment of localization in cell;forebrain cell migration;inner cell mass cell proliferation;intermediate filament cytoskeleton organization;intermediate filament-based process;intracellular transport;localization;locomotion;M phase;M phase of mitotic cell cycle;membrane disassembly;membrane organization;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;mitotic anaphase;mitotic prometaphase;neurofilament cytoskeleton organization;neuron migration;neuron projection morphogenesis;nuclear envelope disassembly;nuclear envelope organization;organelle localization;organelle organization;organelle transport along microtubule;positive regulation of axon extension;positive regulation of axon regeneration;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of Cdc42 GTPase activity;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of neurogenesis;positive regulation of neuron projection development;positive regulation of neuron projection regeneration;positive regulation of Ras GTPase activity;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of Rho GTPase activity;regulation of anatomical structure morphogenesis;regulation of axon extension;regulation of axon regeneration;regulation of axonogenesis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of Cdc42 GTPase activity;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuron projection regeneration;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;retrograde axon cargo transport;telencephalon cell migration;transport;vesicle localization;vesicle transport along microtubule catalytic activity;hydrolase activity;oligopeptidase activity;peptidase activity axon;cell body;cell leading edge;cell part;cell projection;centrosome;chromosomal part;condensed chromosome kinetochore;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;envelope;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinesin complex;kinetochore;macromolecular complex;microtubule;microtubule associated complex;microtubule organizing center;neurofilament cytoskeleton;neuron projection;non-membrane-bounded organelle;nuclear envelope;nuclear part;organelle;organelle envelope;organelle part;protein complex;spindle 2.08E-07 11 3 2 13.8

Q9P2N5 RNA-binding protein 27 RBM27 >sp|Q9P2N5|RBM27_HUMAN RNA-binding protein 27 OS=Homo sapiens GN=RBM27 PE=1 SV=2 0.08 0.46 0.21 0.08 0.14 -0.10 -0.86 -0.23 0.871638918 0.470959194 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part 4.11E-13 1 3 2 4

P78362;P78362-2;H7C5L6 SRSF protein kinase 2;SRSF protein kinase 2 N-terminal;SRSF protein kinase 2 C-terminal SRPK2 >sp|P78362|SRPK2_HUMAN SRSF protein kinase 2 OS=Homo sapiens GN=SRPK2 PE=1 SV=3;>sp|P78362-2|SRPK2_HUMAN Isoform 2 of SRSF protein kinase 2 OS=Homo sapiens GN=SRPK2;>tr|H7C5L6|H7C5L6_HUMAN SRSF protein kinase 2 (Fragment) OS=Homo sapiens GN=SRPK2 PE=4 SV=1 -0.03 0.19 0.11 0.18 -0.56 -0.20 0.00 -0.03 0.953713006 0.30888254 "anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;cell differentiation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular response to stimulus;defense response;developmental process;immune response;immune system process;innate immune response;intracellular protein kinase cascade;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;nuclear body organization;nuclear speck organization;nucleus organization;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell cycle;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of neuron apoptosis;positive regulation of programmed cell death;positive regulation of reproductive process;positive regulation of viral genome replication;positive regulation of viral reproduction;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell death;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of viral genome replication;regulation of viral reproduction;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;signal transduction;spliceosome assembly" "14-3-3 protein binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 1.98E-10 3 3 2 6.7

P61020;P61020-2 Ras-related protein Rab-5B RAB5B >sp|P61020|RAB5B_HUMAN Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1;>sp|P61020-2|RAB5B_HUMAN Isoform 2 of Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B -0.08 0.13 -0.64 0.24 -0.30 0.32 0.01 0.42 0.31635628 -0.203411907 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;endosome organization;establishment of localization;establishment of protein localization;intracellular signal transduction;organelle organization;protein transport;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;GTP-dependent protein binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome membrane;endocytic vesicle;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;vesicle Amoebiasis;Endocytosis;ko05152;Phagosome;Vasopressin-regulated water reabsorption 6.35E-28 2 4 2 20.5

Q9BWF3;E9PB51;Q9BWF3-3;E9PLB0;E9PM61;D6R9K7;J3QRR5;Q9BWF3-4;Q9BWF3-2;Q9BQ04 RNA-binding protein 4;RNA-binding protein 4B RBM4;RBM4B >sp|Q9BWF3|RBM4_HUMAN RNA-binding protein 4 OS=Homo sapiens GN=RBM4 PE=1 SV=1;>tr|E9PB51|E9PB51_HUMAN RNA-binding protein 4 (Fragment) OS=Homo sapiens GN=RBM4 PE=2 SV=1;>sp|Q9BWF3-3|RBM4_HUMAN Isoform 3 of RNA-binding protein 4 OS=Homo sapiens GN=RBM4;>tr| 0.22 0.01 -0.04 -0.07 -0.08 -0.43 -0.17 -0.24 1.111990246 0.259738533 "biological regulation;cap-independent translational initiation;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;circadian regulation of gene expression;circadian rhythm;cytoplasmic translational initiation;developmental process;entrainment of circadian clock;entrainment of circadian clock by photoperiod;intracellular protein kinase cascade;intracellular signal transduction;IRES-dependent translational initiation;macromolecule metabolic process;MAPKKK cascade;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;negative regulation of translation in response to stress;negative regulation of translation involved in gene silencing by miRNA;negative regulation of translation, ncRNA-mediated;negative regulation of translational initiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;photoperiodism;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of muscle cell differentiation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of circadian rhythm;regulation of developmental process;regulation of gene expression;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of translation;regulation of translation in response to stress;regulation of translation, ncRNA-mediated;regulation of translational initiation;regulation of transport;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;rhythmic process;RNA metabolic process;RNA processing;RNA splicing;signal transduction;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;translational initiation"binding;cation binding;ion binding;metal ion binding;miRNA binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;RNA granule;stress granule 1.39E-77 10 4 2 16.5

P61586;E9PLA2;C9J1T2;C9JRM1;Q5JR06;Q5JR07;C9JNR4;C9JX21;Q5JR05 Transforming protein RhoA RHOA >sp|P61586|RHOA_HUMAN Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 0.09 -0.01 0.01 0.07 0.12 0.16 0.16 -0.04 0.448169983 -0.059182144 "actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;anatomical structure development;anatomical structure morphogenesis;androgen receptor signaling pathway;apical junction assembly;axon guidance;biological adhesion;biological regulation;cell activation;cell adhesion;cell cycle process;cell junction assembly;cell junction organization;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;cellular response to stress;chemotaxis;cytoskeleton organization;developmental process;enzyme linked receptor protein signaling pathway;inositol lipid-mediated signaling;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular receptor mediated signaling pathway;intracellular signal transduction;locomotion;microtubule cytoskeleton organization;microtubule-based process;mitotic spindle organization;multicellular organismal process;multi-organism process;muscle tissue development;negative regulation of apoptosis;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of I-kappaB kinase/NF-kappaB cascade;negative regulation of intracellular protein kinase cascade;negative regulation of neurogenesis;negative regulation of neuron apoptosis;negative regulation of neuron differentiation;negative regulation of programmed cell death;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;nerve growth factor receptor signaling pathway;neuron projection morphogenesis;organelle assembly;organelle organization;ossification;ossification involved in bone maturation;phosphatidylinositol-mediated signaling;platelet activation;positive regulation of actin filament bundle assembly;positive regulation of actin filament polymerization;positive regulation of apoptosis;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell cycle cytokinesis;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell growth;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell projection organization;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokinesis;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of neurogenesis;positive regulation of neuron apoptosis;positive regulation of neuron differentiation;positive regulation of NF-kappaB import into nucleus;positive regulation of nucleocytoplasmic transport;positive regulation of organelle organization;positive regulation of peptidase activity;positive regulation of podosome assembly;positive regulation of programmed cell death;positive regulation of protein complex assembly;positive regulation of protein import into nucleus;positive regulation of protein metabolic process;positive regulation of protein polymerization;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress fiber assembly;positive regulation of transcription factor import into nucleus;positive regulation of translation;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of vasoconstriction;posttranscriptional regulation of gene expression;Ras protein signal transduction;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of apoptosis;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcium ion transport;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell cycle cytokinesis;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell division;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokinesis;regulation of cytoskeleton organization;regulation of dendrite development;regulation of developmental process;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of ion transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron apoptosis;regulation of neuron differentiation;regulation of neuron projection development;regulation of NF-kappaB import into nucleus;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organelle organization;regulation of osteoblast proliferation;regulation of peptidase activity;regulation of podosome assembly;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein polymerization;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of steroid hormone receptor signaling pathway;regulation of stress fiber assembly;regulation of system process;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of transmembrane transport;regulation of transport;regulation of vasoconstriction;reproductive process;response to abiotic stimulus;response to acid;response to amine stimulus;response to amino acid stimulus;response to carbohydrate stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to glucocorticoid stimulus;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to hypoxia;response to mechanical stimulus;response to monosaccharide stimulus;response to organic nitrogen;response to organic substance;response to oxygen levels;response to steroid hormone stimulus;response to stimulus;response to stress;Rho protein signal transduction;signal transduction;skeletal muscle tissue development;small GTPase mediated signal transduction;spindle assembly;spindle assembly involved in mitosis;spindle organization;steroid hormone receptor signaling pathway;stress fiber assembly;stress-activated protein kinase signaling cascade;striated muscle tissue development;taxis;tissue development;trabecula morphogenesis;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproductive process;virus-host interaction" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" apical junction complex;axon;cell cortex;cell division site part;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;cleavage furrow;cytoplasmic part;cytoskeleton;cytosol;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;leading edge membrane;membrane;membrane part;membrane-bounded organelle;midbody;mitochondrion;neuron projection;non-membrane-bounded organelle;nucleus;organelle;plasma membrane;plasma membrane part;ruffle membrane Adherens junction;Axon guidance;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Colorectal cancer;Endocytosis;Focal adhesion;ko05152;Leukocyte transendothelial migration;Neurotrophin signaling pathway;Pancreatic secretion;Pathogenic Escherichia coli infection;Pathways in cancer;Regulation of actin cytoskeleton;T cell receptor signaling pathway;TGF-beta signaling pathway;Tight junction;Vascular smooth muscle contraction;Wnt signaling pathway 2.34E-24 9 4 2 22.3

Q8IXI1;H3BST5;Q8IXI1-2;I3L2C6;Q8IXI2-6 Mitochondrial Rho GTPase 2 RHOT2 >sp|Q8IXI1|MIRO2_HUMAN Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2;>tr|H3BST5|H3BST5_HUMAN Mitochondrial Rho GTPase 2 (Fragment) OS=Homo sapiens GN=RHOT2 PE=2 SV=2;>sp|Q8IXI1-2|MIRO2_HUMAN Isoform 2 of Mitochondrial Rho GTPase 2 OS=Homo s -0.67 -0.01 0.13 0.57 0.03 0.11 -0.87 0.11 0.172149589 0.163844814 "apoptosis;biological regulation;catabolic process;cell death;cellular catabolic process;cellular component movement;cellular homeostasis;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cytoskeleton-dependent intracellular transport;death;establishment of localization;establishment of localization in cell;establishment of mitochondrion localization;establishment of mitochondrion localization, microtubule-mediated;establishment of organelle localization;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;intracellular signal transduction;intracellular transport;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrion transport along microtubule;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle transport along microtubule;primary metabolic process;programmed cell death;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process;transport" "binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;integral to membrane;integral to mitochondrial membrane;integral to mitochondrial outer membrane;integral to organelle membrane;intracellular;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to mitochondrial outer membrane;intrinsic to organelle membrane;membrane;membrane part;mitochondrial membrane part;mitochondrial part;organelle part;plasma membrane 2.71E-55 5 4 2 8.1

E9PID8;P33240-2;P33240;E7EWR4 Cleavage stimulation factor subunit 2 CSTF2 >tr|E9PID8|E9PID8_HUMAN Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=2 SV=1;>sp|P33240-2|CSTF2_HUMAN Isoform 2 of Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2;>sp|P33240|CSTF2_HUMAN Cleavage stimulation factor subunit 0.13 0.29 0.13 0.06 -0.10 -0.34 -0.79 -0.10 1.190660572 0.484310982 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA cleavage;mRNA metabolic process;mRNA polyadenylation;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA metabolic process;RNA polyadenylation;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;termination of RNA polymerase II transcription;transcription termination, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cleavage body;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mRNA cleavage and polyadenylation specificity factor complex;mRNA cleavage factor complex;nuclear body;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex mRNA surveillance pathway 1.26E-25 4 5 2 17.6

P17096;P17096-3;H7BYM6;E5RIT9 High mobility group protein HMG-I/HMG-Y HMGA1 >sp|P17096|HMGA1_HUMAN High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3;>sp|P17096-3|HMGA1_HUMAN Isoform HMG-R of High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1;>tr|H7BYM6|H7BYM6_HUMAN High mobility group protein -0.24 0.63 -0.60 0.18 0.82 0.35 -1.27 -0.21 0.047803497 0.074383188 "aging;base-excision repair;biological regulation;biosynthetic process;cell aging;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;cellular senescence;chromatin assembly;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA repair;DNA unwinding involved in replication;heterochromatin formation;heterochromatin organization;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of chromatin silencing;negative regulation of gene expression;negative regulation of gene silencing;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;oncogene-induced senescence;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell aging;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular senescence;positive regulation of developmental process;positive regulation of gene expression;positive regulation of gene expression, epigenetic;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cell aging;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of cellular senescence;regulation of chromatin silencing;regulation of developmental process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of gene silencing;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to biotic stimulus;response to DNA damage stimulus;response to other organism;response to stimulus;response to stress;response to virus;RNA biosynthetic process;RNA metabolic process;senescence-associated heterochromatin focus formation;transcription, DNA-dependent" 5'-deoxyribose-5-phosphate lyase activity;AT DNA binding;binding;carbon-oxygen lyase activity;catalytic activity;DNA binding;DNA-(apurinic or apyrimidinic site) lyase activity;hormone receptor binding;ligand-dependent nuclear receptor transcription coactivator activity;lyase activity;nuclear hormone receptor binding;nucleic acid binding;nucleic acid binding transcription factor activity;peroxisome proliferator activated receptor binding;protein binding;protein binding transcription factor activity;receptor binding;retinoic acid receptor binding;retinoid X receptor binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity cell part;chromatin;chromosomal part;cytoplasmic part;cytosol;heterochromatin;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;senescence-associated heterochromatin focus;transcription factor complex 1.62E-36 4 5 2 33.6

Q6NUQ4-2;Q6NUQ4;H7C0H8;H7C008 Transmembrane protein 214 TMEM214 >sp|Q6NUQ4-2|TM214_HUMAN Isoform 2 of Transmembrane protein 214 OS=Homo sapiens GN=TMEM214;>sp|Q6NUQ4|TM214_HUMAN Transmembrane protein 214 OS=Homo sapiens GN=TMEM214 PE=1 SV=2 0.03 0.14 -0.43 -0.18 0.16 0.07 -0.55 -0.62 0.198531992 0.127233388 cell part;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;microtubule;organelle part;protein complex 1.54E-33 4 5 2 10.7

Q13547;Q5TEE2;F5GXM1 Histone deacetylase 1 HDAC1 >sp|Q13547|HDAC1_HUMAN Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1;>tr|Q5TEE2|Q5TEE2_HUMAN Histone deacetylase 1 (Fragment) OS=Homo sapiens GN=HDAC1 PE=2 SV=1;>tr|F5GXM1|F5GXM1_HUMAN Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=2 SV=1 0.07 0.66 -0.01 0.59 -0.39 -0.13 -1.06 0.13 0.950064303 0.69012392 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;biosynthetic process;blood coagulation;cell cycle;cell differentiation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;coagulation;covalent chromatin modification;developmental process;ectodermal placode formation;embryonic digit morphogenesis;embryonic morphogenesis;enzyme linked receptor protein signaling pathway;epidermal cell differentiation;eyelid development in camera-type eye;fungiform papilla formation;hair follicle placode formation;hemostasis;histone deacetylation;histone H3 deacetylation;histone H4 deacetylation;histone modification;interaction with host;interaction with symbiont;interspecies interaction between organisms;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic cell cycle;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;multicellular organismal process;multi-organism process;negative regulation by host of viral transcription;negative regulation of androgen receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of reproductive process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of viral transcription;nerve growth factor receptor signaling pathway;nitrogen compound metabolic process;Notch signaling pathway;nucleic acid metabolic process;nucleobase-containing compound metabolic process;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of receptor biosynthetic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;primary metabolic process;protein deacetylation;protein deacylation;protein metabolic process;protein modification process;regulation of androgen receptor signaling pathway;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of receptor biosynthetic process;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproductive process;virus-host interaction" "binding;catalytic activity;core promoter binding;deacetylase activity;DNA binding;histone deacetylase activity;histone deacetylase activity (H3-K14 specific);histone deacetylase activity (H3-K9 specific);hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;NAD-dependent histone deacetylase activity;NAD-dependent histone deacetylase activity (H3-K14 specific);NAD-dependent histone deacetylase activity (H3-K9 specific);NAD-dependent histone deacetylase activity (H4-K16 specific);NAD-dependent protein deacetylase activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein binding transcription factor activity;protein deacetylase activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription corepressor activity;RNA polymerase II transcription factor binding transcription factor activity;RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription;sequence-specific DNA binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding;transcription factor binding transcription factor activity;transcription regulatory region DNA binding" cell part;chromatin remodeling complex;chromosomal part;cytoplasmic part;cytosol;histone deacetylase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;protein complex;Sin3 complex;Sin3-type complex;transcriptional repressor complex Cell cycle;Chronic myeloid leukemia;Huntington's disease;Notch signaling pathway;Pathways in cancer 1.74E-44 3 6 2 14.7

P51812;F5GYC4;B4DG22;B7ZB17 Ribosomal protein S6 kinase alpha-3 RPS6KA3 >sp|P51812|KS6A3_HUMAN Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1;>tr|F5GYC4|F5GYC4_HUMAN Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=2 SV=1;>tr|B4DG22|B4DG22_HUMAN Ribosomal protein S6 kinase alpha-3 OS= 0.00 -0.04 0.09 -0.20 0.17 0.09 0.71 0.29 1.001705872 -0.354919134 "activation of immune response;activation of innate immune response;anatomical structure development;axon guidance;biological regulation;cell communication;cell cycle;cell surface receptor linked signaling pathway;cell-cell signaling;cellular process;cellular response to stimulus;cellular response to stress;central nervous system development;chemotaxis;defense response;developmental process;enzyme linked receptor protein signaling pathway;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;intracellular protein kinase cascade;intracellular signal transduction;locomotion;MAPKKK cascade;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nerve growth factor receptor signaling pathway;pattern recognition receptor signaling pathway;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of defense response;positive regulation of developmental process;positive regulation of gene expression;positive regulation of growth;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of developmental process;regulation of DNA-dependent transcription in response to stress;regulation of gene expression;regulation of growth;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of translation in response to stress;response to biotic stimulus;response to chemical stimulus;response to external stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;response to stress;signal transduction;signaling;skeletal system development;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;synaptic transmission;system development;taxis;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;TRIF-dependent toll-like receptor signaling pathway" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;caspase inhibitor activity;caspase regulator activity;catalytic activity;cation binding;cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;peptidase inhibitor activity;peptidase regulator activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;ribosome Long-term potentiation;MAPK signaling pathway;mTOR signaling pathway;Neurotrophin signaling pathway;Oocyte meiosis;Progesterone-mediated oocyte maturation 5.17E-20 4 6 2 8.4

P22528;E7ETD7 Cornifin-B SPRR1B >sp|P22528|SPR1B_HUMAN Cornifin-B OS=Homo sapiens GN=SPRR1B PE=1 SV=2;>tr|E7ETD7|E7ETD7_HUMAN Cornifin-B OS=Homo sapiens GN=SPRR1B PE=2 SV=1 0.85 1.44 -1.77 -0.98 0.93 2.19 0.88 0.85 0.689977186 -1.329228446 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity" cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 2.27E-99 2 6 2 87.6

F5H8J4;F5H564;Q504Z1;O43432;O43432-3;Q5SWD1 Eukaryotic translation initiation factor 4 gamma 3EIF4G3 >tr|F5H8J4|F5H8J4_HUMAN Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=2 SV=1;>tr|F5H564|F5H564_HUMAN Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=2 SV=1;>tr|Q504Z1|Q504Z1_HUMAN EIF4G3 pro 0.21 -0.06 0.11 -0.06 0.12 0.05 0.46 -0.09 0.241586384 -0.084769623 biological regulation;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;gamete generation;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;male gamete generation;meiotic prophase I;metabolic process;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;prophase;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of translation;regulation of translational initiation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA metabolic process;signal transduction;spermatogenesis;viral reproductive process;virus-host interaction "binding;DNA binding;nucleic acid binding;RNA binding;RNA cap binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex RNA transport;Viral myocarditis 5.21E-33 6 8 2 8.2

Q9Y6C9;F5H3Y2 Mitochondrial carrier homolog 2 MTCH2 >sp|Q9Y6C9|MTCH2_HUMAN Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 -0.43 0.69 -0.03 0.90 0.21 0.90 -1.39 0.56 0.129700967 0.214351404 establishment of localization;transport cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part 1.44E-46 2 8 2 37

P11908;P11908-2;B1ALA9;B4DNL6;A6NMS2;D3YTJ7;H7C540 Ribose-phosphate pyrophosphokinase 2;Ribose-phosphate pyrophosphokinase PRPS2;PRPS1>sp|P11908|PRPS2_HUMAN Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2;>sp|P11908-2|PRPS2_HUMAN Isoform 2 of Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2;>tr|B1ALA9|B1ALA9_HUMAN Ribose-phosphate pyrophosphokinase 1 0.23 0.00 -0.15 -0.07 -0.32 -0.71 -0.05 -0.41 0.994887814 0.375071955 5-phosphoribose 1-diphosphate biosynthetic process;5-phosphoribose 1-diphosphate metabolic process;alcohol biosynthetic process;alcohol metabolic process;AMP biosynthetic process;AMP metabolic process;anatomical structure morphogenesis;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;developmental process;D-ribose biosynthetic process;D-ribose metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organ morphogenesis;organ regeneration;pentose biosynthetic process;pentose metabolic process;primary metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regeneration;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;ribose phosphate biosynthetic process;ribose phosphate metabolic process;small molecule biosynthetic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;AMP binding;ATP binding;binding;carbohydrate binding;catalytic activity;cation binding;diphosphotransferase activity;GDP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;identical protein binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;ribose phosphate diphosphokinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" macromolecular complex;protein complex;ribose phosphate diphosphokinase complex Pentose phosphate pathway;Purine metabolism 8.10E-43 7 8 2 29.6

P20290 Transcription factor BTF3 BTF3 >sp|P20290|BTF3_HUMAN Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1 0.17 0.00 0.12 -0.07 -0.05 -0.57 0.25 -0.27 0.497833861 0.215536588 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;in utero embryonic development;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.14E-26 1 9 2 60.2

F8VYE8;P36873;P36873-2;F8W0W8;F8VR82;B4DNE3;F8W0V8;F8WE71 Serine/threonine-protein phosphatase;Serine/threonine-protein phosphatase PP1-gamma catalytic subunit PPP1CC >tr|F8VYE8|F8VYE8_HUMAN Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=2 SV=1;>sp|P36873|PP1G_HUMAN Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Homo sapiens GN=PPP1CC PE=1 SV=1;>sp|P36873-2|PP1G_HUMAN Isoform Gamm 0.07 0.27 0.04 0.29 0.50 0.18 -0.45 0.07 0.170459865 0.095279572 acylglycerol catabolic process;acylglycerol metabolic process;anaphase;biological regulation;carbohydrate metabolic process;catabolic process;cell cycle phase;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular carbohydrate metabolic process;cellular catabolic process;cellular glucan metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;dephosphorylation;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;generation of precursor metabolites and energy;glucan metabolic process;glycerol ether catabolic process;glycerol ether metabolic process;glycerolipid catabolic process;glycerolipid metabolic process;glycogen metabolic process;lipid catabolic process;lipid metabolic process;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;neutral lipid catabolic process;neutral lipid metabolic process;organic ether metabolic process;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;polysaccharide metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of intracellular transport;regulation of localization;regulation of nucleocytoplasmic transport;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transport;response to stimulus;signal transduction;small molecule metabolic process;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;triglyceride catabolic process;triglyceride metabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity" cell division site part;cell part;chromosomal part;cleavage furrow;condensed chromosome kinetochore;cytoplasmic part;cytosol;histone methyltransferase complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane-bounded organelle;methyltransferase complex;midbody;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;MLL5-L complex;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex;protein serine/threonine phosphatase complex;PTW/PP1 phosphatase complex Focal adhesion;Insulin signaling pathway;Long-term potentiation;Meiosis - yeast;Oocyte meiosis;Regulation of actin cytoskeleton;Vascular smooth muscle contraction 8.51E-89 8 9 2 34.2

Q9NUU7;I3L0H8;H3BTB3;B4DRZ7;I3L352;J3QRH0;H3BSL8;H3BP36;H3BP50;H0YD26 ATP-dependent RNA helicase DDX19A DDX19A >sp|Q9NUU7|DD19A_HUMAN ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1;>tr|I3L0H8|I3L0H8_HUMAN ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=2 SV=1;>tr|H3BTB3|H3BTB3_HUMAN ATP-dependent RNA helicase DDX19A OS=Homo sap 0.13 -0.03 0.00 -0.06 0.04 -0.22 0.26 -0.25 0.152871952 0.053381167 biological regulation;establishment of localization;establishment of protein localization;establishment of RNA localization;induction of apoptosis;induction of programmed cell death;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;response to zinc ion;RNA transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding" cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear pore;organelle membrane;organelle part;pore complex;protein complex 6.25E-90 10 10 2 23.6

F8VY35;B3KNT8;F5H4R6;H0YIV4;P55209;F8W020;F8W118;F8VV59;F8W0J6;H0YH88;H0YHC3;B7Z9C2;F8VRJ2;F8VXI6;F8VUX1;F8VVB5;B3KV44 Nucleosome assembly protein 1-like 1 NAP1L1 >tr|F8VY35|F8VY35_HUMAN Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1;>tr|B3KNT8|B3KNT8_HUMAN Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=2 SV=1;>tr|F5H4R6|F5H4R6_HUMAN Nucleosome assembly protein 0.25 0.05 0.01 0.01 0.09 -0.13 0.15 -0.30 0.427299653 0.124188486 biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;DNA metabolic process;DNA replication;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;pigment granule;vesicle 2.12E-198 17 11 2 45.5

Q6UWP8-2;K7ESC4 >sp|Q6UWP8-2|SBSN_HUMAN Isoform 2 of Suprabasin OS=Homo sapiens GN=SBSN -0.65 0.79 0.02 0.46 1.89 2.51 0.14 -0.48 0.461007327 -0.861558417 1.07E-79 2 13 2 57.5

E9PK01;P29692;P29692-2;E9PRY8;E9PQ49;E9PI39;P29692-4;E9PPR1;E9PL12;E9PQZ1;E9PMW7;E9PIZ1;H0YCK7;E9PK06;E9PK72;E9PKK3;H0YE58;H0YE72;E9PNW6;E9PQC9;E9PJD0 Elongation factor 1-delta EEF1D >tr|E9PK01|E9PK01_HUMAN Elongation factor 1-delta (Fragment) OS=Homo sapiens GN=EEF1D PE=2 SV=1;>sp|P29692|EF1D_HUMAN Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5;>sp|P29692-2|EF1D_HUMAN Isoform 2 of Elongation factor 1-delta OS=Homo sapien 0.15 0.05 0.01 -0.07 0.09 -0.16 -0.17 -0.20 0.749323167 0.143400886 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;translational elongation" "binding;DNA binding;molecular transducer activity;nucleic acid binding;RNA binding;signal transducer activity;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex 1.36E-278 21 14 2 53.3

P68133;P68032;P63267;P62736;Q5T8M8;A6NL76;P63267-2;C9JFL5;F6UVQ4;F6QUT6;F8WB63;B8ZZJ2"Actin, alpha skeletal muscle;Actin, alpha cardiac muscle 1;Actin, gamma-enteric smooth muscle;Actin, aortic smooth muscle" ACTA1;ACTC1;ACTG2;ACTA2 ">sp|P68133|ACTS_HUMAN Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1;>sp|P68032|ACTC_HUMAN Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1;>sp|P63267|ACTH_HUMAN Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 P" -0.13 0.46 -0.23 0.47 -0.18 0.21 -0.06 0.57 0.008940299

0.006933041 actin cytoskeleton organization;actin filament organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;actomyosin structure organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptosis;biological regulation;cardiac muscle contraction;cardiac muscle tissue morphogenesis;cardiac myofibril assembly;cell death;cell development;cell growth;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;circulatory system process;cytoskeleton organization;death;developmental process;glomerular mesangial cell development;growth;heart contraction;heart process;mesangial cell development;multicellular organismal process;multi-organism process;muscle adaptation;muscle cell development;muscle contraction;muscle fiber development;muscle filament sliding;muscle system process;muscle tissue morphogenesis;myofibril assembly;organelle organization;programmed cell death;regulation of anatomical structure size;regulation of biological quality;regulation of blood pressure;regulation of blood vessel size;regulation of tube size;response to abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to inorganic substance;response to lithium ion;response to mechanical stimulus;response to metal ion;response to organic substance;response to other organism;response to steroid hormone stimulus;response to stimulus;response to virus;skeletal muscle adaptation;skeletal muscle fiber adaptation;skeletal muscle fiber development;skeletal muscle thin filament assembly;smooth muscle contraction;striated muscle adaptation;striated muscle cell development;striated muscle contraction;system process;tissue morphogenesis;vascular process in circulatory system;vascular smooth muscle contraction;vasoconstriction "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;myosin binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" "actin cytoskeleton;actin filament;actin filament bundle;actomyosin;actomyosin, actin part;cell part;cell periphery;contractile fiber;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;I band;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle part;protein complex;smooth muscle contractile fiber;stress fiber;striated muscle thin filament;vesicle" Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM);Vascular smooth muscle contraction 0 12 22 2 39.5

P13928;Q5T2P8;B4DKI1;Q5VTM3;F5GX16;Q5T2P7;B4DTC9;F5H7X5 Annexin A8;Annexin A8-like protein 1;Annexin ANXA8;ANXA8L1;ANXA8L2 >sp|P13928|ANXA8_HUMAN Annexin A8 OS=Homo sapiens GN=ANXA8 PE=1 SV=3;>sp|Q5T2P8|AXA81_HUMAN Annexin A8-like protein 1 OS=Homo sapiens GN=ANXA8L1 PE=1 SV=1;>tr|B4DKI1|B4DKI1_HUMAN Annexin OS=Homo sapiens GN=ANXA8L1 PE=2 SV=1;>tr|Q5VTM3|Q5VTM3_HUMAN Annexin 0.08 0.09 -0.28 -0.23 -0.98 -0.15 0.57 0.37 0.034386714 -0.037349191 biological regulation;blood coagulation;coagulation;hemostasis;multicellular organismal process;regulation of biological quality;regulation of body fluid levels binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;ion binding;lipid binding;metal ion binding;phospholipid binding 0 8 23 2 70.3

I3L2B0;I3L0P4 CLUH >tr|I3L2B0|I3L2B0_HUMAN Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=2 SV=1 0.33 0.04 0.09 -0.12 -0.75 -0.71 0.06 -0.42 1.079873145 0.538509072 cell part;cytoplasm;intracellular part 2.03E-180 2 23 2 38.9

P31946;Q4VY20;Q4VY19 "14-3-3 protein beta/alpha;14-3-3 protein beta/alpha, N-terminally processed" YWHAB >sp|P31946|1433B_HUMAN 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3 -0.09 0.00 -0.06 0.01 0.02 0.03 0.04 0.15 1.050994373 -0.096194885 "activation of MAPKK activity;activation of protein kinase activity;axon guidance;biological regulation;cell surface receptor linked signaling pathway;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemotaxis;cytoplasmic sequestering of protein;defense response;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;fibroblast growth factor receptor signaling pathway;gene expression;hippo signaling cascade;immune response;immune system process;innate immune response;insulin receptor signaling pathway;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;MAPKKK cascade;membrane organization;metabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of dephosphorylation;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of protein dephosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein transport;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;negative regulation of transport;nerve growth factor receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein metabolic process;protein modification process;protein oligomerization;protein phosphorylation;protein targeting;protein transport;Ras protein signal transduction;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of establishment of protein localization;regulation of gene expression;regulation of kinase activity;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein transport;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;RNA metabolic process;signal transduction;small GTPase mediated signal transduction;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport" protein binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;nuclear part;nucleoplasm part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;pigment granule;protein complex;transcriptional repressor complex;vesicle;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis 0 3 23 2 68.7

P09493-3;P09493-4;P09493-10;P09493-9;P09493;Q6ZN40;H0YL52;P09493-8;H0YKX5;P09493-7;P09493-6;H0YKP3;H0YL80;H0YL42;H0YK20;H0YKZ6 Tropomyosin alpha-1 chain TPM1 >sp|P09493-3|TPM1_HUMAN Isoform 3 of Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1;>sp|P09493-4|TPM1_HUMAN Isoform 4 of Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1;>sp|P09493-10|TPM1_HUMAN Isoform 10 of Tropomyosin alpha-1 chain OS=Homo sapiens G -0.73 -0.12 -0.97 -0.16 -0.11 1.64 0.94 2.34 1.243277467 -1.696059255 actin cytoskeleton organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;actomyosin structure organization;anatomical structure morphogenesis;biological regulation;cardiac muscle contraction;cardiac muscle tissue morphogenesis;cell projection organization;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;chordate embryonic development;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;in utero embryonic development;multicellular organismal process;muscle contraction;muscle filament sliding;muscle system process;muscle tissue morphogenesis;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;organelle organization;positive regulation of actin filament bundle assembly;positive regulation of ATPase activity;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of heart rate by epinephrine;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of organelle organization;positive regulation of stress fiber assembly;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of ATPase activity;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of heart contraction;regulation of heart rate;regulation of heart rate by chemical signal;regulation of hydrolase activity;regulation of localization;regulation of locomotion;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of stress fiber assembly;regulation of system process;response to chemical stimulus;response to inorganic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;response to wounding;ruffle organization;sarcomere organization;striated muscle contraction;system process;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis;wound healing actin binding;binding;cytoskeletal protein binding;protein binding;structural constituent of cytoskeleton;structural constituent of muscle;structural molecule activity actin cytoskeleton;actin filament bundle;actomyosin;bleb;cell part;cell projection;cell projection membrane;cell projection part;contractile fiber;contractile fiber part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;muscle thin filament tropomyosin;myofibril;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;protein complex;ruffle membrane;stress fiber Cardiac muscle contraction;Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM) 3.77E-249 16 27 2 56.7

Q14157;Q14157-5;Q14157-3;F8W726;Q5VU77;Q5VU78;Q5VU81;Q5VU80;Q5VU79;H0Y5H6;H7C2T8 Ubiquitin-associated protein 2-likeUBAP2L >sp|Q14157|UBP2L_HUMAN Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L PE=1 SV=2;>sp|Q14157-5|UBP2L_HUMAN Isoform 5 of Ubiquitin-associated protein 2-like OS=Homo sapiens GN=UBAP2L;>sp|Q14157-3|UBP2L_HUMAN Isoform 3 of Ubiquitin-associated pr 0.06 -0.01 0.10 -0.05 0.17 -0.01 0.03 -0.22 0.119655177 0.029568682 binding of sperm to zona pellucida;cell recognition;cell-cell recognition;cellular process;cellular process involved in reproduction;reproductive process;sperm-egg recognition 0 11 27 2 38.8

Q16851-2;C9JNZ1;C9JVG3;C9JWG0;C9JUW1;C9JTZ5;F2Z3H1;C9J3M0;F2Z3P4;F8WC70 >sp|Q16851-2|UGPA_HUMAN Isoform 2 of UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 0.30 0.03 0.05 -0.16 0.24 0.10 0.45 -0.02 0.394388933 -0.135461095 "catalytic activity;nucleotidyltransferase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" 0 10 30 2 67.4

B4DXX7;O15523;B4E132;C9J081 ATP-dependent RNA helicase DDX3Y DDX3Y >tr|B4DXX7|B4DXX7_HUMAN Uncharacterized protein OS=Homo sapiens GN=DDX3Y PE=2 SV=1;>sp|O15523|DDX3Y_HUMAN ATP-dependent RNA helicase DDX3Y OS=Homo sapiens GN=DDX3Y PE=1 SV=2;>tr|B4E132|B4E132_HUMAN Uncharacterized protein OS=Homo sapiens GN=DDX3Y PE=2 SV=1 0.33 0.49 0.35 0.39 -2.78 -2.36 -0.44 0.89 0.781150536 1.565270729 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle RIG-I-like receptor signaling pathway 0 4 31 2 48.7

O60506;O60506-2;F6UXX1 Heterogeneous nuclear ribonucleoprotein Q SYNCRIP >sp|O60506|HNRPQ_HUMAN Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2;>sp|O60506-2|HNRPQ_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP -0.13 0.32 -0.05 0.35 -0.20 -0.18 -0.62 -0.19 1.079094091 0.417450146 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;CRD-mediated mRNA stabilization;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of translation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization;viral reproductive process;virus-host interaction" binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;RNA binding;single-stranded RNA bindingcatalytic step 2 spliceosome;cell part;CRD-mediated mRNA stability complex;cytoplasm;cytoplasmic part;endoplasmic reticulum;histone pre-mRNA 3'end processing complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex 0 3 33 2 54.7

P68371;Q3ZCM7;M0R2D3;M0QY85;M0R0X0;M0QY37;M0QX14;M0QZL7 Tubulin beta-4B chain TUBB4B >sp|P68371|TBB4B_HUMAN Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 0.23 0.03 -0.42 -0.05 -0.15 -0.02 0.22 0.01 0.155551877 -0.066842935 biological regulation;cell cycle process;cell killing;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;defense response;G2/M transition of mitotic cell cycle;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;leukocyte mediated cytotoxicity;leukocyte mediated immunity;lymphocyte mediated immunity;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to stimulus;response to stress "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;MHC class I protein binding;MHC protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity;unfolded protein binding" cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 8 33 2 76.6

P63261;I3L3I0;I3L1U9;I3L4N8;K7EM38;I3L3R2;J3KT65"Actin, cytoplasmic 2;Actin, cytoplasmic 2, N-terminally processed" ACTG1 ">sp|P63261|ACTG_HUMAN Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1;>tr|I3L3I0|I3L3I0_HUMAN Actin, cytoplasmic 2, N-terminally processed (Fragment) OS=Homo sapiens GN=ACTG1 PE=2 SV=1;>tr|I3L1U9|I3L1U9_HUMAN Actin, cytoplasmic 2, N-terminally proc" -0.04 0.39 -0.81 0.50 -0.75 0.13 -0.01 0.37 0.065753108 0.073792928 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;adherens junction organization;axon guidance;cell junction assembly;cell junction organization;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;chemotaxis;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;locomotion;membrane organization;organelle organization;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;sarcomere organization;taxis adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity cell part;contractile fiber;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;myofibril;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Dilated cardiomyopathy;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Phagosome;Phototransduction - fly;Regulation of actin cytoskeleton;Shigellosis;Tight junction;Vibrio cholerae infection;Viral myocarditis 0 7 37 2 82.1

P02545-2;Q5TCI8 LMNA >sp|P02545-2|LMNA_HUMAN Isoform C of Prelamin-A/C OS=Homo sapiens GN=LMNA;>tr|Q5TCI8|Q5TCI8_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=2 SV=1-0.25 0.30 0.19 0.45 0.12 0.02 -1.62 -0.33 0.6169512 0.624313527 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex 0 2 67 2 83

O75369-8 >sp|O75369-8|FLNB_HUMAN Isoform 8 of Filamin-B OS=Homo sapiens GN=FLNB 0.13 0.19 -0.11 -0.06 -0.40 0.23 0.23 0.35 0.12873837 -0.066394312 0 1 196 2 81.6

Q9NRN7;B4DDW7;E9PNF3;E9PLW6 L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase AASDHPPT >sp|Q9NRN7|ADPPT_HUMAN L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase OS=Homo sapiens GN=AASDHPPT PE=1 SV=2 0.35 -0.01 0.19 -0.01 -0.29 -0.67 0.20 -0.63 0.930854962 0.478969375 amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;fatty acid biosynthetic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;pantothenate metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "binding;catalytic activity;cation binding;holo-[acyl-carrier-protein] synthase activity;ion binding;magnesium ion binding;metal ion binding;phosphotransferase activity, for other substituted phosphate groups;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part Pantothenate and CoA biosynthesis 1.10E-14 4 3 3 12.9

P28288-2;F5GYC1;P28288;E7EUE1 ATP-binding cassette sub-family D member 3 ABCD3 >sp|P28288-2|ABCD3_HUMAN Isoform 2 of ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3;>tr|F5GYC1|F5GYC1_HUMAN ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=2 SV=1;>sp|P28288|ABCD3_HUMAN ATP-binding cassette sub- 0.03 0.30 -0.46 -0.04 0.45 0.59 -0.63 0.24 0.24871069 -0.20374537 ATP catabolic process;ATP metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;heterocycle catabolic process;heterocycle metabolic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;peroxisome organization;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule catabolic process;small molecule metabolic process;transmembrane transport;transport;very long-chain fatty acid catabolic process;very long-chain fatty acid metabolic process "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;cytosol;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part ABC transporters;Peroxisome 2.53E-10 4 3 3 6.7

P52594-2;P52594-3;P52594;P52594-4;C9J2I0;B8ZZY2 Arf-GAP domain and FG repeat-containing protein 1 AGFG1 >sp|P52594-2|AGFG1_HUMAN Isoform 2 of Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens GN=AGFG1;>sp|P52594-3|AGFG1_HUMAN Isoform 3 of Arf-GAP domain and FG repeat-containing protein 1 OS=Homo sapiens GN=AGFG1;>sp|P52594|AGFG1_HUMAN Arf-GAP 0.08 0.11 -0.11 -0.21 0.08 -0.11 0.12 0.29 0.449378688 -0.123963516 biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;establishment of localization;establishment of localization in cell;establishment of RNA localization;gamete generation;intracellular transport;male gamete generation;mRNA export from nucleus;mRNA transport;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;nuclear export;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;regulation of ARF GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;reproductive process;RNA export from nucleus;RNA transport;spermatogenesis;transport ARF GTPase activator activity;binding;cation binding;DNA binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase regulator activity;RNA binding;small GTPase regulator activity;transition metal ion binding;zinc ion binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nuclear part;nuclear pore;organelle;organelle part;pore complex;protein complex;vesicle 2.19E-11 6 3 3 14

Q92625;B4DQW8 Ankyrin repeat and SAM domain-containing protein 1A ANKS1A >sp|Q92625|ANS1A_HUMAN Ankyrin repeat and SAM domain-containing protein 1A OS=Homo sapiens GN=ANKS1A PE=1 SV=4 0.14 0.06 0.47 -0.04 0.04 0.14 0.30 -0.06 0.130476533 0.049083238 biological regulation;cell maturation;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component movement;cellular developmental process;cellular process;cellular response to stimulus;developmental maturation;developmental process;enzyme linked receptor protein signaling pathway;ephrin receptor signaling pathway;locomotion;neuron maturation;neuron remodeling;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;substrate-dependent cell migration;transmembrane receptor protein tyrosine kinase signaling pathway cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;neuron projection;nucleus;organelle 2.53E-07 2 3 3 3.3

O75915;F8WF90;C9JQU6;F8WF33 PRA1 family protein 3 ARL6IP5 >sp|O75915|PRAF3_HUMAN PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=1 SV=1;>tr|F8WF90|F8WF90_HUMAN PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=2 SV=1;>tr|C9JQU6|C9JQU6_HUMAN PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=2 SV=1;>tr|F8WF -0.51 -0.15 -0.29 -0.14 0.71 0.18 -0.25 0.33 0.999439914 -0.513026766 acidic amino acid transport;amine transport;amino acid transport;anion transport;biological regulation;carboxylic acid transport;establishment of localization;ion transport;L-glutamate transport;negative regulation of biological process;negative regulation of transport;nitrogen compound transport;organic acid transport;organic anion transport;organic substance transport;regulation of biological process;regulation of localization;regulation of transport;transport cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 8.65E-82 4 3 3 20.7

G3V2S6;Q9Y5K8;H0YJ55;H0YJS0;G3V559;G3V5S7;G3V3T8;G3V2V6;H0YJH8 V-type proton ATPase subunit D ATP6V1D >tr|G3V2S6|G3V2S6_HUMAN V-type proton ATPase subunit D OS=Homo sapiens GN=ATP6V1D PE=2 SV=1;>sp|Q9Y5K8|VATD_HUMAN V-type proton ATPase subunit D OS=Homo sapiens GN=ATP6V1D PE=1 SV=1;>tr|H0YJ55|H0YJ55_HUMAN V-type proton ATPase subunit D (Fragment) OS=Homo -0.20 0.33 -0.57 0.45 -0.46 0.48 -0.37 0.14 0.059288113 0.056725003 biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organelle organization;phagosome maturation;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;pyrophosphatase activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane part;organelle part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting V-type ATPase complex;vacuolar part;vacuolar proton-transporting V-type ATPase complex Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection 3.70E-17 9 3 3 19.3

F8VR84;F8VQQ3;Q9HB07;H3BPH3 "UPF0160 protein MYG1, mitochondrial" C12orf10 ">tr|F8VR84|F8VR84_HUMAN UPF0160 protein MYG1, mitochondrial OS=Homo sapiens GN=C12orf10 PE=2 SV=1;>tr|F8VQQ3|F8VQQ3_HUMAN UPF0160 protein MYG1, mitochondrial OS=Homo sapiens GN=C12orf10 PE=2 SV=1;>sp|Q9HB07|MYG1_HUMAN UPF0160 protein MYG1, mitochondrial OS" -0.07 0.00 0.17 0.03 0.06 -0.20 -1.23 -0.54 0.764809766 0.509821232 pigmentation cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle 9.15E-23 4 3 3 15

Q5T6V5 UPF0553 protein C9orf64 C9orf64 >sp|Q5T6V5|CI064_HUMAN UPF0553 protein C9orf64 OS=Homo sapiens GN=C9orf64 PE=1 SV=1 0.21 -0.02 -0.01 0.04 -0.20 -0.59 0.19 -0.66 0.775880767 0.368909168 8.34E-09 1 3 3 8.5

C9J0A7;Q9UQN3;Q9UQN3-2 Charged multivesicular body protein 2b CHMP2B >tr|C9J0A7|C9J0A7_HUMAN Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B PE=2 SV=1;>sp|Q9UQN3|CHM2B_HUMAN Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B PE=1 SV=1;>sp|Q9UQN3-2|CHM2B_HUMAN Isoform 2 of Charged multivesicula 0.09 -0.09 -0.01 0.07 -0.19 -0.21 0.24 0.03 0.139880979 0.043906524 cell death;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;death;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;membrane organization;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;cytosol;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome membrane;membrane;membrane-bounded organelle;mitochondrion;nucleus;organelle;organelle membrane;organelle part Endocytosis 8.90E-19 3 3 3 16.9

Q9Y3Y2-4;Q9Y3Y2;Q9Y3Y2-3;Q5T7Y7 Chromatin target of PRMT1 protein CHTOP >sp|Q9Y3Y2-4|CHTOP_HUMAN Isoform 3 of Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP;>sp|Q9Y3Y2|CHTOP_HUMAN Chromatin target of PRMT1 protein OS=Homo sapiens GN=CHTOP PE=1 SV=2;>sp|Q9Y3Y2-3|CHTOP_HUMAN Isoform 2 of Chromatin target of PRMT1 pro -0.39 0.80 0.39 0.97 -0.25 0.05 -1.47 -0.04 0.796655789 0.866713115 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;nucleic acid binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part 1.56E-100 4 3 3 20.8

Q12860-2;Q12860;H0YIJ1;Q12860-3 Contactin-1 CNTN1 >sp|Q12860-2|CNTN1_HUMAN Isoform 2 of Contactin-1 OS=Homo sapiens GN=CNTN1;>sp|Q12860|CNTN1_HUMAN Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1 -0.80 -0.02 0.39 1.02 -1.04 -0.28 -0.54 -0.56 0.78273512 0.755017822 anatomical structure development;axon guidance;biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cerebellum development;chemotaxis;developmental process;locomotion;Notch signaling pathway;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of gene expression;positive regulation of ion transport;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of neuron projection development;positive regulation of sodium ion transport;positive regulation of transport;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of ion transport;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of sodium ion transport;regulation of transport;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis binding;carbohydrate binding anchored to membrane;cell part;intrinsic to membrane;membrane;membrane part;plasma membrane Cell adhesion molecules (CAMs) 7.14E-08 4 3 3 3

Q96JB2;Q96JB2-2 Conserved oligomeric Golgi complex subunit 3 COG3 >sp|Q96JB2|COG3_HUMAN Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 PE=1 SV=3;>sp|Q96JB2-2|COG3_HUMAN Isoform 2 of Conserved oligomeric Golgi complex subunit 3 OS=Homo sapiens GN=COG3 0.19 0.24 -0.07 0.11 -0.06 -0.06 -0.23 0.03 0.97651522 0.196977282 "biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;localization;macromolecule glycosylation;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein glycosylation;protein localization;protein localization to organelle;protein metabolic process;protein modification process;protein stabilization;protein transport;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle-mediated transport" protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cis-Golgi network;cytoplasmic part;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi transport complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;plasma membrane;protein complex 3.27E-12 2 3 3 4.8

Q96HY6-2;Q96HY6 DDRGK domain-containing protein 1 DDRGK1 >sp|Q96HY6-2|DDRGK_HUMAN Isoform 2 of DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1;>sp|Q96HY6|DDRGK_HUMAN DDRGK domain-containing protein 1 OS=Homo sapiens GN=DDRGK1 PE=1 SV=2 0.04 0.02 0.18 0.04 0.34 -0.01 -0.36 -0.33 0.39094667 0.160183134 cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle 1.05E-23 2 3 3 14.7

Q96EY1-2;Q96EY1;E7ES32 "DnaJ homolog subfamily A member 3, mitochondrial" DNAJA3 ">sp|Q96EY1-2|DNJA3_HUMAN Isoform 2 of DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3;>sp|Q96EY1|DNJA3_HUMAN DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3 PE=1 SV=2;>tr|E7ES32|E7ES32_HUMAN DnaJ homolo" -0.06 0.56 -0.01 0.29 0.00 -0.02 -0.99 -0.26 0.80069195 0.511397752 "activation of caspase activity;activation-induced cell death of T cells;aging;apoptosis;biological regulation;biosynthetic process;cell activation;cell aging;cell death;cell differentiation;cellular biosynthetic process;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to stimulus;death;developmental process;DNA metabolic process;DNA replication;DNA-dependent DNA replication;embryo development;immune system process;intracellular signal transduction;leukocyte activation;leukocyte apoptosis;leukocyte differentiation;localization;lymphocyte activation;lymphocyte apoptosis;lymphocyte differentiation;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial DNA metabolic process;mitochondrial DNA replication;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine-mediated signaling pathway;negative regulation of gene expression;negative regulation of hydrolase activity;negative regulation of I-kappaB kinase/NF-kappaB cascade;negative regulation of interferon-gamma-mediated signaling pathway;negative regulation of intracellular protein kinase cascade;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of response to cytokine stimulus;negative regulation of response to interferon-gamma;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;neuromuscular junction development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of hydrolase activity;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of leukocyte proliferation;positive regulation of lymphocyte activation;positive regulation of lymphocyte proliferation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of mononuclear cell proliferation;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of T cell activation;positive regulation of T cell proliferation;postsynaptic membrane organization;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein folding;protein localization;protein localization in membrane;protein metabolic process;protein stabilization;receptor clustering;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-gamma-mediated signaling pathway;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein ubiquitination;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of T cell activation;regulation of T cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;response to abiotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to heat;response to interferon-gamma;response to organic substance;response to stimulus;response to stress;response to temperature stimulus;signal transduction;skeletal muscle nicotinic acetylcholine receptor clustering;small GTPase mediated signal transduction;synapse organization;T cell activation;T cell apoptosis;T cell differentiation;T cell differentiation in thymus" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cation binding;cytokine receptor binding;enzyme regulator activity;GTPase regulator activity;interferon-gamma receptor binding;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;small GTPase regulator activity cell junction;cell part;cytoplasmic part;cytosol;extrinsic to membrane;extrinsic to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial nucleoid;mitochondrial part;neuromuscular junction;non-membrane-bounded organelle;nucleoid;nucleus;organelle;organelle lumen;organelle part;plasma membrane part;postsynaptic membrane;synapse;synapse part;synaptic membrane 1.68E-30 3 3 3 9.3

J3QRI9;J3QKW7;A8MZF9;P55039;J3QR71;J3QL90;J3KRL5;J3QKV7 Developmentally-regulated GTP-binding protein 2 DRG2 >tr|J3QRI9|J3QRI9_HUMAN Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens GN=DRG2 PE=4 SV=1;>tr|J3QKW7|J3QKW7_HUMAN Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens GN=DRG2 PE=4 SV=1;>tr|A8MZF9|A8MZF9_HUMAN Developmentally-regu 0.11 -0.13 -0.32 -0.02 -0.06 0.02 0.47 -0.19 0.355670915 -0.15029147 biological regulation;cellular process;cellular response to stimulus;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 1.47E-28 8 3 3 25.6

Q99848;H7C2Q8 Probable rRNA-processing protein EBP2 EBNA1BP2 ">sp|Q99848|EBP2_HUMAN Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2;>tr|H7C2Q8|H7C2Q8_HUMAN EBNA1 binding protein 2, isoform CRA_d OS=Homo sapiens GN=EBNA1BP2 PE=2 SV=1" -0.18 1.26 0.35 1.16 -0.71 -0.08 -1.40 -0.39 1.210384866 1.293026583 cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 6.09E-08 2 3 3 10.5

P42126-2;P42126;Q96DC0;H3BS70 "Enoyl-CoA delta isomerase 1, mitochondrial" ECI1;DCI ">sp|P42126-2|ECI1_HUMAN Isoform 2 of Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1;>sp|P42126|ECI1_HUMAN Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1;>tr|Q96DC0|Q96DC0_HUMAN DCI protein OS=Homo sapiens G" -0.33 -0.54 0.46 0.29 -0.32 -0.63 0.01 -0.55 0.510804039 0.340711484 carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "catalytic activity;dodecenoyl-CoA delta-isomerase activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, transposing C=C bonds;isomerase activity" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part Fatty acid metabolism 6.40E-21 4 3 3 12.6

O94919 Endonuclease domain-containing 1 protein ENDOD1>sp|O94919|ENDD1_HUMAN Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2 0.03 -0.06 0.44 0.12 0.48 0.90 0.29 0.61 1.100794927 -0.440863981 cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process "binding;catalytic activity;cation binding;endonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nuclease activity;nucleic acid binding" extracellular region Apoptosis 1.47E-18 1 3 3 7.6

Q5NDL2;B4E243;A8K2U1;Q5NDL2-3;C9J4G5;C9JQM7;F5H225;Q5NDL2-2 EGF domain-specific O-linked N-acetylglucosamine transferase EOGT >sp|Q5NDL2|EOGT_HUMAN EGF domain-specific O-linked N-acetylglucosamine transferase OS=Homo sapiens GN=EOGT PE=2 SV=1;>tr|B4E243|B4E243_HUMAN EGF domain-specific O-linked N-acetylglucosamine transferase OS=Homo sapiens GN=EOGT PE=2 SV=1;>tr|A8K2U1|A8K2U1_HU 0.06 -0.25 0.46 -0.55 0.43 -0.34 0.82 0.46 0.525593473 -0.409030654 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein O-linked glycosylation "acetylglucosaminyltransferase activity;catalytic activity;protein N-acetylglucosaminyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;UDP-glycosyltransferase activity" cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part 8.14E-11 8 3 3 6.6

P13726;P13726-2 Tissue factor F3 >sp|P13726|TF_HUMAN Tissue factor OS=Homo sapiens GN=F3 PE=1 SV=10.77 0.59 -0.96 -0.30 -0.84 -0.20 -0.18 0.59 0.132751606 0.183953341 "activation of blood coagulation via clotting cascade;activation of caspase activity;activation of plasma proteins involved in acute inflammatory response;biological regulation;blood coagulation, extrinsic pathway;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;positive regulation of angiogenesis;positive regulation of behavior;positive regulation of biological process;positive regulation of blood coagulation;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of coagulation;positive regulation of developmental process;positive regulation of endothelial cell proliferation;positive regulation of epithelial cell proliferation;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of locomotion;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of peptidase activity;positive regulation of platelet-derived growth factor receptor signaling pathway;positive regulation of positive chemotaxis;positive regulation of protein kinase B signaling cascade;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein activation cascade;protein maturation;protein metabolic process;protein processing;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of blood coagulation;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of chemotaxis;regulation of coagulation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of peptidase activity;regulation of platelet-derived growth factor receptor signaling pathway;regulation of positive chemotaxis;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of wound healing;response to stimulus" binding;cell surface binding;lipid binding;phospholipid binding cell part;extracellular matrix;extracellular region part;extracellular space;integral to membrane;intrinsic to external side of plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Complement and coagulation cascades 5.37E-31 2 3 3 16.9

B4DT23;Q8NCA5-2;Q8NCA5;E9PH82 Protein FAM98A FAM98A >tr|B4DT23|B4DT23_HUMAN Protein FAM98A OS=Homo sapiens GN=FAM98A PE=2 SV=1;>sp|Q8NCA5-2|FA98A_HUMAN Isoform 2 of Protein FAM98A OS=Homo sapiens GN=FAM98A;>sp|Q8NCA5|FA98A_HUMAN Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1;>tr|E9PH82|E9PH82_HUMAN Prot 0.35 -0.10 0.09 -0.13 0.34 0.20 0.06 -0.15 0.155229667 -0.065008042 1.05E-28 4 3 3 15.2

Q14318;Q14318-2;J3KQ73;C8C9T5;M0R2K9 Peptidyl-prolyl cis-trans isomerase FKBP8 FKBP8 >sp|Q14318|FKBP8_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2;>sp|Q14318-2|FKBP8_HUMAN Isoform 2 of Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8;>tr|J3KQ73|J3KQ73_HUMAN Peptidyl-prolyl cis-trans i -0.33 0.16 0.19 0.18 0.38 -0.24 -0.85 0.14 0.246332444 0.190526638 apoptosis;biological regulation;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;death;interaction with host;interspecies interaction between organisms;intracellular signal transduction;macromolecule metabolic process;metabolic process;multi-organism process;primary metabolic process;programmed cell death;protein folding;protein metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to stimulus;signal transduction;viral reproductive process;virus-host interaction binding;catalytic activity;cis-trans isomerase activity;drug binding;FK506 binding;isomerase activity;macrolide binding;peptidyl-prolyl cis-trans isomerase activity cell part;cytoplasmic part;endoplasmic reticulum part;envelope;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;mitochondrial envelope;mitochondrial membrane;mitochondrial part;organelle envelope;organelle membrane;organelle part 3.83E-59 5 3 3 9.7

Q9UJY5-3;Q9UJY5;Q6IC75;Q9UJY5-4;Q9UJY5-2;B0QYR9;B0QYS0;B0QYS1;B0QYS2;B0QYS3;B0QYR5;J3QRS8;B0QYS4;B0QYS5;H3BPI3;J3QRP3;B7Z1E9;H3BMM6;B0QYR6;Q9UJY4;J3KSS7;Q9NZ52-4;Q9NZ52 ADP-ribosylation factor-binding protein GGA1 GGA1 >sp|Q9UJY5-3|GGA1_HUMAN Isoform 3 of ADP-ribosylation factor-binding protein GGA1 OS=Homo sapiens GN=GGA1;>sp|Q9UJY5|GGA1_HUMAN ADP-ribosylation factor-binding protein GGA1 OS=Homo sapiens GN=GGA1 PE=1 SV=1;>tr|Q6IC75|Q6IC75_HUMAN ADP-ribosylation factor-b 0.08 0.06 0.14 0.26 0.06 0.08 0.27 0.72 0.378759518 -0.14993855 cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;transport;vesicle-mediated transport ADP-ribosylation factor binding;binding;enzyme binding;GTPase binding;protein binding;small GTPase binding AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endosomal part;endosome membrane;Golgi apparatus;Golgi apparatus part;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;protein complex;trans-Golgi network;vesicle Lysosome 1.01E-10 23 3 3 8.3

Q9HD26-2;Q9HD26;F5H1Y4;Q9HD26-3 Golgi-associated PDZ and coiled-coil motif-containing protein GOPC >sp|Q9HD26-2|GOPC_HUMAN Isoform 2 of Golgi-associated PDZ and coiled-coil motif-containing protein OS=Homo sapiens GN=GOPC;>sp|Q9HD26|GOPC_HUMAN Golgi-associated PDZ and coiled-coil motif-containing protein OS=Homo sapiens GN=GOPC PE=1 SV=1;>tr|F5H1Y4|F5H1 0.10 -0.16 0.04 0.12 -0.17 -0.03 -0.22 -0.17 0.970591919 0.174690953 apical protein localization;asymmetric protein localization;biological regulation;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular process involved in reproduction;cytoplasmic sequestering of CFTR protein;cytoplasmic sequestering of protein;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi to plasma membrane transport;Golgi vesicle transport;intracellular transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;negative regulation of biological process;negative regulation of cellular process;negative regulation of Golgi to plasma membrane CFTR protein transport;negative regulation of Golgi to plasma membrane protein transport;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of protein transport;negative regulation of transport;nucleus organization;organelle organization;post-Golgi vesicle-mediated transport;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein localization;protein oligomerization;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of Golgi to plasma membrane CFTR protein transport;regulation of Golgi to plasma membrane protein transport;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of protein localization;regulation of protein transport;regulation of transport;regulation of vesicle-mediated transport;reproductive process;spermatid nucleus differentiation;transport;vesicle-mediated transport enzyme regulator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;small GTPase regulator activity cell junction;cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;Golgi apparatus;Golgi apparatus part;Golgi membrane;Golgi-associated vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane;postsynaptic density;postsynaptic membrane;protein complex;synapse part;synaptic membrane;trans-Golgi network transport vesicle;transport vesicle;vesicle 1.76E-07 4 3 3 9.3

Q96QA5 Gasdermin-A GSDMA >sp|Q96QA5|GSDMA_HUMAN Gasdermin-A OS=Homo sapiens GN=GSDMA PE=2 SV=4 -0.03 0.48 -0.13 0.01 1.36 1.84 0.96 0.37 1.266556406 -1.050770637 apoptosis;biological regulation;cell death;cellular process;death;induction of apoptosis;induction of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death	cell part;cytoplasmic part;intracellular part;perinuclear region of cytoplasm		1.29E-40	1	3	3	10.8

Q7Z4V5-2;Q7Z4V5;K7EPS6;K7EQZ6;Q7Z4V5-3;M0R0J3	Hepatoma-derived growth factor-related protein 2	HDGFRP2	>sp|Q7Z4V5-2|HDGR2_HUMAN Isoform 2 of Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2;>sp|Q7Z4V5|HDGR2_HUMAN Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFRP2 PE=1 SV=1;>tr|K7EPS6|K7EPS6_HUMAN Hepatoma-	-0.34	0.03	0.09	0.18	0.50	0.04	-0.94	-0.23	0.169804808	0.147874956	"biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent"	binding;DNA binding;nucleic acid binding	cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle		2.18E-32	6	3	3	6

Q5T447;Q5T447-2	E3 ubiquitin-protein ligase HECTD3	HECTD3	>sp|Q5T447|HECD3_HUMAN E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens GN=HECTD3 PE=1 SV=1	-0.15	-0.37	0.10	0.17	0.11	0.46	0.22	0.14	0.854388346	-0.295306373	catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process	"acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;ubiquitin-protein ligase activity"	cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm		1.95E-13	2	3	3	5.5

Q8TCT9-5;Q8TCT9;Q8TCT9-4;Q8TCT9-2	Minor histocompatibility antigen H13	HM13	>sp|Q8TCT9-5|HM13_HUMAN Isoform 5 of Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13;>sp|Q8TCT9|HM13_HUMAN Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1;>sp|Q8TCT9-4|HM13_HUMAN Isoform 4 of Minor histocompatibility ant	-1.07	0.51	-0.56	-0.38	1.74	0.93	-1.97	0.09	0.257421885	-0.574514609	macromolecule metabolic process;membrane protein proteolysis;metabolic process;primary metabolic process;protein metabolic process;proteolysis	"aspartic endopeptidase activity, intramembrane cleaving;aspartic-type endopeptidase activity;aspartic-type peptidase activity;binding;catalytic activity;endopeptidase activity;hydrolase activity;identical protein binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;protein dimerization activity;protein homodimerization activity"	cell part;cell surface;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum part;integral to cytosolic side of endoplasmic reticulum membrane;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle part;plasma membrane;rough endoplasmic reticulum		1.44E-29	4	3	3	13.7

Q1M185;Q1M188;Q1M186;F5H2U8;Q1M187;P52926-2;P52926;F5H2A4;F5H6H0	High mobility group protein HMGI-C	HMGA2	>tr|Q1M185|Q1M185_HUMAN HMGA2d OS=Homo sapiens GN=HMGA2 PE=2 SV=1;>tr|Q1M188|Q1M188_HUMAN HMGA2c OS=Homo sapiens GN=HMGA2 PE=2 SV=1;>tr|Q1M186|Q1M186_HUMAN HMGA2d OS=Homo sapiens GN=HMGA2 PE=2 SV=1;>tr|F5H2U8|F5H2U8_HUMAN High mobility group protein HMGI-	-0.51	0.86	-0.13	0.85	-1.16	-0.10	-1.45	0.32	0.676834665	0.866362093	"adipose tissue development;adrenal gland development;aging;anatomical structure development;anatomical structure morphogenesis;base-excision repair;biological regulation;cell aging;cell communication;cell cycle checkpoint;cell cycle phase;cell cycle process;cell differentiation;cell division;cell morphogenesis;cell morphogenesis involved in differentiation;cell proliferation;cell proliferation in forebrain;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cellular senescence;chondrocyte differentiation;chondrocyte proliferation;chromatin assembly;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromosome breakage;chromosome condensation;chromosome organization;covalent chromatin modification;detection of stimulus;developmental process;developmental process involved in reproduction;DNA conformation change;DNA damage checkpoint;DNA damage response, detection of DNA damage;DNA integrity checkpoint;DNA metabolic process;DNA packaging;DNA repair;endodermal cell differentiation;epithelial to mesenchymal transition;fat cell differentiation;fat pad development;G2/M transition checkpoint;G2/M transition DNA damage checkpoint;G2/M transition of mitotic cell cycle;gamete generation;gland development;gonad development;heterochromatin formation;heterochromatin organization;histone H2A-S139 phosphorylation;histone modification;histone phosphorylation;histone-serine phosphorylation;interaction with symbiont;interspecies interaction between organisms;macromolecule metabolic process;macromolecule modification;male gamete generation;male gonad development;mesodermal cell differentiation;mesodermal-endodermal cell signaling;metabolic process;mitosis;mitotic cell cycle checkpoint;mitotic cell cycle G2/M transition checkpoint;mitotic cell cycle G2/M transition DNA damage checkpoint;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;negative regulation by host of viral transcription;negative regulation of apoptosis;negative regulation of astrocyte differentiation;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA binding;negative regulation of DNA metabolic process;negative regulation of DNA repair;negative regulation of double-strand break repair;negative regulation of double-strand break repair via nonhomologous end joining;negative regulation of glial cell differentiation;negative regulation of gliogenesis;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of neurogenesis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of reproductive process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of retroviral genome replication;negative regulation of RNA metabolic process;negative regulation of viral genome replication;negative regulation of viral reproduction;negative regulation of viral transcription;neural precursor cell proliferation;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oncogene-induced senescence;organ development;organelle fission;organelle organization;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;pituitary gland development;positive regulation of apoptosis;positive regulation of binding;positive regulation of biological process;positive regulation of cell aging;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of cellular response to X-ray;positive regulation of cellular senescence;positive regulation of developmental process;positive regulation of DNA binding;positive regulation of growth;positive regulation of molecular function;positive regulation of multicellular organism growth;positive regulation of multicellular organismal process;positive regulation of programmed cell death;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of stem cell proliferation;positive regulation of transcription regulatory region DNA binding;positive regulation of viral reproduction;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of apoptosis;regulation of astrocyte differentiation;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell aging;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to drug;regulation of cellular response to stress;regulation of cellular response to X-ray;regulation of cellular senescence;regulation of developmental process;regulation of DNA binding;regulation of DNA metabolic process;regulation of DNA repair;regulation of double-strand break repair;regulation of double-strand break repair via nonhomologous end joining;regulation of G2/M transition of mitotic cell cycle;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of growth;regulation of growth hormone secretion;regulation of hormone secretion;regulation of interphase of mitotic cell cycle;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organism growth;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of response to DNA damage stimulus;regulation of response to drug;regulation of response to stimulus;regulation of response to stress;regulation of retroviral genome replication;regulation of RNA metabolic process;regulation of secretion;regulation of signaling;regulation of stem cell differentiation;regulation of stem cell maintenance;regulation of stem cell proliferation;regulation of transcription regulatory region DNA binding;regulation of transcription, DNA-dependent;regulation of transport;regulation of viral genome replication;regulation of viral reproduction;regulation of viral transcription;reproductive process;reproductive structure development;response to biotic stimulus;response to DNA damage stimulus;response to other organism;response to stimulus;response to stress;response to virus;senescence-associated heterochromatin focus formation;signaling;somatic stem cell maintenance;spermatogenesis;stem cell differentiation;stem cell maintenance;tissue development" "5'-deoxyribose-5-phosphate lyase activity;AT DNA binding;binding;C2H2 zinc finger domain binding;cAMP response element binding;carbon-oxygen lyase activity;catalytic activity;chromatin binding;chromatin DNA binding;core promoter binding;DNA bending activity;DNA binding;DNA-(apurinic or apyrimidinic site) lyase activity;DNA-dependent protein kinase activity;kinase activity;lyase activity;MH1 domain binding;MH2 domain binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleosomal DNA binding;nucleosome binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein domain specific binding;protein kinase activity;protein serine/threonine kinase activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;structure-specific DNA binding;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;chromatin;chromosomal part;chromosome;heterochromatin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleus;organelle;organelle part;protein complex;protein-DNA complex;senescence-associated heterochromatin focus;SMAD protein complex 2.02E-58 9 3 3 41.9

O43837;O43837-3;O43837-2 "Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial" IDH3B ">sp|O43837|IDH3B_HUMAN Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2;>sp|O43837-3|IDH3B_HUMAN Isoform C of Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B;>sp|O43837-2|IDH3" 0.24 0.00 0.09 -0.22 -0.36 -0.18 -0.08 0.00 0.612798108 0.179040409 2-oxoglutarate metabolic process;acetyl-CoA catabolic process;acetyl-CoA metabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;heterocycle metabolic process;isocitrate metabolic process;metabolic process;NAD metabolic process;NADH metabolic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule metabolic process;tricarboxylic acid cycle "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;electron carrier activity;ion binding;isocitrate dehydrogenase (NAD+) activity;isocitrate dehydrogenase activity;magnesium ion binding;metal ion binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part Citrate cycle (TCA cycle) 1.26E-17 3 3 3 11.9

Q9BY89;Q9BY89-2 Uncharacterized protein KIAA1671 KIAA1671 >sp|Q9BY89|K1671_HUMAN Uncharacterized protein KIAA1671 OS=Homo sapiens GN=KIAA1671 PE=1 SV=2 0.08 0.01 -0.04 0.08 -0.02 0.01 0.26 0.03 0.212051222 -0.040209735 4.21E-08 2 3 3 2.7

E5RGR0;O75608-2;O75608;E5RJ48;E5RI35 Acyl-protein thioesterase 1 LYPLA1 >tr|E5RGR0|E5RGR0_HUMAN Acyl-protein thioesterase 1 (Fragment) OS=Homo sapiens GN=LYPLA1 PE=2 SV=1;>sp|O75608-2|LYPA1_HUMAN Isoform 2 of Acyl-protein thioesterase 1 OS=Homo sapiens GN=LYPLA1;>sp|O75608|LYPA1_HUMAN Acyl-protein thioesterase 1 OS=Homo sapien 0.33 0.04 0.28 -0.15 -0.40 -0.26 0.64 0.16 0.118825812 0.08609665 biological regulation;carboxylic acid metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid metabolic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;nitric oxide metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of nitric-oxide synthase activity;regulation of oxidoreductase activity;small molecule metabolic process "carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;lysophospholipase activity;palmitoyl-(protein) hydrolase activity;phospholipase activity;thiolester hydrolase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Glycerophospholipid metabolism 1.08E-35 5 3 3 16.2

Q15773;F5H0Y3;F5H7L5;F5H800 Myeloid leukemia factor 2 MLF2 >sp|Q15773|MLF2_HUMAN Myeloid leukemia factor 2 OS=Homo sapiens GN=MLF2 PE=1 SV=1;>tr|F5H0Y3|F5H0Y3_HUMAN Myeloid leukemia factor 2 (Fragment) OS=Homo sapiens GN=MLF2 PE=2 SV=1 -0.06 0.76 0.05 0.61 -0.77 0.12 -0.70 -0.04 0.957043475 0.682755907 defense response;response to stimulus;response to stress cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 5.26E-07 4 3 3 15.7

P50281 Matrix metalloproteinase-14 MMP14 >sp|P50281|MMP14_HUMAN Matrix metalloproteinase-14 OS=Homo sapiens GN=MMP14 PE=1 SV=3 0.16 -0.06 -0.58 -0.01 -0.18 -0.29 0.06 0.17 0.120023076 -0.064215449 anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;astrocyte cell migration;biological regulation;branching morphogenesis of a tube;cell migration;cell motility;cell proliferation;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;developmental process;endothelial cell proliferation;epithelial cell proliferation;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;glial cell migration;locomotion;lung development;macromolecule metabolic process;metabolic process;morphogenesis of a branching structure;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell-matrix adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of focal adhesion assembly;organ development;ossification;ovarian follicle development;ovulation cycle process;positive regulation of biological process;positive regulation of cell growth;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of growth;positive regulation of locomotion;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;regulation of biological process;regulation of cell adhesion;regulation of cell growth;regulation of cell migration;regulation of cell motility;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of focal adhesion assembly;regulation of growth;regulation of localization;regulation of locomotion;response to abiotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to external stimulus;response to hormone stimulus;response to hypoxia;response to mechanical stimulus;response to organic substance;response to oxidative stress;response to oxygen levels;response to steroid hormone stimulus;response to stimulus;response to stress;rhythmic process;tissue remodeling;tube morphogenesis;zymogen activation "binding;calcium ion binding;catalytic activity;cation binding;endopeptidase activity;enzyme activator activity;enzyme regulator activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;nucleic acid binding transcription factor activity;peptidase activator activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;peptidase regulator activity;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular matrix;extracellular region part;Golgi apparatus part;Golgi lumen;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;plasma membrane part;vesicle GnRH signaling pathway 6.54E-16 1 3 3 6.7

K7ELQ0;Q9BYD3-2;K7ES61;Q9BYD3;K7EKI4;K7ELF1;K7EJ73 "39S ribosomal protein L4, mitochondrial" MRPL4 ">tr|K7ELQ0|K7ELQ0_HUMAN 39S ribosomal protein L4, mitochondrial OS=Homo sapiens GN=MRPL4 PE=4 SV=1;>sp|Q9BYD3-2|RM04_HUMAN Isoform 2 of 39S ribosomal protein L4, mitochondrial OS=Homo sapiens GN=MRPL4;>tr|K7ES61|K7ES61_HUMAN 39S ribosomal protein L4, mitoc" -0.12 0.28 0.19 0.17 -0.23 -0.34 -1.47 -0.36 1.01741732 0.730784949 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome 3.66E-63 7 3 3 21.4

O75592-2;O75592;J3KPZ3;H7C3U4 Probable E3 ubiquitin-protein ligase MYCBP2 MYCBP2 >sp|O75592-2|MYCB2_HUMAN Isoform 2 of Probable E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2;>sp|O75592|MYCB2_HUMAN Probable E3 ubiquitin-protein ligase MYCBP2 OS=Homo sapiens GN=MYCBP2 PE=1 SV=3;>tr|J3KPZ3|J3KPZ3_HUMAN Probable E3 ubiquitin 0.15 0.00 -0.19 0.29 0.28 0.62 0.19 0.38 0.941835974 -0.303776283 "anatomical structure morphogenesis;axon guidance;axonogenesis;biological regulation;biosynthetic process;branchiomotor neuron axon guidance;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular biosynthetic process;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic

process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;central nervous system neuron axonogenesis;central nervous system projection neuron
axonogenesis;chemotaxis;developmental process;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;motor axon guidance;neuron projection
morphogenesis;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein metabolic process;protein modification by small
protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;regulation of biological process;regulation of biosynthetic process;regulation of cellular
biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton
organization;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen
compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of protein localization;regulation of RNA
metabolic process;regulation of transcription, DNA-dependent;response to chemical stimulus;response to external stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;taxis;transcription, DNA-dependent" "acid-amino acid ligase activity;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;small conjugating protein ligase
activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" axon;cell part;cell projection;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded
organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microtubule cytoskeleton;neuron projection;non-membrane-bounded organelle;nucleus;organelle 8.09E-07 4 3 3 0.9
E9PL57;F8VSA6;Q15843;E9PS38;Q86V88-3;Q86V88-2;Q86V88 NEDD8 NEDD8-MDP1;NEDD8 >tr|E9PL57|E9PL57_HUMAN Protein NEDD8-MDP1 (Fragment) OS=Homo sapiens GN=NEDD8-MDP1 PE=2
SV=1;>tr|F8VSA6|F8VSA6_HUMAN NEDD8 OS=Homo sapiens GN=NEDD8 PE=2 SV=1;>sp|Q15843|NEDD8_HUMAN NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1;>tr|E9PS38|E9PS38_HUMAN Protein N
0.42 0.35 -1.03 0.04 0.58 0.82 0.27 0.67 0.777125928 -0.643176984 "anatomical structure morphogenesis;biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic
process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;dephosphorylation;developmental process;localization;macromolecule catabolic
process;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic
process;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein localization;protein metabolic
process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein neddylation;proteolysis;proteolysis involved in cellular protein
catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic
process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen
compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II
promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to organic cyclic compound;response to organic substance;response to stimulus;ubiquitin-dependent protein catabolic process"
"binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase
activity;protein tyrosine phosphatase activity" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.38E-06 7 3 3
18.8
O43809;H3BND3 Cleavage and polyadenylation specificity factor subunit 5 NUDT21 >sp|O43809|CPSF5_HUMAN Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1
0.08 0.02 -0.07 0.11 0.18 -0.50 -0.55 -0.71 0.90808376 0.425059789 "biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component
organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex
subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA metabolic process;mRNA polyadenylation;mRNA processing;nitrogen compound metabolic process;nuclear mRNA
splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein
oligomerization;protein tetramerization;RNA 3'-end processing;RNA biosynthetic process;RNA metabolic process;RNA polyadenylation;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA
splicing, via transesterification reactions with bulged adenosine as nucleophile;termination of RNA polymerase II transcription;transcription termination, DNA-dependent" AU-rich element binding;binding;catalytic
activity;hydrolase activity;mRNA binding;nucleic acid binding;RNA binding cell part;centrosome;cytoplasmic part;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle
part;intracellular part;macromolecular complex;microtubule organizing center;mRNA cleavage factor complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm part;organelle;organelle
part;paraspeckles;protein complex mRNA surveillance pathway 4.98E-08 2 3 3 9.7
G3V3Z8;P49757-4;P49757-2;P49757-3;P49757;B1P2N8;B1P2N7;B1P2N6;B1P2N5 Protein numb homolog NUMB >tr|G3V3Z8|G3V3Z8_HUMAN Protein numb homolog OS=Homo sapiens GN=NUMB PE=2
SV=1;>sp|P49757-4|NUMB_HUMAN Isoform 4 of Protein numb homolog OS=Homo sapiens GN=NUMB;>sp|P49757-2|NUMB_HUMAN Isoform 2 of Protein numb homolog OS=Homo sapiens GN=NUMB;>sp|P49757-3|
-0.20 -0.03 0.30 -0.04 0.32 0.09 -0.24 0.88 0.405670612 -0.256691424 adherens junction organization;anatomical structure development;anatomical structure morphogenesis;axon
guidance;axonogenesis;biological regulation;cell differentiation;cell division;cell junction organization;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling
pathway;cell-cell junction organization;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component
organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;chemotaxis;developmental process;epithelial cell differentiation;forebrain neuroblast division;lateral
ventricle development;locomotion;lung cell differentiation;lung epithelial cell differentiation;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative
regulation of Notch signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;neuroblast division;neuroblast division in subventricular zone;neuron
projection morphogenesis;Notch signaling pathway;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cellular process;positive
regulation of developmental process;positive regulation of epithelial cell differentiation;positive regulation of neurogenesis;positive regulation of polarized epithelial cell differentiation;regulation of anatomical structure
morphogenesis;regulation of biological process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of
epithelial cell differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of Notch signaling
pathway;regulation of organ morphogenesis;regulation of polarized epithelial cell differentiation;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response
to external stimulus;response to stimulus;signal transduction;somatic stem cell division;stem cell division;taxis apical part of cell;basolateral plasma membrane;cell part;cytoplasmic part;early
endosome;endosome;extrinsic to membrane;extrinsic to plasma membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to
membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane part Notch signaling pathway 3.80E-40 9 3 3 9.7
E7EV56;Q15154-2;E7ETA6;Q15154;A6NNN6;H0YBA1 Pericentriolar material 1 protein PCM1 >tr|E7EV56|E7EV56_HUMAN Methyl-CpG-binding domain protein 1 OS=Homo sapiens GN=PCM1 PE=2
SV=1;>sp|Q15154-2|PCM1_HUMAN Isoform 2 of Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1;>tr|E7ETA6|E7ETA6_HUMAN Methyl-CpG-binding domain protein 1 OS=Homo -0.11 0.07 -0.64
0.08 -0.96 -0.56 -0.27 -0.75 0.918118178 0.483592588 anatomical structure formation involved in morphogenesis;biological regulation;cell cycle process;cell projection assembly;cell projection
organization;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component organization;cellular component organization at cellular
level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;centrosome
organization;cilium assembly;cytoskeleton organization;developmental process;G2/M transition of mitotic cell cycle;interkinetic nuclear migration;localization;macromolecule localization;maintenance of location;maintenance of
location in cell;maintenance of protein location;maintenance of protein location in cell;microtubule anchoring;microtubule anchoring at centrosome;microtubule anchoring at microtubule organizing center;microtubule
cytoskeleton organization;microtubule organizing center organization;microtubule-based process;negative regulation of biological process;negative regulation of cell development;negative regulation of cell
differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neurogenesis;neuronal stem cell maintenance;nucleus localization;organelle localization;organelle
organization;protein localization;protein localization to centrosome;protein localization to organelle;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell
differentiation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system
development;regulation of neurogenesis;stem cell maintenance binding;identical protein binding;protein binding cell part;centriolar satellite;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;microtubule organizing center;microtubule organizing center part;non-membrane-bounded organelle;nuclear
membrane;nuclear part;organelle;organelle membrane;organelle part;pericentriolar material 9.58E-10 6 3 3 2.6
Q96S52-2;Q96S52;F5H019;G3V1A9;P42695 GPI transamidase component PIG-S PIGS >sp|Q96S52-2|PIGS_HUMAN Isoform 2 of GPI transamidase component PIG-S OS=Homo sapiens

GN=PIGS;>sp|Q96S52|PIGS_HUMAN GPI transamidase component PIG-S OS=Homo sapiens GN=PIGS PE=1 SV=3;>tr|F5H019|F5H019_HUMAN GPI transamidase component PIG-S OS=Homo sapiens -0.33 -0.09 0.07 -0.01 0.40 0.03 -0.50 -0.16 0.053321818 -0.032734071 attachment of GPI anchor to protein;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chromosome condensation;chromosome organization;C-terminal protein amino acid modification;C-terminal protein lipidation;DNA conformation change;DNA metabolic process;DNA packaging;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic chromosome condensation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;post-translational protein modification;primary metabolic process;protein lipidation;protein metabolic process;protein modification process binding;catalytic activity;GPI-anchor transamidase activity;histone binding;hydrolase activity;methylated histone residue binding;protein binding cell part;centromeric heterochromatin;chromatin;chromosomal part;condensin complex;cytoplasmic part;endoplasmic reticulum part;GPI-anchor transamidase complex;heterochromatin;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear centromeric heterochromatin;nuclear chromatin;nuclear chromosome part;nuclear condensin complex;nuclear heterochromatin;nuclear part;organelle part;protein complex Glycosylphosphatidylinositol(GPI)-anchor biosynthesis 3.61E-52 5 3 3 8.2

F8WCX5;Q9BY77-2;Q9BY77;Q6R954;F8WEE2;B4DMM2 Polymerase delta-interacting protein 3 POLDIP3;PDIP46 >tr|F8WCX5|F8WCX5_HUMAN Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=2 SV=1;>sp|Q9BY77-2|PDIP3_HUMAN Isoform 2 of Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3;>sp|Q9BY77|PDIP3_HUMAN Polymerase delta-interacting 0.03 0.70 -0.01 1.07 -0.31 0.36 -1.25 -0.09 0.765316224 0.7697081 biological regulation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part 1.04E-15 6 3 3 17.4

F8WEG8;G5E9Q4;C9JMM3;O75569-3;O75569-2;O75569 Interferon-inducible double stranded RNA-dependent protein kinase activator A PRKRA >tr|F8WEG8|F8WEG8_HUMAN Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Homo sapiens GN=PRKRA PE=2 SV=1;>tr|G5E9Q4|G5E9Q4_HUMAN Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Homo sapiens G -0.44 -0.01 -0.03 0.13 0.17 0.07 -0.37 -0.56 0.146936568 0.086500865 anatomical structure morphogenesis;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to dsRNA;cellular response to organic substance;cellular response to stimulus;developmental process;dsRNA fragmentation;embryonic morphogenesis;immune response;immune system process;induction of apoptosis;induction of programmed cell death;macromolecule metabolic process;macromolecule modification;metabolic process;middle ear morphogenesis;multi-organism process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ morphogenesis;outer ear morphogenesis;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;production of siRNA involved in RNA interference;production of small RNA involved in gene silencing by RNA;protein metabolic process;protein modification process;protein phosphorylation;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of programmed cell death;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;RNA metabolic process;RNA processing;skeletal system morphogenesis "binding;catalytic activity;double-stranded RNA binding;enzyme activator activity;enzyme regulator activity;kinase activity;nucleic acid binding;RNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular;intracellular part;perinuclear region of cytoplasm 9.12E-10 6 3 3 38.9

C9JBI3;P78330 Phosphoserine phosphatase PSPH >tr|C9JBI3|C9JBI3_HUMAN Phosphoserine phosphatase (Fragment) OS=Homo sapiens GN=PSPH PE=2 SV=1;>sp|P78330|SERB_HUMAN Phosphoserine phosphatase OS=Homo sapiens GN=PSPH PE=1 SV=2 -0.06 -0.64 -0.12 -0.15 -0.55 -0.94 0.72 -0.19 0.001815821 -0.002156073 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;dephosphorylation;L-serine biosynthetic process;L-serine metabolic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;response to abiotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to mechanical stimulus;response to nutrient levels;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to testosterone stimulus;serine family amino acid biosynthetic process;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule metabolic process "binding;calcium ion binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;magnesium ion binding;metal ion binding;phosphatase activity;phosphoric ester hydrolase activity;phosphoserine phosphatase activity" cell part;cell projection;cytoplasmic part;cytosol;intracellular part;neuron projection"Glycine, serine and threonine metabolism;Methane metabolism" 1.38E-08 2 3 3 15.5

Q96PU8-5;Q96PU8-9;Q96PU8-8;Q96PU8-6;Q96PU8-3;Q96PU8;H0YGD6;H0YG47;F5H5U6;F5H8C8;F5GXS8;F5GYM3 Protein quaking QKI >sp|Q96PU8-5|QKI_HUMAN Isoform 3 of Protein quaking OS=Homo sapiens GN=QKI;>sp|Q96PU8-9|QKI_HUMAN Isoform 6 of Protein quaking OS=Homo sapiens GN=QKI;>sp|Q96PU8-8|QKI_HUMAN Isoform 5 of Protein quaking OS=Homo sapiens GN=QKI;>sp|Q96PU8-6|QKI_HUMAN Isoform 0.01 0.72 -0.23 0.48 0.63 0.36 -0.93 -0.05 0.231365944 0.245278585 anatomical structure development;axon ensheathment;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cell development;cell differentiation;cellular biosynthetic process;cellular developmental process;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;developmental process;developmental process involved in reproduction;ensheathment of neurons;establishment of localization;establishment of RNA localization;fatty acid biosynthetic process;fatty acid metabolic process;germ cell development;lipid biosynthetic process;lipid metabolic process;long-chain fatty acid biosynthetic process;long-chain fatty acid metabolic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;mRNA metabolic process;mRNA processing;mRNA transport;muscle cell differentiation;myelination;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;reproductive process;RNA metabolic process;RNA processing;RNA splicing;RNA transport;small molecule biosynthetic process;small molecule metabolic process;spermatid development;transport;vasculogenesis binding;nucleic acid binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.88E-12 12 3 3 14.2

Q9UL25 Ras-related protein Rab-21 RAB21 >sp|Q9UL25|RAB21_HUMAN Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21 PE=1 SV=30.28 0.09 0.40 -0.07 0.23 0.06 -0.15 0.09 0.37156371 0.119251871 biological regulation;cellular process;cellular response to stimulus;establishment of localization;establishment of protein localization;intracellular signal transduction;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell division site part;cell part;cleavage furrow;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endosomal part;endosome;endosome membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;vesicle membrane 7.34E-36 1 3 3 18.7

B7Z7F3;Q9H6Z4-3;Q9H6Z4-2;Q9H6Z4;K7EJV3;F5H4C2;K7ENJ2;K7EID7;K7ENB9;K7EPW1;K7EIJ4;K7EN31 Ran-binding protein 3 RANBP3 >tr|B7Z7F3|B7Z7F3_HUMAN Ran-binding protein 3 OS=Homo sapiens
GN=RANBP3 PE=2 SV=1;>sp|Q9H6Z4-3|RANB3_HUMAN Isoform 3 of Ran-binding protein 3 OS=Homo sapiens GN=RANBP3;>sp|Q9H6Z4-2|RANB3_HUMAN Isoform 2 of Ran-binding protein 3 OS=Homo sapiens
GN=RANBP3;>s 0.16 -0.04 0.08 0.01 0.02 -0.12 -0.16 -0.47 0.908562755 0.237481556 establishment of localization;establishment of localization in cell;establishment of protein
localization;intracellular transport;protein transport;transport binding;enzyme binding;GTPase binding;protein binding;Ran GTPase binding;Ras GTPase binding;small GTPase binding cell part;cytoplasm;intracellular
membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.02E-19 12 3 3 9.9
Q9H7B2;Q5VXN0;Q5VXM9 Ribosome production factor 2 homolog RPF2 >sp|Q9H7B2|RPF2_HUMAN Ribosome production factor 2 homolog OS=Homo sapiens GN=RPF2 PE=1
SV=2;>tr|Q5VXN0|Q5VXN0_HUMAN Ribosome production factor 2 homolog (Fragment) OS=Homo sapiens GN=RPF2 PE=2 SV=1 -0.10 1.10 0.11 0.95 -0.48 0.26 -1.36 0.31 0.723316906 0.831892526
cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 9.37E-09 3
3 3 10.5
P42677;Q5T4L4;Q71UM5;H0YMV8;C9J1C5;C9JLI6 40S ribosomal protein S27;40S ribosomal protein S27-like RPS27;RPS27L >sp|P42677|RS27_HUMAN 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27
PE=1 SV=3;>tr|Q5T4L4|Q5T4L4_HUMAN 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=2 SV=1;>sp|Q71UM5|RS27L_HUMAN 40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=
0.22 0.18 0.85 2.39 -3.12 -1.44 0.02 -0.25 1.013640896 2.109429194 "anaphase;biological regulation;biosynthetic process;catabolic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell
proliferation;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular
level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular
macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process
involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cotranslational protein targeting to membrane;DNA damage
checkpoint;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction
resulting in induction of apoptosis;DNA integrity checkpoint;DNA metabolic process;DNA repair;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein
localization in endoplasmic reticulum;establishment of protein localization to organelle;G1/S transition checkpoint;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell
death;intracellular protein transport;intracellular signal transduction;intracellular transport;M phase;M phase of mitotic cell cycle;macromolecular complex disassembly;macromolecular complex subunit
organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mitotic anaphase;mitotic cell cycle checkpoint;mitotic cell cycle G1/S transition
checkpoint;mitotic cell cycle G1/S transition DNA damage checkpoint;mitotic prometaphase;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic
process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of
biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex disassembly;protein complex subunit
organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell
cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular process;regulation of G1/S transition of mitotic cell cycle;regulation of interphase of mitotic cell cycle;regulation of mitotic cell
cycle;regulation of programmed cell death;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;signal
transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;SRP-dependent cotranslational protein targeting
to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" "apoptotic protease activator activity;binding;caspase activator activity;caspase regulator
activity;cation binding;DNA binding;enzyme activator activity;enzyme regulator activity;ion binding;metal ion binding;nucleic acid binding;peptidase activator activity;peptidase regulator activity;structural constituent of
ribosome;structural molecule activity;transition metal ion binding;translation activator activity;translation regulator activity;translation regulator activity, nucleic acid binding;zinc ion binding" cell part;cytoplasmic
part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular
complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 2.56E-11 6 3 3 40.5
Q14684-2;Q14684 Ribosomal RNA processing protein 1 homolog B RRP1B >sp|Q14684-2|RRP1B_HUMAN Isoform 2 of Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens
GN=RRP1B;>sp|Q14684|RRP1B_HUMAN Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3-0.15 0.84 0.18 1.03 -0.13 0.15 -0.97 0.05 0.799822199 0.701461945
biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic
process;ncRNA processing;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;nitrogen compound metabolic
process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic
process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate
metabolic process;regulation of phosphorus metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing "cell part;chromatin;chromosomal part;cytoplasmic
part;cytosol;euchromatin;heterochromatin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear
part;nucleolus;organelle;organelle part;preribosome;preribosome, small subunit precursor;ribonucleoprotein complex" 1.69E-10 2 3 3 6.1
E9PPY3;O43159 Ribosomal RNA-processing protein 8 RRP8 >tr|E9PPY3|E9PPY3_HUMAN Ribosomal RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=2 SV=1;>sp|O43159|RRP8_HUMAN Ribosomal
RNA-processing protein 8 OS=Homo sapiens GN=RRP8 PE=1 SV=2 -0.25 1.03 0.60 1.19 -0.20 0.20 -1.75 0.31 0.74625875 1.003804807 "biological regulation;biosynthetic process;carbon catabolite
regulation of transcription;cell communication;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component
organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular
response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient;cellular response to nutrient levels;cellular
response to starvation;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromatin silencing;chromatin silencing at rDNA;chromosome organization;gene silencing;induction
of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;metabolic
process;methylation;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of
cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of gene expression,
epigenetic;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic
process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic
process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive
regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;regulation of
apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular biosynthetic
process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of
macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic
process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription by glucose;regulation of transcription, DNA-dependent;response to chemical
stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to starvation;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic
process;RNA processing;rRNA metabolic process;rRNA processing;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;small molecule
metabolic process;transcription, DNA-dependent" "binding;catalytic activity;histone binding;methylated histone residue binding;methyltransferase activity;protein binding;S-adenosylmethionine-dependent methyltransferase
activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;chromatin;chromatin remodeling complex;chromatin silencing complex;chromosomal part;cytoplasm;heterochromatin;intracellular
non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle
part;plasma membrane;protein complex;rDNA heterochromatin 1.19E-13 2 3 3 16
O00442;O00442-2 RNA 3-terminal phosphate cyclase RTCA >sp|O00442|RTCA_HUMAN RNA 3-terminal phosphate cyclase OS=Homo sapiens GN=RTCA PE=1 SV=1;>sp|O00442-2|RTCA_HUMAN Isoform 2 of

RNA 3-terminal phosphate cyclase OS=Homo sapiens GN=RTCA 0.01 0.08 -0.36 -0.20 0.09 -0.08 0.36 0.13 0.775618412 -0.243881883 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cyclase activity;ligase activity;ligase activity, forming phosphoric ester bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;RNA-3'-phosphate cyclase activity" cell part;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part 6.88E-13 2 3 3 9

Q9HB40;I3L4Z9;Q9HB40-2 Retinoid-inducible serine carboxypeptidase SCPEP1 >sp|Q9HB40|RISC_HUMAN Retinoid-inducible serine carboxypeptidase OS=Homo sapiens GN=SCPEP1 PE=1 SV=1;>tr|I3L4Z9|I3L4Z9_HUMAN Retinoid-inducible serine carboxypeptidase (Fragment) OS=Homo sapiens GN=SCPEP1 PE=4 SV=1 -0.66 -0.49 -0.02 0.19 -0.01 -0.26 0.55 0.05 0.518853181 -0.324328313 biological regulation;carboxylic acid metabolic process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;diterpenoid metabolic process;fat-soluble vitamin metabolic process;hormone metabolic process;isoprenoid metabolic process;lipid metabolic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein metabolic process;proteolysis;regulation of biological quality;regulation of hormone levels;retinoic acid metabolic process;retinoid metabolic process;small molecule metabolic process;terpenoid metabolic process;vitamin A metabolic process;vitamin metabolic process "carboxypeptidase activity;catalytic activity;exopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type carboxypeptidase activity;serine-type exopeptidase activity;serine-type peptidase activity" cell part;cytoplasmic part;cytosol;extracellular region;intracellular part 1.74E-16 3 3 3 7.7

P18827;E9PHH3;H7C1K4 Syndecan-1 SDC1 >sp|P18827|SDC1_HUMAN Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3 0.17 0.18 0.19 -0.06 -0.38 -0.16 0.11 -0.51 1.020934237 0.356819904 "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;canonical Wnt receptor signaling pathway;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell development;cell surface receptor linked signaling pathway;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;developmental process involved in reproduction;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;lipoprotein metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;muscle cell development;myoblast development;nitrogen compound metabolic process;odontogenesis;organ morphogenesis;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to abiotic stimulus;response to calcium ion;response to cAMP;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to light stimulus;response to metal ion;response to organic substance;response to oxidative stress;response to radiation;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;response to toxin;response to wounding;retinoid metabolic process;Sertoli cell development;signal transduction;striated muscle cell development;sulfur compound metabolic process;terpenoid metabolic process;tube development;ureteric bud development;Wnt receptor signaling pathway;wound healing" adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;external side of plasma membrane;extracellular region;focal adhesion;Golgi apparatus part;Golgi lumen;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane part;protein complex;vacuolar lumen;vacuolar part Cell adhesion molecules (CAMs);ECM-receptor interaction;Malaria 2.14E-17 3 3 3 16.1

P30825;Q5JR49;P52569;P52569-3 High affinity cationic amino acid transporter 1 SLC7A1 >sp|P30825|CTR1_HUMAN High affinity cationic amino acid transporter 1 OS=Homo sapiens GN=SLC7A1 PE=1 SV=1 0.53 0.37 -0.24 -0.32 -0.31 -0.04 -0.46 -0.28 0.660974028 0.358051449 amine metabolic process;amine transport;amino acid transport;biological regulation;biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;cell activation;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;immune system process;leukocyte activation;macrophage activation;metabolic process;multicellular organismal process;myeloid leukocyte activation;nitric oxide biosynthetic process;nitric oxide metabolic process;nitric oxide production involved in inflammatory response;nitrogen compound metabolic process;nitrogen compound transport;organic acid metabolic process;organic acid transport;organic substance transport;oxoacid metabolic process;primary metabolic process;production of molecular mediator involved in inflammatory response;regulation of biological process;regulation of cell activation;regulation of cellular process;regulation of defense response;regulation of immune system process;regulation of inflammatory response;regulation of leukocyte activation;regulation of macrophage activation;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;small molecule metabolic process;transmembrane transport;transport active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;arginine transmembrane transporter activity;basic amino acid transmembrane transporter activity;carboxylic acid transmembrane transporter activity;high affinity arginine transmembrane transporter activity;high affinity basic amino acid transmembrane transporter activity;L-amino acid transmembrane transporter activity;L-lysine transmembrane transporter activity;L-ornithine transmembrane transporter activity;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasm;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane part 7.71E-24 4 3 3 6.8

Q8N0X7 Spartin SPG20 >sp|Q8N0X7|SPG20_HUMAN Spartin OS=Homo sapiens GN=SPG20 PE=1 SV=1 0.17 -0.11 0.06 -0.06 0.23 -0.49 0.19 0.81 0.237820187 -0.169821998 abscission;adipose tissue development;anatomical structure development;biological regulation;cell death;cell division;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular process;chemical homeostasis;cytokinesis;death;developmental process;homeostatic process;ion homeostasis;lipid particle organization;multicellular organismal process;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of BMP signaling pathway;negative regulation of cell communication;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of collateral sprouting;negative regulation of collateral sprouting in absence of injury;negative regulation of developmental growth;negative regulation of developmental process;negative regulation of growth;negative regulation of neurogenesis;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;neurological system process;neuromuscular process;organelle organization;regulation of anatomical structure morphogenesis;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of BMP signaling pathway;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of collateral sprouting;regulation of collateral sprouting in absence of injury;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of membrane potential;regulation of mitochondrial membrane potential;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;system process;tissue development cell part;cytoplasmic part;intracellular organelle part;intracellular part;lipid particle;membrane;midbody;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane;synapse 4.20E-24 1 3 3 5.1

O15270 Serine palmitoyltransferase 2 SPTLC2 >sp|O15270|SPTC2_HUMAN Serine palmitoyltransferase 2 OS=Homo sapiens GN=SPTLC2 PE=1 SV=1 0.34 0.18 0.02 0.14 0.28 0.38 -0.16 -0.27 0.261240535 0.115644327 alcohol biosynthetic process;alcohol metabolic process;amine metabolic process;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;ceramide biosynthetic process;ceramide metabolic process;lipid biosynthetic process;lipid metabolic process;membrane lipid biosynthetic process;membrane lipid metabolic process;metabolic process;nitrogen compound metabolic process;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;sphinganine biosynthetic process;sphinganine metabolic process;sphingoid biosynthetic process;sphingoid metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process;sphingomyelin biosynthetic process;sphingomyelin metabolic process;sphingosine biosynthetic process;sphingosine metabolic process "binding;C-acyltransferase activity;catalytic activity;cofactor binding;C-palmitoyltransferase activity;palmitoyltransferase activity;pyridoxal phosphate binding;serine C-palmitoyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;endoplasmic reticulum palmitoyltransferase complex;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle part;palmitoyltransferase complex;protein complex;serine C-palmitoyltransferase complex Sphingolipid metabolism 1.19E-89 1 3 3 10.1

Q5T760;Q05519-2;Q05519;B4DWT1;B4DTC1;Q5T757 Serine/arginine-rich splicing factor 11 SRSF11 >tr|Q5T760|Q5T760_HUMAN Serine/arginine-rich splicing factor 11 (Fragment) OS=Homo sapiens GN=SRSF11 PE=2 SV=1;>sp|Q05519-2|SRS11_HUMAN Isoform 2 of Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11;>sp|Q05519|SRS11_HUMAN Serine/arginine-ri -0.03 0.30 0.12 0.23 0.00 -0.64 -1.13 -0.56 1.248293146 0.73610385 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part 5.51E-23 6 3 3 10

C9J3L8;C9J5W0;P43307;E9PAL7;C9IZQ1;P43307-2;F5H5Y2 Translocon-associated protein subunit alpha SSR1 >tr|C9J3L8|C9J3L8_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1;>tr|C9J5W0|C9J5W0_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=2 SV=1;>sp|P43307|SSRA_HUMAN Translocon-associated protein -0.27 0.21 -0.23 0.10 0.81 0.61 -0.64 0.19 0.341590396 -0.293139273 activation of signaling protein activity involved in unfolded protein response;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;SRP-dependent cotranslational protein targeting to membrane;translation;transport cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Protein processing in endoplasmic reticulum 3.09E-32 7 3 3 12.8

O00186 Syntaxin-binding protein 3 STXBP3 >sp|O00186|STXB3_HUMAN Syntaxin-binding protein 3 OS=Homo sapiens GN=STXBP3 PE=1 SV=2 0.00 -0.03 -0.28 0.02 0.54 0.27 -0.03 -0.14 0.580704121 -0.232834645 biological adhesion;biological regulation;cell activation;cell activation involved in immune response;cell adhesion;cell-cell adhesion;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;homotypic cell-cell adhesion;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;leukocyte degranulation;macromolecular complex assembly;macromolecular complex subunit organization;membrane docking;membrane organization;myeloid cell activation involved in immune response;myeloid leukocyte activation;negative regulation of biological process;negative regulation of calcium ion-dependent exocytosis;negative regulation of cellular process;negative regulation of exocytosis;negative regulation of secretion;negative regulation of transport;neutrophil activation;neutrophil activation involved in immune response;neutrophil degranulation;platelet aggregation;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;protein transport;regulated secretory pathway;regulation of biological process;regulation of calcium ion-dependent exocytosis;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;secretion;secretion by cell;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle-mediated transport apical plasma membrane;basolateral plasma membrane;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;plasma membrane;plasma membrane part;platelet alpha granule;specific granule;stored secretory granule;tertiary granule;vesicle 2.95E-10 1 3 3 5.1

O15260-2;Q5T8U5;O15260;B7Z6A4 Surfeit locus protein 4 SURF4 >sp|O15260-2|SURF4_HUMAN Isoform 2 of Surfeit locus protein 4 OS=Homo sapiens GN=SURF4;>tr|Q5T8U5|Q5T8U5_HUMAN Surfeit 4 OS=Homo sapiens GN=SURF4 PE=2 SV=1;>sp|O15260|SURF4_HUMAN Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3;>tr|B7Z6A4|B7Z6A4_ 0.37 -0.09 -0.33 -0.55 1.11 0.56 -0.04 -0.10 0.657167652 -0.533303626 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;Golgi organization;organelle organization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of organelle organization;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of organelle organization cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 1.08E-54 4 3 3 25.8

Q9BZK7;C9JLJ1;C9JCK0;C9JBN1;C9IYU9 F-box-like/WD repeat-containing protein TBL1XR1 TBL1XR1 >sp|Q9BZK7|TBL1R_HUMAN F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens GN=TBL1XR1 PE=1 SV=1;>tr|C9JLJ1|C9JLJ1_HUMAN F-box-like/WD repeat-containing protein TBL1XR1 (Fragment) OS=Homo sapiens GN=TBL1XR1 PE=2 SV=1;>tr|C9JCK0|C9JCK0_HUMAN F-bo -0.03 0.03 0.00 -0.01 -0.04 -0.30 -0.92 -0.37 0.931946549 0.403978375 "biological regulation;biosynthetic process;canonical Wnt receptor signaling pathway;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;lipid metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;Notch signaling pathway;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;small molecule metabolic process;transcription, DNA-dependent;ubiquitin-dependent protein catabolic process;Wnt receptor signaling pathway" binding;DNA binding;histone binding;nucleic acid binding;protein binding;protein binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding cell part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;spindle microtubule;transcriptional repressor complex Wnt signaling pathway 7.38E-29 5 3 3 8.4

Q9BVC6;Q6N065;Q8IZQ8-2;Q8IZQ8;Q8IZQ8-3 Transmembrane protein 109 TMEM109 >sp|Q9BVC6|TM109_HUMAN Transmembrane protein 109 OS=Homo sapiens GN=TMEM109 PE=1 SV=1 0.24 -0.04 -0.31 0.16 0.63 0.52 -0.31 -0.28 0.165688665 -0.126684877 "anatomical structure development;anatomical structure morphogenesis;artery morphogenesis;biological regulation;blood vessel morphogenesis;cardiac cell differentiation;cardiac chamber development;cardiac muscle cell differentiation;cardiac ventricle development;cell activation;cell differentiation;cell growth;cell growth involved in cardiac muscle cell development;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to hypoxia;cellular response to organic substance;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;developmental cell growth;developmental growth;developmental process;developmental process involved in reproduction;digestive tract development;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;ductus arteriosus closure;fibroblast activation;growth;hepatic stellate cell activation;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;lung alveolus development;muscle cell differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cardiac muscle cell apoptosis;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cyclin-dependent protein kinase activity;negative regulation of developmental process;negative regulation of gene expression;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of muscle cell apoptosis;negative regulation of muscle cell differentiation;negative regulation of myotube differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of RNA metabolic process;negative regulation of skeletal muscle cell differentiation;negative regulation of striated muscle cell apoptosis;negative regulation of striated muscle cell differentiation;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;organ development;positive regulation of apoptosis;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cardiac muscle cell differentiation;positive regulation of cardiac vascular smooth muscle cell differentiation;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of DNA binding;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle cell differentiation;positive regulation of muscle contraction;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smooth muscle cell differentiation;positive regulation of smooth muscle contraction;positive regulation of striated muscle cell differentiation;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation;positive regulation of transcription from RNA polymerase II promoter involved in smooth muscle cell differentiation;positive regulation of transcription, DNA-dependent;positive regulation of transforming growth factor beta receptor signaling pathway;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cardiac muscle cell apoptosis;regulation of cardiac muscle cell differentiation;regulation of cardiac muscle tissue development;regulation of cardiac vascular smooth muscle cell differentiation;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell growth by extracellular stimulus;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of cyclin-dependent protein kinase activity;regulation of developmental process;regulation of DNA binding;regulation of gene expression;regulation of growth;regulation of histone acetylation;regulation of histone modification;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell apoptosis;regulation of muscle cell differentiation;regulation of muscle contraction;regulation of muscle organ development;regulation of muscle system process;regulation of myoblast differentiation;regulation of myotube differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-lysine acetylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of smooth muscle cell differentiation;regulation of smooth muscle contraction;regulation of striated muscle cell apoptosis;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;regulation of system process;regulation of transcription from RNA polymerase II promoter;regulation of transcription from RNA polymerase II promoter involved in myocardial precursor cell differentiation;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;reproductive process;reproductive structure development;response to chemical stimulus;response to DNA damage stimulus;response to growth factor stimulus;response to hypoxia;response to organic substance;response to oxygen levels;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;striated muscle cell differentiation;urinary bladder development;uterus development;vasculogenesis;ventricular cardiac muscle cell differentiation" binding;core promoter binding;core promoter sequence-specific DNA binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein binding transcription factor activity;protein domain specific binding;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription;RNA polymerase II transcription factor binding transcription factor activity;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nuclear membrane;nuclear outer membrane;nuclear part;nucleus;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;sarcoplasmic reticulum membrane 6.44E-18 5 3 3 11.1

D6RAA6;P57088;H0Y8N0 Transmembrane protein 33 TMEM33 >tr|D6RAA6|D6RAA6_HUMAN Transmembrane protein 33 (Fragment) OS=Homo sapiens GN=TMEM33 PE=2 SV=1;>sp|P57088|TMM33_HUMAN Transmembrane protein 33 OS=Homo sapiens GN=TMEM33 PE=1 SV=2;>tr|H0Y8N0|H0Y8N0_HUMAN Transmembrane protein 33 (Fragment) OS=Homo sapiens -0.38 0.41 0.30 0.91 -3.55 -0.58 -0.92 -0.01 0.813882532 1.577172489 cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;vesicle 6.17E-27 3 3 3 14

Q9NS69 Mitochondrial import receptor subunit TOM22 homolog TOMM22 >sp|Q9NS69|TOM22_HUMAN Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3 -0.26 1.04 -0.10 1.29 -0.02 0.91 -1.46 0.70 0.268017569 0.458695954 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;organelle organization;outer mitochondrial membrane organization;primary metabolic process;protein import;protein import into mitochondrial outer membrane;protein metabolic process;protein targeting;protein targeting to membrane;protein targeting to mitochondrion;protein transport;transport macromolecule transmembrane transporter activity;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial outer membrane translocase complex;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex 1.87E-152 1 3 3 40.8

H0YNH8;Q9BZF9-2;Q9BZF9;F5H2B9;H0YN48 Uveal autoantigen with coiled-coil domains and ankyrin repeats UACA >tr|H0YNH8|H0YNH8_HUMAN Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens GN=UACA PE=2 SV=1;>sp|Q9BZF9-2|UACA_HUMAN Isoform 2 of Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Homo sapiens GN=UACA;>sp|Q9BZF9| -0.03 0.13 0.12 0.14 0.13 0.46 -0.43 -0.24 0.208043218 0.111725247 "biological regulation;cellular process;cellular response to stimulus;cellular response to stress;DNA damage response, signal transduction resulting in induction of apoptosis;induction of apoptosis;induction of apoptosis by intracellular signals;induction of apoptosis by oxidative stress;induction of programmed cell death;intracellular signal transduction;negative regulation of biological process;negative regulation of cellular process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of NF-kappaB import into nucleus;negative regulation of nucleocytoplasmic transport;negative regulation of protein import into nucleus;negative regulation of protein transport;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of transcription factor import into nucleus;negative regulation of transmembrane transport;negative regulation of transport;positive regulation of apoptosis;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of molecular function;positive regulation of nucleocytoplasmic transport;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of transmembrane transport;positive regulation of transport;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular localization;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of defense response;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of hydrolase activity;regulation of inflammatory response;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of NF-kappaB import into nucleus;regulation of nucleocytoplasmic transport;regulation of peptidase activity;regulation of programmed cell death;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of transcription factor import into nucleus;regulation of transmembrane transport;regulation of transport;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;signal transduction;signal transduction in response to DNA damage" apoptosome;cell part;cytoplasmic part;cytoskeleton;cytosolic part;envelope;extracellular region;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleus;organelle;organelle envelope;organelle part;perinuclear region of cytoplasm;protein complex 1.26E-11 5 3 3 2.1

Q05086-2;Q05086-3;Q05086 Ubiquitin-protein ligase E3A UBE3A >sp|Q05086-2|UBE3A_HUMAN Isoform I of Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A;>sp|Q05086-3|UBE3A_HUMAN Isoform III of Ubiquitin-protein ligase E3A OS=Homo sapiens GN=UBE3A;>sp|Q05086|UBE3A_HUMAN Ubiquitin-protein ligase E3A OS=Homo sapiens GN 0.20 -0.10 0.16 -0.08 0.06 -0.09 0.00 -0.18 0.418353585 0.098347552 "anatomical structure development;androgen receptor signaling pathway;biological regulation;brain development;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to stimulus;developmental growth;developmental process;developmental process involved in reproduction;endocytosis;establishment of localization;growth;interaction with host;interspecies interaction between organisms;intracellular receptor mediated signaling pathway;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;metabolic process;multi-organism process;organ development;ovarian follicle development;ovulation cycle process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;prostate gland growth;protein K48-linked ubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphatidylinositol 3-kinase cascade;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to stimulus;rhythmic process;signal transduction;sperm entry;steroid hormone receptor signaling pathway;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction" "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;protein binding transcription factor activity;small conjugating protein ligase activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;ubiquitin-protein ligase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;proteasome complex;protein complex Ubiquitin mediated proteolysis 6.39E-31 3 3 3 4.6

Q92575;F8WB86;Q6PJ80;C9JLR4 UBX domain-containing protein 4 UBXN4 >sp|Q92575|UBXN4_HUMAN UBX domain-containing protein 4 OS=Homo sapiens GN=UBXN4 PE=1 SV=2 0.03 0.01 0.07 0.15 0.05 0.10 -0.15 0.28 0.017340293 -0.004972863 response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;nuclear envelope;nuclear part;nucleus;organelle;organelle envelope;organelle membrane;organelle part 3.97E-36 4 3 3 10

Q9Y5J1;J3QLD6;J3QRG0;J3QR85;J3KSR7 U3 small nucleolar RNA-associated protein 18 homolog UTP18 >sp|Q9Y5J1|UTP18_HUMAN U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens GN=UTP18 PE=1 SV=3-0.07 1.06 0.06 1.00 -0.83 -0.08 -1.16 -0.16 1.128266671 1.069247311 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part Ribosome biogenesis in eukaryotes 4.88E-09 5 3 3 8.5

Q08AM6;H3BUU8 Protein VAC14 homolog VAC14 >sp|Q08AM6|VAC14_HUMAN Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=1 SV=1;>tr|H3BUU8|H3BUU8_HUMAN Protein VAC14 homolog OS=Homo sapiens GN=VAC14 PE=2 SV=1-0.08 -0.39 -0.15 0.16 -0.14 0.27 0.04 -0.07 0.390538441 -0.138927788 biological regulation;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;interaction with host;interspecies interaction between organisms;lipid biosynthetic process;lipid metabolic process;metabolic process;multi-organism process;organophosphate metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to stimulus;signal transduction;small molecule metabolic process;viral reproductive process;virus-host interaction enzyme activator activity;enzyme regulator activity;kinase activator activity;kinase regulator activity;receptor activity cell part;cytoplasmic part;early endosome membrane;endoplasmic reticulum;endosomal part;endosome membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome membrane;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part 2.39E-09 2 3 3 5.8

Q8NI36;D6RFM8;D6R922 WD repeat-containing protein 36 WDR36 >sp|Q8NI36|WDR36_HUMAN WD repeat-containing protein 36 OS=Homo sapiens GN=WDR36 PE=1 SV=1 -0.19 1.09 -0.35 1.62 0.33 -0.78 -1.84 0.35 0.614852017 1.03198396 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;multicellular organismal process;ncRNA metabolic process;ncRNA processing;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;response to stimulus;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;sensory perception;sensory perception of light stimulus;system process;visual perception cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;ribonucleoprotein complex;small-subunit processome Ribosome biogenesis in eukaryotes 4.16E-10 3 3 3 4

Q5HYZ1;A2ABB6;H0Y6G3;O15213 WD repeat-containing protein 46 WDR46 >tr|Q5HYZ1|Q5HYZ1_HUMAN WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=2

SV=2;>tr|A2ABB6|A2ABB6_HUMAN WD repeat-containing protein 46 (Fragment) OS=Homo sapiens GN=WDR46 PE=2 SV=1;>tr|H0Y6G3|H0Y6G3_HUMAN WD repeat-containing protein -0.50 1.19 -0.18 1.41 -1.11 0.06 -1.25 0.94 0.484947744 0.823669647 2.55E-40 4 3 3 18.9

B4DP38;Q9BQA1;H0Y711 Methylosome protein 50 WDR77 >tr|B4DP38|B4DP38_HUMAN Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=2 SV=1;>sp|Q9BQA1|MEP50_HUMAN Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1 0.26 0.12 -0.12 0.07 -0.35 -0.42 0.10 -0.31 0.978253702 0.327343164 "biological regulation;cell differentiation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;columnar/cuboidal epithelial cell differentiation;developmental process;developmental process involved in reproduction;epithelial cell differentiation;epithelial cell differentiation involved in prostate gland development;glandular epithelial cell differentiation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epithelial cell proliferation;negative regulation of epithelial cell proliferation involved in prostate gland development;negative regulation of reproductive process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of epithelial cell proliferation;regulation of epithelial cell proliferation involved in prostate gland development;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;secretory columnal luminar epithelial cell differentiation involved in prostate glandular acinus development;spliceosomal snRNP assembly" ligand-dependent nuclear receptor transcription coactivator activity;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;cytoplasmic part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 7.75E-14 3 3 3 12.2

O43670-2;O43670;J3QRS9;O43670-4;J3KS31;O43670-3;J3QS27;J3KTL1;J3KRB6;J3KRW6;H0Y3M2 Zinc finger protein 207 ZNF207 >sp|O43670-2|ZN207_HUMAN Isoform 2 of Zinc finger protein 207 OS=Homo sapiens GN=ZNF207;>sp|O43670|ZN207_HUMAN Zinc finger protein 207 OS=Homo sapiens GN=ZNF207 PE=1 SV=1;>tr|J3QRS9|J3QRS9_HUMAN Zinc finger protein 207 OS=Homo sapiens GN=ZNF207 PE=4 SV=1;> 0.15 0.02 0.07 -0.05 0.22 -0.59 -0.40 -0.74 0.844191877 0.423478104 binding;carbohydrate binding;cation binding;DNA binding;glycosaminoglycan binding;heparin binding;ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;pattern binding;polysaccharide binding;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.50E-19 11 3 3 9.9

Q5BKZ1;Q5BKZ1-3 DBIRD complex subunit ZNF326 ZNF326 >sp|Q5BKZ1|ZN326_HUMAN DBIRD complex subunit ZNF326 OS=Homo sapiens GN=ZNF326 PE=1 SV=2 0.08 1.05 -0.06 1.06 0.18 0.89 -1.14 0.45 0.332093087 0.442339489 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription elongation, DNA-dependent;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;transcription, DNA-dependent" basal RNA polymerase II transcription machinery binding;basal transcription machinery binding;binding;cation binding;DNA binding;enzyme binding;ion binding;metal ion binding;nucleic acid binding;protein binding;RNA polymerase binding;RNA polymerase core enzyme binding;RNA polymerase II core binding;transition metal ion binding;zinc ion binding cell part;intracellular organelle part;intracellular part;nuclear matrix;nuclear part;organelle part 7.98E-26 2 3 3 6.7

Q86UK7-2;Q86UK7-3;Q86UK7;H3BQQ2 Zinc finger protein 598 ZNF598 >sp|Q86UK7-2|ZN598_HUMAN Isoform 2 of Zinc finger protein 598 OS=Homo sapiens GN=ZNF598;>sp|Q86UK7-3|ZN598_HUMAN Isoform 3 of Zinc finger protein 598 OS=Homo sapiens GN=ZNF598;>sp|Q86UK7|ZN598_HUMAN Zinc finger protein 598 OS=Homo sapiens GN=ZNF598 PE=1 SV 0.06 -0.09 0.45 -0.02 0.26 -0.15 -0.06 -0.35 0.41362933 0.177632526 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding 2.46E-27 4 3 3 4.4

Q9Y224;H0YJB9;G3V4C6;Q96L16;A6NFL8 UPF0568 protein C14orf166 C14orf166 >sp|Q9Y224|CN166_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1;>tr|H0YJB9|H0YJB9_HUMAN UPF0568 protein C14orf166 (Fragment) OS=Homo sapiens GN=C14orf166 PE=2 SV=1;>tr|G3V4C6|G3V4C6_HUMAN UPF0568 protein C14orf166 OS=Homo sapiens GN -0.04 0.13 -0.27 0.05 -0.08 -0.07 -0.26 -0.21 0.508540103 0.118879555 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;interaction with host;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;viral reproductive process;virus-host interaction" basal RNA polymerase II transcription machinery binding;basal transcription machinery binding;binding;enzyme binding;protein binding;RNA polymerase binding;RNA polymerase core enzyme binding;RNA polymerase II core binding cell part;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule organizing center;nucleus;organelle;organelle part;perinuclear region of cytoplasm;protein complex;tRNA-splicing ligase complex 8.82E-58 5 4 3 19.3

H3BV90;Q6FI81-3;Q6FI81;H3BUG4;H3BT65;Q6FI81-2;H3BQ23 Anamorsin CIAPIN1 >tr|H3BV90|H3BV90_HUMAN Anamorsin OS=Homo sapiens GN=CIAPIN1 PE=2 SV=1;>sp|Q6FI81-3|CPIN1_HUMAN Isoform 3 of Anamorsin OS=Homo sapiens GN=CIAPIN1;>sp|Q6FI81|CPIN1_HUMAN Anamorsin OS=Homo sapiens GN=CIAPIN1 PE=1 SV=2;>tr|H3BUG4|H3BUG4_HUMAN Anamorsin OS=Hom 0.08 -0.10 -0.13 0.20 -0.35 -0.24 0.35 -0.14 0.243180151 0.109309964 anatomical structure development;apoptosis;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular metabolic process;cellular process;cofactor biosynthetic process;cofactor metabolic process;death;developmental process;hemopoiesis;hemopoietic or lymphoid organ development;iron-sulfur cluster assembly;metabolic process;metallo-sulfur cluster assembly;methylation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;one-carbon metabolic process;organ development;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;small molecule metabolic process"binding;catalytic activity;iron-sulfur cluster binding;metal cluster binding;methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 1.99E-27 7 4 3 15.9

Q10570 Cleavage and polyadenylation specificity factor subunit 1 CPSF1 >sp|Q10570|CPSF1_HUMAN Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2 0.65 0.21 -0.07 -0.25 0.62 0.33 -0.33 -0.11 0.007412708 0.006692661 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA cleavage;mRNA export from nucleus;mRNA metabolic process;mRNA polyadenylation;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA polyadenylation;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;mRNA cleavage and polyadenylation specificity factor complex;mRNA cleavage factor complex;nuclear part;nucleoplasm part;organelle part;protein complex mRNA surveillance pathway 2.00E-13 1 4 3 4.2

Q02487-2;Q02487 Desmocollin-2 DSC2 >sp|Q02487-2|DSC2_HUMAN Isoform 2B of Desmocollin-2 OS=Homo sapiens GN=DSC2;>sp|Q02487|DSC2_HUMAN Desmocollin-2 OS=Homo sapiens GN=DSC2 PE=1 SV=1 -0.13 0.81 0.19 0.60 -0.15 1.27 -0.26 0.67 0.011525629 -0.014908932 biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;desmosome;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Arrhythmogenic right ventricular cardiomyopathy (ARVC) 1.77E-72 2 4 3 6.7

Q8WXI9 Transcriptional repressor p66-beta GATAD2B >sp|Q8WXI9|P66B_HUMAN Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1 0.08 0.26 0.09 0.47 -0.16 -0.27 -1.01 0.07 0.970643337 0.570139633 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part 3.94E-30 1 4 3 12.1

J3QRU8;Q9Y2X7;Q9Y2X7-3;J3QLH1 ARF GTPase-activating protein GIT1 GIT1 >tr|J3QRU8|J3QRU8_HUMAN ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=4 SV=1;>sp|Q9Y2X7|GIT1_HUMAN ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2;>sp|Q9Y2X7-3|GIT1_HUMAN Isoform 3 of ARF GTPase-activating protein GIT1 0.11 -0.04 0.22 0.16 -0.49 -0.24 -0.15 0.14 0.890410581 0.292690622 biological regulation;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;regulation of ARF GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of G-protein coupled receptor protein signaling pathway;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling ARF GTPase activator activity;binding;cation binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;small GTPase regulator activity;transition metal ion binding;zinc ion binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;focal adhesion;intracellular part Endocytosis;Epithelial cell signaling in Helicobacter pylori infection;Regulation of actin cytoskeleton 8.42E-26 4 4 3 7.2

P50148;B1AM21 Guanine nucleotide-binding protein G(q) subunit alpha GNAQ >sp|P50148|GNAQ_HUMAN Guanine nucleotide-binding protein G(q) subunit alpha OS=Homo sapiens GN=GNAQ PE=1 SV=4;>tr|B1AM21|B1AM21_HUMAN Guanine nucleotide-binding protein G(q) subunit alpha (Fragment) OS=Homo sapiens GN=GNAQ PE=2 SV=1 0.18 0.26 -0.04 0.09 -0.09 0.18 -0.29 -0.13 0.744081897 0.20427594 "activation of adenylate cyclase activity;activation of adenylate cyclase activity by G-protein signaling pathway;activation of phospholipase C activity;activation of phospholipase C activity by dopamine receptor signaling pathway;activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger;anatomical structure development;anatomical structure morphogenesis;behavior;biological regulation;cAMP-mediated signaling;catabolic process;cell activation;cell development;cell maturation;cell surface receptor linked signaling pathway;cellular catabolic process;cellular chemical homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;central nervous system neuron development;chemical homeostasis;cyclic-nucleotide-mediated signaling;developmental maturation;developmental pigmentation;developmental process;dopamine receptor signaling pathway;embryonic digit morphogenesis;embryonic morphogenesis;forebrain neuron development;glutamate signaling pathway;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;GTP catabolic process;GTP metabolic process;heart development;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;inositol phosphate-mediated signaling;intracellular signal transduction;ion homeostasis;metabolic process;negative regulation of catalytic activity;negative regulation of kinase activity;negative regulation of molecular function;negative regulation of protein kinase activity;negative regulation of transferase activity;neuron development;neuron maturation;neuron remodeling;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organ development;pigmentation;platelet activation;positive regulation of adenylate cyclase activity;positive regulation of adenylate cyclase activity by G-protein signaling pathway;positive regulation of catalytic activity;positive regulation of cyclase activity;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of lyase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;post-embryonic development;posttranscriptional regulation of gene expression;primary metabolic process;protein stabilization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of action potential;regulation of adenylate cyclase activity;regulation of adenylate cyclase activity involved in G-protein signaling pathway;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of catenin import into nucleus;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of developmental pigmentation;regulation of developmental process;regulation of establishment of protein localization;regulation of gene expression;regulation of hydrolase activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of lipase activity;regulation of localization;regulation of lyase activity;regulation of macromolecule metabolic process;regulation of melanocyte differentiation;regulation of membrane potential;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of pigment cell differentiation;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein transport;regulation of transferase activity;regulation of transmembrane transport;regulation of transport;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;second-messenger-mediated signaling;signal transduction;skeletal system development;small molecule metabolic process;system development" "binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activator activity;GTPase activity;GTPase regulator activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleoside-triphosphatase regulator activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity" cell part;cytoplasm;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;organelle membrane;organelle part;plasma membrane part;protein complex African trypanosomiasis;Alzheimer's disease;Amoebiasis;Calcium signaling pathway;Chagas disease (American trypanosomiasis);Endocrine and other factor-regulated calcium reabsorption;Gap junction;Gastric acid secretion;GnRH signaling pathway;Huntington's disease;Long-term depression;Long-term potentiation;Melanogenesis;Pancreatic secretion;Phototransduction - fly;Salivary secretion;Vascular smooth muscle contraction 1.94E-22 2 4 3 16.7

Q9Y608-2;Q9Y608-4;A8MXR0;Q9Y608;Q9Y608-3;C9JSU1;C9JJC9;C9JC17;C9J321;C9J0U5 Leucine-rich repeat flightless-interacting protein 2 LRRFIP2 >sp|Q9Y608-2|LRRF2_HUMAN Isoform 2 of Leucine-rich

repeat flightless-interacting protein 2 OS=Homo sapiens GN=LRRFIP2;>sp|Q9Y608-4|LRRF2_HUMAN Isoform 4 of Leucine-rich repeat flightless-interacting protein 2 OS=Homo sapiens GN=LRRFIP2;>tr|A8MXR0|A8MXR0_HU 0.33 -0.14 -0.11 0.03 0.21 0.26 0.22 0.01 0.492778709 -0.144894178 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;Wnt receptor signaling pathway 1.89E-41 10 4 3 14.2
Q16539-2;Q16539;B4E0K5;Q16539-3;Q16539-4;C9JWQ4;E7EX54;Q5R3E6;B5TY33;B7Z630;D7R525;A6NF29;P45984-5;Q5U4A5;P53779-4;B5MDL5;Q308M2;Q499Y8;A8MWW6;H0Y9H3;J3KNK1;Q15759;P53778;P45984-3;P45984-2;P45983-3;P45983-2;Q86YV6;P53779-2;P45984-4;P45984;P53779-3;P45983-4;P45983;P53779;Q32MK0-4;Q9H1R3;B4DUE3;Q32MK0;Q15746-7;Q15746-4;Q15746-5;Q15746-2;Q15746-3;Q15746-6;Q15746Mitogen-activated protein kinase 14 MAPK14>sp|Q16539-2|MK14_HUMAN Isoform CSBP1 of Mitogen-activated protein kinase 14 OS=Homo sapiens GN=MAPK14;>sp|Q16539|MK14_HUMAN Mitogen-activated protein kinase 14 OS=Homo sapiens GN=MAPK14 PE=1 SV=3;>tr|B4E0K5|B4E0K5_HUMAN Mitogen-activated protein kinase 14 0.10 0.03 0.03 -0.14 0.25 -0.24 0.91 -0.01 0.357587516 -0.22589953 "3'-UTR-mediated mRNA stabilization;actin cytoskeleton organization;actin filament-based process;activation of immune response;activation of innate immune response;activation of MAPK activity;actomyosin structure organization;aging;alcohol metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;aorta smooth muscle tissue morphogenesis;apoptosis;apoptotic mitochondrial changes;biological regulation;biosynthetic process;bleb assembly;carbohydrate metabolic process;carboxylic acid metabolic process;cardiac cell differentiation;cardiac muscle cell differentiation;cardiac muscle contraction;cardiac muscle tissue morphogenesis;cardiac myofibril assembly;cell activation;cell aging;cell communication;cell cycle arrest;cell cycle checkpoint;cell cycle process;cell death;cell differentiation;cell morphogenesis;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-cell signaling;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular hypotonic response;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to external stimulus;cellular response to growth factor stimulus;cellular response to interleukin-1;cellular response to ionizing radiation;cellular response to light stimulus;cellular response to lipopolysaccharide;cellular response to mechanical stimulus;cellular response to molecule of bacterial origin;cellular response to organic substance;cellular response to osmotic stress;cellular response to radiation;cellular response to stimulus;cellular response to stress;cellular response to tumor necrosis factor;cellular response to UV;cellular response to vascular endothelial growth factor stimulus;cellular senescence;central nervous system development;chemotaxis;chondrocyte differentiation;circulatory system process;cytoskeleton organization;death;defense response;developmental process;DNA damage checkpoint;DNA damage induced protein phosphorylation;DNA integrity checkpoint;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;fatty acid metabolic process;fatty acid oxidation;gene expression;glucose metabolic process;hexose metabolic process;hypotonic response;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;leukocyte differentiation;lipid metabolic process;lipid modification;lipid oxidation;lipopolysaccharide-mediated signaling pathway;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;mitochondrial transport;mitochondrion organization;monocarboxylic acid metabolic process;monosaccharide metabolic process;mRNA metabolic process;mRNA stabilization;multicellular organismal process;muscle cell differentiation;muscle contraction;muscle organ development;muscle structure development;muscle system process;muscle tissue development;muscle tissue morphogenesis;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;myeloid cell differentiation;myeloid leukocyte differentiation;myoblast differentiation;myofibril assembly;negative regulation of apoptosis;negative regulation of binding;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cellular process;negative regulation of molecular function;negative regulation of programmed cell death;negative regulation of protein binding;nerve growth factor receptor signaling pathway;neuromuscular synaptic transmission;neuron projection development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle organization;organic acid metabolic process;ossification;osteoclast differentiation;oxidation-reduction process;oxoacid metabolic process;pattern recognition receptor signaling pathway;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;peptidyl-threonine modification;peptidyl-threonine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of calcium ion transport;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell morphogenesis involved in differentiation;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemokine production;positive regulation of cytokine production;positive regulation of cytoskeleton organization;positive regulation of deacetylase activity;positive regulation of defense response;positive regulation of determination of dorsal identity;positive regulation of developmental process;positive regulation of erythrocyte differentiation;positive regulation of fatty acid biosynthetic process;positive regulation of fatty acid metabolic process;positive regulation of fatty acid transport;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of icosanoid secretion;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of ion transport;positive regulation of kinase activity;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of lipid transport;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of macrophage derived foam cell differentiation;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle cell differentiation;positive regulation of myeloid cell differentiation;positive regulation of nitric oxide biosynthetic process;positive regulation of nitric-oxide synthase biosynthetic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of organelle organization;positive regulation of organic acid transport;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of prostaglandin biosynthetic process;positive regulation of prostaglandin secretion;positive regulation of protein import into nucleus;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of protein transport;positive regulation of reactive oxygen species metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of sarcomere organization;positive regulation of secretion;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of wound healing;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein autophosphorylation;protein import;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein targeting to mitochondrion;protein transport;Ras protein signal transduction;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcium ion transport;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chemokine production;regulation of cytokine production;regulation of cytoskeleton organization;regulation of defense response;regulation of determination of dorsal identity;regulation of developmental process;regulation of erythrocyte differentiation;regulation of establishment of protein localization;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of fatty acid transport;regulation of gene expression;regulation of homeostatic process;regulation of hydrolase activity;regulation of icosanoid secretion;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of ion transport;regulation of JNK cascade;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of lipid transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of macrophage derived foam cell differentiation;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of mRNA stability;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of muscle contraction;regulation of muscle filament sliding;regulation of muscle system process;regulation of myeloid cell differentiation;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase biosynthetic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organelle organization;regulation of organic acid transport;regulation of phosphate metabolic

process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of prostaglandin biosynthetic process;regulation of prostaglandin secretion;regulation of protein binding;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of protein ubiquitination;regulation of reactive oxygen species metabolic process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA stability;regulation of sarcomere organization;regulation of secretion;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of striated muscle cell differentiation;regulation of system process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmembrane transport;regulation of transport;regulation of vascular permeability;regulation of vascular permeability involved in acute inflammatory response;regulation of wound healing;release of cytochrome c from mitochondria;response to abiotic stimulus;response to amine stimulus;response to biotic stimulus;response to cadmium ion;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to growth factor stimulus;response to inorganic substance;response to interleukin-1;response to ionizing radiation;response to light stimulus;response to lipopolysaccharide;response to mechanical stimulus;response to metal ion;response to molecule of bacterial origin;response to muramyl dipeptide;response to organic nitrogen;response to organic substance;response to osmotic stress;response to peptidoglycan;response to radiation;response to stimulus;response to stress;response to toxin;response to tumor necrosis factor;response to UV;RNA biosynthetic process;RNA metabolic process;RNA stabilization;sarcomere organization;sarcomerogenesis;satellite cell differentiation;signal transduction;signal transduction in response to DNA damage;signaling;skeletal muscle cell differentiation;skeletal muscle tissue development;small GTPase mediated signal transduction;small molecule metabolic process;smooth muscle contraction;stem cell differentiation;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;stress-induced premature senescence;striated muscle cell differentiation;striated muscle contraction;striated muscle tissue development;synaptic transmission;system development;system process;taxis;tissue development;tissue morphogenesis;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;tonic smooth muscle contraction;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;transport;TRIF-dependent toll-like receptor signaling pathway;vascular endothelial growth factor receptor signaling pathway;vascular process in circulatory system" "adenyl nucleotide binding;adenyl ribonucleotide binding;apoptotic protease activator activity;ATP binding;binding;calmodulin binding;calmodulin-dependent protein kinase activity;caspase activator activity;caspase regulator activity;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;histone deacetylase regulator activity;ion binding;JUN kinase activity;kinase activity;magnesium ion binding;MAP kinase activity;MAP kinase kinase activity;metal ion binding;molecular transducer activity;myosin light chain kinase activity;NFAT protein binding;nucleotide binding;peptidase activator activity;peptidase regulator activity;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein serine/threonine kinase activity;protein serine/threonine/tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;ribonucleotide binding;SAP kinase activity;signal transducer activity;transcription factor binding;transferase activity;transferase activity, transferring phosphorus-containing groups" actin cytoskeleton;actin filament bundle;actomyosin;cell division site part;cell part;cell projection;cleavage furrow;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;cytosolic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane;sarcomere;spindle pole;stress fiber Adipocytokine signaling pathway;Amyotrophic lateral sclerosis (ALS);Calcium signaling pathway;Chagas disease (American trypanosomiasis);Colorectal cancer;Epithelial cell signaling in Helicobacter pylori infection;ErbB signaling pathway;Fc epsilon RI signaling pathway;Focal adhesion;Gastric acid secretion;GnRH signaling pathway;Hepatitis C;Insulin signaling pathway;ko05152;Leishmaniasis;Leukocyte transendothelial migration;MAPK signaling pathway;MAPK signaling pathway - yeast;Neurotrophin signaling pathway;NOD-like receptor signaling pathway;Osteoclast differentiation;Pancreatic cancer;Pathways in cancer;Progesterone-mediated oocyte maturation;Protein processing in endoplasmic reticulum;Regulation of actin cytoskeleton;RIG-I-like receptor signaling pathway;Shigellosis;T cell receptor signaling pathway;Toll-like receptor signaling pathway;Toxoplasmosis;Type II diabetes mellitus;Vascular smooth muscle contraction;VEGF signaling pathway;Wnt signaling pathway 2.26E-11 46 4 3 10

Q9NYL2;C9J3F7;Q9NYL2-3 Mitogen-activated protein kinase kinase kinase MLT MLTK >sp|Q9NYL2|MLTK_HUMAN Mitogen-activated protein kinase kinase kinase MLT OS=Homo sapiens GN=MLTK PE=1 SV=3 0.01 -0.39 0.70 0.15 -1.41 -0.72 -0.32 -0.39 1.040115648 0.825836829 activation of JUN kinase activity;activation of MAPK activity;activation of MAPKK activity;activation of protein kinase activity;biological regulation;cell cycle arrest;cell cycle checkpoint;cell cycle process;cell death;cell differentiation;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cytoskeleton organization;death;developmental process;DNA damage checkpoint;DNA integrity checkpoint;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of JUN kinase activity;positive regulation of kinase activity;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;response to abiotic stimulus;response to DNA damage stimulus;response to radiation;response to stimulus;response to stress;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;MAP kinase kinase kinase activity;metal ion binding;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle MAPK signaling pathway;Tight junction 4.50E-19 3 4 3 6.5

Q9BPW8;H7C2U6;C9JDV8;F8WCR5 Protein NipSnap homolog 1 NIPSNAP1 >sp|Q9BPW8|NIPS1_HUMAN Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1;>tr|H7C2U6|H7C2U6_HUMAN Protein NipSnap homolog 1 (Fragment) OS=Homo sapiens GN=NIPSNAP1 PE=4 SV=1 -0.09 -0.04 0.07 0.04 0.01 0.13 0.07 0.11 0.797559571 -0.082721853 multicellular organismal process;neurological system process;sensory perception;sensory perception of pain;system processbinding;neurotransmitter binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part;synapse part;synaptic membrane 6.47E-14 4 4 3 18.7

Q08752 Peptidyl-prolyl cis-trans isomerase D PPID >sp|Q08752|PPID_HUMAN Peptidyl-prolyl cis-trans isomerase D OS=Homo sapiens GN=PPID PE=1 SV=30.22 0.10 -0.26 -0.03 -0.46 -0.74 0.13 -1.06 0.846540701 0.539975487 "apoptosis;biological regulation;cell death;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to light stimulus;cellular response to radiation;cellular response to stimulus;cellular response to UV;cellular response to UV-A;chaperone-mediated protein folding;death;establishment of localization;establishment of protein localization;lipid particle organization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of reproductive process;positive regulation of secretion;positive regulation of transport;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;programmed cell death;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein transport;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of establishment of protein localization;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of reproductive process;regulation of RNA metabolic process;regulation of secretion;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transport;regulation of viral genome replication;regulation of viral reproduction;release of virus from host;reproductive process;response to abiotic stimulus;response to light stimulus;response to radiation;response to stimulus;response to UV;response to UV-A;transport;viral reproductive process"binding;catalytic activity;cis-trans isomerase activity;cyclosporin A binding;drug binding;estrogen receptor binding;heat shock protein binding;hormone receptor binding;Hsp70 protein binding;Hsp90 protein binding;isomerase activity;nuclear hormone receptor binding;peptide binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;receptor binding;steroid hormone receptor binding;transcription factor binding cell part;cytoplasm;cytoskeleton;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part Calcium signaling pathway;Huntington's disease;Parkinson's disease 1.20E-08 1 4 3 10.5

B4DPM9;P34896-2;P34896;P34896-3 "Serine hydroxymethyltransferase;Serine hydroxymethyltransferase, cytosolic" SHMT1 ">tr|B4DPM9|B4DPM9_HUMAN Serine hydroxymethyltransferase OS=Homo sapiens GN=SHMT1 PE=2 SV=1;>sp|P34896-2|GLYC_HUMAN Isoform 2 of Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1;>sp|P34896|GLYC_HUMAN Serine hydroxymethyltransferase, cytos" -0.69 -0.36 0.95 0.46 -1.13 -1.43 -0.53 -0.97 1.111724124 1.10697034 amine biosynthetic process;amine catabolic process;amine metabolic process;betaine biosynthetic process;betaine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;carnitine biosynthetic process;carnitine metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;folic acid metabolic process;folic acid-containing compound metabolic process;glycine biosynthetic process;glycine biosynthetic process from serine;glycine metabolic process;heterocycle metabolic process;L-serine catabolic process;L-serine metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;one-carbon metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;pigment biosynthetic process;pigment metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;pteridine-containing compound metabolic process;purine base biosynthetic process;purine base metabolic process;purine-containing compound metabolic process;serine family amino acid biosynthetic process;serine family amino acid catabolic process;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;tetrahydrofolate interconversion;tetrahydrofolate metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "aldehyde-lyase activity;amine binding;amino acid binding;binding;carbon-carbon lyase activity;carboxylic acid binding;catalytic activity;cofactor binding;glycine hydroxymethyltransferase activity;hydroxymethyl-, formyl- and related transferase activity;identical protein binding;L-allo-threonine aldolase activity;lyase activity;methyltransferase activity;protein binding;protein dimerization activity;protein homodimerization activity;pyridoxal phosphate binding;threonine aldolase activity;transferase activity;transferase activity, transferring one-carbon groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle "Cyanoamino acid metabolism;Glycine, serine and threonine metabolism;Methane metabolism;One carbon pool by folate" 4.22E-58 4 4 3 17.4

Q13033-2;Q13033;G3V340;G3V3G7;M0QXN2;M0R2A7;M0QYS2;M0R0W8 Striatin-3 STRN3 >sp|Q13033-2|STRN3_HUMAN Isoform Alpha of Striatin-3 OS=Homo sapiens GN=STRN3;>sp|Q13033|STRN3_HUMAN Striatin-3 OS=Homo sapiens GN=STRN3 PE=1 SV=3;>tr|G3V340|G3V340_HUMAN Striatin-3 OS=Homo sapiens GN=STRN3 PE=2 SV=1;>tr|G3V3G7|G3V3G7_HUMAN Striatin-3 (Fra 0.00 0.02 -0.30 0.00 -0.75 -0.29 -0.17 0.30 0.269520853 0.159777893 "biological regulation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of estrogen receptor signaling pathway;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to hormone stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus" binding;calmodulin binding;enzyme binding;nucleic acid binding transcription factor activity;phosphatase binding;protein binding;protein complex binding;protein phosphatase 2A binding;protein phosphatase binding;sequence-specific DNA binding transcription factor activitycell body;cell part;cell projection;cytoplasm;cytoplasmic part;dendrite;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;neuron projection;neuronal cell body;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane;protein complex 6.20E-21 8 4 3 8

F5GYK2;Q9NRL3;F8VYA6;M0R0P4;B4DQH7;R4GN16;M0R317 Striatin-4 STRN4 >tr|F5GYK2|F5GYK2_HUMAN Striatin-4 OS=Homo sapiens GN=STRN4 PE=2 SV=1;>sp|Q9NRL3|STRN4_HUMAN Striatin-4 OS=Homo sapiens GN=STRN4 PE=1 SV=2;>tr|F8VYA6|F8VYA6_HUMAN Striatin-4 OS=Homo sapiens GN=STRN4 PE=2 SV=1;>tr|M0R0P4|M0R0P4_HUMAN Striatin-4 (Fragment) O -0.09 0.14 0.01 0.15 -0.05 0.14 -0.05 -0.04 0.274922275 0.051816947 binding;calmodulin binding;enzyme binding;phosphatase binding;protein binding;protein complex binding;protein phosphatase 2A binding;protein phosphatase binding cell part;cell projection;cell projection part;cytoplasm;dendritic spine;intracellular part;macromolecular complex;membrane;neuron projection;neuron spine;protein complex 2.38E-13 7 4 3 7.7

Q9H2K8;H0YF68;G3V1Q8 Serine/threonine-protein kinase TAO3 TAOK3 >sp|Q9H2K8|TAOK3_HUMAN Serine/threonine-protein kinase TAO3 OS=Homo sapiens GN=TAOK3 PE=1 SV=2 -0.05 0.06 0.07 0.00 0.48 0.27 0.25 0.02 0.991553424 -0.232511699 biological regulation;cell cycle checkpoint;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA damage checkpoint;DNA integrity checkpoint;DNA metabolic process;DNA repair;G2/M transition checkpoint;G2/M transition DNA damage checkpoint;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of intracellular protein kinase cascade;negative regulation of JNK cascade;negative regulation of MAPKKK cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of stress-activated protein kinase signaling cascade;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of JNK cascade;positive regulation of JUN kinase activity;positive regulation of kinase activity;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of transferase activity;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme inhibitor activity;enzyme regulator activity;kinase activity;kinase inhibitor activity;kinase regulator activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle;plasma membrane MAPK signaling pathway 8.26E-17 3 4 3 6.6

Q12800-2;Q12800-3;Q12800-4;Q12800;F8VX55;F8VWL0;C9JWL3Alpha-globin transcription factor CP2 TFCP2 >sp|Q12800-2|TFCP2_HUMAN Isoform 2 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2;>sp|Q12800-3|TFCP2_HUMAN Isoform 3 of Alpha-globin transcription factor CP2 OS=Homo sapiens GN=TFCP2;>sp|Q12800-4|TFCP2_HUMAN Isoform 4 of Alpha-globin tra -0.12 -0.17 0.27 0.01 0.03 -0.15 0.21 -0.28 0.112067233 0.04644212 "anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.40E-27 7 4 3 14.2

Q6ZXV5-2;Q6ZXV5 Transmembrane and TPR repeat-containing protein 3 TMTC3 >sp|Q6ZXV5-2|TMTC3_HUMAN Isoform 2 of Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3;>sp|Q6ZXV5|TMTC3_HUMAN Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2 -0.03 0.36 -0.50 -0.01 0.61 0.88 -0.11 1.02 0.893390257 -0.644241142 anatomical structure development;axis elongation;biological regulation;branch elongation of an epithelium;bud outgrowth involved in lung branching;cell development;cellular developmental process;cellular process;developmental growth;developmental growth involved in morphogenesis;developmental process;growth;lung alveolus development;muscle cell development;muscle fiber development;post-embryonic development;regulation of biological process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;striated muscle cell development cell part;integral to membrane;intrinsic to membrane;membrane part 7.88E-24 2 4 3 5.6

Q712K3 Ubiquitin-conjugating enzyme E2 R2 UBE2R2 >sp|Q712K3|UB2R2_HUMAN Ubiquitin-conjugating enzyme E2 R2 OS=Homo sapiens GN=UBE2R2 PE=1 SV=1 0.13 -0.04 -0.02 -0.23 0.04 -0.21 0.43 -0.03 0.239119442 -0.095702904 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein K48-linked ubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein polyubiquitination;protein ubiquitination"acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small conjugating protein ligase activity;ubiquitin-protein ligase activity" Ubiquitin mediated proteolysis 4.18E-11 1 4 3 16.4

B7ZB63;P84077;P61204;F5H423;H0YGG7 ADP-ribosylation factor 1;ADP-ribosylation factor 3 ARF3;ARF1 >tr|B7ZB63|B7ZB63_HUMAN ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=2 SV=1;>sp|P84077|ARF1_HUMAN ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2;>sp|P61204|ARF3_HUMAN ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2;>tr|F5H4 -0.10 0.05 -1.04 0.18 -0.44 0.19 -0.01 0.06 0.219585779 -0.178741118 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;biosynthetic process;cation homeostasis;cellular biosynthetic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular copper ion homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chemical homeostasis;COPI coating of Golgi vesicle;copper ion homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;Golgi transport vesicle coating;Golgi vesicle transport;homeostatic process;immune system process;intracellular signal transduction;intracellular transport;ion homeostasis;lipid biosynthetic process;lipid metabolic process;metabolic process;organelle organization;organophosphate metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;post-Golgi vesicle-mediated transport;primary metabolic process;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;response to stimulus;retrograde vesicle-mediated transport, Golgi to ER;signal transduction;small GTPase mediated signal transduction;transport;vesicle coating;vesicle organization;vesicle-mediated transport;viral reproduction" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor signaling protein activity;ribonucleotide binding;signal transducer activity" cell part;contractile fiber part;cytoplasmic part;cytosol;Golgi apparatus part;Golgi membrane;intracellular;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;sarcomere Vibrio cholerae infection 4.24E-97 5 5 3 34.7

P84085;C9J1Z8;F5H1V1;F5H6T5;F8WCJ5;F8WDB3;F5H0C7;I3L2E4;I3L1V5;Q8IVW1-2;Q8IVW1;I3L3L1;Q969Q4;Q8IVW1-4 ADP-ribosylation factor 5 ARF5 >sp|P84085|ARF5_HUMAN ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2;>tr|C9J1Z8|C9J1Z8_HUMAN ADP-ribosylation factor 5 (Fragment) OS=Homo sapiens GN=ARF5 PE=2 SV=1 0.09 -0.17 -0.22 0.01 -0.24 -0.14 0.33 0.05 0.184520928 -0.071723921 biological regulation;cellular process;cellular response to stimulus;establishment of localization;establishment of protein localization;intracellular signal transduction;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;Golgi apparatus;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle;perinuclear region of cytoplasm;plasma membrane 4.41E-28 14 5 3 27.8

Q13557-8;Q13557-12;Q13557-9;Q13557-10;Q13557-5;D6R938;Q13557;Q13557-3;E9PBG7;Q13557-6;Q13557-4;Q13557-11;E9PF82;B7Z1Z6;Q13554-7;Q9UQM7;Q13554-4;Q9UQM7-2;Q13554-6;Q13554-3;Q13554-8;Q13554-5;Q13554-2;Q13554;H0Y9J2;H0Y9C2;H7BXS4;D6RHX9;E9PBE8;E7EQE4;H7BZC6 Calcium/calmodulin-dependent protein kinase type II subunit delta;Calcium/calmodulin-dependent protein kinase type II subunit alpha;Calcium/calmodulin-dependent protein kinase type II subunit beta CAMK2D;CAMK2B;CAMK2A >sp|Q13557-8|KCC2D_HUMAN Isoform Delta 6 of Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo sapiens GN=CAMK2D;>sp|Q13557-12|KCC2D_HUMAN Isoform Delta 12 of Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Homo 0.00 -0.09 0.07 0.23 0.81 0.46 0.18 0.72 1.291692961 -0.492347474 "activation of meiosis involved in egg activation;biological regulation;calcium ion transport;calcium-mediated signaling;cardiac muscle contraction;cation transport;cell communication;cell cycle process;cell surface receptor linked signaling pathway;cell-cell signaling;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;G1/S transition of mitotic cell cycle;inhibitory G-protein coupled receptor phosphorylation;interferon-gamma-mediated signaling pathway;intracellular signal transduction;ion transport;macromolecule metabolic process;macromolecule modification;metabolic process;metal ion transport;multicellular organismal process;muscle contraction;muscle system process;neurological system process;neuromuscular process;neuromuscular process controlling balance;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cardiac muscle hypertrophy;positive regulation of cell cycle process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of dendritic spine development;positive regulation of dendritic spine morphogenesis;positive regulation of developmental process;positive regulation of meiosis;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle hypertrophy;positive regulation of neuron projection development;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of synapse maturation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cardiac muscle hypertrophy;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of dendritic spine development;regulation of dendritic spine morphogenesis;regulation of developmental process;regulation of gene expression;regulation of growth;regulation of heart contraction;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of long-term neuronal synaptic plasticity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of meiosis;regulation of meiotic cell cycle;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle adaptation;regulation of muscle contraction;regulation of muscle hypertrophy;regulation of muscle system process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of neurotransmitter secretion;regulation of neurotransmitter transport;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of RNA metabolic process;regulation of ryanodine-sensitive calcium-release channel activity;regulation of secretion;regulation of sequence-specific DNA binding transcription factor activity;regulation of signaling;regulation of skeletal muscle adaptation;regulation of sodium ion transport;regulation of striated muscle contraction;regulation of synapse maturation;regulation of synapse organization;regulation of synapse structural plasticity;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of synaptic transmission, cholinergic;regulation of system process;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transmission of nerve impulse;regulation of transport;regulation of transporter activity;response to cadmium ion;response to chemical stimulus;response to cytokine stimulus;response to inorganic substance;response to interferon-gamma;response to metal ion;response to organic substance;response to stimulus;second-messenger-mediated signaling;signal transduction;signaling;striated muscle contraction;synaptic transmission;system process;transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calmodulin-dependent protein kinase activity;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" axon part;calcium- and calmodulin-dependent protein kinase complex;cell body;cell junction;cell part;cell projection part;cell-cell contact zone;cell-cell junction;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endocytic vesicle membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;initial segment;intercalated disc;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;microtubule organizing center;neuromuscular junction;neuronal cell body;nuclear part;nucleoplasm;organelle membrane;organelle part;plasma membrane;plasma membrane part;presynaptic membrane;protein complex;sarcoplasmic reticulum membrane;spindle midzone;synapse;synapse part;synaptic membrane;T-tubule;vesicle membrane Calcium signaling pathway;ErbB signaling pathway;Gastric acid secretion;Glioma;GnRH signaling pathway;ko05152;Long-term potentiation;Melanogenesis;Neurotrophin signaling pathway;Olfactory transduction;Oocyte meiosis;Phototransduction - fly;Wnt signaling pathway 2.74E-32 31 5 3 13.4

E5RHW4;O94905;E5RJ09 Erlin-2 ERLIN2 >tr|E5RHW4|E5RHW4_HUMAN Erlin-2 (Fragment) OS=Homo sapiens GN=ERLIN2 PE=2 SV=1;>sp|O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 -0.52 0.31 -0.32 0.82 0.09 0.28 -0.59 0.40 0.023404505 0.026935052 catabolic process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;death;ER-associated protein catabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;protein complex 4.46E-28 3 5 3 18

P51116 Fragile X mental retardation syndrome-related protein 2 FXR2 >sp|P51116|FXR2_HUMAN Fragile X mental retardation syndrome-related protein 2 OS=Homo sapiens GN=FXR2 PE=1 SV=2 0.04 0.07 0.07 0.05 -0.02 0.08 -0.40 -0.52 0.793641194 0.270229509 binding;nucleic acid binding;RNA binding cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex 1.80E-20 1 5 3 10

P46926;B7Z3X4;D6RAY7;D6R9P4;D6R917;D6RB13;E7EVU7;D6RFF8 Glucosamine-6-phosphate isomerase 1 GNPDA1 >sp|P46926|GNPI1_HUMAN Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1;>tr|B7Z3X4|B7Z3X4_HUMAN Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=2 SV=1;>tr|D6RAY7|D6RAY7_HUMAN Glucosamine-6-phosphate isomerase 1 (Frag 0.01 -0.20 -0.49 0.02 -0.35 -0.21 0.28 -0.26 0.058494695 -0.031999997 alcohol catabolic process;alcohol metabolic process;amino sugar catabolic process;amino sugar metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;fertilization;generation of precursor metabolites and energy;glucosamine catabolic process;glucosamine metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;N-acetylglucosamine metabolic process;primary metabolic process;reproductive process;single fertilization;small molecule catabolic process;small molecule metabolic process "catalytic activity;deaminase activity;glucosamine-6-phosphate deaminase activity;hydrolase activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting aldoses and ketoses;isomerase activity" cell part;cytoplasm;intracellular part Amino sugar and nucleotide sugar metabolism 1.31E-35 8 5 3 20.8

O95104-3;O95104;O95104-2 "Splicing factor, arginine/serine-rich 15" SCAF4 ">sp|O95104-3|SFR15_HUMAN Isoform 3 of Splicing factor, arginine/serine-rich 15 OS=Homo sapiens GN=SCAF4;>sp|O95104|SFR15_HUMAN Splicing factor, arginine/serine-rich 15 OS=Homo sapiens GN=SCAF4 PE=1 SV=3;>sp|O95104-2|SFR15_HUMAN Isoform 2 of Splicing factor" -0.12 0.40 0.25 0.37 -0.09 0.25 -0.99 -0.31 0.755702931 0.507975891 binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.23E-24 3 5 3 8

Q13043;Q13043-2;F5H5B4 Serine/threonine-protein kinase 4;Serine/threonine-protein kinase 4 37kDa subunit;Serine/threonine-protein kinase 4 18kDa subunit STK4 >sp|Q13043|STK4_HUMAN Serine/threonine-protein kinase 4 OS=Homo sapiens GN=STK4 PE=1 SV=2;>sp|Q13043-2|STK4_HUMAN Isoform 2 of Serine/threonine-protein kinase 4 OS=Homo sapiens GN=STK4;>tr|F5H5B4|F5H5B4_HUMAN Serine/threonine-protein kinase 4 OS=Homo sapie 0.25 -0.05 0.09 -0.10 -0.29 -0.34 0.33 -0.09 0.334471846 0.143923322 anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptosis;biological regulation;branching morphogenesis of a tube;cell death;cell differentiation;cell differentiation involved in embryonic placenta development;cell morphogenesis;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;central nervous system development;death;developmental process;embryonic epithelial tube formation;embryonic hemopoiesis;embryonic organ development;endocardium development;epidermal cell differentiation;epithelial cell differentiation;epithelial tube formation;hemopoiesis;hemopoietic or lymphoid organ development;hippo signaling cascade;induction of apoptosis;induction of programmed cell death;intracellular protein kinase cascade;intracellular signal transduction;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of growth;negative regulation of organ growth;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;neural tube formation;organ development;pattern specification process;patterning of blood vessels;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;primitive hemopoiesis;programmed cell death;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of apoptosis;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of growth;regulation of organ growth;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of Wnt receptor signaling pathway;response to stimulus;signal transduction;system development;tissue morphogenesis;tube formation;tube morphogenesis "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;identical protein binding;ion binding;kinase activator activity;kinase activity;kinase regulator activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein dimerization activity;protein homodimerization activity;protein kinase activator activity;protein kinase activity;protein kinase regulator activity;protein serine/threonine kinase activator activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle MAPK signaling pathway;Non-small cell lung cancer;Pathways in cancer 5.97E-48 3 5 3 15.4

Q92599-2;A6NMH6;A6NFQ9;F6W7K9;F8W8I8;Q92599;Q92599-3;C9JV02;H7C604;C9J4G8 Septin-8 08-Sep >sp|Q92599-2|SEPT8_HUMAN Isoform 2 of Septin-8 OS=Homo sapiens GN=SEPT8;>tr|A6NMH6|A6NMH6_HUMAN Septin-8 OS=Homo sapiens GN=SEPT8 PE=2 SV=1;>tr|A6NFQ9|A6NFQ9_HUMAN Septin-8 OS=Homo sapiens GN=SEPT8 PE=2 SV=1;>tr|F6W7K9|F6W7K9_HUMAN Septin-8 OS=Homo sapiens 0.12 -0.20 -0.08 0.00 -0.17 -0.07 -0.31 -0.12 0.626479355 0.126743181 cell cycle;cellular process binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell cortex part;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex;septin complex 2.01E-18 10 6 3 16.1

O75223;M0QZK8;O75223-3;O75223-2;O75223-4 Gamma-glutamylcyclotransferase GGCT >sp|O75223|GGCT_HUMAN Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1;>tr|M0QZK8|M0QZK8_HUMAN Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=4 SV=1;>sp|O75223-3|GGCT_HUMAN Isoform 3 of Gamma-glutamylcyclotransferase OS=Homo sapi 0.14 0.27 0.04 -0.08 0.03 0.01 0.43 -0.49 0.177603432 0.097394047 amine biosynthetic process;amine metabolic process;apoptotic mitochondrial changes;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutathione biosynthetic process;glutathione metabolic process;metabolic process;mitochondrion organization;nitrogen compound metabolic process;organelle organization;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptide biosynthetic process;peptide metabolic process;primary metabolic process;release of cytochrome c from mitochondria;small molecule biosynthetic process;small molecule metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;xenobiotic metabolic process "binding;catalytic activity;gamma-glutamylcyclotransferase activity;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring amino-acyl groups" cell part;cytoplasmic part;cytosol;intracellular part Glutathione metabolism 9.51E-72 5 6 3 37.2

O43896;E7ERX9;Q9NQT8 Kinesin-like protein KIF1C KIF1C >sp|O43896|KIF1C_HUMAN Kinesin-like protein KIF1C OS=Homo sapiens GN=KIF1C PE=1 SV=3 -0.03 -0.06 0.65 0.00 0.01 0.19 0.50 0.20 0.162577342 -0.087965616 "biological regulation;cell activation;cellular component movement;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;leukocyte activation;lymphocyte activation;microtubule-based movement;microtubule-based process;protein targeting;protein transport;regulation of anatomical structure morphogenesis;regulation of axonogenesis;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;response to stimulus;retrograde vesicle-mediated transport, Golgi to ER;signal transduction;T cell activation;transport;vesicle-mediated transport" "14-3-3 protein binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" axon;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;microtubule associated complex;neuron projection;organelle;organelle part;protein complex 1.12E-25 3 6 3 5.7

O75179-6;H0YM23;E7EUV3;O75179-2;O75179;O75179-3;O75179-5;O75179-4;H0YLQ3;Q8IWZ3-5;Q8IWZ3-2;H0YMS3;D6RHC4;Q8IWZ3-3 Ankyrin repeat domain-containing protein 17 ANKRD17 >sp|O75179-6|ANR17_HUMAN Isoform 6 of Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17;>tr|H0YM23|H0YM23_HUMAN Ankyrin repeat domain-containing protein 17 (Fragment) OS=Homo sapiens GN=ANKRD17 PE=4 SV=1;>tr|E7EUV3|E7EUV3_HUMAN Ankyrin 0.47 0.12 0.03 -0.04 -0.43 -0.36 -0.04 0.04 0.904455211 0.339749314 anatomical structure maturation;biological regulation;blood vessel maturation;developmental maturation;developmental process;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of muscle cell differentiation;negative regulation of smooth muscle cell differentiation;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of muscle cell differentiation;regulation of smooth muscle cell differentiation;reproductive process;viral reproductive process;virus-host interaction binding;nucleic acid binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.26E-157 14 7 3 5

O95716;M0R257;Q96E17 Ras-related protein Rab-3D RAB3D >sp|O95716|RAB3D_HUMAN Ras-related protein Rab-3D OS=Homo sapiens GN=RAB3D PE=1 SV=1 -0.12 -0.01 1.30 0.05 0.07 -0.33 -0.44 -0.42 0.70907447 0.587002515 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;intracellular signal transduction;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;one-carbon metabolic process;peptidyl-amino acid modification;peptidyl-cysteine methylation;peptidyl-cysteine modification;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;secretion;secretion by cell;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;plasma membrane;stored secretory granule;synapse part;synaptic vesicle;transport vesicle;vesicle;zymogen granule Pancreatic secretion 2.38E-72 3 7 3 35.2

P35321 Cornifin-A SPRR1A >sp|P35321|SPR1A_HUMAN Cornifin-A OS=Homo sapiens GN=SPRR1A PE=1 SV=2 0.03 0.62 -0.09 -0.01 1.32 1.96 0.84 0.04 0.886112366 -0.903626266 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity" cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 9.72E-113 1 7 3 95.5

O43865;O43865-2 Putative adenosylhomocysteinase 2 AHCYL1>sp|O43865|SAHH2_HUMAN Putative adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2;>sp|O43865-2|SAHH2_HUMAN Isoform 2 of Putative adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 0.10 0.05 -0.53 -0.07 0.28 0.11 0.39 -0.04 0.739412703 -0.299135252 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA metabolic process;mRNA polyadenylation;mRNA processing;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;one-carbon metabolic process;positive regulation of biological process;positive regulation of ion transport;positive regulation of sodium ion transport;positive regulation of transport;primary metabolic process;protein export from nucleus;protein targeting;protein transport;regulation of anion transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of mRNA 3'-end processing;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of sodium ion transport;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;RNA 3'-end processing;RNA metabolic process;RNA polyadenylation;RNA processing;small molecule metabolic process;transport "adenosylhomocysteinase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ether bonds;trialkylsulfonium hydrolase activity" cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle Cysteine and methionine metabolism 3.30E-19 2 8 3 13.6

P52294;C9JYI4;C9J352;C9JWD9;F2Z3G4;C9J4U1;H0Y3K0;Q5TD90 Importin subunit alpha-1KPNA1 >sp|P52294|IMA5_HUMAN Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3;>tr|C9JYI4|C9JYI4_HUMAN Importin subunit alpha-1 (Fragment) OS=Homo sapiens GN=KPNA1 PE=2 SV=1;>tr|C9J352|C9J352_HUMAN Importin subunit alpha-1 (Fragment) OS=Homo sapiens GN= 0.03 -0.05 0.05 0.07 -0.10 0.16 0.11 -0.09 0.042603686 0.009282411 "biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;positive regulation of biological process;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of transmembrane transport;positive regulation of transport;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA recombination;regulation of establishment of protein localization;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of transmembrane transport;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction;transport;viral infectious cycle;viral reproductive process" binding;nuclear localization sequence binding;peptide binding;protein transporter activity;signal sequence binding;substrate-specific transporter activity;transporter activity cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;dendrite;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;neuron projection;nuclear part;nuclear pore;nucleoplasm;nucleus;organelle;organelle part;pore complex;protein complex 3.09E-57 8 8 3 16.5

P12931;P12931-2 Proto-oncogene tyrosine-protein kinase Src SRC >sp|P12931|SRC_HUMAN Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC PE=1 SV=3;>sp|P12931-2|SRC_HUMAN Isoform 2 of Proto-oncogene tyrosine-protein kinase Src OS=Homo sapiens GN=SRC 0.06 0.18 -0.25 0.26 -0.36 0.03 -0.52 0.11 0.553184227 0.248111836 anatomical structure development;anatomical structure homeostasis;anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;bone resorption;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a tube;cell activation;cell adhesion;cell cycle;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to progesterone stimulus;cellular response to steroid hormone stimulus;cellular response to stimulus;chemotaxis;circulatory system process;defense response;developmental process;developmental process involved in reproduction;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;female gamete generation;fibroblast growth factor receptor signaling pathway;forebrain development;gamete generation;homeostatic process;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular receptor mediated signaling pathway;intracellular signal transduction;leukocyte migration;locomotion;lymphocyte costimulation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;membrane organization;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell adhesion;negative regulation of cell death;negative regulation of cell-matrix adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of focal adhesion assembly;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of protein complex assembly;negative regulation of protein homooligomerization;negative regulation of protein oligomerization;nerve growth factor receptor signaling pathway;oogenesis;organ development;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of biological process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of ERK1 and ERK2 cascade;positive regulation of immune system process;positive regulation of integrin activation;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of MAPKKK cascade;positive regulation of podosome assembly;positive regulation of protein complex assembly;positive regulation of protein kinase B signaling cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of T cell activation;positive regulation of Wnt receptor signaling pathway;primary metabolic process;progesterone receptor signaling pathway;protein autophosphorylation;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regulation of anoikis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of bone remodeling;regulation of bone resorption;regulation of canonical Wnt receptor signaling pathway;regulation of catalytic activity;regulation of cell activation;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of ERK1 and ERK2 cascade;regulation of estrogen receptor signaling pathway;regulation of focal adhesion assembly;regulation of homeostatic process;regulation of hydrolase activity;regulation of immune system process;regulation of integrin activation;regulation of intracellular protein kinase cascade;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of peptidase activity;regulation of podosome assembly;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein homooligomerization;regulation of protein kinase B signaling cascade;regulation of protein oligomerization;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of T cell activation;regulation of tissue remodeling;regulation of vascular permeability;regulation of Wnt receptor signaling pathway;reproductive process;reproductive structure development;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to interleukin-1;response to organic substance;response to progesterone stimulus;response to steroid hormone stimulus;response to stimulus;response to stress;signal complex assembly;signal transduction;small GTPase mediated signal transduction;steroid hormone receptor signaling pathway;system process;T cell costimulation;taxis;tissue homeostasis;tissue morphogenesis;transmembrane receptor protein tyrosine kinase signaling pathway;tube morphogenesis;uterus development;vascular process in circulatory system;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;binding, bridging;catalytic activity;cation binding;heme binding;integrin binding;ion binding;iron ion binding;kinase activity;metal ion binding;non-membrane spanning protein tyrosine kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein binding, bridging;protein complex binding;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor

binding;ribonucleotide binding;SH3/SH2 adaptor activity;signaling adaptor activity;tetrapyrrole binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding"
caveola;cell part;cytoplasmic part;cytoskeleton;cytosol;endosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late
endosome;lysosome;lytic vacuole;membrane;membrane part;membrane raft;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;non-membrane-bounded
organelle;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane part;vacuole Adherens junction;Bacterial invasion of epithelial cells;Endocytosis;Epithelial cell signaling in
Helicobacter pylori infection;ErbB signaling pathway;Focal adhesion;Gap junction;GnRH signaling pathway;ko05152;Tight junction;VEGF signaling pathway 1.74E-28 2 8 3 16.6
Q8N4C8-5;Q8N4C8-2;Q8N4C8-3;Q8N4C8-4;Q8N4C8;Q9UKE5-8;Q9UKE5-5;Q9UKE5-7;Q9UKE5-3;F5H5M9;Q9UKE5-6;Q9UKE5-2;F5H865;Q9UKE5-4;Q9UKE5;C9J338;I3L2I2;E7ETN6;I3L1U1 Misshapen-like kinase
1;TRAF2 and NCK-interacting protein kinase MINK1;TNIK >sp|Q8N4C8-5|MINK1_HUMAN Isoform 5 of Misshapen-like kinase 1 OS=Homo sapiens GN=MINK1;>sp|Q8N4C8-2|MINK1_HUMAN Isoform 1 of
Misshapen-like kinase 1 OS=Homo sapiens GN=MINK1;>sp|Q8N4C8-3|MINK1_HUMAN Isoform 2 of Misshapen-like kinase 1 OS=Homo sapiens GN=M 0.18 0.14 0.25 -0.20 -0.21 -0.01 0.08 -0.01
0.468459045 0.133071925 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;activation of JNKK activity;activation of MAPKK activity;activation of protein kinase
activity;anatomical structure morphogenesis;biological regulation;cell communication;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cell-cell
signaling;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at
cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to
stress;cytoskeleton organization;dendrite morphogenesis;developmental process;immune system process;intracellular protein kinase cascade;intracellular signal transduction;JNK cascade;macromolecule metabolic
process;macromolecule modification;MAPKKK cascade;metabolic process;negative T cell selection;negative thymic T cell selection;neuron projection morphogenesis;organelle organization;phosphate-containing compound
metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cellular
process;positive regulation of intracellular protein kinase cascade;positive regulation of JNK cascade;positive regulation of kinase activity;positive regulation of MAPKKK cascade;positive regulation of molecular
function;positive regulation of protein kinase activity;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase
signaling cascade;positive regulation of transferase activity;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of catalytic activity;regulation of cell
adhesion;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in
differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cell-cell adhesion;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cellular component
movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of
dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of
localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal
development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of
phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic
process;regulation of protein modification process;regulation of protein phosphorylation;regulation of receptor activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation
of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;response to stimulus;response to stress;signal transduction;signaling;stress-activated protein kinase signaling
cascade;synaptic transmission;T cell selection;thymic T cell selection;Wnt receptor signaling pathway "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme regulator
activity;GTPase regulator activity;kinase activity;nucleoside-triphosphatase regulator activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase
activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small GTPase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" axon;cell junction;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;endosome;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma
membrane;postsynaptic density;postsynaptic membrane;recycling endosome;synapse part;synaptic membrane 1.17E-24 19 9 3 9.6
P23497;P23497-7;P23497-6;E9PHV6;P23497-5;E9PBK3;P23497-2;P23497-3;E7EUA7;P23497-4;C9JBL0;Q9H930-3 Nuclear autoantigen Sp-100 SP100 >sp|P23497|SP100_HUMAN Nuclear autoantigen Sp-100
OS=Homo sapiens GN=SP100 PE=1 SV=3;>sp|P23497-7|SP100_HUMAN Isoform 7 of Nuclear autoantigen Sp-100 OS=Homo sapiens GN=SP100;>sp|P23497-6|SP100_HUMAN Isoform 6 of Nuclear autoantigen Sp-100
OS=Homo sapiens -0.06 0.95 -0.01 0.63 -1.05 -0.09 -1.46 0.25 0.875824138 0.962401787 "anatomical structure homeostasis;biological regulation;cell surface receptor linked signaling
pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule
metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cellular response to type I interferon;chromosome organization;cytokine-mediated signaling pathway;DNA damage response,
signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator;DNA damage response, signal transduction resulting in
transcription;DNA metabolic process;homeostatic process;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;intracellular receptor mediated signaling
pathway;intracellular signal transduction;macromolecule metabolic process;metabolic process;multi-organism process;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic
process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular biosynthetic process;negative regulation of cellular component movement;negative regulation of cellular
macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA binding;negative regulation of endothelial cell migration;negative
regulation of gene expression;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of locomotion;negative regulation of macromolecule biosynthetic
process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative
regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of protein export from nucleus;negative regulation of protein transport;negative regulation
of reproductive process;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of transcription from RNA polymerase II
promoter;negative regulation of transcription, DNA-dependent;negative regulation of transport;negative regulation of viral transcription;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular
metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive
regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation
of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;primary metabolic
process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell
migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation
of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA binding;regulation of endothelial cell migration;regulation of establishment of protein localization;regulation of
gene expression;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule
metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic
process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein
localization;regulation of protein transport;regulation of reproductive process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription from RNA
polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transport;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to chemical stimulus;response to cytokine
stimulus;response to DNA damage stimulus;response to external stimulus;response to extracellular stimulus;response to interferon-gamma;response to nutrient;response to nutrient levels;response to organic substance;response to
retinoic acid;response to stimulus;response to stress;response to type I interferon;response to vitamin;response to vitamin A;retinoic acid receptor signaling pathway;signal transduction;signal transduction by p53 class
mediator;signal transduction in response to DNA damage;telomere maintenance;telomere organization;type I interferon-mediated signaling pathway;viral reproductive process;virus-host interaction" binding;DNA
binding;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity

cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded
organelle;nuclear body;nuclear part;nuclear periphery;nucleolus;nucleoplasm part;nucleus;organelle;organelle part;PML body 1.18E-69 12 9 3 10.6
O15294;O15294-3;O15294-4;C9JZL3;H7C2T7 UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OGT >sp|O15294|OGT1_HUMAN UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase
110 kDa subunit OS=Homo sapiens GN=OGT PE=1 SV=3;>sp|O15294-3|OGT1_HUMAN Isoform 1 of UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit OS
-0.04 0.08 0.21 0.02 0.36 -0.04 -0.19 0.01 0.084608973 0.031164323 "apoptosis;biological regulation;carbohydrate metabolic process;cell communication;cell death;cellular carbohydrate metabolic
process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule
metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular
response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;chromatin modification;chromatin
organization;chromosome organization;covalent chromatin modification;death;glycosylation;histone acetylation;histone H3-K4 methylation;histone H3-K4 trimethylation;histone H4 acetylation;histone H4-K16
acetylation;histone H4-K5 acetylation;histone H4-K8 acetylation;histone lysine methylation;histone methylation;histone modification;induction of apoptosis;induction of programmed cell death;inositol lipid-mediated
signaling;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;intracellular signal transduction;macromolecule glycosylation;macromolecule metabolic process;macromolecule methylation;macromolecule
modification;metabolic process;methylation;one-carbon metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine methylation;peptidyl-lysine modification;peptidyl-lysine
trimethylation;phosphatidylinositol-mediated signaling;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive
regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular
process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of granulocyte differentiation;positive regulation of histone
H3-K4 methylation;positive regulation of histone methylation;positive regulation of histone modification;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic
process;positive regulation of metabolic process;positive regulation of myeloid cell differentiation;positive regulation of myeloid leukocyte differentiation;positive regulation of nitrogen compound metabolic process;positive
regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of
protein modification process;positive regulation of proteolysis;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary
metabolic process;programmed cell death;protein acetylation;protein acylation;protein alkylation;protein glycosylation;protein metabolic process;protein methylation;protein modification process;protein O-linked
glycosylation;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic
process;regulation of cell death;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of
cellular catabolic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular
protein metabolic process;regulation of chromosome organization;regulation of developmental process;regulation of gene expression;regulation of generation of precursor metabolites and energy;regulation of glucose metabolic
process;regulation of glycolysis;regulation of granulocyte differentiation;regulation of histone H3-K4 methylation;regulation of histone methylation;regulation of histone modification;regulation of immune system
process;regulation of insulin receptor signaling pathway;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal
development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing
compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein
modification process;regulation of proteolysis;regulation of Rac protein signal transduction;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of RNA metabolic process;regulation of
signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical
stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to insulin stimulus;response to nutrient;response to nutrient levels;response to
organic substance;response to peptide hormone stimulus;response to retinoic acid;response to stimulus;response to vitamin;response to vitamin A;signal transduction;small molecule metabolic process"
"acetylglucosaminyltransferase activity;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;lipid binding;phosphatidylinositol binding;phosphatidylinositol-3,4,5-trisphosphate binding;phospholipid
binding;protein N-acetylglucosaminyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;UDP-glycosyltransferase activity" cell
part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;histone acetyltransferase complex;histone methyltransferase complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded
organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;methyltransferase complex;microtubule organizing center;mitochondrion;MLL5-L
complex;non-membrane-bounded organelle;nuclear part;nucleoplasm part;organelle;organelle part;plasma membrane;protein complex Other types of O-glycan biosynthesis 8.35E-53 5 10 3 12.9
Q09028-3;Q09028;Q09028-2;Q09028-4;E9PNS2;E9PIC4;E9PNS6;C9JAJ9 Histone-binding protein RBBP4 RBBP4 >sp|Q09028-3|RBBP4_HUMAN Isoform 3 of Histone-binding protein RBBP4 OS=Homo sapiens
GN=RBBP4;>sp|Q09028|RBBP4_HUMAN Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3;>sp|Q09028-2|RBBP4_HUMAN Isoform 2 of Histone-binding protein RBBP4 OS=Homo -0.13
0.35 -0.17 0.34 -0.12 -0.47 -0.84 -0.45 1.155413742 0.568849275 "ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cell cycle;cellular biosynthetic process;cellular
component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization
or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular
metabolic process;cellular nitrogen compound metabolic process;cellular process;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin
organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;DNA metabolic process;DNA replication;DNA replication-independent nucleosome assembly;DNA replication-independent
nucleosome organization;histone exchange;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitotic cell
cycle;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing
compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of
biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic
process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen
compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA
biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;histone binding;protein binding CAF-1 complex;cell part;chromatin assembly complex;chromatin remodeling complex;chromosomal
part;ESC/E(Z) complex;histone deacetylase complex;histone methyltransferase complex;intracellular organelle part;intracellular part;ISWI complex;macromolecular complex;methyltransferase complex;nuclear chromosome
part;nuclear part;nucleoplasm part;NuRD complex;NURF complex;organelle part;PcG protein complex;protein complex;Sin3 complex;Sin3-type complex;transcriptional repressor complex 3.79E-46 8 10 3 23.2
Q92922;F8WE13 SWI/SNF complex subunit SMARCC1 SMARCC1 >sp|Q92922|SMRC1_HUMAN SWI/SNF complex subunit SMARCC1 OS=Homo sapiens GN=SMARCC1 PE=1 SV=3 -0.25 0.61 -0.59
0.72 -1.03 0.04 -1.00 -0.48 0.772310632 0.737068407 "anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;cell surface receptor linked signaling
pathway;cellular biosynthetic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component
organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic
process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous
stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chromatin
modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;enzyme linked receptor protein signaling pathway;insulin receptor signaling pathway;macromolecular complex
disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nervous system development;nitrogen compound metabolic process;nucleic
acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;organ morphogenesis;organelle organization;positive regulation of biological process;positive
regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive
regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation
of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary
metabolic process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic

process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;system development;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway"	binding;chromatin binding;DNA binding;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity	cell part;chromatin remodeling complex;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;nBAF complex;non-membrane-bounded organelle;npBAF complex;nuclear part;organelle;organelle part;protein complex;sex chromosome;SWI/SNF complex;SWI/SNF-type complex;WINAC complex;XY body		1.47E-45 2	11	3	11

P16402	Histone H1.3	HIST1H1D	>sp|P16402|H13_HUMAN Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	-0.97	1.34 0.07 0.83 -0.45	-0.57	-2.54	-1.25		0.932481137 1.516134474	cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization	binding;DNA binding;nucleic acid binding	cell part;chromatin;chromosomal part;intracellular organelle part;intracellular part;macromolecular complex;nuclear chromatin;nuclear chromosome part;nuclear part;nucleosome;organelle part;protein-DNA complex		3.05E-78 1	13	3	37.6

Q14151;K7EQU4;K7ERX3	Scaffold attachment factor B2	SAFB2	>sp|Q14151|SAFB2_HUMAN Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	-0.10	0.67 0.07 0.97 -0.06	0.75 -0.68	0.61	0.227465043	0.248048738	"biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent"	binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding	cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle		6.59E-84 3	13	3	16.1

P51991;H7C1J8	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	>sp|P51991|ROA3_HUMAN Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 -0.18	0.76 -0.06	0.79 -0.02	0.19 -1.25	0.02	0.594441043	0.594308548	"cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile"	binding;nucleic acid binding;nucleotide binding;RNA binding	catalytic step 2 spliceosome;cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome	1.27E-99 2	15	3	30.2

Q8WVM8;J3KNG4;G3V4I1;G3V5F3;G3V2M8;G3V3K9;G3V363;H0YJS6	Sec1 family domain-containing protein 1	SCFD1	>sp|Q8WVM8|SCFD1_HUMAN Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4	-0.02	0.09 0.02 0.10 0.12 0.27 0.04 0.05	0.516775031	-0.07523294	"biological regulation;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;membrane docking;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of ER to Golgi vesicle-mediated transport;regulation of intracellular transport;regulation of localization;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;response to toxin;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle-mediated transport"	binding;protein binding;SNARE binding;syntaxin binding	cell part;cis-Golgi network;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi transport complex;Golgi-associated vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane;protein complex;vesicle		1.01E-128	8	16	3	37.4

E9PLY5		MACF1	">tr|E9PLY5|E9PLY5_HUMAN Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Fragment) OS=Homo sapiens GN=MACF1 PE=2 SV=1"	0.28 0.13 0.27 -0.11	-0.14	-0.31 0.12 0.68	0.078092038	0.053246878				7.93E-290	1	46	3	40.1

P04259	"Keratin, type II cytoskeletal 6B"	KRT6B	">sp|P04259|K2C6B_HUMAN Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5"	-2.35	-0.20	-0.23	1.67 -0.09	1.50 -0.61 0.97	0.297271208	-0.719668617	anatomical structure development;developmental process;ectoderm development;tissue development	structural constituent of cytoskeleton;structural molecule activity	cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;organelle part;protein complex		0	1	73	3	73.8

Q15149-4;Q15149-7;Q15149-8;Q15149-9;Q15149-5;Q15149-6			>sp|Q15149-4|PLEC_HUMAN Isoform 4 of Plectin OS=Homo sapiens GN=PLEC;>sp|Q15149-7|PLEC_HUMAN Isoform 7 of Plectin OS=Homo sapiens GN=PLEC;>sp|Q15149-8|PLEC_HUMAN Isoform 8 of Plectin OS=Homo sapiens GN=PLEC;>sp|Q15149-9|PLEC_HUMAN Isoform 9 of Plectin OS=H	0.05 0.33 0.13 0.35 -0.12	0.29 -0.08	0.19 0.486883327	0.147927972				0	6	463	3	78.4

Q9NRG9-2;Q9NRG9;F8VZ44;F8VUB6;H3BU82	Aladin	AAAS	>sp|Q9NRG9-2|AAAS_HUMAN Isoform 2 of Aladin OS=Homo sapiens GN=AAAS;>sp|Q9NRG9|AAAS_HUMAN Aladin OS=Homo sapiens GN=AAAS PE=1 SV=1;>tr|F8VZ44|F8VZ44_HUMAN Aladin OS=Homo sapiens GN=AAAS PE=2 SV=1;>tr|F8VUB6|F8VUB6_HUMAN Aladin (Fragment) OS=Homo sapiens GN	0.38 0.35 -0.78	0.13 -0.71 -0.32	-0.65	-0.55		0.869140812	0.58176513	behavior;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cognition;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;fertilization;glucose transport;hexose transport;intracellular transport;learning;learning or memory;metabolic process;monosaccharide transport;multicellular organismal process;neurological system process;nuclear transport;nucleocytoplasmic transport;organic substance transport;primary metabolic process;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of glucose transport;regulation of intracellular transport;regulation of localization;regulation of nucleocytoplasmic transport;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction;small molecule metabolic process;system process;transmembrane transport;transport;viral reproductive process		cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;microtubule organizing center;non-membrane-bounded organelle;nuclear membrane;nuclear part;nuclear pore;organelle;organelle membrane;organelle part;pore complex;protein complex	RNA transport1.41E-19 5	4	4	9.9

Q9NY61	Protein AATF	AATF	>sp|Q9NY61|AATF_HUMAN Protein AATF OS=Homo sapiens GN=AATF PE=1 SV=1	-0.38	1.15 0.41 1.17 -0.29	0.09 -1.37	0.29	0.745561134	0.908118028 "biological adhesion;biological regulation;cell adhesion;cell division;cell surface receptor linked signaling pathway;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;cellular response to stress;embryonic cleavage;enzyme linked receptor protein signaling pathway;negative regulation of amyloid precursor protein biosynthetic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of glycoprotein biosynthetic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;negative regulation of reactive oxygen species metabolic process;negative regulation of superoxide anion generation;nerve growth factor receptor signaling pathway;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of amyloid precursor protein biosynthetic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of glycoprotein biosynthetic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of reactive oxygen species metabolic process;regulation of RNA metabolic process;regulation of superoxide anion generation;regulation of superoxide metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;ribonucleoprotein complex biogenesis;ribosome biogenesis;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway" nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;focal adhesion;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 1.02E-20 1 4 4 9.5

P24666;G5E9R5;B5MCC7;F2Z2Q9;P24666-3;P24666-2;D3YTI2 Low molecular weight phosphotyrosine protein phosphatase ACP1 ">sp|P24666|PPAC_HUMAN Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3;>tr|G5E9R5|G5E9R5_HUMAN Acid phosphatase 1, soluble, isoform CRA_d OS=Homo sapiens GN=ACP1 PE=2 SV=1;>tr|B5MCC7|B5MCC7_HUMAN Low molecular weig" 0.19 0.01 -0.09 -0.27 0.07 -0.02 0.55 0.13 0.593405944 -0.222416648 cell communication;cell-cell signaling;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;dephosphorylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;signaling;synaptic transmission "acid phosphatase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;non-membrane spanning protein tyrosine phosphatase activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein tyrosine phosphatase activity" cell part;cell projection;cytoplasm;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane part;membrane-bounded organelle;neuron projection;nucleus;organelle;plasma membrane part Riboflavin metabolism 4.07E-59 7 4 4 31.6

Q03154-4;Q03154;B4DNW0;C9JMV9;Q03154-2;Q03154-3;F8WC59;C9JYZ0 Aminoacylase-1 ACY1;ABHD14A-ACY1 >sp|Q03154-4|ACY1_HUMAN Isoform 4 of Aminoacylase-1 OS=Homo sapiens GN=ACY1;>sp|Q03154|ACY1_HUMAN Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1;>tr|B4DNW0|B4DNW0_HUMAN Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=2 SV=1;>tr|C9JMV9|C9JMV9_HUMAN Protein ABHD 0.08 -0.17 -0.03 0.06 -0.72 -1.01 0.03 -0.72 1.079877477 0.588404332 amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein metabolic process;proteolysis;small molecule metabolic process "aminoacylase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Arginine and proline metabolism 1.58E-14 8 4 4 16.4

Q16186 Proteasomal ubiquitin receptor ADRM1 ADRM1 >sp|Q16186|ADRM1_HUMAN Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2 0.20 0.01 0.04 0.00 -0.07 -0.15 0.04 -0.40 0.866759212 0.208022933 "biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;proteasome assembly;protein complex assembly;protein complex subunit organization;RNA biosynthetic process;RNA metabolic process;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent" binding;endopeptidase activator activity;endopeptidase regulator activity;enzyme activator activity;enzyme regulator activity;peptidase activator activity;peptidase regulator activity;proteasome binding;protein binding;protein complex binding cell part;cytoplasm;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane part;proteasome complex;protein complex 7.00E-16 1 4 4 12

Q9NQW6-2;Q9NQW6;C9JJT6;H7C1K5 Actin-binding protein anillin ANLN >sp|Q9NQW6-2|ANLN_HUMAN Isoform 2 of Actin-binding protein anillin OS=Homo sapiens GN=ANLN;>sp|Q9NQW6|ANLN_HUMAN Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2;>tr|C9JJT6|C9JJT6_HUMAN Actin-binding protein anillin (Fragment) OS=Homo sapien 0.79 -0.01 -0.13 -0.14 0.00 -0.73 -0.92 -1.09 1.054404374 0.816183435 biological regulation;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytokinesis;macromolecular complex assembly;macromolecular complex subunit organization;mitosis;nuclear division;organelle fission;organelle organization;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of cell cycle;regulation of cell cycle process;regulation of cellular process;regulation of exit from mitosis;regulation of mitotic cell cycle;septin ring assembly actin binding;binding;cytoskeletal protein binding;lipid binding;phospholipid binding;protein binding actomyosin contractile ring;cell cortex part;cell division site part;cell part;contractile ring;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nucleus;organelle;organelle part 3.73E-10 4 4 4 6.9

Q9BTT0;E9PPH5;Q9BTT0-3;Q5TB19;E9PLC4;E9PI45;Q5TB25;Q9BTT0-2 Acidic leucine-rich nuclear phosphoprotein 32 family member E ANP32E >sp|Q9BTT0|AN32E_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1;>tr|E9PPH5|E9PPH5_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member E (Fragment) OS=Homo sapiens GN=ANP32E PE=2 SV=1;>s 0.06 0.04 -0.24 -0.05 0.19 -0.39 -0.27 -0.79 0.518952993 0.266445057 enzyme inhibitor activity;enzyme regulator activity;phosphatase inhibitor activity;phosphatase regulator activity cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;vesicle 1.20E-45 8 4 4 14.6

Q9NVJ2;Q96BM9;B4DI85 ADP-ribosylation factor-like protein 8B;ADP-ribosylation factor-like protein 8A ARL8B;ARL8A >sp|Q9NVJ2|ARL8B_HUMAN ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1;>sp|Q96BM9|ARL8A_HUMAN ADP-ribosylation factor-like protein 8A OS=Homo sapiens GN=ARL8A PE=1 SV=1 -0.15 0.11 -0.39 0.18 0.41 0.54 -0.01 0.40 0.959971878 -0.396623909 biological regulation;cell cycle;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;chromosome segregation;intracellular signal transduction;mitosis;nuclear division;organelle fission;organelle organization;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction "alpha-tubulin binding;beta-tubulin binding;binding;catalytic activity;cytoskeletal protein binding;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;tubulin binding" cell part;cytoplasm;cytoplasmic part;cytoskeletal part;endosomal part;endosome membrane;intracellular;intracellular organelle part;intracellular part;late endosome membrane;lysosomal membrane;membrane;midbody;organelle membrane;organelle part;spindle midzone;vacuolar membrane;vacuolar part 4.59E-12 3 4 4 19.9

O95671-2;O95671;E7ER97;O95671-3 N-acetylserotonin O-methyltransferase-like protein ASMTL >sp|O95671-2|ASML_HUMAN Isoform 2 of N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL;>sp|O95671|ASML_HUMAN N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3;>tr|E7ER97|E7ER97_HUMAN N-acetylser -0.16 -0.20 0.01 -0.08 0.51 0.26 0.24 -0.04 1.197561593 -0.349284892 "catalytic activity;methyltransferase activity;O-methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasm;intracellular part 6.81E-22 4 4 4 10.1

Q9NT62;Q9NT62-2;F8WDI0 Ubiquitin-like-conjugating enzyme ATG3 ATG3 >sp|Q9NT62|ATG3_HUMAN Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1;>sp|Q9NT62-2|ATG3_HUMAN Isoform 2 of Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3;>tr|F8WDI0|F8WDI0_HUMAN Ubiquitin-like-conjugating enzyme ATG 0.32 -0.04 0.08 -0.03 0.08 -0.11 0.12 -0.45 0.464033356 0.172915811 apoptotic mitochondrial changes;autophagic vacuole assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;macromolecule metabolic process;macromolecule modification;metabolic process;mitochondrial fission;mitochondrial fragmentation involved in apoptosis;mitochondrion organization;organelle assembly;organelle fission;organelle organization;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein targeting;protein targeting to membrane;protein transport;protein ubiquitination;transport;vacuole organization "acid-amino acid ligase activity;Atg12 ligase activity;Atg8 ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity" cell part;cytoplasmic part;cytoplasmic ubiquitin ligase complex;cytosol;intracellular part;macromolecular complex;protein complex;ubiquitin ligase complex Regulation of autophagy 8.89E-45 3 4 4 15.9

H7C3E1;B7Z413;B7Z9I3;O75787;H0Y750;B7Z1I9;H7C240 Renin receptor ATP6AP2 >tr|H7C3E1|H7C3E1_HUMAN Renin receptor (Fragment) OS=Homo sapiens GN=ATP6AP2 PE=4 SV=1;>tr|B7Z413|B7Z413_HUMAN Renin receptor OS=Homo sapiens GN=ATP6AP2 PE=2 SV=1;>tr|B7Z9I3|B7Z9I3_HUMAN Renin receptor OS=Homo sapiens GN=ATP6AP2 PE=2 SV=1;>sp|O75787|RENR_H 0.02 0.15 0.13 -0.03 0.39 0.05 -0.25 -0.11 0.117060669 0.047474408 angiotensin maturation;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;hormone metabolic process;macromolecule metabolic process;metabolic process;peptide hormone processing;positive regulation of biological process;positive regulation of cytokine production;positive regulation of multicellular organismal process;positive regulation of transforming growth factor beta production;positive regulation of transforming growth factor beta1 production;primary metabolic process;protein maturation;protein metabolic process;protein processing;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of cytokine production;regulation of hormone levels;regulation of intracellular protein kinase cascade;regulation of MAPKKK cascade;regulation of multicellular organismal process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta production;regulation of transforming growth factor beta1 production "aspartic-type endopeptidase activity;aspartic-type peptidase activity;catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;receptor activity" cell body;cell part;cell projection;external side of plasma membrane;integral to membrane;intrinsic to membrane;membrane part;neuron projection;plasma membrane part 4.63E-37 7 4 4 20.8

Q93050-1;Q93050;F5H569;Q93050-3;B7Z641;B7Z2A9;K7EM24;K7EN36;K7EPG4;K7ELZ6;F5H1T6V-type proton ATPase 116 kDa subunit a isoform 1 ATP6V0A1 >sp|Q93050-1|VPP1_HUMAN Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1;>sp|Q93050|VPP1_HUMAN V-type proton ATPase 116 kDa subunit a isoform 1 OS=Homo sapiens GN=ATP6V0A1 PE=1 SV=3;>tr|F5H569|F5H569_HUMAN V-type pr 0.03 1.09 -0.96 -0.26 0.94 0.57 0.35 0.54 0.594744161 -0.622776189 "ATP hydrolysis coupled proton transport;biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organelle organization;phagosome maturation;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity "cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;endosomal part;endosome membrane;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle membrane;organelle part;phagocytic vesicle membrane;pigment granule;plasma membrane;protein complex;proton-transporting two-sector ATPase complex, proton-transporting domain;proton-transporting V-type ATPase, V0 domain;vacuolar part;vacuolar proton-transporting V-type ATPase, V0 domain;vesicle;vesicle membrane" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection 1.09E-10 11 4 4 5.8

Q9HA77;H0YFV1;F5H623;H0YFF0 "Probable cysteine--tRNA ligase, mitochondrial" CARS2 ">sp|Q9HA77|SYCM_HUMAN Probable cysteine--tRNA ligase, mitochondrial OS=Homo sapiens GN=CARS2 PE=1 SV=1" 0.33 0.09 -0.27 -0.12 -0.21 0.02 0.11 -0.39 0.282240688 0.125299249 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cysteinyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;cation binding;cysteine-tRNA ligase activity;ion binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part Aminoacyl-tRNA biosynthesis 5.04E-10 4 4 4 9.4

Q9Y3E7;Q9Y3E7-2;Q9Y3E7-4;Q9Y3E7-3 Charged multivesicular body protein 3 CHMP3 >sp|Q9Y3E7|CHMP3_HUMAN Charged multivesicular body protein 3 OS=Homo sapiens GN=CHMP3 PE=1 SV=3;>sp|Q9Y3E7-2|CHMP3_HUMAN Isoform 2 of Charged multivesicular body protein 3 OS=Homo sapiens GN=CHMP3;>sp|Q9Y3E7-4|CHMP3_HUMAN Isoform 4 of Charged multivesicula 0.03 -0.02 0.25 0.08 -0.15 0.06 0.39 0.20 0.109209101 -0.039838368 apoptosis;cell cycle;cell death;cell division;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;death;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;membrane organization;programmed cell death;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;cytosol;endosomal part;endosome membrane;intracellular organelle part;intracellular part;late endosome membrane;membrane;organelle membrane;organelle part Endocytosis 2.68E-19 4 4 4 18.5

O75175-2;O75175;O75175-3;H0Y5X7;H7C148 CCR4-NOT transcription complex subunit 3 CNOT3 >sp|O75175-2|CNOT3_HUMAN Isoform 2 of CCR4-NOT transcription complex subunit 3 OS=Homo sapiens GN=CNOT3;>sp|O75175|CNOT3_HUMAN CCR4-NOT transcription complex subunit 3 OS=Homo sapiens GN=CNOT3 PE=1 SV=1;>sp|O75175-3|CNOT3_HUMAN Isoform 3 of CCR4-NOT transc 0.18 0.08 -0.02 0.07 0.06 -0.08 -0.22 -0.12 1.010565061 0.168720937 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of stem cell differentiation;regulation of stem cell maintenance;regulation of transcription, DNA-dependent;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;transcription, DNA-dependent" CCR4-NOT complex;cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;RNA granule;transcription factor complex RNA degradation 4.82E-45 5 4 4 10.7

Q9H9Q2;J3KQ34;Q9H9Q2-2;J3QT73;Q9H9Q2-3;J3KQ41;J3KQV6;J3QT67;J3QT66;J3QT69;J3QT50;J3QT43;J3QT95 COP9 signalosome complex subunit 7b COPS7B >sp|Q9H9Q2|CSN7B_HUMAN COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1;>tr|J3KQ34|J3KQ34_HUMAN COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=4 SV=1;>sp|Q9H9Q2-2|CSN7B_HUMAN Isoform 2 of COP9 signalosome complex su 0.00 0.07 -0.04 0.11 0.02 -0.15 -0.06 -0.15 0.949136269 0.121473785 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cullin deneddylation;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein deneddylation;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;protein complex;signalosome 1.49E-34 13 4 4 23.9

P61923;F8VVA7;F8W651;F8VWL5;F8VYK5;F8VXB1;F8VUC5;F8W156;B4DHZ0;B4DDX8;F8VS17;F8VYZ4;F8VXR1 Coatomer subunit zeta-1 COPZ1 >sp|P61923|COPZ1_HUMAN Coatomer subunit zeta-1 OS=Homo sapiens GN=COPZ1 PE=1 SV=1;>tr|F8VVA7|F8VVA7_HUMAN Coatomer subunit zeta-1 OS=Homo sapiens GN=COPZ1 PE=2 SV=1;>tr|F8W651|F8W651_HUMAN Coatomer subunit zeta-1 OS=Homo sapiens GN=COPZ1 PE=2 SV=1;>tr|F8VW 0.11 0.03 -0.18 0.33 0.22 0.20 0.08 0.14 0.321058756 -0.088640625 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;organelle organization;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;protein complex;vesicle coat 9.26E-67 13 4 4 26.6

P36551;H0YA22 "Coproporphyrinogen-III oxidase, mitochondrial" CPOX ">sp|P36551|HEM6_HUMAN Coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3;>tr|H0YA22|H0YA22_HUMAN Coproporphyrinogen-III oxidase, mitochondrial (Fragment) OS=Homo sapiens GN=CPOX PE=4 SV=1" -0.07 -0.14 0.24 0.04 0.09 -0.30 0.10 -0.47 0.39103798 0.16013839 biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cofactor biosynthetic process;cofactor metabolic process;heme biosynthetic process;heme metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;pigment biosynthetic process;pigment metabolic process;porphyrin-containing compound biosynthetic process;porphyrin-containing compound metabolic process;protoporphyrinogen IX biosynthetic process;protoporphyrinogen IX metabolic process;response to arsenic-containing substance;response to chemical stimulus;response to inorganic substance;response to insecticide;response to iron ion;response to lead ion;response to metal ion;response to methylmercury;response to organic substance;response to stimulus;response to toxin;small molecule metabolic process;tetrapyrrole biosynthetic process;tetrapyrrole metabolic process "binding;catalytic activity;coproporphyrinogen oxidase activity;identical protein binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, oxygen as acceptor;protein binding;protein dimerization activity;protein homodimerization activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial part;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part Porphyrin and chlorophyll metabolism 3.42E-14 2 4 4 9.3

P08574 "Cytochrome c1, heme protein, mitochondrial" CYC1 ">sp|P08574|CY1_HUMAN Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3" -0.20 0.55 0.06 0.73 0.34 0.68 -1.33 0.09 0.26720907 0.338203721 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process "binding;cation binding;electron carrier activity;electron transporter, transferring electrons from CoQH2-cytochrome c reductase complex and cytochrome c oxidase complex activity;heme binding;ion binding;iron ion binding;metal ion binding;tetrapyrrole binding;transition metal ion binding" cell junction;cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;respiratory chain Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 4.16E-13 1 4 4 15.4

Q3LXA3;I3L252;H0YCY6 Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);ATP-dependent dihydroxyacetone kinase;FAD-AMP lyase (cyclizing)DAK >sp|Q3LXA3|DHAK_HUMAN Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2;>tr|I3L252|I3L252_HUMAN FAD-AMP lyase (cyclizing) (Fragment) OS=Homo sapiens GN=DAK PE=2 SV=1;>tr|H0YCY6|H0YCY6_HUMAN FAD-AM -0.26 -0.28 0.08 0.12 0.41 -0.26 0.17 -0.89 0.06738231 0.05989293 alcohol metabolic process;alditol metabolic process;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;defense response;glycerol metabolic process;immune response;immune system process;innate immune response;metabolic process;polyol metabolic process;primary metabolic process;response to stimulus;response to stress;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;cyclase activity;FAD-AMP lyase (cyclizing) activity;glycerone kinase activity;ion binding;kinase activity;lyase activity;metal ion binding;nucleotide binding;phosphorus-oxygen lyase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups;triokinase activity" cell part;cytoplasmic part;cytosol;intracellular part Glycerolipid metabolism;Methane metabolism;RIG-I-like receptor signaling pathway 2.72E-23 3 4 4 12.2

Q96PD2;Q96PD2-2 "Discoidin, CUB and LCCL domain-containing protein 2" DCBLD2 ">sp|Q96PD2|DCBD2_HUMAN Discoidin, CUB and LCCL domain-containing protein 2 OS=Homo sapiens GN=DCBLD2 PE=1 SV=1;>sp|Q96PD2-2|DCBD2_HUMAN Isoform 2 of Discoidin, CUB and LCCL domain-containing protein 2 OS=Homo sapiens GN=DCBLD2" 0.45 0.42 -0.24 -0.37 -0.95 -0.38 -0.17 0.15 0.534885628 0.403282851 biological adhesion;biological regulation;cell adhesion;cellular process;cellular response to stimulus;intracellular receptor mediated signaling pathway;negative regulation of biological process;negative regulation of cell growth;negative regulation of cellular process;negative regulation of growth;regulation of biological process;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth;response to stimulus;response to stress;response to wounding;signal transduction;wound healing cell part;cell surface;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part 2.72E-23 2 4 4 11

Q9H2U1-3;Q9H2U1-2;F5GZS0;Q9H2U1;E7EWK3;H7C5F5 Probable ATP-dependent RNA helicase DHX36 DHX36 >sp|Q9H2U1-3|DHX36_HUMAN Isoform 3 of Probable ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36;>sp|Q9H2U1-2|DHX36_HUMAN Isoform 2 of Probable ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36;>tr|F5GZS0|F5GZS0_HUMAN Probable ATP-dependent 0.21 0.15 0.08 -0.03 -0.03 0.00 -0.01 -0.15 1.011267435 0.147912704 multi-organism process;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to virus "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;double-stranded RNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle RNA degradation 8.57E-18 6 4 4 5.4

O60884;H3BMW5 DnaJ homolog subfamily A member 2 DNAJA2 >sp|O60884|DNJA2_HUMAN DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1 0.16 -0.09 -0.11 -0.42 -0.10 -0.51 0.20 0.05 0.04163436 -0.024270994 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cation binding;ion binding;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;membrane Protein processing in endoplasmic reticulum 7.76E-27 2 4 4 12.9

Q08554-2;Q08554 Desmocollin-1DSC1 >sp|Q08554-2|DSC1_HUMAN Isoform 1B of Desmocollin-1 OS=Homo sapiens GN=DSC1;>sp|Q08554|DSC1_HUMAN Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2 -0.39 1.55 -0.51 -0.35 1.14 1.71 -1.62 0.80 0.182345804 -0.433325507 biological adhesion;cell adhesion;cell-cell adhesion;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;desmosome;gap junction;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane 4.11E-18 2 4 4 6.3

P98172 Ephrin-B1 EFNB1 >sp|P98172|EFNB1_HUMAN Ephrin-B1 OS=Homo sapiens GN=EFNB1 PE=1 SV=1 0.03 0.05 -0.16 0.09 -1.53 -1.42 -0.12 -0.53 1.096037703 0.906145487 ameboidal cell migration;axon guidance;biological adhesion;biological regulation;cell adhesion;cell communication;cell migration;cell motility;cell-cell signaling;cellular component movement;cellular process;chemotaxis;developmental process;embryonic pattern specification;locomotion;neural crest cell migration;pattern specification process;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of leukocyte proliferation;positive regulation of lymphocyte activation;positive regulation of lymphocyte proliferation;positive regulation of mononuclear cell proliferation;positive regulation of T cell activation;positive regulation of T cell proliferation;regulation of biological process;regulation of cell activation;regulation of cell proliferation;regulation of cellular process;regulation of immune system process;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of mononuclear cell proliferation;regulation of T cell activation;regulation of T cell proliferation;response to chemical stimulus;response to external stimulus;response to stimulus;signaling;taxis binding;ephrin receptor binding;protein binding;receptor bindingcell part;cytoplasm;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane raft;membrane-bounded organelle;nucleus;organelle;plasma membrane part;synapse Axon guidance 1.62E-37 1 4 4 17.9

P49770;H0YJJ8;G3V5E5 Translation initiation factor eIF-2B subunit beta EIF2B2 >sp|P49770|EI2BB_HUMAN Translation initiation factor eIF-2B subunit beta OS=Homo sapiens GN=EIF2B2 PE=1 SV=3 0.14 0.11 0.09 -0.12 -0.02 -0.06 0.11 -0.02 0.304978326 0.053238514 anatomical structure development;axon ensheathment;biological regulation;cell development;cellular developmental process;cellular metabolic process;cellular process;cellular response to stimulus;developmental process;ensheathment of neurons;glial cell development;metabolic process;myelination;oligodendrocyte development;ovarian follicle development;ovulation cycle process;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;response to abiotic stimulus;response to carbohydrate stimulus;response to chemical stimulus;response to endogenous stimulus;response to glucose stimulus;response to heat;response to hexose stimulus;response to hormone stimulus;response to monosaccharide stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;rhythmic process;translational initiation "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 2B complex;intracellular part;macromolecular complex;protein complexRNA transport9.17E-17 3 4 4 17.4

O95834;O95834-2;O95834-3;K7EIK7;K7EII6;K7EKG3;C9JRL6 Echinoderm microtubule-associated protein-like 2 EML2 >sp|O95834|EMAL2_HUMAN Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2 PE=2 SV=1;>sp|O95834-2|EMAL2_HUMAN Isoform 2 of Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens GN=EML2;>sp|O95834-3|EMAL2_HUMAN Isoform 3 of E 0.32 0.02 0.08 -0.37 -0.14 -0.45 0.51 -0.62 0.253873755 0.188869861 metabolic process;multicellular organismal process;neurological system process;sensory perception;sensory perception of light stimulus;sensory perception of mechanical stimulus;sensory perception of sound;system process;visual perception catalytic activity cell part;cytoplasm;cytoskeletal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;microtubule associated complex;organelle;organelle part;protein complex 1.81E-14 7 4 4 6.5

Q969X5-2;Q969X5Endoplasmic reticulum-Golgi intermediate compartment protein 1 ERGIC1 >sp|Q969X5-2|ERGI1_HUMAN Isoform 2 of Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens GN=ERGIC1;>sp|Q969X5|ERGI1_HUMAN Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens GN=ERGIC1 PE=1 SV=1 -0.54 -0.25 0.09 0.13 1.01 0.56 -0.57 -0.18 0.363174325 -0.351025263 cellular process;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;transport;vesicle-mediated transport cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 1.24E-13 2 4 4 21.2

Q9Y3I1;Q9Y3I1-3;Q9Y3I1-2;F8WBR0;F8WDR9 F-box only protein 7 FBXO7 >sp|Q9Y3I1|FBX7_HUMAN F-box only protein 7 OS=Homo sapiens GN=FBXO7 PE=1 SV=1;>sp|Q9Y3I1-3|FBX7_HUMAN Isoform 3 of F-box only protein 7 OS=Homo sapiens GN=FBXO7;>sp|Q9Y3I1-2|FBX7_HUMAN Isoform 2 of F-box only protein 7 OS=Homo sapiens GN=FBXO7 0.21 0.15 0.02 -0.19 -0.05 -0.68 -0.07 -0.63 0.893873196 0.405384182 biological regulation;catabolic process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;death;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability;ubiquitin-dependent protein catabolic process "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;ubiquitin-protein ligase activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;ubiquitin ligase complex 3.91E-15 5 4 4 11.5

Q5VW36 Focadhesin FOCAD >sp|Q5VW36|FOCAD_HUMAN Focadhesin OS=Homo sapiens GN=FOCAD PE=1 SV=1 0.23 -0.12 -0.57 -0.08 0.35 0.27 0.49 -0.29 0.599110391 -0.337305278 adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;focal adhesion;integral to membrane;intrinsic to membrane;membrane part 2.11E-20 1 4 4 2.9

Q92522 Histone H1x H1FX >sp|Q92522|H1X_HUMAN Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1 -0.59 0.47 0.66 0.59 -0.73 -0.69 -2.59 -0.95 1.173528889 1.521494627 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organizationbinding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex 4.84E-42 1 4 4 26.3

Q13325;B4DDV1 Interferon-induced protein with tetratricopeptide repeats 5 IFIT5 >sp|Q13325|IFIT5_HUMAN Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 PE=1 SV=1;>tr|B4DDV1|B4DDV1_HUMAN Interferon-induced protein with tetratricopeptide repeats 5 OS=Homo sapiens GN=IFIT5 PE=2 SV=1 0.35 0.23 -0.19 -0.12 -0.79 -0.93 0.03 -0.11 0.813566659 0.520281953 defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;multi-organism process;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus binding;nucleic acid binding;RNA binding;single-stranded RNA binding;tRNA binding actin cytoskeleton;apical part of cell;cell part;cell projection membrane;cell projection part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;leading edge membrane;membrane part;non-membrane-bounded organelle;organelle;plasma membrane part;ruffle membrane 8.82E-20 2 4 4 9.5

P78318 Immunoglobulin-binding protein 1IGBP1 >sp|P78318|IGBP1_HUMAN Immunoglobulin-binding protein 1 OS=Homo sapiens GN=IGBP1 PE=1 SV=1 0.10 -0.04 0.12 -0.24 0.21 0.06 0.35 -0.20 0.329586193 -0.119903273 "B cell activation;biological regulation;cell activation;cellular process;cellular response to stimulus;immune system process;leukocyte activation;lymphocyte activation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of dephosphorylation;negative regulation of gene expression;negative regulation of hydrolase activity;negative regulation of intracellular protein kinase cascade;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAPKKK cascade;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of peptidase activity;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of programmed cell death;negative regulation of protein dephosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of stress-activated MAPK cascade;negative regulation of stress-activated protein kinase signaling cascade;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of dephosphorylation;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of dephosphorylation;regulation of endopeptidase activity;regulation of gene expression;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of microtubule-based movement;regulation of microtubule-based process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to cytokine stimulus;response to interleukin-1;response to organic substance;response to stimulus;response to tumor necrosis factor;signal transduction" enzyme regulator activity;phosphatase regulator activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity cell part;cytoplasm;intracellular part 8.32E-16 1 4 4 13.6

Q96CN7;D6RGE2 Isochorismatase domain-containing protein 1 ISOC1 >sp|Q96CN7|ISOC1_HUMAN Isochorismatase domain-containing protein 1 OS=Homo sapiens GN=ISOC1 PE=1 SV=3;>tr|D6RGE2|D6RGE2_HUMAN Isochorismatase domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ISOC1 PE=2 SV=1 0.03 -0.02 -0.14 0.19 -0.55 -0.50 0.02 -0.49 1.110226803 0.396271702 catalytic activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microbody;organelle;peroxisome 5.58E-28 2 4 4 17.4

Q96ST2-2;Q96ST2-3;Q96ST2 Protein IWS1 homolog IWS1 >sp|Q96ST2-2|IWS1_HUMAN Isoform 2 of Protein IWS1 homolog OS=Homo sapiens GN=IWS1;>sp|Q96ST2-3|IWS1_HUMAN Isoform 3 of Protein IWS1 homolog OS=Homo sapiens GN=IWS1;>sp|Q96ST2|IWS1_HUMAN Protein IWS1 homolog OS=Homo sapiens GN=IWS1 PE=1 SV=2 -0.14 0.31 0.03 0.03 0.06 -0.30 -0.89 -0.49 0.902427123 0.463000037 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.99E-10 3 4 4 9.3

O60341;O60341-2;F6S0T5;R4GMP9 Lysine-specific histone demethylase 1A KDM1A >sp|O60341|KDM1A_HUMAN Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=2;>sp|O60341-2|KDM1A_HUMAN Isoform 2 of Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A;>tr|F6S0T5|F6S0T5_HUMAN Lysine-specific histone demethyla 0.19 0.47 -0.06 0.40 -0.38 -0.13 -0.88 0.10 1.005110737 0.572335416 "anatomical structure development;biological regulation;biosynthetic process;blood coagulation;cell development;cell differentiation;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chordate embryonic development;chromatin modification;chromatin organization;chromosome organization;coagulation;covalent chromatin modification;demethylation;developmental process;embryo development;embryo development ending in birth or egg hatching;gland development;granulocyte differentiation;hemostasis;histone demethylation;histone H3-K4 demethylation;histone lysine demethylation;histone modification;in utero embryonic development;leukocyte differentiation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;muscle cell development;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of apoptosis;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of DNA binding;negative regulation of DNA damage response, signal transduction by p53 class mediator;negative regulation of gene expression;negative regulation of histone H3-K4 methylation;negative regulation of histone H3-K9 methylation;negative regulation of histone methylation;negative regulation of histone modification;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of programmed cell death;negative regulation of protein binding;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organ development;organelle organization;pituitary gland development;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of erythrocyte differentiation;positive regulation of gene expression;positive regulation of hormone biosynthetic process;positive regulation of hormone metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of megakaryocyte differentiation;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of myeloid cell differentiation;positive regulation of neural precursor cell proliferation;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of stem cell proliferation;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein dealkylation;protein demethylation;protein metabolic process;protein modification process;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome organization;regulation of developmental process;regulation of DNA binding;regulation of DNA damage response, signal transduction by p53 class mediator;regulation of embryonic development;regulation of erythrocyte differentiation;regulation of gene expression;regulation of histone H3-K4 methylation;regulation of histone H3-K9 methylation;regulation of histone methylation;regulation of histone modification;regulation of homeostatic process;regulation of hormone biosynthetic process;regulation of hormone metabolic process;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of megakaryocyte differentiation;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of neural precursor cell proliferation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of primitive erythrocyte differentiation;regulation of programmed cell death;regulation of protein binding;regulation of protein metabolic process;regulation of protein modification process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of stem cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;transcription, DNA-dependent" androgen receptor binding;bHLH transcription factor binding;binding;catalytic activity;chromatin binding;coenzyme binding;cofactor binding;demethylase activity;DNA binding;flavin adenine dinucleotide binding;histone demethylase activity;histone demethylase activity (H3-dimethyl-K4 specific);histone demethylase activity (H3-K4 specific);histone demethylase activity (H3-K9 specific);hormone receptor binding;ligand-dependent nuclear receptor transcription coactivator activity;MRF binding;nuclear hormone receptor binding;nucleic acid binding;nucleic acid binding transcription factor activity;oxidoreductase activity;protein binding;protein binding transcription factor activity;receptor binding;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding transcription factor activity;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;transcription regulatory region DNA binding cell part;chromatin;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;transcription factor complex 7.60E-13 4 4 4 5.2

Q9P260;Q9P260-2 LisH domain and HEAT repeat-containing protein KIAA1468 KIAA1468 >sp|Q9P260|K1468_HUMAN LisH domain and HEAT repeat-containing protein KIAA1468 OS=Homo sapiens GN=KIAA1468 PE=1 SV=2;>sp|Q9P260-2|K1468_HUMAN Isoform 2 of LisH domain and HEAT repeat-containing protein KIAA1468 OS=Homo sapiens GN=KIAA1468 0.15 0.20 0.27 -0.10 0.40 0.39 0.06 -0.23 0.044051817 -0.022601476 1.71E-29 2 4 4 4.8

Q9P206;Q9P206-3;Q9P206-2;Q9P206-4 Uncharacterized protein KIAA1522 KIAA1522 >sp|Q9P206|K1522_HUMAN Uncharacterized protein KIAA1522 OS=Homo sapiens GN=KIAA1522 PE=1 SV=2;>sp|Q9P206-3|K1522_HUMAN Isoform 3 of Uncharacterized protein KIAA1522 OS=Homo sapiens GN=KIAA1522;>sp|Q9P206-2|K1522_HUMAN Isoform 2 of Uncharacterized protein K -0.43 -0.13 0.57 0.18 -1.25 -0.50 -0.29 -0.09 0.751933186 0.583015312 4.02E-15 4 4 4 6.6

Q8NC56;H0Y9B7;D6RBV0;Q8NC56-2;H7C2Z0 LEM domain-containing protein 2 LEMD2 >sp|Q8NC56|LEMD2_HUMAN LEM domain-containing protein 2 OS=Homo sapiens GN=LEMD2 PE=1 SV=1 -0.33 0.34 0.37 0.49 0.41 0.18 -0.85 -0.14 0.387212082 0.317087263 biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;muscle cell differentiation;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of intracellular protein kinase cascade;negative regulation of MAPKKK cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of intracellular protein kinase cascade;regulation of MAPKKK cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;skeletal muscle cell differentiation;striated muscle cell differentiation cell part;integral to membrane;integral to nuclear inner membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to nuclear inner membrane;intrinsic to organelle membrane;membrane;membrane part;nuclear membrane;nuclear membrane part;nuclear part;organelle membrane;organelle part 9.11E-31 5 4 4 15.1

B4DGZ6;Q14693;Q14693-2;E7ESE7;F5GY24;H7C3T1;B4DET9;A8MU38 Phosphatidate phosphatase LPIN1 LPIN1 >tr|B4DGZ6|B4DGZ6_HUMAN Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 PE=2 SV=1;>sp|Q14693|LPIN1_HUMAN Phosphatidate phosphatase LPIN1 OS=Homo sapiens GN=LPIN1 PE=1 SV=2;>sp|Q14693-2|LPIN1_HUMAN Isoform 2 of Phosphatidate phosphatase LPIN1 OS=Ho -0.02 -0.12 0.13 0.01 -0.07 -0.28 0.10 0.41 0.093959824 -0.041812515 "actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;acylglycerol biosynthetic process;acylglycerol metabolic process;alcohol metabolic process;amine biosynthetic process;amine metabolic process;anatomical structure morphogenesis;biological regulation;biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell projection organization;cellular amine metabolic process;cellular biogenic amine biosynthetic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytoskeleton organization;developmental process;ethanolamine biosynthetic process;ethanolamine metabolic process;ethanolamine-containing compound metabolic process;fatty acid catabolic process;fatty acid metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrial fission;mitochondrion organization;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;neutral lipid biosynthetic process;neutral lipid metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ morphogenesis;organ regeneration;organelle fission;organelle organization;organic acid catabolic process;organic acid metabolic process;organic ether metabolic process;organophosphate metabolic process;oxoacid metabolic process;phosphatidylcholine biosynthetic process;phosphatidylcholine metabolic process;phosphatidylethanolamine biosynthetic process;phosphatidylethanolamine metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of histone deacetylation;positive regulation of histone modification;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of protein deacetylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regeneration;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of developmental process;regulation of fat cell differentiation;regulation of gene expression;regulation of histone deacetylation;regulation of histone modification;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of protein deacetylation;regulation of protein metabolic process;regulation of protein modification process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;ruffle organization;small molecule catabolic process;small molecule metabolic process;transcription, DNA-dependent;triglyceride biosynthetic process;triglyceride metabolic process;triglyceride mobilization" "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphatidate phosphatase activity;phosphoric ester hydrolase activity;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nucleoplasm part;organelle membrane;organelle part;protein complex;transcription factor complex 3.33E-32 8 4 4 14

Q9NZL9-4;Q9NZL9-2;Q9NZL9;Q9NZL9-3;H7C0X7;E5RFS9;Q9NZL9-5;E5RJR3 Methionine adenosyltransferase 2 subunit beta MAT2B >sp|Q9NZL9-4|MAT2B_HUMAN Isoform 4 of Methionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B;>sp|Q9NZL9-2|MAT2B_HUMAN Isoform 2 of Methionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B;>sp|Q9NZL9|MAT2B_HUMAN Methionine aden 0.26 -0.12 -0.10 -0.02 0.40 -0.16 0.21 -0.48 0.017189571 0.01128961 amine biosynthetic process;amine metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;extracellular polysaccharide biosynthetic process;extracellular polysaccharide metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;methylation;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;one-carbon metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside biosynthetic process;ribonucleoside metabolic process;S-adenosylmethionine biosynthetic process;S-adenosylmethionine metabolic process;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;xenobiotic metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;dTDP-4-dehydrorhamnose reductase activity;enzyme regulator activity;methionine adenosyltransferase regulator activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;methionine adenosyltransferase complex;mitochondrion;nucleus;organelle;protein complex Cysteine and methionine metabolism 3.35E-46 8 4 4 19.3

Q13505-3;Q13505;Q13505-2;H0Y6Y5 Metaxin-1 MTX1 >sp|Q13505-3|MTX1_HUMAN Isoform 3 of Metaxin-1 OS=Homo sapiens GN=MTX1;>sp|Q13505|MTX1_HUMAN Metaxin-1 OS=Homo sapiens GN=MTX1 PE=1 SV=2;>sp|Q13505-2|MTX1_HUMAN Isoform 2 of Metaxin-1 OS=Homo sapiens GN=MTX1;>tr|H0Y6Y5|H0Y6Y5_HUMAN Metaxin-1 (Fragment) OS= -0.12 0.02 0.14 0.20 -0.01 -0.03 -0.59 -0.15 0.720465292 0.255672025 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transport cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle

part;outer membrane 2.11E-38 4 4 4 16.7
F5H8H2;Q03426;F5H163;F5H368;F5GXC0;F5H092;B7Z1C2 Mevalonate kinase MVK >tr|F5H8H2|F5H8H2_HUMAN Mevalonate kinase OS=Homo sapiens GN=MVK PE=2 SV=1;>sp|Q03426|KIME_HUMAN
Mevalonate kinase OS=Homo sapiens GN=MVK PE=1 SV=1;>tr|F5H163|F5H163_HUMAN Mevalonate kinase OS=Homo sapiens GN=MVK PE=2 SV=1;>tr|F5H368|F5H368_HUMAN Mevalonat -0.09 0.12 -0.30
0.04 -0.45 -0.28 0.42 -0.27 0.155756304 0.091075581 "acetyl-CoA metabolic process;alcohol metabolic process;biological regulation;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic
process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;coenzyme metabolic process;cofactor metabolic process;isopentenyl diphosphate biosynthetic process;isopentenyl
diphosphate biosynthetic process, mevalonate pathway;isopentenyl diphosphate metabolic process;isoprenoid biosynthetic process;isoprenoid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic
process;negative regulation of biological process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of response to external stimulus;negative regulation of response to
stimulus;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;regulation of biological process;regulation of defense response;regulation of
inflammatory response;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol
biosynthetic process;sterol metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;mevalonate kinase activity;nucleotide binding;phosphotransferase
activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-
containing groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Peroxisome;Terpenoid backbone biosynthesis 3.50E-19 7 4 4 18.3
Q4G0N4-3;B7Z8V7;Q4G0N4-2;Q4G0N4 "NAD kinase domain-containing protein 1, mitochondrial" NADKD1 ">sp|Q4G0N4-3|NAKD2_HUMAN Isoform 3 of NAD kinase 2, mitochondrial OS=Homo sapiens
GN=NADK2;>tr|B7Z8V7|B7Z8V7_HUMAN Protein NADK2 OS=Homo sapiens GN=NADK2 PE=2 SV=1;>sp|Q4G0N4-2|NAKD2_HUMAN Isoform 2 of NAD kinase 2, mitochondrial OS=Homo sapiens GN=NADK2;>"
-0.41 -0.19 -0.07 -0.01 1.55 1.13 0.06 -0.16 0.827591557 -0.816769755 biosynthetic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular
nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;heterocycle biosynthetic process;heterocycle metabolic
process;metabolic process;NAD metabolic process;NADP biosynthetic process;NADP metabolic process;nicotinamide nucleotide biosynthetic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic
process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide
biosynthetic process;nucleotide metabolic process;oxidoreduction coenzyme metabolic process;primary metabolic process;pyridine nucleotide biosynthetic process;pyridine nucleotide metabolic process;pyridine-containing
compound biosynthetic process;pyridine-containing compound metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;identical
protein binding;kinase activity;NAD+ kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide
binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular
membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 2.40E-31 4 4 4 19
A2RRP1-2;A2RRP1;H0Y5G7 Neuroblastoma-amplified sequence NBAS >sp|A2RRP1-2|NBAS_HUMAN Isoform 2 of Neuroblastoma-amplified sequence OS=Homo sapiens
GN=NBAS;>sp|A2RRP1|NBAS_HUMAN Neuroblastoma-amplified sequence OS=Homo sapiens GN=NBAS PE=1 SV=2;>tr|H0Y5G7|H0Y5G7_HUMAN Neuroblastoma-amplified sequence (Fragment) OS=Ho -0.13
-0.25 -0.07 -0.01 0.64 0.48 0.21 -0.43 0.596608112 -0.339993657 cell part;cytoplasm;intracellular part 2.47E-13 3 4 4 2.4
E9PHA2;Q15003;B4E189;C9J470;H7C415;C9JZP1 Condensin complex subunit 2 NCAPH >tr|E9PHA2|E9PHA2_HUMAN Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=2
SV=1;>sp|Q15003|CND2_HUMAN Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=1 SV=3;>tr|B4E189|B4E189_HUMAN Condensin complex subunit 2 OS=Homo sapiens GN=NCAPH PE=2 SV 0.65
0.29 -0.03 -0.14 0.24 -0.66 -0.29 -0.34 0.745654372 0.452835713 cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular
level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic
process;cellular process;chromosome condensation;chromosome organization;DNA conformation change;DNA metabolic process;DNA packaging;M phase;M phase of mitotic cell cycle;macromolecule metabolic
process;metabolic process;mitosis;mitotic chromosome condensation;mitotic prometaphase;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic
process;organelle fission;organelle organization;primary metabolic process cell part;chromosomal part;condensin complex;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;intracellular membrane-bounded
organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-
bounded organelle;nucleus;organelle;organelle part;protein complex Cell cycle - yeast 5.18E-26 6 4 4 7.3
Q8WTT2;A6NJZ9;F5H677 Nucleolar complex protein 3 homolog NOC3L >sp|Q8WTT2|NOC3L_HUMAN Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1
SV=1;>tr|A6NJZ9|A6NJZ9_HUMAN Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=2 SV=1;>tr|F5H677|F5H677_HUMAN Nucleolar complex protein 3 homolog OS=Homo 0.05 1.13 0.47
-0.17 -0.37 0.55 -0.75 0.78 0.265860721 0.317816815 cell differentiation;cellular developmental process;cellular process;developmental process;fat cell differentiation cell part;intracellular non-
membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part
1.92E-81 3 4 4 8.2
G3V2V8;B4DQV7;J3KMY5;P61916;G3V3E8;E7EMS2;G3V3D1;H0YIZ1 Epididymal secretory protein E1 NPC2 >tr|G3V2V8|G3V2V8_HUMAN Epididymal secretory protein E1 (Fragment) OS=Homo sapiens
GN=NPC2 PE=2 SV=1;>tr|B4DQV7|B4DQV7_HUMAN Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=2 SV=1;>tr|J3KMY5|J3KMY5_HUMAN Epididymal secretory protein E1 OS=Homo s -0.04
-0.23 -0.65 0.04 -0.30 -0.35 0.26 -0.39 0.033941766 -0.022265724 alcohol metabolic process;biological regulation;chemical homeostasis;cholesterol efflux;cholesterol homeostasis;cholesterol
metabolic process;cholesterol transport;establishment of localization;establishment of localization in cell;glycolipid transport;homeostatic process;intracellular cholesterol transport;intracellular lipid transport;intracellular sterol
transport;intracellular transport;lipid homeostasis;lipid metabolic process;lipid transport;metabolic process;multi-organism process;organic substance transport;phospholipid transport;primary metabolic process;regulation of
biological process;regulation of biological quality;regulation of cellular metabolic process;regulation of cellular process;regulation of isoprenoid metabolic process;regulation of lipid metabolic process;regulation of metabolic
process;regulation of primary metabolic process;response to biotic stimulus;response to other organism;response to stimulus;response to virus;small molecule metabolic process;steroid metabolic process;sterol homeostasis;sterol
metabolic process;sterol transport;transport binding;cholesterol binding;lipid binding;steroid binding;sterol binding cell part;cytoplasmic part;endoplasmic reticulum;extracellular region;intracellular membrane-bounded
organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane-bounded organelle;organelle;vacuole Lysosome 5.40E-83 8 4 4 36.1
Q9H0P0-3;Q9H0P0-2;Q9H0P0-1;Q9H0P0;B9A035 Cytosolic 5-nucleotidase 3 NT5C3 >sp|Q9H0P0-3|5NT3A_HUMAN Isoform 4 of Cytosolic 5-nucleotidase 3A OS=Homo sapiens GN=NT5C3A;>sp|Q9H0P0-
2|5NT3A_HUMAN Isoform 3 of Cytosolic 5-nucleotidase 3A OS=Homo sapiens GN=NT5C3A;>sp|Q9H0P0-1|5NT3A_HUMAN Isoform 1 of Cytosolic 5-nucleotidase 3A OS= 0.12 1.05 0.42 0.18 -0.34 -0.08 -0.68
0.83 0.559937581 0.51460081 catabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen
compound metabolic process;cellular process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound
catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside catabolic process;nucleoside metabolic process;nucleoside phosphate metabolic
process;nucleotide metabolic process;primary metabolic process;pyrimidine base metabolic process;pyrimidine nucleoside catabolic process;pyrimidine nucleoside metabolic process;pyrimidine-containing compound catabolic
process;pyrimidine-containing compound metabolic process;small molecule metabolic process"2'-phosphotransferase activity;5'-nucleotidase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity,
acting on ester bonds;ion binding;magnesium ion binding;metal ion binding;nucleotidase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity;transferase activity" cell part;cytoplasm;cytoplasmic
part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Nicotinate and nicotinamide metabolism;Purine
metabolism;Pyrimidine metabolism 1.53E-17 5 4 4 17.2
Q96IZ0;H0YHP5;F8W1M8 PRKC apoptosis WT1 regulator protein PAWR >sp|Q96IZ0|PAWR_HUMAN PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1
SV=1;>tr|H0YHP5|H0YHP5_HUMAN PRKC apoptosis WT1 regulator protein (Fragment) OS=Homo sapiens GN=PAWR PE=2 SV=1 0.23 0.28 0.08 0.23 -1.30 -0.42 -0.11 0.01 0.94023617 0.656428397
"actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;apoptosis;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular
component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization
or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytokine
biosynthetic process;cytokine metabolic process;cytoskeleton organization;death;induction of apoptosis;induction of programmed cell death;interleukin-2 biosynthetic process;macromolecule biosynthetic process;macromolecule
metabolic process;metabolic process;negative regulation of antigen receptor-mediated signaling pathway;negative regulation of B cell activation;negative regulation of B cell proliferation;negative regulation of biological

process;negative regulation of biosynthetic process;negative regulation of cell activation;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mononuclear cell proliferation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of T cell activation;negative regulation of T cell proliferation;negative regulation of T cell receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of amyloid precursor protein biosynthetic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of glycoprotein biosynthetic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of programmed cell death;primary metabolic process;programmed cell death;protein metabolic process;regulation of amyloid precursor protein biosynthetic process;regulation of antigen receptor-mediated signaling pathway;regulation of apoptosis;regulation of B cell activation;regulation of B cell proliferation;regulation of biological process;regulation of biosynthetic process;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of glycoprotein biosynthetic process;regulation of immune system process;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mononuclear cell proliferation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of T cell activation;regulation of T cell proliferation;regulation of T cell receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" actin binding;binding;cytoskeletal protein binding;enzyme binding;protein binding;protein binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 2.39E-15 3 4 4 17.1

O43314-2;O43314;Q6PFW1-6;Q6PFW1-5;Q6PFW1-7;Q6PFW1-4;Q6PFW1-3;F8W9A8;B7WPL9;Q6PFW1-2;Q6PFW1;D6RFG4;H0Y9S9;D6RBU4 Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2;Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 1 PPIP5K2;PPIP5K1 >sp|O43314-2|VIP2_HUMAN Isoform 2 of Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2 OS=Homo sapiens GN=PPIP5K2;>sp|O43314|VIP2_HUMAN Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2 OS=Homo sapiens GN=P -0.35 -0.45 0.37 -0.06 0.68 0.15 0.57 -0.16 0.68122948 -0.429991888 alcohol metabolic process;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;inositol metabolic process;inositol phosphate metabolic process;metabolic process;organophosphate metabolic process;polyol metabolic process;primary metabolic process;small molecule metabolic process "acid phosphatase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;diphosphoinositol-pentakisphosphate kinase activity;hydrolase activity;hydrolase activity, acting on ester bonds;inositol 1,3,4,5,6-pentakisphosphate kinase activity;inositol hexakisphosphate 1-kinase activity;inositol hexakisphosphate 3-kinase activity;inositol hexakisphosphate 5-kinase activity;inositol hexakisphosphate kinase activity;inositol or phosphatidylinositol kinase activity;inositol pyrophosphate synthase activity;kinase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity;phosphotransferase activity, phosphate group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 7.31E-15 14 4 4 5.2

B7ZKK9;Q16537;J3KQN6;Q15173-2;Q15173 Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform PPP2R5E>tr|B7ZKK9|B7ZKK9_HUMAN PPP2R5E protein OS=Homo sapiens GN=PPP2R5E PE=2 SV=1;>sp|Q16537|2A5E_HUMAN Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform OS=Homo sapiens GN=PPP2R5E PE=1 SV=1;>tr|J3KQN6|J3KQN6_HUMAN Serine/threoni -0.11 0.02 -0.59 0.14 -0.32 0.23 0.24 -0.07 0.285668303 -0.152002046 activation of signaling protein activity involved in unfolded protein response;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;macromolecule metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;signal transduction enzyme regulator activity;phosphatase regulator activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;organelle;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;Wnt signaling pathway 3.74E-20 5 4 4 10.2

P41743 Protein kinase C iota type PRKCI >sp|P41743|KPCI_HUMAN Protein kinase C iota type OS=Homo sapiens GN=PRKCI PE=1 SV=2 0.43 0.03 -0.44 -0.85 0.13 0.06 0.76 1.37 0.819887796 -0.791577521 "actin cytoskeleton organization;actin filament organization;actin filament-based process;anatomical structure development;biological regulation;cell development;cell junction assembly;cell junction organization;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytoskeleton organization;developmental process;enzyme linked receptor protein signaling pathway;establishment of apical/basal cell polarity;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of monopolar cell polarity;establishment of protein localization;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;establishment or maintenance of epithelial cell apical/basal polarity;establishment or maintenance of monopolar cell polarity;eye photoreceptor cell development;Golgi vesicle budding;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotion;membrane budding;membrane organization;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of glial cell apoptosis;negative regulation of neuron apoptosis;negative regulation of programmed cell death;nerve growth factor receptor signaling pathway;neuron development;organelle organization;photoreceptor cell development;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of endothelial cell apoptosis;positive regulation of establishment of protein localization in plasma membrane;positive regulation of glial cell proliferation;positive regulation of gliogenesis;positive regulation of glucose import;positive regulation of glucose transport;positive regulation of molecular function;positive regulation of neurogenesis;positive regulation of neuron projection development;positive regulation of NF-kappaB transcription factor activity;positive regulation of programmed cell death;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transport;protein targeting;protein targeting to membrane;protein transport;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of endothelial cell apoptosis;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of gene expression;regulation of glial cell apoptosis;regulation of glial cell proliferation;regulation of gliogenesis;regulation of glucose import;regulation of glucose transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron apoptosis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein localization;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-

dependent;regulation of transport;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to interleukin-1;response to organic substance;response to peptide hormone stimulus;response to stimulus;secretion;signal transduction;tight junction assembly;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle organization;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;lipid binding;metal ion binding;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein kinase C activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;zinc ion binding" apical plasma membrane;cell cortex part;cell leading edge;cell part;cytoplasmic part;cytosol;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane;plasma membrane part;polarisome;protein complex;Schmidt-Lanterman incisure Endocytosis;Insulin signaling pathway;Tight junction 1.90E-19 1 4
4 8.1

P49720;J3KSM3;J3KRR2;J3QKR3 Proteasome subunit beta type-3 PSMB3 >sp|P49720|PSB3_HUMAN Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2;>tr|J3KSM3|J3KSM3_HUMAN Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=3 SV=1;>tr|J3KRR2|J3KRR2_HUMAN Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB -0.11 0.00 -0.10 0.10 -0.28 0.06 -0.05 -0.03 0.212893256 0.049033411 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome core complex;protein complexProteasome 7.15E-45 4 4 4
24.9

Q99436;B4E0P1;Q5TBG5 Proteasome subunit beta type-7;Proteasome subunit beta type PSMB7 ">sp|Q99436|PSB7_HUMAN Proteasome subunit beta type-7 OS=Homo sapiens GN=PSMB7 PE=1 SV=1;>tr|B4E0P1|B4E0P1_HUMAN Proteasome (Prosome, macropain) subunit, beta type, 7, isoform CRA_b OS=Homo sapiens GN=PSMB7 PE=2 SV=1;>tr|Q5TBG5|Q5TBG5_HUMAN Proteasome subun" -0.13 0.07 -0.41 0.03 -0.19 0.00 -0.33 -0.02 0.072842889 0.028279376 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome core complex;protein complex Proteasome 2.34E-73 3 4 4 18.8

P15151-3;P15151-2;P15151-4;P15151 Poliovirus receptor PVR>sp|P15151-3|PVR_HUMAN Isoform Gamma of Poliovirus receptor OS=Homo sapiens GN=PVR;>sp|P15151-2|PVR_HUMAN Isoform Beta of Poliovirus receptor OS=Homo sapiens GN=PVR;>sp|P15151-4|PVR_HUMAN Isoform Delta of Poliovirus receptor OS=Homo sapiens GN=PVR;>sp|P151 -0.15 -0.17 0.24 -0.19 0.38 -0.15 0.46 0.16 0.69781611 -0.27896937 adherens junction organization;biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell motility;cell-cell adhesion;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;interaction with host;interspecies interaction between organisms;locomotion;multi-organism process;positive regulation of adaptive immune response;positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;positive regulation of biological process;positive regulation of cell killing;positive regulation of defense response;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune response to tumor cell;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of leukocyte mediated cytotoxicity;positive regulation of leukocyte mediated immunity;positive regulation of lymphocyte mediated immunity;positive regulation of natural killer cell mediated cytotoxicity;positive regulation of natural killer cell mediated cytotoxicity directed against tumor cell target;positive regulation of natural killer cell mediated immune response to tumor cell;positive regulation of natural killer cell mediated immunity;positive regulation of response to biotic stimulus;positive regulation of response to stimulus;positive regulation of response to tumor cell;positive regulation of T cell mediated cytotoxicity;positive regulation of T cell mediated immunity;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of biological process;regulation of cell killing;regulation of defense response;regulation of immune effector process;regulation of immune response;regulation of immune response to tumor cell;regulation of immune system process;regulation of innate immune response;regulation of leukocyte mediated cytotoxicity;regulation of leukocyte mediated immunity;regulation of lymphocyte mediated immunity;regulation of natural killer cell mediated cytotoxicity;regulation of natural killer cell mediated cytotoxicity directed against tumor cell target;regulation of natural killer cell mediated immune response to tumor cell;regulation of natural killer cell mediated immunity;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of response to tumor cell;regulation of T cell mediated cytotoxicity;regulation of T cell mediated immunity;reproductive process;susceptibility to natural killer cell mediated cytotoxicity;susceptibility to T cell mediated cytotoxicity;viral reproductive process;virus-host interaction receptor activity cell junction;cell part;cell surface;cytoplasm;extracellular region part;extracellular space;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane Cell adhesion molecules (CAMs) 1.74E-08 4 4 4 14.8

P32322-2;P32322;B4DMU0;J3QL24;J3KQ22;E2QRB3;J3KTA8;J3QKT3;J3QRZ0;J3QLK9;J3QL23;J3QL32;J3QR88;J3QKT4 "Pyrroline-5-carboxylate reductase 1, mitochondrial;Pyrroline-5-carboxylate reductase" PYCR1 ">sp|P32322-2|P5CR1_HUMAN Isoform 2 of Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1;>sp|P32322|P5CR1_HUMAN Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2;>tr|B4DMU0|B4DMU0_HUMAN Pyrroline"-0.88 -0.20 -0.70 -0.17 0.19 -0.37 -0.01 -0.33 0.67745513 -0.356079315 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;glutamine family amino acid biosynthetic process;glutamine family amino acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;L-proline biosynthetic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;proline biosynthetic process;proline metabolic process;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;small molecule biosynthetic process;small molecule metabolic process "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH group of donors;oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;pyrroline-5-carboxylate reductase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Arginine and proline metabolism 1.80E-32 14 4 4 14.9

Q9BZG1-4;Q9BZG1;A8MYQ9;J3KQW8;C9JBG0;Q9BZG1-2;C9JY26;E7ES60;K7EJW7;K7EIF2;J3QLC6;H7C0Y7 Ras-related protein Rab-34 RAB34 ">sp|Q9BZG1-4|RAB34_HUMAN Isoform 4 of Ras-related protein Rab-34 OS=Homo sapiens GN=RAB34;>sp|Q9BZG1|RAB34_HUMAN Ras-related protein Rab-34 OS=Homo sapiens GN=RAB34 PE=1 SV=1;>tr|A8MYQ9|A8MYQ9_HUMAN Ras-related protein Rab-34, isoform NARR OS=Homo sapiens"-0.04 -0.06 -0.26 -0.14 0.56 0.01 -0.22 -0.10 0.435939642 -0.189033626 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular response to stimulus;endocytosis;establishment of localization;establishment of protein localization;intracellular signal transduction;membrane invagination;membrane organization;organelle fusion;organelle organization;phagosome-lysosome fusion;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome;endocytic vesicle;endocytic vesicle membrane;endosome;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;phagocytic vesicle;phagocytic vesicle membrane;ruffle;vesicle;vesicle membrane 5.03E-38 12 4 4 19.4

P98175-4;P98175-3;P98175-2;P98175 RNA-binding protein 10 RBM10 >sp|P98175-4|RBM10_HUMAN Isoform 4 of RNA-binding protein 10 OS=Homo sapiens GN=RBM10;>sp|P98175-3|RBM10_HUMAN Isoform 3 of RNA-binding protein 10 OS=Homo sapiens GN=RBM10;>sp|P98175-2|RBM10_HUMAN Isoform 2 of RNA-binding protein 10 OS=Homo sapiens GN=RBM1 0.01 0.41 0.06 0.53 0.59 0.28 -0.86 -0.46 0.41944577 0.365213898 "3'-UTR-mediated mRNA stabilization;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of muscle cell apoptosis;positive regulation of programmed cell death;positive regulation of smooth muscle cell apoptosis;posttranscriptional regulation of gene expression;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of muscle cell apoptosis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of RNA stability;regulation of smooth muscle cell apoptosis;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA metabolic process;RNA processing;RNA splicing;RNA stabilization" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.09E-13 4 4 4 7.6

Q96T37-2;Q96T37-3;Q96T37 Putative RNA-binding protein 15 RBM15 >sp|Q96T37-2|RBM15_HUMAN Isoform 2 of Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15;>sp|Q96T37-3|RBM15_HUMAN Isoform 3 of Putative RNA-binding protein 15 OS=Homo sapiens GN=RBM15;>sp|Q96T37|RBM15_HUMAN Putative RNA-binding protein 15 OS=Homo sap 0.11 0.30 0.42 0.29 -0.02 -0.26 -1.21 -0.36 1.166709347 0.741215928 "anatomical structure development;anatomical structure morphogenesis;biological regulation;blood vessel development;branching morphogenesis of a tube;cardiac septum morphogenesis;developmental process;hemopoietic or lymphoid organ development;interaction with host;interspecies interaction between organisms;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;multi-organism process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of myeloid cell differentiation;organ development;pattern specification process;patterning of blood vessels;placenta blood vessel development;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription of Notch receptor target;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;spleen development;tissue morphogenesis;tube morphogenesis;ventricular septum morphogenesis;viral reproductive process;virus-host interaction"binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.62E-10 3 4 4 8.2

Q14699;G3XAJ6;C9JHG2;C9JWQ9;F8WAR1;C9JRN3 Raftlin RFTN1 ">sp|Q14699|RFTN1_HUMAN Raftlin OS=Homo sapiens GN=RFTN1 PE=1 SV=4;>tr|G3XAJ6|G3XAJ6_HUMAN Raft-linking protein, isoform CRA_c OS=Homo sapiens GN=RFTN1 PE=2 SV=1;>tr|C9JHG2|C9JHG2_HUMAN Raftlin (Fragment) OS=Homo sapiens GN=RFTN1 PE=2 SV=1" -0.02 0.44 0.04 0.40 0.64 0.59 0.28 0.58 0.897662268 -0.305803522 cell part;membrane;membrane part;membrane raft;plasma membrane 8.39E-23 6 4 4 14

P62266;D6RD47;D6RDJ2;D6RIX0;D6R9I740S ribosomal protein S23 RPS23 >sp|P62266|RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3;>tr|D6RD47|D6RD47_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=2 SV=1;>tr|D6RDJ2|D6RDJ2_HUMAN 40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=2 SV=1;>tr -0.01 0.00 -0.07 -0.20 -0.49 -0.77 -0.12 -0.40 1.103456819 0.375119267 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 5.96E-17 5 4 4 28.7

P60903 Protein S100-A10 S100A10 >sp|P60903|S10AA_HUMAN Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2 -0.03 0.24 -1.06 -0.51 -0.17 0.21 0.25 0.11 0.625576846 -0.442069019 biological regulation;cellular process;cellular response to acid;cellular response to chemical stimulus;cellular response to stimulus;positive regulation of binding;positive regulation of molecular function;regulation of binding;regulation of biological process;regulation of cellular process;regulation of molecular function;response to acid;response to chemical stimulus;response to stimulus;signal transduction binding;calcium ion binding;cation binding;ion binding;metal ion binding;protein binding;receptor binding cell part;extrinsic to membrane;extrinsic to plasma membrane;membrane part;plasma membrane part 8.37E-42 1 4 4 51.5

M0QX65;M0QZS6;Q9UBE0-2;Q9UBE0-3;B3KNJ4;Q9UBE0;M0R286;M0QYM8;M0R054 SUMO-activating enzyme subunit 1 SAE1 >tr|M0QX65|M0QX65_HUMAN SUMO-activating enzyme subunit 1 (Fragment) OS=Homo sapiens GN=SAE1 PE=4 SV=1;>tr|M0QZS6|M0QZS6_HUMAN SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=4 SV=1;>sp|Q9UBE0-2|SAE1_HUMAN Isoform 2 of SUMO-activating enzyme sub -0.17 -0.09 -0.06 0.02 0.07 -0.49 -0.77 -0.77 0.884374369 0.418515467 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein sumoylation;protein ubiquitination ATP-dependent protein binding;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;ligase activity;protein binding;protein C-terminus binding;protein dimerization activity;protein heterodimerization activity;small protein activating enzyme activity;ubiquitin activating enzyme activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Ubiquitin mediated proteolysis 5.29E-22 9 4 4 23.4

O14828;O14828-2 Secretory carrier-associated membrane protein 3 SCAMP3>sp|O14828|SCAM3_HUMAN Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 PE=1 SV=3;>sp|O14828-2|SCAM3_HUMAN Isoform 2 of Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 0.73 -0.01 -0.03 -0.49 0.85 0.90 0.30 0.10 0.643872741 -0.487159309 cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;post-Golgi vesicle-mediated transport;protein transport;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to retinoic acid;response to stimulus;response to vitamin;response to vitamin A;transport;vesicle-mediated transport cell part;cytoplasmic part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part 3.90E-58 2 4 4 19

O00767 Acyl-CoA desaturase SCD>sp|O00767|ACOD_HUMAN Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2 0.86 0.26 -0.80 -1.30 -0.32 -0.36 0.06 -0.20 0.026510774 -0.0403687 biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid biosynthetic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process"binding;catalytic activity;cation binding;CoA desaturase activity;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water;stearoyl-CoA 9-desaturase activity;transition metal ion binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Biosynthesis of unsaturated fatty acids;PPAR signaling pathway 9.97E-14 1 4 4 15.9

Q96KG9-3;E9PS17;E9PK59;Q96KG9-4;Q96KG9-2;Q96KG9;Q96KG9-5;E9PPN3;Q96KG9-6;H0YCI6;H0YDH0 N-terminal kinase-like protein SCYL1 >sp|Q96KG9-3|NTKL_HUMAN Isoform 3 of N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1;>tr|E9PS17|E9PS17_HUMAN N-terminal kinase-like protein OS=Homo sapiens GN=SCYL1 PE=2 SV=1;>tr|E9PK59|E9PK59_HUMAN N-terminal kinase-like protein OS=Homo sapiens GN 0.08 0.08 -0.17 0.12 0.37 0.30 0.06 -0.24 0.242458608 -0.096461391 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;retrograde vesicle-mediated transport, Golgi to ER;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;transport;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;kinase activity;nucleic acid binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cis-Golgi network;COPI vesicle coat;cytoplasm;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;endoplasmic reticulum-Golgi intermediate compartment;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;membrane-bounded organelle;microtubule organizing center;nucleus;organelle;organelle part;protein complex;vesicle coat 1.36E-11 11 4 4 10.2

F8VSC5;Q6P3W7;H0YIK6 SCY1-like protein 2 SCYL2 >tr|F8VSC5|F8VSC5_HUMAN SCY1-like protein 2 (Fragment) OS=Homo sapiens GN=SCYL2 PE=2 SV=1;>sp|Q6P3W7|SCYL2_HUMAN SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1 0.10 0.08 0.11 -0.05 -0.21 -0.26 0.22 -0.03 0.466299499 0.129188447 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;endocytosis;endosome to lysosome transport;endosome transport;establishment of localization;establishment of localization in cell;intracellular transport;lysosomal transport;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of clathrin-mediated endocytosis;positive regulation of endocytosis;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of receptor internalization;positive regulation of receptor-mediated endocytosis;positive regulation of transport;receptor internalization;receptor internalization involved in canonical Wnt receptor signaling pathway;receptor metabolic process;receptor-mediated endocytosis;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of clathrin-mediated endocytosis;regulation of endocytosis;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of receptor internalization;regulation of receptor-mediated endocytosis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of vesicle-mediated transport;regulation of Wnt receptor signaling pathway;transport;vacuolar transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endosomal part;endosome membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;vesicle 2.70E-14 3 4 4 10.3

P55735-2;P55735;B4DXJ1;A8MXL6;E7ERC8 Protein SEC13 homolog SEC13 >sp|P55735-2|SEC13_HUMAN Isoform 2 of Protein SEC13 homolog OS=Homo sapiens GN=SEC13;>sp|P55735|SEC13_HUMAN Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=1 SV=3;>tr|B4DXJ1|B4DXJ1_HUMAN Protein SEC13 homolog OS=Homo sapiens GN=SEC13 PE=2 SV=1;>tr|A8MXL6 0.03 0.06 -0.70 0.02 -0.50 0.28 0.06 0.18 0.226689105 -0.151159304 anaphase;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cell cycle phase;cell cycle process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glycosylation;immune system process;intracellular protein transport;intracellular transport;M phase;M phase of mitotic cell cycle;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;mitotic prometaphase;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;RNA transport;transport;vesicle coating;vesicle organization cell part;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;ER to Golgi transport vesicle membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear part;Nup107-160 complex;organelle membrane;organelle part;protein complex;transport vesicle membrane;vesicle membrane Protein processing in endoplasmic reticulum;RNA transport 1.06E-70 5 4 4 20.1

P29353-2;P29353-7;P29353;P29353-6;H0Y539;P29353-5;P29353-3;Q5T181;Q5T182;Q5T188 SHC-transforming protein 1 SHC1 >sp|P29353-2|SHC1_HUMAN Isoform p52Shc of SHC-transforming protein 1 OS=Homo sapiens GN=SHC1;>sp|P29353-7|SHC1_HUMAN Isoform 7 of SHC-transforming protein 1 OS=Homo sapiens GN=SHC1;>sp|P29353|SHC1_HUMAN SHC-transforming protein 1 OS=Homo sapiens GN=SHC1 PE -0.22 -0.09 0.10 0.36 -0.10 -0.08 0.35 -0.19 0.089708922 0.044742087 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;activation of MAPK activity;activation of signaling protein activity involved in unfolded protein response;anatomical structure development;anatomical structure formation involved in morphogenesis;angiogenesis;biological adhesion;biological regulation;cell activation;cell adhesion;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytoskeleton organization;defense response;developmental process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway;heart development;immune response;immune system process;innate immune response;insulin receptor signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;leukocyte migration;locomotion;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;nerve growth factor receptor signaling pathway;organ development;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nuclease activity;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of DNA metabolic process;regulation of DNA replication;regulation of epidermal growth factor receptor signaling pathway;regulation of epidermal growth factor-activated receptor activity;regulation of growth;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein tyrosine kinase activity;regulation of receptor activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transferase activity;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway "binding;binding, bridging;catalytic activity;epidermal growth factor receptor binding;growth factor receptor binding;kinase activity;lipid binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein binding, bridging;protein kinase activity;protein tyrosine kinase activity;receptor binding;receptor tyrosine kinase binding;signaling adaptor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein tyrosine kinase adaptor activity" cell part;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part;plasma membrane part;protein complex;Shc-EGFR complex Bacterial invasion of epithelial cells;Chemokine signaling pathway;Chronic myeloid leukemia;ErbB signaling pathway;Focal adhesion;Glioma;Insulin signaling pathway;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway 5.78E-29 10 4 4 12.7

P53985;Q5T8R3;Q49A45;Q5T8R5 Monocarboxylate transporter 1 SLC16A1 >sp|P53985|MOT1_HUMAN Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3;>tr|Q5T8R3|Q5T8R3_HUMAN Monocarboxylate transporter 1 (Fragment) OS=Homo sapiens GN=SLC16A1 PE=2 SV=1;>tr|Q49A45|Q49A45_HUMAN Monocarboxylate transporter 1 OS=Homo sap -1.01 0.19 -0.47 0.47 -2.75 -1.74 -1.58 -0.24 0.954786719 1.374591734 biological regulation;blood coagulation;carboxylic acid metabolic process;cell migration;cell motility;cellular component movement;cellular ketone metabolic process;cellular metabolic process;cellular process;coagulation;establishment of localization;hemostasis;immune system process;leukocyte migration;locomotion;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;organic acid metabolic process;oxoacid metabolic process;pyruvate metabolic process;regulation of biological quality;regulation of body fluid levels;small molecule metabolic process;transmembrane transport;transport active transmembrane transporter activity;carboxylic acid transmembrane transporter activity;mevalonate transmembrane transporter activity;monocarboxylic acid transmembrane transporter activity;organic acid transmembrane transporter activity;secondary active monocarboxylate transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;plasma membrane 2.00E-16 4 4 4 11.2

Q9Y6M7-6;D3K174;Q9Y6M7-8;Q9Y6M7-7;E9PDL9;Q9Y6M7-11;Q9Y6M7-10;Q9Y6M7-5;F8W7E6;H7C3C4;Q9Y6M7-4;Q9Y6M7-3;C9JRP1;Q9Y6M7-2;Q9Y6M7-9;E9PGC1;E9PFN4;Q9Y6M7 Sodium bicarbonate cotransporter 3 SLC4A7 >sp|Q9Y6M7-6|S4A7_HUMAN Isoform 6 of Sodium bicarbonate cotransporter 3 OS=Homo sapiens GN=SLC4A7;>tr|D3K174|D3K174_HUMAN Sodium bicarbonate cotransporter 3 OS=Homo sapiens GN=SLC4A7 PE=2 SV=1;>sp|Q9Y6M7-8|S4A7_HUMAN Isoform 8 of Sodium bicarbonate cotrans 0.39 0.07 -0.15 -0.37 0.21 0.15 0.28 0.13 0.53296183 -0.209488582 anatomical structure development;anatomical structure morphogenesis;auditory receptor cell development;cell death;cell development;cellular developmental process;cellular process;cochlear nucleus development;death;developmental process;developmental programmed cell death;inner ear receptor cell development;neural nucleus development;neuron development;programmed cell death;retina vasculature morphogenesis in camera-type eye;retinal cell programmed cell death active transmembrane transporter activity;anion transmembrane transporter activity;anion:anion antiporter activity;anion:cation symporter activity;antiporter activity;bicarbonate transmembrane transporter activity;cation transmembrane transporter activity;inorganic anion exchanger activity;inorganic anion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;secondary active transmembrane transporter activity;sodium ion transmembrane transporter activity;sodium:bicarbonate symporter activity;solute:cation symporter activity;solute:solute antiporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity apical plasma membrane;basolateral plasma membrane;cell part;cell projection;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;microvillus;organelle part;plasma membrane;plasma membrane part;stereocilium 2.40E-19 18 4 4 5.5

Q01650 Large neutral amino acids transporter small subunit 1 SLC7A5 >sp|Q01650|LAT1_HUMAN Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2 -0.70 0.11 -0.29 0.09 -1.19 -1.53 -0.93 0.25 0.646226464 0.654846309 amine metabolic process;anatomical structure development;biological regulation;blood coagulation;carboxylic acid metabolic process;cell differentiation;cell migration;cell motility;cellular amine metabolic process;cellular amino acid metabolic process;cellular component movement;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coagulation;developmental process;hemostasis;immune system process;leukocyte migration;locomotion;metabolic process;multicellular organismal process;nervous system development;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of biological quality;regulation of body fluid levels;small molecule metabolic process;system development active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;antigen binding;binding;carboxylic acid transmembrane transporter activity;L-amino acid transmembrane transporter activity;neutral amino acid transmembrane transporter activity;organic acid transmembrane transporter activity;peptide antigen binding;peptide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity apical plasma membrane;cell part;cytoplasmic part;cytosol;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;plasma membrane;plasma membrane part 2.41E-57 1 4 4 11.2

Q16637-4;Q16637-2;Q16637-3;Q16637;E7EQZ4;B4DP61;H0YBZ9 Survival motor neuron protein SMN1;SMN2 >sp|Q16637-4|SMN_HUMAN Isoform SMN-delta57 of Survival motor neuron protein OS=Homo sapiens GN=SMN1;>sp|Q16637-2|SMN_HUMAN Isoform SMN-delta5 of Survival motor neuron protein OS=Homo sapiens GN=SMN1;>sp|Q16637-3|SMN_HUMAN Isoform SMN-delta7 of Survival mot -0.12 0.07 -0.51 0.08 -0.65 0.01 -0.33 0.08 0.172330756 0.101359969 cell death;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA processing;spliceosomal snRNP assembly;spliceosome assembly binding;nucleic acid binding;RNA binding Cajal body;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex RNA transport 1.24E-11 7 4 4 26.8

Q2TAY7 WD40 repeat-containing protein SMU1 SMU1 >sp|Q2TAY7|SMU1_HUMAN WD40 repeat-containing protein SMU1 OS=Homo sapiens GN=SMU1 PE=1 SV=2 0.16 0.41 0.29 0.26 0.24 -0.25 -1.18 -0.61 1.020227205 0.731282018 cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.10E-13 1 4 4 7

Q9Y5X1 Sorting nexin-9 SNX9 >sp|Q9Y5X1|SNX9_HUMAN Sorting nexin-9 OS=Homo sapiens GN=SNX9 PE=1 SV=1 0.38 -0.13 0.24 0.02 0.46 0.03 -0.08 -0.22 0.146563408 0.075303275 biological regulation;cell communication;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;lipid tube assembly;macromolecular complex assembly;macromolecular complex subunit organization;membrane invagination;membrane organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular component organization;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of protein complex assembly;positive regulation of protein oligomerization;protein transport;receptor-mediated endocytosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein oligomerization;regulation of purine nucleotide catabolic process;transport;vesicle-mediated transport 1-phosphatidylinositol binding;binding;lipid binding;phosphatidylinositol binding;phospholipid binding cell part;cell projection;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;plasma membrane part;ruffle;trans-Golgi network;vesicle;vesicle membrane 3.12E-56 1 4 4 9.6

O60248;B4DWU7 Protein SOX-15 SOX15 >sp|O60248|SOX15_HUMAN Protein SOX-15 OS=Homo sapiens GN=SOX15 PE=1 SV=1;>tr|B4DWU7|B4DWU7_HUMAN Protein SOX-15 OS=Homo sapiens GN=SOX15 PE=2 SV=1 0.32 0.50 -0.37 0.12 -1.90 -1.49 -1.02 -0.17 1.271605394 1.286722127 "anatomical structure development;anatomical structure morphogenesis;biological regulation;cell development;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;chromatin organization;chromosome organization;developmental growth;developmental process;developmental process involved in reproduction;gonad development;growth;male gonad development;myoblast development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of muscle organ development;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of striated muscle tissue development;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;organ development;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell activation;positive regulation of cell cycle;positive regulation of cell cycle process;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of G0 to G1 transition;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of myoblast proliferation;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of satellite cell activation involved in skeletal muscle regeneration;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regeneration;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biosynthetic process;regulation of cell activation;regulation of cell cycle;regulation of cell cycle process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of G0 to G1 transition;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of myoblast proliferation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of satellite cell activation involved in skeletal muscle regeneration;regulation of skeletal muscle tissue regeneration;regulation of striated muscle tissue development;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of wound healing;reproductive process;reproductive structure development;skeletal muscle tissue regeneration;tissue development;tissue regeneration" binding;chromatin binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 7.18E-54 2 4 4 37.3

Q86XZ4;F8VS10 Spermatogenesis-associated serine-rich protein 2 SPATS2 >sp|Q86XZ4|SPAS2_HUMAN Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens GN=SPATS2 PE=1 SV=1;>tr|F8VS10|F8VS10_HUMAN Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens GN=SPATS2 PE=2 SV=1 0.44 0.15 0.18 0.07 -0.21 -0.60 -0.48 0.42 0.758001577 0.42900613 cell part;cytoplasm;intracellular part 1.54E-24 2 4 4 9.9

E9PL01;Q15005;E9PI68;H0YE04 Signal peptidase complex subunit 2 SPCS2 >tr|E9PL01|E9PL01_HUMAN Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=2 SV=1;>sp|Q15005|SPCS2_HUMAN Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3;>tr|E9PI68|E9PI68_HUMAN Signal peptidase complex subunit 2 OS=Homo sa 0.05 0.17 -0.35 -0.63 -0.05 -0.38 -0.45 0.12 0.00390447 0.002770474 biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;peptide metabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;proteolysis;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;signal peptide processing;SRP-dependent cotranslational protein targeting to membrane;translation;transport catalytic activity;hydrolase activity;peptidase activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;protein complex;signal peptidase complex Protein export 3.68E-23 4 4 4 31.8

E7EVQ6;Q14534;H0YBN7;E5RJH9 Squalene monooxygenase SQLE >tr|E7EVQ6|E7EVQ6_HUMAN Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=2 SV=1;>sp|Q14534|ERG1_HUMAN Squalene monooxygenase OS=Homo sapiens GN=SQLE PE=1 SV=3;>tr|H0YBN7|H0YBN7_HUMAN Squalene monooxygenase (Fragment) OS=Homo sapiens GN=SQLE PE=2 SV=1 0.49 0.15 -0.60 -0.51 0.82 0.37 0.39 -0.31 0.524338101 -0.43950773 alcohol metabolic process;biosynthetic process;cellular aromatic compound metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;response to chemical stimulus;response to organic substance;response to stimulus;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;squalene monooxygenase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part Steroid biosynthesis 1.30E-17 4 4 4 12.1

F8WAK8;Q8N3U4;Q8N3U4-2;Q68DW7;Q6P275;Q8WVM7;B1AMT4;F5H1C4 Cohesin subunit SA-2;Cohesin subunit SA-1STAG2;DKFZp781D1416;STAG1 >tr|F8WAK8|F8WAK8_HUMAN Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2 PE=2 SV=1;>sp|Q8N3U4|STAG2_HUMAN Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2 PE=1 SV=3;>sp|Q8N3U4-2|STAG2_HUMAN Isoform 2 of Cohesin subunit SA-2 OS=Homo sapiens GN=STAG2;>tr|Q68DW7|Q6 -0.05 0.56 0.14 0.58 -0.05 -0.06 -0.88 -0.14 0.988157643 0.58872779 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chromosome organization;chromosome segregation;cytokinesis;developmental process;M phase;M phase of mitotic cell cycle;meiosis;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA endoreduplication;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;organelle organization;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA endoreduplication;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;S phase;S phase of mitotic cell cycle;sister chromatid cohesion;stem cell maintenance "cell junction;cell part;chromatin;chromosomal part;chromosome, centromeric region;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part" Cell cycle;Cell cycle - yeast;Meiosis - yeast 4.27E-12 8 4 4 4.5

Q8TCJ2 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B STT3B >sp|Q8TCJ2|STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1 0.55 0.15 -0.45 -0.05 1.78 -1.02 0.31 -0.51 0.044439714 -0.085745447 carbohydrate metabolic process;catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;co-translational protein modification;ER-associated protein catabolic process;glycoprotein catabolic process;glycoprotein metabolic process;glycosylation;macromolecule catabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;proteolysis;proteolysis involved in cellular protein catabolic process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;ubiquitin-dependent protein catabolic process "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;oligosaccharyltransferase complex;organelle part;protein complex N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis 1.35E-13 1 4 4 6.1

Q15582;G8JLA8;H0Y8L3;H0YAB8;D6RBX4;H0YAH8;H0Y9D7 Transforming growth factor-beta-induced protein ig-h3 TGFBI >sp|Q15582|BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1;>tr|G8JLA8|G8JLA8_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=2 SV=1;>tr|H0Y8L3|H0Y8L3_HUMAN Transfor -1.10 0.31 0.19 0.60 -0.17 1.26 0.18 2.38 0.55786903 -0.912491381 anatomical structure formation involved in morphogenesis;angiogenesis;biological adhesion;biological regulation;cell adhesion;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;extracellular matrix organization;extracellular structure organization;multicellular organismal process;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;neurological system process;regulation of biological process;regulation of cell adhesion;regulation of cellular process;response to stimulus;sensory perception;sensory perception of light stimulus;system process;visual perception binding;extracellular matrix binding;integrin binding;protein binding;protein complex binding;receptor binding cell part;extracellular matrix;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;proteinaceous

extracellular matrix;vesicle 4.46E-16 7 4 4 7.9
O75663;O75663-2 TIP41-like protein TIPRL >sp|O75663|TIPRL_HUMAN TIP41-like protein OS=Homo sapiens GN=TIPRL PE=1 SV=2;>sp|O75663-2|TIPRL_HUMAN Isoform 2 of TIP41-like protein OS=Homo sapiens GN=TIPRL0.01 -0.08 0.30 -0.21 0.29 -0.16 0.33 -0.05 0.232986989 -0.099617371 biological regulation;cell cycle checkpoint;cellular process;cellular response to stimulus;cellular response to stress;DNA damage checkpoint;DNA integrity checkpoint;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;negative regulation of phosphoprotein phosphatase activity;negative regulation of protein phosphatase type 2A activity;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of lipase activity;regulation of lipoprotein lipase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of protein phosphatase type 2A activity;response to DNA damage stimulus;response to stimulus;response to stress cell part;cytoplasm;intracellular part 1.83E-10 2 4 4 13.6
H0Y612;Q9UPN9-2;Q9UPN9;E7EN20 E3 ubiquitin-protein ligase TRIM33 TRIM33 >tr|H0Y612|H0Y612_HUMAN E3 ubiquitin-protein ligase TRIM33 (Fragment) OS=Homo sapiens GN=TRIM33 PE=4 SV=1;>sp|Q9UPN9-2|TRI33_HUMAN Isoform Beta of E3 ubiquitin-protein ligase TRIM33 OS=Homo sapiens GN=TRIM33;>sp|Q9UPN9|TRI33_HUMAN E3 ubiquitin-protein liga 0.12 -0.02 0.21 0.00 0.05 -0.26 -0.69 -0.63 1.071484571 0.459801458 "biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of BMP signaling pathway;negative regulation of cell communication;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of BMP signaling pathway;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway" "acid-amino acid ligase activity;binding;catalytic activity;cation binding;DNA binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleic acid binding;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part 1.04E-16 4 4 4 5.4
Q15645;Q15645-2;H0YAL2 Pachytene checkpoint protein 2 homolog TRIP13 >sp|Q15645|PCH2_HUMAN Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2 0.38 0.17 0.23 -0.11 -0.24 -1.10 -0.13 -1.13 1.184050589 0.819400145 "anatomical structure development;biosynthetic process;cell cycle phase;cell cycle process;cell development;cell maturation;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;cellular response to stress;chromosome organization;chromosome organization involved in meiosis;developmental maturation;developmental process;developmental process involved in reproduction;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;female gamete generation;female meiosis I;gamete generation;germ cell development;macromolecule biosynthetic process;macromolecule metabolic process;male gamete generation;male meiosis I;meiosis I;metabolic process;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oocyte maturation;oogenesis;organelle organization;pachytene;primary metabolic process;reciprocal DNA recombination;reciprocal meiotic recombination;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;spermatid development;spermatogenesis;synaptonemal complex assembly;synaptonemal complex organization;transcription from RNA polymerase II promoter;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;germ cell nucleus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;male germ cell nucleus;membrane-bounded organelle;nucleus;organelle 5.83E-16 3 4 4 11.6
Q15650;H0YL91 Activating signal cointegrator 1 TRIP4 >sp|Q15650|TRIP4_HUMAN Activating signal cointegrator 1 OS=Homo sapiens GN=TRIP4 PE=1 SV=4;>tr|H0YL91|H0YL91_HUMAN Activating signal cointegrator 1 OS=Homo sapiens GN=TRIP4 PE=2 SV=1 0.13 0.07 -0.08 -0.15 -0.22 0.15 0.29 0.16 0.307863871 -0.09986461 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;cation binding;ion binding;ligand-dependent nuclear receptor binding;metal ion binding;protein binding;protein binding transcription factor activity;receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;nucleus;organelle;organelle part 7.48E-12 2 4 4 9.6
Q8TBC4-2;Q8TBC4;F8W8D4;B7Z5F6;F8WF86 NEDD8-activating enzyme E1 catalytic subunit UBA3 >sp|Q8TBC4-2|UBA3_HUMAN Isoform 2 of NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3;>sp|Q8TBC4|UBA3_HUMAN NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=2;>tr|F8W8D4|F8W8D4_HUMAN NEDD8-activating enzyme E0.18 0.00 -0.06 0.07 -0.16 -0.36 0.21 -0.17 0.540054684 0.167656521 "biological regulation;cell cycle;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;endomitotic cell cycle;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic cell cycle;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein neddylation;proteolysis;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic

process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent" "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;NEDD8 activating enzyme activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small protein activating enzyme activity" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Ubiquitin mediated proteolysis 3.66E-15 5 4 4 10.2

P61088;F8VSD4;Q5JXB2;F8VZ29;F8VQQ8;F8VV71 Ubiquitin-conjugating enzyme E2 N;Putative ubiquitin-conjugating enzyme E2 N-like UBE2N;UBE2NL >sp|P61088|UBE2N_HUMAN Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1;>tr|F8VSD4|F8VSD4_HUMAN Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=2 SV=1;>sp|Q5JXB2|UE2NL_HUMAN Putative ubiquitin-conjugating enzyme E2 N-like 0.01 0.32 -0.87 1.00 0.14 0.92 -0.03 0.22 0.164327696 -0.19687345 "activation of immune response;activation of innate immune response;antigen receptor-mediated signaling pathway;biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;cytokine-mediated signaling pathway;cytoplasmic pattern recognition receptor signaling pathway;defense response;DNA catabolic process;DNA catabolic process, exonucleolytic;DNA double-strand break processing;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via homologous recombination;histone modification;histone ubiquitination;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;intracellular receptor mediated signaling pathway;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;MyD88-dependent toll-like receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;nucleotide-binding oligomerization domain containing signaling pathway;organelle organization;pattern recognition receptor signaling pathway;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of defense response;positive regulation of DNA metabolic process;positive regulation of DNA repair;positive regulation of histone modification;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein kinase cascade;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of ubiquitin-protein ligase activity;postreplication repair;primary metabolic process;protein K63-linked ubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;recombinational repair;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome organization;regulation of defense response;regulation of DNA metabolic process;regulation of DNA repair;regulation of gene expression;regulation of histone modification;regulation of histone ubiquitination;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of ligase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of ubiquitin-protein ligase activity;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to organic substance;response to stimulus;response to stress;signal transduction;T cell receptor signaling pathway;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;ubiquitin-dependent protein catabolic process" "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small conjugating protein binding;small conjugating protein ligase activity;ubiquitin binding;ubiquitin-protein ligase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;UBC13-MMS2 complex;UBC13-UEV1A complex;ubiquitin conjugating enzyme complex;ubiquitin ligase complex Ubiquitin mediated proteolysis 3.76E-40 6 4 4 24.3

Q9HAU5;Q9HAU5-2 Regulator of nonsense transcripts 2 UPF2 >sp|Q9HAU5|RENT2_HUMAN Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 PE=1 SV=1;>sp|Q9HAU5-2|RENT2_HUMAN Isoform 2 of Regulator of nonsense transcripts 2 OS=Homo sapiens GN=UPF2 -0.18 -0.01 -0.24 -0.11 0.04 -0.09 0.09 -0.51 0.038313404 -0.016708273 "anatomical structure development;anatomical structure morphogenesis;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;establishment of localization;establishment of localization in cell;establishment of RNA localization;gene expression;intracellular transport;liver development;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;organ development;organ morphogenesis;organ regeneration;primary metabolic process;regeneration;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA transport;transport" binding;DNA binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;exon-exon junction complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;perinuclear region of cytoplasm;protein complex mRNA surveillance pathway;RNA transport 1.90E-10 2 4 4 3.3

Q9H9H4;F5H4M0;F5H1F6 Vacuolar protein sorting-associated protein 37B VPS37B >sp|Q9H9H4|VP37B_HUMAN Vacuolar protein sorting-associated protein 37B OS=Homo sapiens GN=VPS37B PE=1 SV=1;>tr|F5H4M0|F5H4M0_HUMAN Vacuolar protein sorting-associated protein 37B (Fragment) OS=Homo sapiens GN=VPS37B PE=2 SV=1;>tr|F5H1F6|F5H1F6_HUMAN Vacuol -0.06 0.07 -0.11 -0.10 -0.14 0.04 0.12 0.14 0.480755541 -0.087556863 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular process involved in reproduction;egress of virus within host cell;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;macromolecule metabolic process;membrane organization;metabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;protein transport;reproductive process;transport;vesicle-mediated transport;viral protein processing;viral reproductive process;virion assembly cell part;cytoplasmic part;endosomal part;endosome membrane;intracellular organelle part;intracellular part;late endosome membrane;membrane;midbody;organelle membrane;organelle part Endocytosis 1.21E-60 3 4 4 22.8

M0QY97;Q9UPT8 Zinc finger CCCH domain-containing protein 4 ZC3H4 >tr|M0QY97|M0QY97_HUMAN Zinc finger CCCH domain-containing protein 4 (Fragment) OS=Homo sapiens GN=ZC3H4 PE=4 SV=1;>sp|Q9UPT8|ZC3H4_HUMAN Zinc finger CCCH domain-containing protein 4 OS=Homo sapiens GN=ZC3H4 PE=1 SV=3 0.16 0.00 0.19 -0.28 0.26 -0.30 -0.58 -0.29 0.489131425 0.243326192 binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding 3.74E-25 2 4 4 9.2

Q969S3 Zinc finger protein 622 ZNF622 >sp|Q969S3|ZN622_HUMAN Zinc finger protein 622 OS=Homo sapiens GN=ZNF622 PE=1 SV=1 0.02 -0.08 0.30 0.20 0.46 -0.04 0.03 0.20 0.133436286 -0.052016292 biological regulation;induction of apoptosis;induction of apoptosis by intracellular signals;induction of apoptosis by oxidative stress;induction of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell death;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of JNK cascade;positive regulation of kinase activity;positive regulation of MAPKKK cascade;positive regulation of molecular function;positive regulation of programmed cell death;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of transferase activity;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of programmed cell death;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 3.17E-45 1 4 4 13.8

P62158;H0Y7A7;E7ETZ0;E7EMB3;G3V361;Q96HY3;F8WBR5;G3V226;M0QZ52;G3V479;C9J7T9;P02585 Calmodulin CALM1;CALM2;CALM3 >sp|P62158|CALM_HUMAN Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2;>tr|H0Y7A7|H0Y7A7_HUMAN Calmodulin (Fragment) OS=Homo sapiens GN=CALM2 PE=2 SV=1;>tr|E7ETZ0|E7ETZ0_HUMAN Calmodulin OS=Homo sapiens GN=CALM1 PE=2 SV=1;>tr|E7EMB3|E7EMB3_HUMAN Calmodulin OS 0.04 -0.01 -0.35 0.41 -0.02 0.31 0.15 0.22 0.327651968 -0.140257716 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;activation of phospholipase C activity;alcohol metabolic process;biological regulation;calcium-mediated signaling;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell activation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;defense response;detection of calcium ion;detection of chemical stimulus;detection of stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;fibroblast growth factor receptor signaling pathway;generation of precursor metabolites and energy;glucan catabolic process;glucan metabolic process;glucose metabolic process;glycogen catabolic process;glycogen metabolic process;G-protein coupled receptor protein signaling pathway;hexose metabolic process;immune response;immune system process;innate immune response;inositol phosphate metabolic process;intracellular signal transduction;macromolecule catabolic process;macromolecule metabolic process;membrane organization;metabolic process;monosaccharide metabolic process;multicellular organismal process;muscle contraction;muscle filament sliding;muscle system process;negative regulation of biological process;negative regulation of ion transmembrane transporter activity;negative regulation of molecular function;negative regulation of ryanodine-sensitive calcium-release channel activity;negative regulation of transport;negative regulation of transporter activity;nerve growth factor receptor signaling pathway;nitric oxide metabolic process;nitrogen compound metabolic process;organophosphate metabolic process;oxidation-reduction process;platelet activation;platelet degranulation;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cyclic nucleotide metabolic process;positive regulation of cyclic-nucleotide phosphodiesterase activity;positive regulation of dephosphorylation;positive regulation of hydrolase activity;positive regulation of ion transmembrane transporter activity;positive regulation of lipase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleotide metabolic process;positive regulation of phosphatase activity;positive regulation of phosphate metabolic process;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphoprotein phosphatase activity;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of ryanodine-sensitive calcium-release channel activity;positive regulation of transport;positive regulation of transporter activity;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of catalytic activity;regulation of cell division;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclic nucleotide metabolic process;regulation of cyclic-nucleotide phosphodiesterase activity;regulation of cytokinesis;regulation of dephosphorylation;regulation of heart contraction;regulation of heart rate;regulation of homeostatic process;regulation of hydrolase activity;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of lipase activity;regulation of lipoprotein lipase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide metabolic process;regulation of oxidoreductase activity;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to stimulus;response to stress;second-messenger-mediated signaling;secretion;secretion by cell;signal transduction;signaling;skeletal muscle contraction;small molecule metabolic process;striated muscle contraction;synaptic transmission;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport "binding;calcium ion binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;ion binding;kinase activity;metal ion binding;phosphatase activator activity;phosphatase regulator activity;protein phosphatase activator activity;protein phosphatase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;centrosome;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;plasma membrane;protein complex;sarcomere;spindle microtubule;spindle pole;troponin complex Alzheimer's disease;Calcium signaling pathway;Gastric acid secretion;Glioma;GnRH signaling pathway;Insulin signaling pathway;ko05152;Long-term potentiation;Melanogenesis;Neurotrophin signaling pathway;Olfactory transduction;Oocyte meiosis;Phosphatidylinositol signaling system;Phototransduction;Phototransduction - fly;Plant-pathogen interaction;Salivary secretion;Vascular smooth muscle contraction 2.62E-93 12 5 4 28.9

P60953;E7ETU3;P60953-1;Q5JYX0;F8WET9;B1AH79;G3V4H1;G3V476;Q9H4E5-2;P17081;Q9H4E5 Cell division control protein 42 homolog CDC42 >sp|P60953|CDC42_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2;>tr|E7ETU3|E7ETU3_HUMAN Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=2 SV=1;>sp|P60953-1|CDC42_HUMAN Isoform 1 of Cell division contr -0.10 0.11 -0.92 0.09 -0.51 0.18 0.01 0.26 0.243689915 -0.189268926 "actin cytoskeleton organization;actin filament branching;actin filament bundle assembly;actin filament organization;actin filament-based process;adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;axon guidance;biological adhesion;biological regulation;blood coagulation;canonical Wnt receptor signaling pathway;cardiac conduction system development;cell adhesion;cell communication;cell development;cell differentiation;cell fate determination;cell junction organization;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell junction organization;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemotaxis;circulatory system process;coagulation;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;cytoskeleton-dependent intracellular transport;defense response;developmental process;ectodermal placode formation;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epithelial cell development;epithelial cell-cell adhesion;epithelial-mesenchymal cell signaling;establishment of Golgi localization;establishment of localization;establishment of localization in cell;establishment of nucleus localization;establishment of organelle localization;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;filopodium assembly;Golgi organization;growth;hair cycle process;hair follicle morphogenesis;hair follicle placode formation;heart contraction;heart process;hemostasis;immune response;immune system process;innate immune response;insulin receptor signaling pathway;intracellular signal transduction;intracellular transport;keratinization;keratinocyte development;leukocyte differentiation;localization;locomotion;lymphocyte costimulation;macromolecule localization;macrophage differentiation;microspike assembly;microtubule-based movement;microtubule-based process;microtubule-based transport;molting cycle;molting cycle process;multicellular organism growth;multicellular organismal process;muscle cell differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of establishment of protein localization in plasma membrane;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein complex assembly;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;neuron fate determination;nuclear migration;organelle organization;organelle transport along microtubule;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell cycle cytokinesis;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell division;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokinesis;positive regulation of developmental process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of filopodium assembly;positive regulation of gene expression;positive regulation of glucose import;positive regulation of glucose transport;positive regulation of hair follicle cell proliferation;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JNK cascade;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of metalloenzyme activity;positive regulation of molecular function;positive regulation of muscle cell differentiation;positive regulation of neuron apoptosis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidyl-serine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein transport;positive regulation of pseudopodium assembly;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of stress-activated protein kinase signaling cascade;positive regulation of synapse structural plasticity;positive regulation of T cell activation;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of transport;posttranscriptional regulation of gene expression;protein localization;Ras protein signal transduction;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of attachment of spindle microtubules to kinetochore;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell cycle cytokinesis;regulation of cell cycle process;regulation of cell death;regulation of cell differentiation;regulation of cell division;regulation of cell morphogenesis;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cell shape;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome segregation;regulation of cytokinesis;regulation of cytoskeleton organization;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of epidermal growth factor receptor signaling pathway;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of filopodium assembly;regulation of gene expression;regulation of glucose import;regulation of glucose transport;regulation of hair follicle cell proliferation;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JNK cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of metalloenzyme activity;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of mitosis;regulation of mitotic cell cycle;regulation of molecular function;regulation of muscle cell differentiation;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein binding;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein heterodimerization activity;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of protein transport;regulation of pseudopodium assembly;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of stress-activated protein kinase signaling cascade;regulation of synapse organization;regulation of synapse structural plasticity;regulation of T cell activation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;Rho protein signal transduction;signal transduction;signaling;small GTPase mediated signal transduction;sprouting angiogenesis;submandibular salivary gland formation;system process;T cell costimulation;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;Wnt receptor signaling pathway" "binding;catalytic activity;enzyme binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;kinase binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein kinase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin filament;apical part of cell;cell body;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;filopodium;Golgi apparatus part;Golgi membrane;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;midbody;mitotic spindle;neuron projection;neuronal cell body;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;protein complex;spindle;spindle midzone;stored secretory granule;vesicle Adherens junction;Axon guidance;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Endocytosis;Epithelial cell signaling in Helicobacter pylori infection;Fc gamma R-mediated phagocytosis;Focal adhesion;GnRH signaling pathway;Insulin signaling pathway;Leukocyte transendothelial migration;MAPK signaling pathway;MAPK signaling pathway - yeast;Neurotrophin signaling pathway;Pancreatic cancer;Pathogenic Escherichia coli infection;Pathways in cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;T cell receptor signaling pathway;Tight junction;VEGF signaling pathway 1.84E-35 11 5 4 36.6

P09496-2;P09496-4;P09496-3;P09496;P09496-5;F8WF69;C9J8P9;D6RFZ2;Q0IIM8-2;Q0IIM8-3 Clathrin light chain A CLTA >sp|P09496-2|CLCA_HUMAN Isoform Non-brain of Clathrin light chain A OS=Homo sapiens GN=CLTA;>sp|P09496-4|CLCA_HUMAN Isoform 4 of Clathrin light chain A OS=Homo sapiens GN=CLTA;>sp|P09496-3|CLCA_HUMAN Isoform 3 of Clathrin light chain A OS=Homo sapiens GN=C -0.31 0.05 -0.42 -0.07 1.45 0.80 0.24 0.29 1.217395267 -0.882569449 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;locomotion;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transportbinding;peptide binding;structural molecule activity cell part;clathrin coat;clathrin coat of coated pit;clathrin coat of trans-Golgi network vesicle;clathrin coated vesicle membrane;clathrin vesicle coat;clathrin-coated endocytic vesicle membrane;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endocytic vesicle membrane;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;trans-Golgi network membrane;vesicle coat;vesicle membrane Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease;Lysosome 1.06E-87 10 5 4 24.8

P41240;H3BUM9;H3BU69 Tyrosine-protein kinase CSK CSK>sp|P41240|CSK_HUMAN Tyrosine-protein kinase CSK OS=Homo sapiens GN=CSK PE=1 SV=1 0.08 -0.03 0.09 0.00 0.33 0.06 0.62 -0.03 0.592108917 -0.209802651 activation of immune response;adherens junction organization;anatomical structure development;antigen receptor-mediated signaling pathway;biological regulation;brain development;cell activation;cell differentiation;cell junction organization;cell surface receptor linked signaling pathway;cell-cell junction organization;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;developmental process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;glial cell differentiation;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;lymphocyte costimulation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of bone remodeling;negative regulation of bone resorption;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of endocytosis;negative regulation of ERK1 and ERK2 cascade;negative regulation of Golgi to plasma membrane protein transport;negative regulation of homeostatic process;negative regulation of interleukin-6 production;negative regulation of intracellular protein kinase cascade;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of kinase activity;negative regulation of lipoprotein particle clearance;negative regulation of low-density lipoprotein particle clearance;negative regulation of MAPKKK cascade;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of phagocytosis;negative regulation of protein transport;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of tissue remodeling;negative regulation of transferase activity;negative regulation of transport;oligodendrocyte differentiation;organ development;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cellular process;positive regulation of immune response;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of response to stimulus;positive regulation of T cell activation;positive regulation of transferase activity;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of bone remodeling;regulation of bone resorption;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of endocytosis;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of Fc receptor mediated stimulatory signaling pathway;regulation of Golgi to plasma membrane protein transport;regulation of homeostatic process;regulation of immune response;regulation of immune system process;regulation of interleukin-6 production;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of leukocyte activation;regulation of lipoprotein particle clearance;regulation of localization;regulation of low-density lipoprotein particle clearance;regulation of lymphocyte activation;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell activation;regulation of tissue remodeling;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;T cell costimulation;T cell receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;non-membrane spanning protein tyrosine kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein C-terminus binding;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell junction;cell part;cell-cell junction;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;plasma membrane Chemokine signaling pathway;Epithelial cell signaling in Helicobacter pylori infection;Neurotrophin signaling pathway;Regulation of actin cytoskeleton;Shigellosis 5.22E-14 3 5 4 12.2

Q14574-2;Q14574;J3QRL9 Desmocollin-3 DSC3 >sp|Q14574-2|DSC3_HUMAN Isoform 3B of Desmocollin-3 OS=Homo sapiens GN=DSC3;>sp|Q14574|DSC3_HUMAN Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3 -0.21 0.60 -0.22 0.45 -1.30 0.32 -0.39 0.00 0.505306814 0.4976714 biological adhesion;biological regulation;cell adhesion;cell-cell adhesion;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;homophilic cell adhesion;in utero embryonic development;posttranscriptional regulation of gene expression;protein stabilization;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;cytoplasm;desmosome;extracellular region;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;plasma membrane 7.91E-21 3 5 4 10.6

A0MZ66-8;A0MZ66-4;A0MZ66-5;A0MZ66-6;A0MZ66;A0MZ66-3;A0MZ66-2;A0MZ66-7;REV__A0MZ66-2;REV__A0MZ66-8;REV__A0MZ66-4;REV__A0MZ66-5;REV__A0MZ66-6;REV__A0MZ66;REV__A0MZ66-3 Shootin-1 KIAA1598 >sp|A0MZ66-8|SHOT1_HUMAN Isoform 8 of Shootin-1 OS=Homo sapiens GN=KIAA1598;>sp|A0MZ66-4|SHOT1_HUMAN Isoform 4 of Shootin-1 OS=Homo sapiens GN=KIAA1598;>sp|A0MZ66-5|SHOT1_HUMAN Isoform 5 of Shootin-1 OS=Homo sapiens GN=KIAA1598;>sp|A0MZ66-6|SHOT1_HUMAN Iso -0.11 -0.05 0.42 0.06 -1.30 -0.78 0.15 -0.50 0.903659781 0.687080693 axon guidance;chemotaxis;locomotion;response to chemical stimulus;response to external stimulus;response to stimulus;taxis axon;cell part;cell projection;neuron projection 8.27E-19 15 5 4 11.4

Q5R3E4;O15264 Mitogen-activated protein kinase 13 MAPK13 >tr|Q5R3E4|Q5R3E4_HUMAN Mitogen-activated protein kinase 13 OS=Homo sapiens GN=MAPK13 PE=2 SV=1;>sp|O15264|MK13_HUMAN Mitogen-activated protein kinase 13 OS=Homo sapiens GN=MAPK13 PE=1 SV=1 0.16 0.06 0.31 0.11 -0.40 -0.44 0.12 -0.76 1.157759705 0.528664453 "biological regulation;biosynthetic process;cell cycle;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;nerve growth factor receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of inflammatory response;positive regulation of interleukin-6 production;positive regulation of multicellular organismal process;positive regulation of response to external stimulus;positive regulation of response to stimulus;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of defense response;regulation of gene expression;regulation of inflammatory response;regulation of interleukin-6 production;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to osmotic stress;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;small GTPase mediated signal transduction;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;MAP kinase activity;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part Amyotrophic lateral sclerosis (ALS);Chagas disease (American trypanosomiasis);Epithelial cell signaling in Helicobacter pylori infection;Fc epsilon RI signaling pathway;GnRH signaling pathway;Hepatitis C;ko05152;Leishmaniasis;Leukocyte transendothelial migration;MAPK signaling pathway;MAPK signaling pathway - yeast;Neurotrophin signaling pathway;NOD-like receptor signaling pathway;Osteoclast differentiation;Progesterone-mediated oocyte maturation;RIG-I-like receptor signaling pathway;Shigellosis;T cell receptor signaling pathway;Toll-like receptor signaling pathway;Toxoplasmosis;VEGF signaling pathway 8.69E-14 2 5 4 14.6

O15021-3;O15021-2;O15021-1;E7EWQ5;J3QT34;O15021;F8WAQ9;O60307;H7C1I9;D6RAK1;Q9UKI8-3;J3KRK0;J3QLK5;Q9UKI8-4;Q9UKI8-5;Q86UE8-3;Q86UE8-2;Q9UKI8;Q86UE8;Q9UKI8-2;Q9Y2H9;Q6P0Q8-2;E7ERL6;Q6P0Q8 Microtubule-associated serine/threonine-protein kinase 4 MAST4 >sp|O15021-3|MAST4_HUMAN Isoform 3 of Microtubule-associated serine/threonine-protein kinase 4 OS=Homo sapiens

GN=MAST4;>sp|O15021-2|MAST4_HUMAN Isoform 2 of Microtubule-associated serine/threonine-protein kinase 4 OS=Homo sapiens GN=MAST4;>sp|O15021-1|MAS 0.14 0.01 0.46 -0.25 -0.26 -0.14 0.07 -0.13 0.522775787 0.202892991 biological regulation;cell cycle;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to gamma radiation;cellular response to ionizing radiation;cellular response to radiation;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromosome organization;chromosome segregation;cytoskeleton organization;developmental process;developmental process involved in reproduction;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of autophagy;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of proteasomal ubiquitin-dependent protein catabolic process;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;organelle organization;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;protein transport;regulation of autophagy;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromatin assembly or disassembly;regulation of chromosome organization;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of interleukin-12 biosynthetic process;regulation of interleukin-12 production;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of organelle organization;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of proteolysis;reproductive process;response to abiotic stimulus;response to DNA damage stimulus;response to gamma radiation;response to ionizing radiation;response to radiation;response to stimulus;response to stress;signal transduction;spermatid differentiation;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex 3.36E-11 24 5 4 2.3

P68402;P68402-3;P68402-2;P68402-4;J3KNE3 Platelet-activating factor acetylhydrolase IB subunit beta PAFAH1B2 >sp|P68402|PA1B2_HUMAN Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1;>sp|P68402-3|PA1B2_HUMAN Isoform 3 of Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2;>sp|P68402- -0.26 -0.06 -0.07 -0.03 -0.07 0.11 0.47 0.19 0.972722493 -0.281776399 anatomical structure development;biological regulation;brain development;catabolic process;developmental process;gamete generation;lipid catabolic process;lipid metabolic process;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;organ development;positive regulation of autophagy;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macroautophagy;positive regulation of metabolic process;positive regulation of response to external stimulus;positive regulation of response to extracellular stimulus;positive regulation of response to nutrient levels;positive regulation of response to stimulus;primary metabolic process;regulation of autophagy;regulation of biological process;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of macroautophagy;regulation of metabolic process;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress;reproductive process;spermatogenesis "1-alkyl-2-acetylglycerophosphocholine esterase activity;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane Ether lipid metabolism 1.48E-47 5 5 4 29.7

Q9NTI5-2;Q9NTI5;A9IYQ1 Sister chromatid cohesion protein PDS5 homolog B PDS5B >sp|Q9NTI5-2|PDS5B_HUMAN Isoform 2 of Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B;>sp|Q9NTI5|PDS5B_HUMAN Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1 -0.16 0.29 0.09 0.19 0.50 -0.08 -1.04 -0.65 0.497060712 0.417279208 anaphase;biological regulation;cell cycle phase;cell cycle process;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chromosome organization;cytokinesis;M phase;M phase of mitotic cell cycle;mitotic anaphase;mitotic prometaphase;mitotic sister chromatid cohesion;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;organelle organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process;S phase;S phase of mitotic cell cycle;sister chromatid cohesion adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;DNA binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding "cell part;chromatin;chromosomal part;chromosome, centromeric region;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part" 2.06E-23 3 5 4 5.5

Q00169;F5GWE5;I3L471;I3L4U7;I3L4H1;I3L4C0;I3L459;I3L3W1;I3L2X8 Phosphatidylinositol transfer protein alpha isoform PITPNA >sp|Q00169|PIPNA_HUMAN Phosphatidylinositol transfer protein alpha isoform OS=Homo sapiens GN=PITPNA PE=1 SV=2;>tr|F5GWE5|F5GWE5_HUMAN Phosphatidylinositol transfer protein alpha isoform OS=Homo sapiens GN=PITPNA PE=2 SV=1;>tr|I3L471|I3L471_HUMAN Phosphati -0.02 -0.05 0.46 -0.24 0.76 0.33 0.43 0.40 1.057515115 -0.443653228 axon guidance;chemotaxis;establishment of localization;lipid metabolic process;lipid transport;locomotion;metabolic process;multicellular organismal process;neurological system process;organic substance transport;phospholipid transport;primary metabolic process;response to chemical stimulus;response to external stimulus;response to stimulus;sensory perception;sensory perception of light stimulus;system process;taxis;transport;visual perception binding;carboxylic acid binding;coenzyme binding;cofactor binding;fatty acid binding;fatty-acyl-CoA binding;lipid binding;lipid transporter activity;monocarboxylic acid binding;phosphatidylcholine transmembrane transporter activity;phosphatidylinositol binding;phosphatidylinositol transporter activity;phospholipid binding;phospholipid transporter activity;stearic acid binding;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular;intracellular part 1.36E-31 9 5 4 25.6

Q13136-2;Q13136;E9PJZ7;E9PID5;E9PPF6;H0YD72;H0YEF9;H0YDW2 Liprin-alpha-1 PPFIA1 >sp|Q13136-2|LIPA1_HUMAN Isoform 2 of Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1;>sp|Q13136|LIPA1_HUMAN Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1 PE=1 SV=1;>tr|E9PJZ7|E9PJZ7_HUMAN Liprin-alpha-1 OS=Homo sapiens GN=PPFIA1 PE=2 SV=1 0.25 -0.12 0.06 -0.06 0.13 0.24 -0.09 -0.23 0.046158009 0.018255767 biological adhesion;cell adhesion;cell-matrix adhesion;cell-substrate adhesion;cellular process molecular transducer activity;signal transducer activitycell part;cytoplasm;intracellular part 5.50E-18 8 5 4 6

E9PEQ6;Q9UNP9;E9PKY5;Q9UNP9-2;Q9UNP9-3 Peptidyl-prolyl cis-trans isomerase;Peptidyl-prolyl cis-trans isomerase E PPIE >tr|E9PEQ6|E9PEQ6_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIE PE=2 SV=1;>sp|Q9UNP9|PPIE_HUMAN Peptidyl-prolyl cis-trans isomerase E OS=Homo sapiens GN=PPIE PE=1 SV=1;>tr|E9PKY5|E9PKY5_HUMAN Peptidyl-prolyl cis-trans isomerase (Fragmen -0.03 0.20 -0.09 0.11 -0.32 -0.71 -0.15 -0.06 0.974772465 0.360562197 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;peptidyl-amino acid modification;peptidyl-proline modification;positive regulation of biological process;positive regulation of reproductive process;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;protein folding;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of viral genome replication;regulation of viral reproduction;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;catalytic activity;cis-trans isomerase activity;cyclosporin A binding;drug binding;isomerase activity;nucleic acid binding;nucleotide binding;peptide binding;peptidyl-prolyl cis-trans isomerase activity;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 5.45E-15 5 5 4 19.6

P61019;P61019-2;H7C125;H0YD31;E9PKL7;E9PE37 Ras-related protein Rab-2A RAB2A >sp|P61019|RAB2A_HUMAN Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1;>sp|P61019-2|RAB2A_HUMAN Isoform 2 of Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A -0.07 0.02 -0.48 0.01 0.01 0.45 -0.20 0.22 0.574780217 -0.249229966 biological regulation;cell cycle phase;cell cycle process;cellular process;cellular response to stimulus;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular signal transduction;intracellular transport;M phase;M phase of mitotic cell cycle;mitotic prophase;prophase;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;vesicle 1.49E-153 6 5 4 26.9

Q9Y5X3;Q5QPE4;Q5QPE5;REV__Q6ZSS7 Sorting nexin-5 SNX5 >sp|Q9Y5X3|SNX5_HUMAN Sorting nexin-5 OS=Homo sapiens GN=SNX5 PE=1 SV=1;>tr|Q5QPE4|Q5QPE4_HUMAN Sorting nexin-5 (Fragment) OS=Homo sapiens GN=SNX5 PE=2 SV=1;>tr|Q5QPE5|Q5QPE5_HUMAN Sorting nexin-5 (Fragment) OS=Homo sapiens GN=SNX5 PE=2 SV=1 -0.41 -0.42 -0.10 -0.07 -0.01 -0.06 0.57 -0.20 0.713108404 -0.325429493 cell communication;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;establishment of protein localization;membrane invagination;membrane organization;pinocytosis;protein transport;transport;vesicle-mediated transport binding;lipid binding;phosphatidylinositol binding;phospholipid binding cell part;cell projection;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome membrane;endosomal part;endosome membrane;extrinsic to endosome membrane;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to organelle membrane;extrinsic to plasma membrane;intracellular organelle part;intracellular part;macropinocytic cup;membrane;membrane part;organelle membrane;organelle part;phagocytic cup;plasma membrane part;ruffle;vesicle membrane 7.12E-51 4 5 4 11.9

Q9HD15;REV__O75771-3;B5MCA1;Q96G28;Q96G28-2;REV__Q6QHF9-4;REV__Q6QHF9-2;REV__Q6QHF9;REV__P15924-2 Steroid receptor RNA activator 1 SRA1 >sp|Q9HD15|SRA1_HUMAN Steroid receptor RNA activator 1 OS=Homo sapiens GN=SRA1 PE=1 SV=1 0.45 0.08 0.04 -0.31 -0.01 0.06 0.35 -0.32 0.07261479 0.04378175 "apoptosis;biological regulation;biosynthetic process;cell death;cell differentiation;cell proliferation;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;ligand-dependent nuclear receptor transcription coactivator activity;nucleic acid binding;protein binding transcription factor activity;receptor activator activity;receptor regulator activity;thyroid hormone receptor activator activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell leading edge;cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;transcription factor complex 1.82E-22 9 5 4 25.8

Q9BVK6;F8W7F7 Transmembrane emp24 domain-containing protein 9 TMED9 >sp|Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2 -0.39 0.10 -0.01 0.13 0.46 0.55 -0.49 -0.03 0.241137188 -0.168819294 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of protein localization;Golgi organization;Golgi transport vesicle coating;organelle organization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of organelle organization;protein transport;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of organelle organization;transport;vesicle coating;vesicle organization cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi-associated vesicle;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;trans-Golgi network transport vesicle;transport vesicle;vesicle 7.43E-75 2 5 4 13.6

O95292;E5RK64;O95292-2 Vesicle-associated membrane protein-associated protein B/C VAPB >sp|O95292|VAPB_HUMAN Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3;>tr|E5RK64|E5RK64_HUMAN Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=2 SV=1;>sp|O95292-2|VAPB_HUMAN -0.23 0.21 -0.03 0.11 -0.31 0.08 -0.73 -0.01 0.532782626 0.262124543 activation of signaling protein activity involved in unfolded protein response;biological regulation;biosynthetic process;calcium ion homeostasis;cation homeostasis;cell death;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;chemical homeostasis;death;divalent inorganic cation homeostasis;homeostatic process;interaction with host;interspecies interaction between organisms;ion homeostasis;lipid biosynthetic process;lipid metabolic process;membrane lipid biosynthetic process;membrane lipid metabolic process;metabolic process;metal ion homeostasis;multi-organism process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of reproductive process;positive regulation of transferase activity;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of reproductive process;regulation of transferase activity;regulation of viral genome replication;regulation of viral reproduction;reproductive process;small molecule metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process;viral reproductive process;virus-host interaction beta-tubulin binding;binding;cytoskeletal protein binding;protein binding;structural molecule activity;tubulin binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 1.19E-71 3 5 4 21.4

P47974;G3V2D5;G3V2P5 "Zinc finger protein 36, C3H1 type-like 2" ZFP36L2 ">sp|P47974|TISD_HUMAN Zinc finger protein 36, C3H1 type-like 2 OS=Homo sapiens GN=ZFP36L2 PE=1 SV=3" 0.63 0.30 -0.18 -0.12 -1.55 -1.35 -0.36 -0.45 1.239622857 1.080056848 "biological regulation;catabolic process;cell activation;cell differentiation;cell proliferation;cellular catabolic process;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;immune system process;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of translation;RNA catabolic process;RNA metabolic process;T cell activation;T cell differentiation;T cell differentiation in thymus;vasculogenesis" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;RNA binding;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.31E-37 3 5 4 14

O75477;B0QZ43;O94905-2;O94905-3 Erlin-1 ERLIN1 >sp|O75477|ERLN1_HUMAN Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1;>tr|B0QZ43|B0QZ43_HUMAN Erlin-1 (Fragment) OS=Homo sapiens GN=ERLIN1 PE=2 SV=1 -0.61 0.37 0.17 0.64 0.15 0.17 -1.17 0.09 0.3132294 0.334960062 catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;ER-associated protein catabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;protein complex 5.35E-32 4 6 4 19.9

B4DJA5;P20339 Ras-related protein Rab-5A RAB5A >tr|B4DJA5|B4DJA5_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=2 SV=1;>sp|P20339|RAB5A_HUMAN Ras-related protein Rab-5A OS=Homo sapiens GN=RAB5A PE=1 SV=2 -0.22 0.05 -0.74 0.18 -0.25 0.37 -0.08 0.07 0.355656089 -0.214683321 anatomical structure development;biological regulation;blood coagulation;cell differentiation;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular response to stimulus;coagulation;developmental process;endocytosis;establishment of localization;establishment of protein localization;hemostasis;intracellular signal transduction;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;multicellular organismal process;nervous system development;positive regulation of biological process;positive regulation of cellular process;positive regulation of exocytosis;positive regulation of secretion;positive regulation of transport;protein transport;receptor internalization;receptor internalization involved in canonical Wnt receptor signaling pathway;receptor metabolic process;receptor-mediated endocytosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of filopodium assembly;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;system development;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin cytoskeleton;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;early endosome;early endosome membrane;endocytic vesicle;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;ruffle;vesicle Amoebiasis;Amyotrophic lateral sclerosis (ALS);Endocytosis;ko05152;Phagosome;Vasopressin-regulated water reabsorption 4.67E-54 2 6 4 34.8

Q9UPN6;B7Z888 Protein SCAF8 SCAF8 >sp|Q9UPN6|SCAF8_HUMAN Protein SCAF8 OS=Homo sapiens GN=SCAF8 PE=1 SV=1;>tr|B7Z888|B7Z888_HUMAN Protein SCAF8 OS=Homo sapiens GN=SCAF8 PE=2 SV=1 -0.19 0.12 -0.01 0.26 -0.03 -0.18 -0.59 -0.64 0.970284811 0.404066561 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear matrix;nuclear part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex 8.01E-21 2 6 4 8.3

Q13620-3;Q13620-1;K4DI93;Q13620;A6NE76 Cullin-4B CUL4B ">sp|Q13620-3|CUL4B_HUMAN Isoform 3 of Cullin-4B OS=Homo sapiens GN=CUL4B;>sp|Q13620-1|CUL4B_HUMAN Isoform 2 of Cullin-4B OS=Homo sapiens GN=CUL4B;>tr|K4DI93|K4DI93_HUMAN Cullin 4B, isoform CRA_e OS=Homo sapiens GN=CUL4B PE=3 SV=1;>sp|Q13620|CUL4B_HUMAN Cul" -0.26 0.10 -0.74 0.14 0.09 0.26 -0.24 -0.43 0.154899777 -0.109196354 biological regulation;catabolic process;cell cycle;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell cycle;positive regulation of cell cycle process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitotic cell cycle;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of S phase of mitotic cell cycle;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catabolic process;regulation of cell cycle;regulation of cell cycle process;regulation of cellular process;regulation of interphase of mitotic cell cycle;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of S phase;regulation of S phase of mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;ubiquitin-dependent protein catabolic process cell part;CUL4 RING ubiquitin ligase complex;Cul4B-RING ubiquitin ligase complex;cullin-RING ubiquitin ligase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane;protein complex;ubiquitin ligase complex Nucleotide excision repair;Ubiquitin mediated proteolysis 2.17E-13 5 7 4 11.2

P46934-4;P46934-2;P46934;H0Y8X6;P46934-3 E3 ubiquitin-protein ligase NEDD4;E3 ubiquitin-protein ligase NEDD4 >sp|P46934-4|NEDD4_HUMAN Isoform 4 of E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4;>sp|P46934-2|NEDD4_HUMAN Isoform 2 of E3 ubiquitin-protein ligase NEDD4 OS=Homo sapiens GN=NEDD4;>sp|P46934|NEDD4_HUMAN E3 ubiquitin-protein ligase NEDD4 OS=Ho 0.41 -0.07 0.08 -0.97 0.28 -0.22 0.50 2.85 0.559899808 -0.990851922 "adaptive immune response;anatomical structure development;anatomical structure morphogenesis;biological regulation;blood vessel morphogenesis;catabolic process;cell activation;cell projection organization;cell surface receptor linked signaling pathway;cellular catabolic process;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to light stimulus;cellular response to organic substance;cellular response to radiation;cellular response to stimulus;cellular response to stress;cellular response to UV;chemical homeostasis;corticosteroid receptor signaling pathway;cytokine-mediated signaling pathway;development involved in symbiotic interaction;developmental process;dissemination or transmission of organism from other organism involved in symbiotic interaction;dissemination or transmission of symbiont from host;endocardial cushion development;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;glucocorticoid receptor signaling pathway;homeostatic process;immune response;immune system process;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular transport;ion homeostasis;leukocyte activation;locomotion;lymphocyte activation;lysosomal transport;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;mesenchyme development;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular response to growth factor stimulus;negative regulation of gene expression;negative regulation of ion transport;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of sodium ion transport;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage;negative regulation of transcription, DNA-dependent;negative regulation of transport;negative regulation of vascular endothelial growth factor receptor signaling pathway;neuromuscular junction development;neuron projection development;outflow tract morphogenesis;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of intracellular transport;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transport;primary metabolic process;progesterone receptor signaling pathway;protein K63-linked ubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein polyubiquitination;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;receptor catabolic process;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catabolic process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to growth factor stimulus;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of DNA-dependent transcription in response to stress;regulation of gene expression;regulation of intracellular transport;regulation of ion transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of phosphatidylinositol 3-kinase cascade;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of sodium ion transport;regulation of synapse organization;regulation of transcription from RNA polymerase II promoter;regulation of transcription from RNA polymerase II promoter in response to stress;regulation of transcription from RNA polymerase II promoter in response to UV-induced DNA damage;regulation of transcription, DNA-dependent;regulation of transport;regulation of vascular endothelial growth factor receptor signaling pathway;reproductive process;response to abiotic stimulus;response to calcium ion;response to chemical stimulus;response to cytokine stimulus;response to inorganic substance;response to light stimulus;response to metal ion;response to organic substance;response to radiation;response to stimulus;response to stress;response to UV;signal transduction;steroid hormone receptor signaling pathway;synapse organization;T cell activation;tissue development;transmission of virus;transport;ubiquitin-dependent protein catabolic process;ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway;vacuolar transport;vesicle-mediated transport;viral reproductive process;virus-host interaction"	"acid-amino acid ligase activity;adrenergic receptor binding;amine binding;amino acid binding;beta-2 adrenergic receptor binding;binding;carboxylic acid binding;catalytic activity;channel inhibitor activity;channel regulator activity;G-protein-coupled receptor binding;ion channel inhibitor activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;phosphoprotein binding;phosphoserine binding;phosphothreonine binding;proline-rich region binding;protein binding;protein phosphorylated amino acid binding;receptor binding;small conjugating protein binding;small conjugating protein ligase activity;sodium channel inhibitor activity;sodium channel regulator activity;ubiquitin binding;ubiquitin-protein ligase activity"	apicolateral plasma membrane;cell cortex;cell part;chromatin;chromosomal part;cytoplasmic part;cytosol;Golgi apparatus;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex;ubiquitin ligase complex	Endocytosis;Ubiquitin mediated proteolysis	6.48E-18	5	7	4	11.1

P63000;P63000-2;P60763	Ras-related C3 botulinum toxin substrate 1;Ras-related C3 botulinum toxin substrate 3	RAC1;RAC3	>sp|P63000|RAC1_HUMAN Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1;>sp|P63000-2|RAC1_HUMAN Isoform B of Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1;>sp|P60763|RAC3_HUMAN Ras-related C3 botulinum toxin	0.03	0.20	-0.32	0.19	-0.37	0.01	-0.19	0.10	0.339143404	0.135577455	"actin cytoskeleton organization;actin filament organization;actin filament polymerization;actin filament-based process;actin polymerization or depolymerization;anatomical structure arrangement;anatomical structure homeostasis;anatomical structure morphogenesis;auditory receptor cell morphogenesis;axon guidance;biological adhesion;biological regulation;bone resorption;cell activation;cell adhesion;cell chemotaxis;cell differentiation;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell morphogenesis involved in neuron differentiation;cell motility;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-cell junction organization;cell-matrix adhesion;cell-substrate adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to stimulus;cerebral cortex cell migration;cerebral cortex radially oriented cell migration;chemotaxis;cochlea morphogenesis;cytoskeleton organization;defense response;dendrite morphogenesis;developmental process;dopaminergic neuron differentiation;embryonic morphogenesis;embryonic olfactory bulb interneuron precursor migration;engulfment of apoptotic cell;enzyme linked receptor protein signaling pathway;epithelial cell morphogenesis;forebrain cell migration;homeostatic process;hyperosmotic response;immune response;immune system process;inflammatory response;innate immune response;intracellular signal transduction;lamellipodium assembly;leukocyte chemotaxis;leukocyte migration;localization;localization within membrane;locomotion;lymphocyte costimulation;macromolecular complex assembly;macromolecular complex subunit organization;mast cell chemotaxis;membrane invagination;membrane organization;multicellular organismal process;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of endocytosis;negative regulation of interleukin-23 production;negative regulation of multicellular organismal process;negative regulation of receptor-mediated endocytosis;negative regulation of transport;nerve growth factor receptor signaling pathway;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;neuron projection development;neuron projection morphogenesis;non-canonical Wnt receptor signaling pathway;organelle organization;phagocytosis, engulfment;platelet activation;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell projection organization;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of lamellipodium assembly;positive regulation of leukocyte activation;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of protein complex assembly;positive regulation of protein polymerization;positive regulation of Ras protein signal transduction;positive regulation of response to stimulus;positive regulation of Rho protein signal transduction;positive regulation of signal transduction;positive regulation of signaling;positive regulation of small GTPase mediated signal transduction;positive regulation of T cell activation;positive regulation of transferase activity;protein complex assembly;protein complex subunit organization;protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of cytoskeleton organization;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of endocytosis;regulation of establishment of planar polarity;regulation of hydrogen peroxide metabolic process;regulation of immune effector process;regulation of immune system process;regulation of interleukin-23 production;regulation of kinase activity;regulation of lamellipodium assembly;regulation of leukocyte activation;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein polymerization;regulation of Ras protein signal transduction;regulation of reactive oxygen species metabolic process;regulation of receptor-mediated endocytosis;regulation of respiratory burst;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of T cell activation;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to osmotic stress;response to stimulus;response to stress;response to wounding;ruffle organization;signal transduction;small GTPase mediated signal transduction;substrate adhesion-dependent cell spreading;substrate-independent telencephalic tangential interneuron migration;substrate-independent telencephalic tangential migration;system process;T cell costimulation;tangential migration from the subventricular zone to the olfactory bulb;taxis;telencephalon cell migration;tissue homeostasis;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproduction;Wnt receptor signaling pathway;Wnt receptor signaling pathway, planar cell polarity pathway" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell body;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;endomembrane system;extrinsic to membrane;extrinsic to plasma membrane;filamentous actin;Golgi apparatus part;Golgi membrane;growth cone;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;leading edge membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuronal cell body;organelle;organelle membrane;organelle part;phagocytic cup;pigment granule;plasma membrane;plasma membrane part;protein complex;ruffle membrane;site of polarized growth;trans-Golgi network;vesicle Adherens junction;Amyotrophic lateral sclerosis (ALS);Axon guidance;B cell receptor signaling pathway;Bacterial invasion of epithelial cells;Chemokine signaling pathway;Colorectal cancer;Epithelial cell signaling in Helicobacter pylori infection;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Leukocyte transendothelial migration;MAPK signaling pathway;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Osteoclast differentiation;Pancreatic cancer;Pancreatic secretion;Pathways in cancer;Phagosome;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;Toll-like receptor signaling pathway;VEGF signaling pathway;Viral myocarditis;Wnt signaling pathway 3.86E-38 3 7 4 28.1

Q9Y281;Q9Y281-3;F8WDN3;G3V2U0 Cofilin-2 CFL2 >sp|Q9Y281|COF2_HUMAN Cofilin-2 OS=Homo sapiens GN=CFL2 PE=1 SV=1;>sp|Q9Y281-3|COF2_HUMAN Isoform 3 of Cofilin-2 OS=Homo sapiens GN=CFL2 0.02 0.12 -0.50 0.02 1.32 1.19 0.25 0.17 1.038479827 -0.819925345 actin cytoskeleton organization;actin filament depolymerization;actin filament organization;actin filament-based process;actin polymerization or depolymerization;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex disassembly;cytoskeleton organization;macromolecular complex disassembly;macromolecular complex subunit organization;organelle organization;protein complex disassembly;protein complex subunit organization;protein depolymerization actin cytoskeleton;cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear matrix;nuclear part;organelle;organelle part Axon guidance;Fc gamma R-mediated phagocytosis;Regulation of actin cytoskeleton 2.52E-59 4 8 4 42.2

Q15366-6;Q15366-3;Q15366;Q15366-2;H3BRU6;G3V0E8;F8VZX2;B4DXP5;Q15366-4;Q15366-5;B4DLC0;F8W0G4;J3QT27;P57721-2;P57721-3;P57721-5;E9PFP8;P57721-4;P57721;F8VXH9;F8W1G6;H3BSS4;F8VTZ0;F8VRH0;H3BSP4;C9K0A2;F8WC71;C9IZV9;C9J7A9;C9JSA6;C9J5V4;H3BND9;C9JTY5;C9JZY3;C9J0A4;P57723-2;P57723 Poly(rC)-binding protein 2;Poly(rC)-binding protein 3 PCBP2;PCBP3 >sp|Q15366-6|PCBP2_HUMAN Isoform 6 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2;>sp|Q15366-3|PCBP2_HUMAN Isoform 3 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2;>sp|Q15366|PCBP2_HUMAN Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 P 0.18 0.04 -0.14 0.17 -0.05 -0.34 -0.06 -0.37 0.984489213 0.265864979 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of defense response;negative regulation of defense response to virus;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of multicellular organismal process;negative regulation of multi-organism process;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of type I interferon production;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of immune effector process;regulation of immune system process;regulation of multicellular organismal process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of type I interferon production;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;ubiquitin-dependent protein catabolic process" binding;DNA binding;nucleic acid binding;RNA binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex 7.59E-146 37 8 4 29.9

P11388;P11388-2;P11388-3;P11388-4;J3KTB7 DNA topoisomerase 2-alpha TOP2A >sp|P11388|TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3;>sp|P11388-2|TOP2A_HUMAN Isoform 2 of DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A;>sp|P11388-3|TOP2A_HUMAN Isoform 3 of DNA topoisomerase 2-alpha OS=Homo sapiens GN= 0.28 1.40 -0.12 0.47 -0.32 -0.28 -1.38 0.66 0.676546396 0.837269912 "apoptotic chromosome condensation;biological regulation;biosynthetic process;cell cycle;cell cycle process;cell division;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome condensation;chromosome organization;chromosome segregation;chromosome separation;DNA conformation change;DNA ligation;DNA metabolic process;DNA packaging;DNA recombination;DNA repair;DNA replication;DNA topological change;DNA-dependent DNA replication;embryonic cleavage;inositol lipid-mediated signaling;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;meiotic chromosome separation;metabolic process;mitotic cell cycle;mitotic recombination;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;phosphatidylinositol-mediated signaling;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of reproductive process;positive regulation of retroviral genome replication;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of retroviral genome replication;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral genome replication;regulation of viral reproduction;resolution of meiotic recombination intermediates;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;sister chromatid segregation" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cation binding;chromatin binding;DNA bending activity;DNA binding;DNA topoisomerase (ATP-hydrolyzing) activity;DNA topoisomerase activity;DNA-dependent ATPase activity;drug binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;isomerase activity;magnesium ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;small conjugating protein binding;ubiquitin binding" cell part;chromosomal part;chromosome;condensed chromosome;cytoplasm;DNA topoisomerase complex (ATP-hydrolyzing);intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;protein complex;synaptonemal complex 2.24E-36 5 8 4 6.5

Q9UMX0;Q9UMX0-2;H0YEZ9 Ubiquilin-1 UBQLN1>sp|Q9UMX0|UBQL1_HUMAN Ubiquilin-1 OS=Homo sapiens GN=UBQLN1 PE=1 SV=2;>sp|Q9UMX0-2|UBQL1_HUMAN Isoform 2 of Ubiquilin-1 OS=Homo sapiens GN=UBQLN1 0.19 -0.05 0.12 -0.03 0.11 0.07 0.27 -0.18 0.028829729 -0.009563983 apoptosis;biological regulation;cell death;cellular process;death;programmed cell death;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;proteasome complex;protein complex Protein processing in endoplasmic reticulum 4.73E-148 3 9 4 25

R4GN55;Q7Z739;R4GMX0 YTH domain family protein 3YTHDF3 >tr|R4GN55|R4GN55_HUMAN YTH domain family protein 3 OS=Homo sapiens GN=YTHDF3 PE=4 SV=1;>sp|Q7Z739|YTHD3_HUMAN YTH domain family protein 3 OS=Homo sapiens GN=YTHDF3 PE=1 SV=1;>tr|R4GMX0|R4GMX0_HUMAN YTH domain family protein 3 OS=Homo sapiens GN=YTHDF3 PE= 0.20 -0.05 0.00 -0.18 0.25 0.05 0.18 0.24 0.885134793 -0.188217925 5.25E-69 3 9 4 23.1

Q03135;E9PCT5;P56539 Caveolin-1;Caveolin CAV1 >sp|Q03135|CAV1_HUMAN Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4;>tr|E9PCT5|E9PCT5_HUMAN Caveolin OS=Homo sapiens GN=CAV1 PE=2 SV=1 -1.03 0.55 0.01 0.60 0.22 -0.48 -1.27 -0.07 0.350225861 0.435679526 "actin cytoskeleton organization;actin filament organization;actin filament-based process;acylglycerol metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;angiogenesis;biological regulation;blood coagulation;body fluid secretion;calcium ion homeostasis;calcium ion transport;carbohydrate homeostasis;cardiac cell development;cardiac muscle cell development;cation homeostasis;cation transport;caveola assembly;caveolin-mediated endocytosis;cell communication;cell development;cell differentiation;cell growth;cell migration;cell motility;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein localization;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to hyperoxia;cellular response to nutrient levels;cellular response to oxygen levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;chemical homeostasis;cholesterol homeostasis;cholesterol transport;circulatory system process;coagulation;cytoplasmic microtubule organization;cytoskeleton organization;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of cytosolic calcium ion concentration;endocytosis;establishment of localization;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;gas homeostasis;glucose homeostasis;glycerol ether metabolic process;glycerolipid metabolic process;growth;heart trabecula formation;hemostasis;homeostatic process;immune system process;inactivation of MAPK activity;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;ion homeostasis;ion transport;lactation;leukocyte migration;lipid homeostasis;lipid localization;lipid metabolic process;lipid storage;lipid transport;localization;locomotion;lymphocyte costimulation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;mammary gland involution;MAPKKK cascade;membrane depolarization;membrane invagination;membrane organization;membrane raft assembly;membrane raft organization;metabolic process;metal ion homeostasis;metal ion transport;microtubule cytoskeleton organization;microtubule-based process;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;muscle cell development;muscle cell homeostasis;muscle organ development;muscle structure development;muscle tissue development;myoblast fusion;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of binding;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of BMP signaling pathway;negative regulation of calcium ion transport;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cardiac muscle hypertrophy;negative regulation of cardiac muscle tissue growth;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell growth involved in cardiac muscle cell development;negative regulation of cell proliferation;negative regulation of cell size;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cytokine-mediated signaling pathway;negative regulation of cytoskeleton organization;negative regulation of developmental growth;negative regulation of developmental process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell differentiation;negative regulation of epithelial cell proliferation;negative regulation of gene expression;negative regulation of growth;negative regulation of heart growth;negative regulation of intracellular protein kinase cascade;negative regulation of ion transport;negative regulation of JAK-STAT cascade;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of monooxygenase activity;negative regulation of multicellular organismal process;negative regulation of muscle cell differentiation;negative regulation of muscle hypertrophy;negative regulation of nitric oxide biosynthetic process;negative regulation of nitric-oxide synthase activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organ growth;negative regulation of organelle organization;negative regulation of oxidoreductase activity;negative regulation of peptidyl-serine phosphorylation;negative regulation of peptidyl-tyrosine phosphorylation;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of programmed cell death;negative regulation of protein binding;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of protein serine/threonine kinase activity;negative regulation of protein ubiquitination;negative regulation of response to cytokine stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sarcomere organization;negative regulation of signal transduction;negative regulation of signaling;negative regulation of striated muscle cell differentiation;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of transport;negative regulation of tyrosine phosphorylation of STAT protein;negative regulation of tyrosine phosphorylation of Stat5 protein;negative regulation of Wnt receptor signaling pathway;neutral lipid metabolic process;nitric oxide homeostasis;nitric oxide metabolic process;nitrogen compound metabolic process;nucleus localization;organ development;organelle localization;organelle organization;organic ether metabolic process;organic substance transport;plasma membrane organization;plasma membrane repair;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of calcium ion transport into cytosol;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of homeostatic process;positive regulation of immune system process;positive regulation of ion transport;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of metalloenzyme activity;positive regulation of microtubule polymerization;positive regulation of microtubule polymerization or depolymerization;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle cell differentiation;positive regulation of myotube differentiation;positive regulation of organelle organization;positive regulation of peptidyl-serine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein complex assembly;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein polymerization;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of skeletal muscle cell differentiation;positive regulation of striated muscle cell differentiation;positive regulation of T cell activation;positive regulation of transport;positive regulation of vasoconstriction;positive regulation of Wnt receptor signaling pathway;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein localization;protein localization in membrane;protein localization in plasma membrane;protein oligomerization;receptor internalization;receptor internalization involved in canonical Wnt receptor signaling pathway;receptor metabolic process;receptor-mediated endocytosis;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of anoikis;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood coagulation;regulation of blood vessel size;regulation of BMP signaling pathway;regulation of body fluid levels;regulation of branching involved in mammary gland duct morphogenesis;regulation of calcium ion import;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac muscle cell differentiation;regulation of cardiac muscle contraction;regulation of cardiac muscle hypertrophy;regulation of cardiac muscle tissue development;regulation of cardiac muscle tissue growth;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell growth involved in cardiac muscle cell development;regulation of cell proliferation;regulation of cell size;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular ketone metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of coagulation;regulation of cytokine-mediated signaling pathway;regulation of cytoskeleton organization;regulation of developmental growth;regulation of developmental process;regulation of endothelial cell proliferation;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of fatty acid metabolic process;regulation of gene expression;regulation of growth;regulation of heart contraction;regulation of heart growth;regulation of heart rate;regulation of homeostatic process;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of lipid metabolic process;regulation of localization;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of membrane depolarization;regulation of membrane potential;regulation of membrane repolarization;regulation of metabolic process;regulation of metal ion transport;regulation of metalloenzyme activity;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of molecular function;regulation of monooxygenase activity;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle adaptation;regulation of muscle cell differentiation;regulation of muscle contraction;regulation of muscle hypertrophy;regulation of muscle organ development;regulation of muscle system process;regulation of myotube differentiation;regulation of nerve growth factor receptor activity;regulation of nerve growth factor receptor signaling pathway;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ growth;regulation of organ morphogenesis;regulation of organelle organization;regulation of oxidoreductase activity;regulation of peptidyl-serine phosphorylation;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein binding;regulation of protein complex assembly;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of protein serine/threonine kinase activity;regulation of protein ubiquitination;regulation of receptor activity;regulation of response to cytokine stimulus;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sarcomere organization;regulation of signal transduction;regulation of signal transduction by receptor internalization;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of skeletal muscle contraction;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of smooth muscle contraction;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of striated muscle cell differentiation;regulation of striated muscle contraction;regulation of striated muscle tissue development;regulation of system process;regulation of T cell activation;regulation of the force of heart contraction;regulation of the force of heart contraction by chemical signal;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;regulation of tube size;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat5 protein;regulation of vasoconstriction;regulation of ventricular cardiomyocyte membrane depolarization;regulation of ventricular cardiomyocyte membrane repolarization;regulation of Wnt receptor signaling pathway;regulation of wound healing;reproductive process;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to hyperoxia;response to hypoxia;response to inorganic substance;response to metal ion;response to nutrient levels;response to organic substance;response to oxygen levels;response to progesterone stimulus;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;secretion;signal transduction;skeletal muscle tissue development;small molecule metabolic process;sterol homeostasis;sterol transport;striated muscle tissue development;syncytium formation;syncytium formation by plasma membrane fusion;system process;T cell costimulation;tissue development;tissue remodeling;trabecula formation;transport;triglyceride metabolic process;T-tubule organization;vascular process in circulatory system;vasculogenesis;vasoconstriction;vesicle organization;vesicle-mediated transport;viral reproductive process;virus-host interaction" binding;calcium channel regulator activity;channel regulator activity;cholesterol binding;connexin binding;enzyme activator activity;enzyme regulator activity;lipid binding;peptidase activator activity;peptidase regulator activity;protein binding;protein complex binding;protein complex scaffold;protein C-terminus binding;sodium channel regulator activity;steroid binding;sterol binding;structural molecule activity acrosomal membrane;apical plasma membrane;basolateral plasma membrane;caveola;cell cortex;cell part;cell surface;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;dystrophin-associated glycoprotein complex;endocytic vesicle membrane;endoplasmic reticulum;endoplasmic reticulum part;endosome;Golgi apparatus part;Golgi membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lipid particle;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;neuromuscular junction;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex;secretory granule membrane;synapse;T-tubule;vesicle;vesicle membrane Bacterial invasion of epithelial cells;Endocytosis;Focal adhesion;Viral myocarditis 1.25E-49 3 10 4 52.8

P30154-4;P30154;P30154-2;P30154-5;P30154-3;J3KR29;H0YDG7 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform PPP2R1B >sp|P30154-4|2AAB_HUMAN Isoform 4 of Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B;>sp|P30154|2AAB_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo 0.50 0.25 -0.04 -0.29 -0.33 -0.36 0.07 0.02 0.523397853 0.256710024 Cell cycle - yeast;Chagas disease (American trypanosomiasis);Hepatitis C;Long-term depression;Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;TGF-beta signaling pathway;Tight junction;Wnt signaling pathway 2.68E-110 7 11 4 25.9

Q8TAQ2-2;Q8TAQ2-3;Q8TAQ2;F8VXC8;F8VZW6 SWI/SNF complex subunit SMARCC2 SMARCC2 >sp|Q8TAQ2-2|SMRC2_HUMAN Isoform 2 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2;>sp|Q8TAQ2-3|SMRC2_HUMAN Isoform 3 of SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2;>sp|Q8TAQ2|SMRC2_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo -0.09 0.58 0.06 0.59 -0.19 0.23 -1.04 -0.01 0.699955185 0.537647907 "anatomical structure development;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;system development;transcription, DNA-dependent" binding;chromatin binding;DNA binding;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;chromatin remodeling complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nBAF complex;npBAF complex;nuclear part;nucleus;organelle;organelle part;protein complex;SWI/SNF complex;SWI/SNF-type complex 1.01E-126 5 12 4 14.4

P16403;Q02539;P22492 Histone H1.2 HIST1H1C >sp|P16403|H12_HUMAN Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 -0.85 1.31 0.23 0.67 0.02 -0.30 -2.22 -1.43 0.823264022 1.321484527 binding of sperm to zona pellucida;cell differentiation;cell motility;cell recognition;cell-cell recognition;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular process involved in reproduction;chromatin organization;chromosome organization;developmental process;gamete generation;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;male gamete generation;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization;reproductive process;sperm motility;spermatogenesis;sperm-egg recognition binding;DNA binding;nucleic acid binding cell part;chromatin;chromosomal part;chromosome;condensed chromosome;condensed nuclear chromosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome;nuclear chromosome part;nuclear part;nucleosome;nucleus;organelle;organelle part;protein-DNA complex 4.45E-88 3 14 4 39.4

E7EQG2;Q14240;Q14240-2;Q9NZE6;J3KSN7;J3KT04;E7EMV8;J3QQP0;E9PBH4;F8WE11 Eukaryotic initiation factor 4A-II EIF4A2 >tr|E7EQG2|E7EQG2_HUMAN Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=2 SV=1;>sp|Q14240|IF4A2_HUMAN Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2;>sp|Q14240-2|IF4A2_HUMAN Isoform 2 of Eukaryotic initiation factor -0.57

0.06 -0.70 0.26 -0.80 0.11 -0.15 -0.20 0.023727853 0.021960918 biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;signal transduction;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex RNA transport 2.22E-262 10 17 4 42.5

Q9BQE3;F5H5D3;F8VVB9;Q9H853 Tubulin alpha-1C chain TUBA1C >sp|Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1;>tr|F5H5D3|F5H5D3_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=2 SV=1 -0.09 0.07 -0.70 -0.19 -0.34 0.04 0.85 0.68 0.708434008 -0.534316338 cell division;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cytoskeleton-dependent intracellular transport;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 4 27 4 61.5

P67936-2;K7ENT6;K7ERG3;K7EP68;K7ELP0;H0YLS7 TPM4 >sp|P67936-2|TPM4_HUMAN Isoform 2 of Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4;>tr|K7ENT6|K7ENT6_HUMAN Tropomyosin alpha-4 chain (Fragment) OS=Homo sapiens GN=TPM4 PE=4 SV=1;>tr|K7ERG3|K7ERG3_HUMAN Tropomyosin alpha-4 chain (Fragment) OS=Homo sapie -0.84 -0.39 -0.61 0.59 -1.04 -1.76 1.28 0.20 0.009240198 0.021262839 0 6 37 4 72.9

P14618-2;H3BTN5;Q504U3 Pyruvate kinase PKM;PKM2 >sp|P14618-2|KPYM_HUMAN Isoform M1 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM;>tr|H3BTN5|H3BTN5_HUMAN Pyruvate kinase (Fragment) OS=Homo sapiens GN=PKM PE=2 SV=1;>tr|Q504U3|Q504U3_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM2 PE=2 SV=1 -0.10 -0.42 -0.31 0.03 -0.09 0.96 0.80 0.65 1.276404157 -0.783987367 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "alkali metal ion binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;phosphotransferase activity, alcohol group as acceptor;potassium ion binding;pyruvate kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 0 3 59 4 82.7

P02545;Q6UYC3;P02545-3;D6RAQ3;P02545-4;H0YAB0;REV__F8W912;REV__Q86Z20-2;REV__Q86Z20 Prelamin-A/C;Lamin-A/C LMNA >sp|P02545|LMNA_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1;>tr|Q6UYC3|Q6UYC3_HUMAN Prelamin-A/C OS=Homo sapiens GN=LMNA PE=2 SV=1;>sp|P02545-3|LMNA_HUMAN Isoform ADelta10 of Prelamin-A/C OS=Homo sapiens GN=LMNA;>tr|D6RAQ3|D6RAQ3_HUMAN Prelamin-A/-0.44 0.32 0.31 0.65 0.21 0.11 -1.40 -0.49 0.584979916 0.604567004 activation of signaling protein activity involved in unfolded protein response;anaphase;anatomical structure development;biological regulation;cardiac cell development;cardiac muscle cell development;cell cycle phase;cell cycle process;cell development;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hypoxia;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment or maintenance of cell polarity;establishment or maintenance of cytoskeleton polarity;establishment or maintenance of microtubule cytoskeleton polarity;intracellular protein transport;intracellular transport;localization;M phase;M phase of mitotic cell cycle;macromolecule localization;macromolecule metabolic process;membrane disassembly;membrane organization;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic nuclear envelope disassembly;mitotic nuclear envelope reassembly;mitotic prophase;muscle cell development;muscle organ development;muscle structure development;nuclear envelope disassembly;nuclear envelope organization;nuclear envelope reassembly;nuclear import;nuclear transport;nucleocytoplasmic transport;organ development;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell aging;positive regulation of cellular process;positive regulation of developmental process;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;prophase;protein import;protein import into nucleus;protein localization;protein localization to nucleus;protein localization to organelle;protein metabolic process;protein targeting;protein transport;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell aging;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of hydrolase activity;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;sterol regulatory element binding protein import into nucleus;transport;ventricular cardiac muscle cell development structural molecule activity cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;envelope;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane-bounded organelle;nuclear envelope;nuclear part;nucleoplasm;nucleus;organelle;organelle envelope;organelle part;perinuclear region of cytoplasm;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM) 0 9 69 4 81.6

E9PPU0 EPPK1 >tr|E9PPU0|E9PPU0_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=4 SV=1 0.05 0.72 -0.72 -0.03 0.37 1.07 0.69 0.22 0.711460673 -0.582898903 cell part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 0 1 122 4 64.8

B4DUF5;E9PF16;B4DHT5;Q96CM8;B4DFQ6 "Acyl-CoA synthetase family member 2, mitochondrial" ACSF2 ">tr|B4DUF5|B4DUF5_HUMAN Acyl-CoA synthetase family member 2, mitochondrial OS=Homo sapiens GN=ACSF2 PE=2 SV=1;>tr|E9PF16|E9PF16_HUMAN Acyl-CoA synthetase family member 2, mitochondrial OS=Homo sapiens GN=ACSF2 PE=2 SV=1;>tr|B4DHT5|B4DHT5_HUMAN Acyl-CoA syn" 0.10 0.04 0.39 -0.01 -0.86 -0.42 0.14 -0.20 0.882605146 0.466703288 carboxylic acid metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid metabolic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 2.25E-24 5 5 5 20.7

Q9H2P0;E9PQK8 Activity-dependent neuroprotector homeobox protein ADNP >sp|Q9H2P0|ADNP_HUMAN Activity-dependent neuroprotector homeobox protein OS=Homo sapiens GN=ADNP PE=1 SV=1 -0.03 0.58 0.20 0.59 -0.08 0.09 -1.22 -0.15 0.866999483 0.67626737 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of neuron apoptosis;regulation of programmed cell death;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cation binding;chromatin binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 5.23E-22 2 5 5 7.2

Q9NX46 Poly(ADP-ribose) glycohydrolase ARH3 ADPRHL2 >sp|Q9NX46|ARHL2_HUMAN Poly(ADP-ribose) glycohydrolase ARH3 OS=Homo sapiens GN=ADPRHL2 PE=1 SV=1 0.22 -0.06 0.14 -0.03 0.17 0.00 0.42 -0.16 0.091899558 -0.037091155 "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;ion binding;metal ion binding;poly(ADP-ribose) glycohydrolase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nucleus;organelle;organelle lumen;organelle part 5.80E-56 1 5 5 19.8

P30520 Adenylosuccinate synthetase isozyme 2 ADSS >sp|P30520|PURA2_HUMAN Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3 0.23 -0.11 -0.04 -0.05 -0.04 -0.52 0.36 -0.18 0.19276224 0.101320613 amine metabolic process;AMP biosynthetic process;AMP metabolic process;aspartate family amino acid metabolic process;aspartate metabolic process;biosynthetic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to electrical stimulus;cellular response to stimulus;'de novo' AMP biosynthetic process;GTP catabolic process;GTP metabolic process;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;immune system process;IMP metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;response to abiotic stimulus;response to ammonium ion;response to chemical stimulus;response to electrical stimulus;response to inorganic substance;response to organic cyclic compound;response to organic substance;response to purine-containing compound;response to stimulus;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "adenylosuccinate synthase activity;anion binding;binding;catalytic activity;cation binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;magnesium ion binding;metal ion binding;nucleotide binding;phosphate ion binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane "Alanine, aspartate and glutamate metabolism;Purine metabolism" 2.78E-85 1 5 5 15.4

Q13155;A8MU58;F8W950 Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 AIMP2 >sp|Q13155|AIMP2_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2;>tr|A8MU58|A8MU58_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=2 SV=2 0.03 -0.03 0.11 0.04 -0.74 -0.30 -0.15 -0.14 1.089981418 0.370413033 amine metabolic process;amino acid activation;apoptosis;biological regulation;carboxylic acid metabolic process;cell death;cell differentiation;cellular amine metabolic process;cellular amino acid metabolic process;cellular developmental process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;developmental process;epithelial cell differentiation;lung cell differentiation;lung epithelial cell differentiation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;primary metabolic process;programmed cell death;regulation of biological process;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;Type II pneumocyte differentiation cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 7.01E-86 3 5 5 23.8

F8WBH3;F5H4B6;Q8IZ83-3;Q8IZ83;M0QY06 Aldehyde dehydrogenase family 16 member A1 ALDH16A1 >tr|F8WBH3|F8WBH3_HUMAN Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=2 SV=1;>tr|F5H4B6|F5H4B6_HUMAN Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=2 SV=1;>sp|Q8IZ83-3|A16A1_HUMAN Isoform 3 of Aldehyde -0.37 -0.31 0.52 0.33 -0.23 -0.45 0.02 -0.09 0.373509316 0.227402539 "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor" 4.82E-33 5 5 5 12.7

J3QRD1;P51648;P51648-2;J3QS00;I3L1M4;J3KTD9;I3L2W1;E9PJV0;C9JKT2;C9JMC5;I3L3I9;P48448;A8MYB8;E9PNN6;P43353-2;P30838;P43353Fatty aldehyde dehydrogenase ALDH3A2 >tr|J3QRD1|J3QRD1_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=3 SV=1;>sp|P51648|AL3A2_HUMAN Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1;>sp|P51648-2|AL3A2_HUMAN Isoform 2 of Fatty aldehyde dehydrogenase OS=Homo sa 0.06 -0.05 -0.03 0.04 -0.14 -0.09 0.09 -0.26 0.575832418 0.106554648 aging;alcohol catabolic process;alcohol metabolic process;aldehyde catabolic process;anatomical structure development;biological regulation;catabolic process;cellular aldehyde metabolic process;cellular catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;central nervous system development;developmental process;epidermis development;ethanol catabolic process;ethanol metabolic process;isoprenoid metabolic process;lipid metabolic process;metabolic process;peripheral nervous system development;phytol metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary alcohol catabolic process;primary alcohol metabolic process;primary metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to cAMP;response to chemical stimulus;response to corticosteroid stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to hypoxia;response to nutrient;response to nutrient levels;response to organic substance;response to oxidative stress;response to oxygen levels;response to steroid hormone stimulus;response to stimulus;response to stress;sesquiterpene metabolic process;sesquiterpenoid metabolic process;small molecule catabolic process;small molecule metabolic process;system development;terpene metabolic process;terpenoid metabolic process;tissue development "3-chloroallyl aldehyde dehydrogenase activity;alcohol dehydrogenase (NADP+) activity;aldehyde dehydrogenase (NAD) activity;aldehyde dehydrogenase [NAD(P)+] activity;aldo-keto reductase (NADP) activity;catalytic activity;long-chain-alcohol oxidase activity;long-chain-aldehyde dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, oxygen as acceptor" cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microbody;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle membrane;organelle part;peroxisome "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Chloroalkane and chloroalkene degradation;Drug metabolism - cytochrome P450;Fatty acid metabolism;Glycerolipid metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Limonene and pinene degradation;Lysine degradation;Metabolism of xenobiotics by cytochrome P450;Pentose and glucuronate interconversions;Phenylalanine metabolism;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Tyrosine metabolism;Valine, leucine and isoleucine degradation" 1.20E-27 17 5 5 16

O75843;G3V532;G3V2V9;G3V3Z2 AP-1 complex subunit gamma-like 2 AP1G2 >sp|O75843|AP1G2_HUMAN AP-1 complex subunit gamma-like 2 OS=Homo sapiens GN=AP1G2 PE=1 SV=1 -0.06 -0.04 0.11 0.00 -1.15 -0.55 0.44 -0.12 0.42306024 0.34945972 cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;multi-organism process;protein transport;reproductive process;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction protein transporter activity;substrate-specific transporter activity;transporter activity AP-1 adaptor complex;AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;cytoplasmic part;cytoplasmic vesicle part;endosomal part;endosome membrane;Golgi apparatus;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex 1.46E-16 4 5 5 7

K7EJL1;B4DDG7;Q9BXS5;Q9BXS5-2;E7ENJ6;K7EK69;K7ERH5;K7EL08;K7EQX3;Q9Y6Q5;Q9Y6Q5-2 AP-1 complex subunit mu-1 AP1M1 >tr|K7EJL1|K7EJL1_HUMAN AP-1 complex subunit mu-1 OS=Homo sapiens GN=AP1M1 PE=4 SV=1;>tr|B4DDG7|B4DDG7_HUMAN AP-1 complex subunit mu-1 OS=Homo sapiens GN=AP1M1 PE=2 SV=1;>sp|Q9BXS5|AP1M1_HUMAN AP-1 complex subunit mu-1 OS=Homo sapiens GN=AP1M1 PE=1 SV=3;>s -0.02 -0.28 -0.02 -0.17 0.03 -0.11 0.34 -0.43 0.170334171 -0.079735555 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;endosome to melanosome transport;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;immune system process;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;melanosome organization;membrane organization;multi-organism process;organelle organization;pigment granule organization;post-Golgi vesicle-mediated transport;protein targeting;protein transport;regulation of biological process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;reproductive process;transport;vesicle organization;vesicle targeting;vesicle-mediated transport;viral reproduction;viral reproductive process;virus-host interaction AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;clathrin coated vesicle membrane;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;lysosomal membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;protein complex;trans-Golgi network membrane;vacuolar membrane;vacuolar part;vesicle membrane Lysosome 8.83E-20 11 5 5 19.7

F8VWH9;E7EV62;Q8N6T3;Q8N6T3-2;F8W1U7;B7Z8H8;E5RHT6;Q8N6T3-3;E5RHH7;E5RHC5;F8VWB3 ADP-ribosylation factor GTPase-activating protein 1 ARFGAP1 >tr|F8VWH9|F8VWH9_HUMAN ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=2 SV=1;>tr|E7EV62|E7EV62_HUMAN ADP-ribosylation factor GTPase-activating protein 1 OS=Homo sapiens GN=ARFGAP1 PE=2 SV=1;>sp|Q8N6T3|ARFG1_HUMAN ADP-rib 0.25 -0.07 -0.08 -0.18 0.54 0.13 0.13 0.02 0.651481957 -0.225463351 "activation of signaling protein activity involved in unfolded protein response;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular transport;macromolecule metabolic process;metabolic process;organelle organization;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein transport;regulation of ARF GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of transferase activity;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" ARF GTPase activator activity;binding;cation binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;small GTPase regulator activity;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endoplasmic reticulum;Golgi apparatus part;Golgi membrane;Golgi-associated vesicle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nuclear membrane;nuclear part;organelle;organelle membrane;organelle part;plasma membrane;synapse;vesicle membrane Endocytosis 1.94E-28 11 5 5 19.1

P59998;F8WCF6;F8WDD7;H7C0A3;P59998-3;P59998-2;F8WE39;F8WDW3;R4GN08;P59998-4 Actin-related protein 2/3 complex subunit 4 ARPC4;ARPC4-TTLL3 >sp|P59998|ARPC4_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3;>tr|F8WCF6|F8WCF6_HUMAN Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=2 SV=1;>tr|F8WDD7|F8WDD7_HUMAN Actin-related protein 2/3 c -0.18 0.13 -0.52 0.32 -0.08 0.52 0.32 0.38 0.655205952 -0.345403111 actin cytoskeleton organization;actin filament organization;actin filament polymerization;actin filament-based process;actin nucleation;actin polymerization or depolymerization;Arp2/3 complex-mediated actin nucleation;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;protein complex assembly;protein complex subunit organization;protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stress Arp2/3 protein complex;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis 1.45E-30 10 5 5 30.4

P15289-2;P15289 Arylsulfatase A;Arylsulfatase A component B;Arylsulfatase A component C ARSA >sp|P15289-2|ARSA_HUMAN Isoform 2 of Arylsulfatase A OS=Homo sapiens GN=ARSA;>sp|P15289|ARSA_HUMAN Arylsulfatase A OS=Homo sapiens GN=ARSA PE=1 SV=3 -0.97 -0.77 -0.15 0.41 1.31 1.30 0.02 -0.13 0.842501372 -0.992584234 cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycolipid metabolic process;glycosphingolipid metabolic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;membrane lipid metabolic process;metabolic process;post-translational protein modification;primary metabolic process;protein metabolic process;protein modification process;small molecule metabolic process;sphingolipid metabolic process "arylsulfatase activity;binding;calcium ion binding;catalytic activity;cation binding;cerebroside-sulfatase activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;sulfuric ester hydrolase activity" cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-enclosed lumen;organelle lumen;organelle part;vacuolar lumen;vacuolar part Lysosome;Sphingolipid metabolism 3.43E-62 2 5 5 17.5

O75947-2;O75947;F5H608 "ATP synthase subunit d, mitochondrial" ATP5H ">sp|O75947-2|ATP5H_HUMAN Isoform 2 of ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H;>sp|O75947|ATP5H_HUMAN ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3;>tr|F5H608|F5H608_HUMAN ATP synthase subunit d, mitochondri" -0.44 0.18 -0.04 0.27 0.43 0.26 -1.24 -0.08 0.132741146 0.150440603 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity "cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle part;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 7.77E-55 3 5 5 40.1

R4GN72;P61421;F5GYQ1;J3QL14;H3BQJ1 V-type proton ATPase subunit d 1 ATP6V0D1 >tr|R4GN72|R4GN72_HUMAN V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=4 SV=1;>sp|P61421|VA0D1_HUMAN V-type proton ATPase subunit d 1 OS=Homo sapiens GN=ATP6V0D1 PE=1 SV=1;>tr|F5GYQ1|F5GYQ1_HUMAN V-type proton ATPase subunit d 1 OS=Homo sa -0.16 0.60 -0.37 0.32 0.03 0.71 -0.65 0.47 0.037034103 -0.041316502 "activation of signaling protein activity involved in unfolded protein response;anatomical structure development;ATP hydrolysis coupled proton transport;biological regulation;brain development;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;developmental process;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organ development;organelle organization;phagosome maturation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;hydrogen-exporting ATPase activity, phosphorylative mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "apical plasma membrane;axon part;axon terminus;cell part;cell projection part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuron projection terminus;organelle;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain;proton-transporting V-type ATPase complex;proton-transporting V-type ATPase, V0 domain;synapse part;synaptic vesicle;vacuolar part;vacuolar proton-transporting V-type ATPase complex;vesicle;vesicle membrane" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection 5.39E-20 5 5 5 19

Q9UHR4 Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 BAIAP2L1 >sp|Q9UHR4|BI2L1_HUMAN Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Homo sapiens GN=BAIAP2L1 PE=1 SV=2 0.20 -0.13 -0.19 -0.16 -1.25 -0.75 0.31 -0.12 0.439572076 0.37968942 biological regulation;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;filopodium assembly;microspike assembly;multi-organism process;positive regulation of actin cytoskeleton reorganization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin cytoskeleton reorganization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to bacterium;response to biotic stimulus;response to other organism;response to stimulus;signal transduction binding;proline-rich region binding;protein binding cell junction;cell part;cytoplasmic part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;plasma membrane 5.54E-21 1 5 5 13.3

Q14692 Ribosome biogenesis protein BMS1 homolog BMS1 >sp|Q14692|BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1 -0.04 1.10 -0.07 0.70 -0.71 0.26 -0.88 0.96 0.403562438 0.513847004 catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle assembly;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;ribosome assembly;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes 1.46E-22 1 5 5 5.5

Q08AD1-2;Q08AD1-3;Q08AD1 Calmodulin-regulated spectrin-associated protein 2 CAMSAP2 >sp|Q08AD1-2|CAMP2_HUMAN Isoform 2 of Calmodulin-regulated spectrin-associated protein 2 OS=Homo sapiens GN=CAMSAP2;>sp|Q08AD1-3|CAMP2_HUMAN Isoform 3 of Calmodulin-regulated spectrin-associated protein 2 OS=Homo sapiens GN=CAMSAP2;>sp|Q08AD1|CAMP2_HUMAN C -0.11 0.11 0.18 -0.14 -0.21 -0.24 0.38 0.15 0.018998806 -0.009785034 cell part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;microtubule;organelle part;protein complex 5.72E-22 3 5 5 5.7

Q86X55-1;Q86X55;Q86X55-2;K7EQA8;K7EK20;K7EPK1;K7EQB9 Histone-arginine methyltransferase CARM1 CARM1 >sp|Q86X55-1|CARM1_HUMAN Isoform 1 of Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1;>sp|Q86X55|CARM1_HUMAN Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=3;>sp|Q86X55-2|CARM1_HUMAN Isoform 2 of Histone-arginin 0.49 -0.15 0.18 -0.40 0.69 0.21 0.30 0.20 0.589793801 -0.316273592 "anatomical structure morphogenesis;biological regulation;biosynthetic process;bone morphogenesis;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;developmental process;endochondral bone morphogenesis;estrogen receptor signaling pathway;histone arginine methylation;histone H3-R2 methylation;histone methylation;histone modification;interaction with host;interspecies interaction between organisms;intracellular receptor mediated signaling pathway;lipid metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;multi-organism process;negative regulation of binding;negative regulation of molecular function;negative regulation of protein binding;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;pathogenesis;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of fat cell differentiation;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;regulation of anatomical structure morphogenesis;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cartilage development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of estrogen receptor signaling pathway;regulation of fat cell differentiation;regulation of gene expression;regulation of growth;regulation of growth plate cartilage chondrocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of primary metabolic process;regulation of protein binding;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription, DNA-dependent;reproductive process;response to cAMP;response to chemical stimulus;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;small molecule metabolic process;steroid hormone receptor signaling pathway;transcription, DNA-dependent;viral reproductive process;virus-host interaction" "arginine N-methyltransferase activity;beta-catenin binding;binding;catalytic activity;DNA binding;histone acetyl-lysine binding;histone binding;histone methyltransferase activity;histone methyltransferase activity (H3-R17 specific);histone-arginine N-methyltransferase activity;ligand-dependent nuclear receptor transcription coactivator activity;methyltransferase activity;N-methyltransferase activity;nucleic acid binding;protein binding;protein binding transcription factor activity;protein methyltransferase activity;protein-arginine N-methyltransferase activity;protein-arginine omega-N asymmetric methyltransferase activity;regulatory region DNA binding;regulatory region nucleic acid binding;S-adenosylmethionine-dependent methyltransferase activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part 3.88E-30 7 5 5 10.6

G3V169;P29466-2;P29466;B4DVD8;P29466-3;H0YEC7;P29466-4;P29466-5;E9PQW1;Q5EG05-2;Q5FBZ0;Q5EG05 Caspase;Caspase-1;Caspase-1 subunit p20;Caspase-1 subunit p10 CASP1 >tr|G3V169|G3V169_HUMAN Caspase OS=Homo sapiens GN=CASP1 PE=2 SV=1;>sp|P29466-2|CASP1_HUMAN Isoform Beta of Caspase-1 OS=Homo sapiens GN=CASP1;>sp|P29466|CASP1_HUMAN Caspase-1 OS=Homo sapiens GN=CASP1 PE=1 SV=1;>tr|B4DVD8|B4DVD8_HUMAN Caspase-1 subunit p20 -0.01 -0.21 -0.02 -0.19 -1.15 -0.94 0.87 -0.08 0.175155378 0.219236556 "apoptosis;biological regulation;cell death;cellular process;cellular response to abiotic stimulus;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to mechanical stimulus;cellular response to organic substance;cellular response to stimulus;cytokine production;death;defense response;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;interleukin-1 beta production;interleukin-1 production;intracellular receptor mediated signaling pathway;macromolecule metabolic process;metabolic process;multicellular organismal process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of cytokine secretion;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of interleukin-1 alpha production;positive regulation of interleukin-1 alpha secretion;positive regulation of interleukin-1 beta production;positive regulation of interleukin-1 beta secretion;positive regulation of interleukin-1 production;positive regulation of interleukin-1 secretion;positive regulation of intracellular protein kinase cascade;positive regulation of multicellular organismal process;positive regulation of programmed cell death;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of secretion;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transport;primary metabolic process;programmed cell death;protein maturation;protein metabolic process;protein processing;proteolysis;regulation of apoptosis;regulation of biological process;regulation of cell communication;regulation of cell death;regulation of cellular localization;regulation of cellular process;regulation of cytokine production;regulation of cytokine secretion;regulation of establishment of protein localization;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of interleukin-1 alpha production;regulation of interleukin-1 alpha secretion;regulation of interleukin-1 beta production;regulation of interleukin-1 beta secretion;regulation of interleukin-1 production;regulation of interleukin-1 secretion;regulation of intracellular protein kinase cascade;regulation of localization;regulation of multicellular organismal process;regulation of programmed cell death;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of response to stimulus;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of transport;response to abiotic stimulus;response to ATP;response to chemical stimulus;response to external stimulus;response to hypoxia;response to mechanical stimulus;response to organic substance;response to oxygen levels;response to stimulus;response to stress;signal transduction" "apoptotic protease activator activity;caspase activator activity;caspase regulator activity;catalytic activity;cysteine-type endopeptidase activity;cysteine-type endopeptidase inhibitor activity;cysteine-type peptidase activity;endopeptidase activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme activator activity;enzyme inhibitor activity;enzyme regulator activity;hydrolase activity;peptidase activator activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;peptidase inhibitor activity;peptidase regulator activity" cell part;cytoplasmic part;cytosol;extracellular region;intracellular;intracellular part;IPAF inflammasome complex;macromolecular complex;NALP1 inflammasome complex;NALP3 inflammasome complex;protein complex Amyotrophic lateral sclerosis (ALS);Cytosolic DNA-sensing pathway;NOD-like receptor signaling pathway 7.87E-20 12 5 5 16.9

Q9Y5S2;H0YLY0;H0Y6V3;H0Y7V8;H0Y5V1;Q5VT25-3;Q5VT25-4;F5H5N0;Q5VT25-5;Q5VT25;Q5VT25-2;Q5VT25-6 Serine/threonine-protein kinase MRCK beta CDC42BPB >sp|Q9Y5S2|MRCKB_HUMAN Serine/threonine-protein kinase MRCK beta OS=Homo sapiens GN=CDC42BPB PE=1 SV=2 -0.06 1.09 -0.18 0.69 0.68 0.57 0.30 0.39 0.116954238 -0.103842936 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;actomyosin structure organization;biological regulation;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of nucleus localization;establishment of organelle localization;establishment or maintenance of cell polarity;intracellular signal transduction;locomotion;microtubule cytoskeleton organization;microtubule-based process;nuclear migration;organelle organization;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;enzyme regulator activity;GTPase regulator activity;ion binding;kinase activity;lipid binding;magnesium ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small GTPase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" actomyosin;cell junction;cell leading edge;cell part;cell-cell junction;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;membrane;organelle part;plasma membrane 1.14E-15 12 5 5 3.5

Q9H5V8;Q9H5V8-2;Q9H5V8-3 CUB domain-containing protein 1 CDCP1 >sp|Q9H5V8|CDCP1_HUMAN CUB domain-containing protein 1 OS=Homo sapiens GN=CDCP1 PE=1 SV=3;>sp|Q9H5V8-2|CDCP1_HUMAN Isoform 2 of CUB domain-containing protein 1 OS=Homo sapiens GN=CDCP1 0.36 0.71 -0.13 0.09 0.08 -0.31 0.23 0.33 0.300265092 0.1744239 cell part;extracellular region;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane 4.98E-13 3 5 5 6

Q96JB5;F5H3I5;Q96JB5-2;Q96JB5-3;J3QL86;J3QRM1;J3QQY1;J3QS62 CDK5 regulatory subunit-associated protein 3 CDK5RAP3 >sp|Q96JB5|CK5P3_HUMAN CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=1 SV=2;>tr|F5H3I5|F5H3I5_HUMAN CDK5 regulatory subunit-associated protein 3 OS=Homo sapiens GN=CDK5RAP3 PE=2 SV=1;>sp|Q96JB5-2|CK5P3_HUMAN Isoform 2 of CDK5 -0.16 0.08 0.04 0.17 0.06 0.28 -0.48 -0.31 0.297415519 0.141509777 "anatomical structure development;biological regulation;brain development;developmental process;organ development;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of developmental process;regulation of gene expression;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity" binding;enzyme binding;kinase binding;protein binding;protein kinase binding 5.74E-38 8 5 5 11.1

Q9H444 Charged multivesicular body protein 4b CHMP4B >sp|Q9H444|CHM4B_HUMAN Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B PE=1 SV=1 -0.03 0.07 0.00 0.05 0.36 0.18 0.23 0.00 0.934757802 -0.169513275 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;membrane organization;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;cytosol;endosomal part;endosome membrane;intracellular organelle part;intracellular part;late endosome membrane;membrane;organelle membrane;organelle part Endocytosis 1.15E-76 1 5 5 27.2

Q9NZZ3;Q9NZZ3-2 Charged multivesicular body protein 5 CHMP5 >sp|Q9NZZ3|CHMP5_HUMAN Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 PE=1 SV=1;>sp|Q9NZZ3-2|CHMP5_HUMAN Isoform 2 of Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5 0.09 0.16 -0.07 0.03 0.16 0.17 0.06 0.04 0.369235418 -0.053287394 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;endosome to lysosome transport;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;lysosomal transport;lysosome organization;membrane organization;organelle organization;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of receptor recycling;regulation of signaling;transport;vacuolar transport;vacuole organization;vesicle-mediated transport cell part;cytoplasmic part;cytosol;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part Endocytosis 8.36E-41 2 5 5 22.4

E9PBL8;Q8WTW3;J3QKY9;J3QLT5 Conserved oligomeric Golgi complex subunit 1 COG1 >tr|E9PBL8|E9PBL8_HUMAN Conserved oligomeric Golgi complex subunit 1 (Fragment) OS=Homo sapiens GN=COG1 PE=4 SV=2;>sp|Q8WTW3|COG1_HUMAN Conserved oligomeric Golgi complex subunit 1 OS=Homo sapiens GN=COG1 PE=1 SV=1 0.13 0.39 0.33 0.00 0.04 -0.09 -0.24 -0.12 1.227355828 0.318244184 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi organization;Golgi vesicle transport;intracellular transport;intra-Golgi vesicle-mediated transport;organelle organization;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;Golgi apparatus part;Golgi membrane;Golgi transport complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;organelle membrane;organelle part;protein complex 1.51E-10 4 5 5 7.3

B3KSY4;P57737-2;P57737-4;P57737;P57737-3;I3L212;E7EP81;I3L167 Coronin;Coronin-7 CORO7 >tr|B3KSY4|B3KSY4_HUMAN Coronin OS=Homo sapiens GN=CORO7 PE=2 SV=1;>sp|P57737-2|CORO7_HUMAN Isoform 2 of Coronin-7 OS=Homo sapiens GN=CORO7;>sp|P57737-4|CORO7_HUMAN Isoform 4 of Coronin-7 OS=Homo sapiens GN=CORO7;>sp|P57737|CORO7_HUMAN Coronin-7 OS=Homo sa0.25 -0.09 0.24 0.15 -0.25 -0.02 -0.10 -0.16 1.20908549 0.268758046 cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;Golgi apparatus;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;vesicle 4.83E-26 8 5 5 13.3

Q16630-3;F8WJN3;Q16630;Q16630-2;F8W084 Cleavage and polyadenylation specificity factor subunit 6 CPSF6 >sp|Q16630-3|CPSF6_HUMAN Isoform 3 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6;>tr|F8WJN3|F8WJN3_HUMAN Cleavage and polyadenylation-specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=2 SV=1;>sp|Q16630|CPSF6_H 0.02 0.05 -0.08 -0.04 0.05 -0.31 -0.39 -0.33 0.943487737 0.231942839 cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA metabolic process;mRNA polyadenylation;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein tetramerization;RNA 3'-end processing;RNA metabolic process;RNA polyadenylation;RNA processing binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mRNA cleavage factor complex;nuclear body;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;paraspeckles;protein complex;ribonucleoprotein complex mRNA surveillance pathway 1.72E-146 5 5 5 16.1

F5H669;Q8N684-2;Q8N684;Q8N684-3;J3QT54;F5H6M0;F5H047;F5H5B7;F5H1W4;F5H2K8;F5H6P5;F5H6A8;F5GXA3;C9JM38;C9J286;C9J323 Cleavage and polyadenylation specificity factor subunit 7 CPSF7 >tr|F5H669|F5H669_HUMAN Cleavage and polyadenylation-specificity factor subunit 7 (Fragment) OS=Homo sapiens GN=CPSF7 PE=2 SV=1;>sp|Q8N684-2|CPSF7_HUMAN Isoform 2 of Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens GN=CPSF7;>sp|Q8N 0.19 0.00 0.12 0.13 0.31 -0.25 -0.53 -0.35 0.728368638 0.315871912 "biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein tetramerization;RNA 3'-end processing;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;termination of RNA polymerase II transcription;transcription termination, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;mRNA cleavage factor complex;nuclear part;nucleoplasm part;organelle part;protein complex mRNA surveillance pathway 7.19E-45 16 5 5 18.2

Q9P2B4;B1AMN7 CTTNBP2 N-terminal-like protein CTTNBP2NL >sp|Q9P2B4|CT2NL_HUMAN CTTNBP2 N-terminal-like protein OS=Homo sapiens GN=CTTNBP2NL PE=1 SV=2 0.25 0.27 0.46 -0.13 0.04 -0.07 0.05 0.04 0.67371529 0.198638301 actin cytoskeleton;cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 2.18E-12 2 5 5 12.1

P35659;D6R9L5;P35659-2;B4DFG0;D6RDA2;H0Y993 Protein DEK DEK >sp|P35659|DEK_HUMAN Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1;>tr|D6R9L5|D6R9L5_HUMAN Protein DEK (Fragment)

OS=Homo sapiens GN=DEK PE=2 SV=1;>sp|P35659-2|DEK_HUMAN Isoform 2 of Protein DEK OS=Homo sapiens GN=DEK;>tr|B4DFG0|B4DFG0_HUMAN Protein DEK OS= 0.01 0.19 -0.02 0.11 0.22 -0.64 -1.01 -0.89 0.981823015 0.650987421 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of double-strand break repair;regulation of double-strand break repair via nonhomologous end joining;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription from RNA polymerase II promoter;transcription, DNA-dependent;viral genome replication;viral reproductive process" binding;DNA binding;histone binding;nucleic acid binding;protein binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.35E-26 6 5 5 15.2

Q9UBM7;E9PRL8;E9PQ71;E9PIP9;E9PJ54;H0YE57;E9PMT8;E9PM00;E9PLZ2 7-dehydrocholesterol reductase DHCR7 >sp|Q9UBM7|DHCR7_HUMAN 7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1 -1.46 -0.18 0.63 1.25 -1.69 -1.94 -1.76 -0.77 1.053302345 1.599696957 alcohol metabolic process;anatomical structure development;biological regulation;biosynthetic process;blood vessel development;cell differentiation;cellular developmental process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;growth;lipid biosynthetic process;lipid metabolic process;lung development;metabolic process;multicellular organism growth;multicellular organismal process;organ development;post-embryonic development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular process;regulation of cholesterol biosynthetic process;regulation of cholesterol metabolic process;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of steroid biosynthetic process;regulation of steroid metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "7-dehydrocholesterol reductase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nuclear membrane;nuclear outer membrane;nuclear part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane Steroid biosynthesis 1.15E-12 9 5 5 10.1

Q12959-5;Q12959-3;Q12959-6;Q12959-4;Q12959;Q12959-7;Q12959-2;E7EQD7;Q12959-8;Q12959-9;B4E2H8;C9IYP1;C9JUA9;C9JN61;C9JCP6;A8MUT6;H7C166Disks large homolog 1 DLG1 >sp|Q12959-5|DLG1_HUMAN Isoform 5 of Disks large homolog 1 OS=Homo sapiens GN=DLG1;>sp|Q12959-3|DLG1_HUMAN Isoform 3 of Disks large homolog 1 OS=Homo sapiens GN=DLG1;>sp|Q12959-6|DLG1_HUMAN Isoform 6 of Disks large homolog 1 OS=Homo sapiens GN=DLG1;>sp|Q12 -0.14 0.09 0.25 -0.07 -0.27 -0.27 -0.05 0.41 0.164681012 0.081860784 actin cytoskeleton organization;actin filament organization;actin filament-based process;activation of protein kinase activity;adaptive immune response;adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;amyloid precursor protein metabolic process;anatomical structure development;anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;cell activation;cell adhesion;cell communication;cell cycle checkpoint;cell junction assembly;cell junction organization;cell proliferation;cell recognition;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cell-cell recognition;cell-cell signaling;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;chemical homeostasis;chemotaxis;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytokine production;cytokine production involved in immune response;cytoskeleton organization;developmental process;developmental process involved in reproduction;embryonic morphogenesis;embryonic organ morphogenesis;embryonic skeletal system morphogenesis;endothelial cell proliferation;epithelial cell proliferation;establishment or maintenance of cell polarity;glycoprotein metabolic process;hard palate development;homeostatic process;immune effector process;immune response;immune system process;immunological synapse formation;interaction with host;interspecies interaction between organisms;ion homeostasis;lens development in camera-type eye;leukocyte activation;leukocyte mediated immunity;localization;locomotion;lymphocyte activation;lymphocyte mediated immunity;macromolecule localization;macromolecule metabolic process;membrane organization;membrane raft organization;metabolic process;mitotic cell cycle checkpoint;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;multi-organism process;muscle contraction;muscle system process;muscle tissue development;negative regulation of biological process;negative regulation of cell activation;negative regulation of cell cycle;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epithelial cell proliferation;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of mitotic cell cycle;negative regulation of mononuclear cell proliferation;negative regulation of T cell activation;negative regulation of T cell proliferation;organ morphogenesis;organelle organization;peristalsis;phasic smooth muscle contraction;plasma membrane organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of establishment of protein localization in plasma membrane;positive regulation of ion transport;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of potassium ion transport;positive regulation of protein complex assembly;positive regulation of protein kinase activity;positive regulation of protein polymerization;positive regulation of transferase activity;positive regulation of transport;production of molecular mediator of immune response;protein localization;protein localization in membrane;protein localization in plasma membrane;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell activation;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of epithelial cell proliferation;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of immune system process;regulation of ion transport;regulation of kinase activity;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of localization;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of metal ion transport;regulation of mitotic cell cycle;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of potassium ion transport;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of T cell activation;regulation of T cell proliferation;regulation of transferase activity;regulation of transport;reproductive process;reproductive structure development;response to chemical stimulus;response to external stimulus;response to stimulus;signaling;skeletal system morphogenesis;smooth muscle contraction;smooth muscle tissue development;synaptic transmission;system process;T cell activation;T cell cytokine production;T cell mediated immunity;taxis;tight junction assembly;tissue development;tissue morphogenesis;tube morphogenesis;viral reproductive process;virus-host interaction "binding;catalytic activity;channel regulator activity;cytoskeletal protein binding;guanylate kinase activity;hydrolase activity;hydrolase activity, acting on ester bonds;kinase activity;nucleobase-containing compound kinase activity;nucleotide kinase activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;phosphotransferase activity, phosphate group as acceptor;potassium channel regulator activity;protein binding;transferase activity;transferase activity, transferring phosphorus-containing groups" axon part;basolateral plasma membrane;cell junction;cell part;cell projection membrane;cell projection part;cell-cell junction;cytoplasmic part;cytoskeletal part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;immunological synapse;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral loop;lateral plasma membrane;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;microtubule;MPP7-DLG1-LIN7 complex;myelin sheath abaxonal region;neuromuscular junction;node of Ranvier;nucleus;occluding junction;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;postsynaptic density;postsynaptic membrane;protein complex;sarcolemma;synapse;synapse part;synaptic membrane;tight junction T cell receptor signaling pathway 5.21E-19 17 5 5 11.5

O75937 DnaJ homolog subfamily C member 8 DNAJC8 >sp|O75937|DNJC8_HUMAN DnaJ homolog subfamily C member 8 OS=Homo sapiens GN=DNAJC8 PE=1 SV=2 -0.03 0.11 -0.20 0.18 0.24 -0.22 -0.57 -0.54 0.592091757 0.288787541 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" cell part;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part 6.38E-69 1 5 5 20.6

Q6XZF7;Q5SVK8;Q6XZF7-2;B4E0Q3 Dynamin-binding protein DNMBP >sp|Q6XZF7|DNMBP_HUMAN Dynamin-binding protein OS=Homo sapiens GN=DNMBP PE=1 SV=1;>tr|Q5SVK8|Q5SVK8_HUMAN Dynamin-binding protein OS=Homo sapiens GN=DNMBP PE=2 SV=1;>sp|Q6XZF7-2|DNMBP_HUMAN Isoform 2 of Dynamin-binding protein OS=Homo sapiens GN=DNMBP;>tr| -0.05 -0.09 0.11 0.51 -0.10 0.64 -0.50 -0.28 0.250719677 0.182866834 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;regulation of biological process;regulation of cellular process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;signal transduction enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity;Ras guanyl-nucleotide exchange factor activity;Rho guanyl-nucleotide exchange factor activity;small GTPase regulator activity cell junction;cell part;cytoplasm;cytoplasmic part;cytoskeleton;Golgi apparatus part;Golgi stack;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;synapse 4.86E-30 4 5 5 4.3

Q9H7D0;Q9H7D0-2;H0Y7N4 Dedicator of cytokinesis protein 5 DOCK5 >sp|Q9H7D0|DOCK5_HUMAN Dedicator of cytokinesis protein 5 OS=Homo sapiens GN=DOCK5 PE=1 SV=3 0.14 0.13 -0.30 -0.42 0.08 0.13 0.26 0.19 0.804886936 -0.280406471 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity cell part;cytoplasm;intracellular part 2.04E-11 3 5 5 3

O60762;Q5QPK2;H0Y368;E9PHH5;Q5QPJ9 Dolichol-phosphate mannosyltransferase DPM1 >sp|O60762|DPM1_HUMAN Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=1 SV=1;>tr|Q5QPK2|Q5QPK2_HUMAN Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=2 SV=1;>tr|H0Y368|H0Y368_HUMAN Dolichol-phosphate mannosyltransferase (-0.20 -0.08 -0.09 0.17 0.46 0.24 -0.39 -0.03 0.226090653 -0.118377857 alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;C-terminal protein amino acid modification;C-terminal protein lipidation;dolichol metabolic process;dolichol-linked oligosaccharide biosynthetic process;GDP-mannose metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;glycosylation;GPI anchor biosynthetic process;GPI anchor metabolic process;hexose metabolic process;isoprenoid metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;mannose metabolic process;metabolic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;organophosphate metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;polyprenol metabolic process;post-translational protein modification;prenol metabolic process;primary metabolic process;protein glycosylation;protein lipidation;protein mannosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein O-linked glycosylation;protein O-linked mannosylation;small molecule metabolic process "alcohol binding;binding;carbohydrate binding;catalytic activity;dolichyl-phosphate beta-D-mannosyltransferase activity;dolichyl-phosphate-mannose-protein mannosyltransferase activity;mannose binding;mannosyltransferase activity;monosaccharide binding;sugar binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;dolichol-phosphate-mannose synthase complex;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;macromolecular complex;mannosyltransferase complex;membrane;membrane part;organelle membrane;organelle part;protein complex N-Glycan biosynthesis 4.92E-33 5 5 5 21.9

Q8NDI1-3;Q8NDI1-2;Q8NDI1;H7C1E6;H7BZ98 EH domain-binding protein 1 EHBP1 >sp|Q8NDI1-3|EHBP1_HUMAN Isoform 3 of EH domain-binding protein 1 OS=Homo sapiens GN=EHBP1;>sp|Q8NDI1-2|EHBP1_HUMAN Isoform 2 of EH domain-binding protein 1 OS=Homo sapiens GN=EHBP1;>sp|Q8NDI1|EHBP1_HUMAN EH domain-binding protein 1 OS=Homo sapiens GN=EHBP 0.22 0.13 -0.84 -0.22 0.51 -0.08 0.20 0.18 0.600483416 -0.382848935 cell part;cytoplasm;intracellular part;membrane 2.04E-12 5 5 5 6.1

P41214;P41214-2;Q5SY38 Eukaryotic translation initiation factor 2D EIF2D >sp|P41214|EIF2D_HUMAN Eukaryotic translation initiation factor 2D OS=Homo sapiens GN=EIF2D PE=1 SV=3;>sp|P41214-2|EIF2D_HUMAN Isoform 2 of Eukaryotic translation initiation factor 2D OS=Homo sapiens GN=EIF2D 0.12 -0.10 0.06 0.02 -0.53 -0.46 0.06 -0.09 0.795369564 0.280536798 establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;transport "binding;nucleic acid binding;receptor activity;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;intracellular part 4.23E-34 3 5 5 13.4

Q15006;H0YAS9;E5RGJ2 ER membrane protein complex subunit 2 EMC2 >sp|Q15006|EMC2_HUMAN ER membrane protein complex subunit 2 OS=Homo sapiens GN=EMC2 PE=1 SV=1 -0.13 0.32 0.04 0.05 0.48 0.13 -0.80 0.61 0.037081428 -0.036989731 cell part;cytoplasmic part;ER membrane protein complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nucleus;organelle;protein complex 1.27E-28 3 5 5 22.2

Q9HC35-2;Q9HC35;B5MBZ0;F2Z2B5 Echinoderm microtubule-associated protein-like 4 EML4 >sp|Q9HC35-2|EMAL4_HUMAN Isoform 2 of Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4;>sp|Q9HC35|EMAL4_HUMAN Echinoderm microtubule-associated protein-like 4 OS=Homo sapiens GN=EML4 PE=1 SV=3;>tr|B5MBZ0|B5MBZ0_HUMAN Echinoderm micr -0.09 -0.01 -0.09 -0.34 0.25 0.04 0.08 0.02 1.107202307 -0.230990953 cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;microtubule-based process;mitosis;nuclear division;organelle fission;organelle organization cell part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;microtubule;organelle part;protein complex 1.42E-31 4 5 5 6.8

Q9NV70-2;Q9NV70 Exocyst complex component 1 EXOC1 >sp|Q9NV70-2|EXOC1_HUMAN Isoform 2 of Exocyst complex component 1 OS=Homo sapiens GN=EXOC1;>sp|Q9NV70|EXOC1_HUMAN Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4 -0.11 0.05 0.11 -0.06 0.11 0.20 0.09 0.09 0.985575224 -0.125979238 cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;macromolecule metabolic process;membrane organization;metabolic process;primary metabolic process;protein metabolic process;protein transport;secretion;secretion by cell;transport;vesicle-mediated transport cell cortex part;cell part;cytoplasmic part;exocyst;intracellular part;macromolecular complex;membrane;plasma membrane;protein complex 2.67E-51 2 5 5 8.4

Q96KP1 Exocyst complex component 2 EXOC2 >sp|Q96KP1|EXOC2_HUMAN Exocyst complex component 2 OS=Homo sapiens GN=EXOC2 PE=1 SV=1 -0.11 -0.05 0.33 0.12 -0.03 0.15 0.19 0.09 0.088355702 -0.02779104 cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;macromolecule metabolic process;membrane organization;metabolic process;primary metabolic process;protein metabolic process;protein transport;secretion;secretion by cell;transport;vesicle-mediated transport cell part;membrane;plasma membrane 1.46E-18 1 5 5 7.5

Q9Y624;B7Z5W1;B7Z941 Junctional adhesion molecule A F11R >sp|Q9Y624|JAM1_HUMAN Junctional adhesion molecule A OS=Homo sapiens GN=F11R PE=1 SV=1;>tr|B7Z5W1|B7Z5W1_HUMAN Junctional adhesion molecule A OS=Homo sapiens GN=F11R PE=2 SV=1;>tr|B7Z941|B7Z941_HUMAN Junctional adhesion molecule A OS=Homo sapiens GN=F11R P -0.09 -0.05 -0.26 0.15 -1.09 -1.00 0.08 -0.07 0.614777696 0.459797814 biological adhesion;biological regulation;blood coagulation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;coagulation;defense response;developmental process;enzyme linked receptor protein signaling pathway;epithelial cell differentiation;hemostasis;immune system process;inflammatory response;interaction with host;interspecies interaction between organisms;leukocyte migration;locomotion;multicellular organismal process;multi-organism process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;reproductive process;response to stimulus;response to stress;response to wounding;signal transduction;tight junction assembly;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;viral reproductive process;virus-host interaction cell junction;cell part;cell-cell junction;integral to membrane;intrinsic to membrane;membrane;membrane part;occluding junction;plasma membrane;tight junctionCell adhesion molecules (CAMs);Epithelial cell signaling in Helicobacter pylori infection;Leukocyte transendothelial migration;Tight junction 8.31E-45 3 5 5 26.4

Q01469;I6L8B7 "Fatty acid-binding protein, epidermal" FABP5 ">sp|Q01469|FABP5_HUMAN Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3" -0.21 0.01 0.22 0.03 0.03 0.97 0.96 -0.25 0.534980744 -0.41684001 alcohol metabolic process;amine metabolic process;anatomical structure development;biosynthetic process;carbohydrate metabolic process;carbohydrate transport;cellular amine metabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;epidermis development;establishment of localization;ethanolamine-containing compound metabolic process;glucose metabolic process;glucose transport;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;hexose metabolic process;hexose transport;lipid biosynthetic process;lipid metabolic process;metabolic process;monosaccharide metabolic process;monosaccharide transport;nitrogen compound metabolic process;organic substance transport;organophosphate metabolic process;phosphatidylcholine biosynthetic process;phosphatidylcholine metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;small molecule metabolic process;tissue development;transport binding;carboxylic acid binding;fatty acid binding;lipid binding;monocarboxylic acid binding;transporter activity cell part;cytoplasm;intracellular part PPAR signaling pathway 2.24E-53 2 5 5 26.7

Q8WUP2-3;Q8WUP2;Q8WUP2-2;E7EWE8;D6RAI6;E7EPI5;E7EN81;D6R9I4;D6RA19;D6R9V9 Filamin-binding LIM protein 1 FBLIM1 >sp|Q8WUP2-3|FBLI1_HUMAN Isoform 3 of Filamin-binding LIM protein 1 OS=Homo sapiens GN=FBLIM1;>sp|Q8WUP2|FBLI1_HUMAN Filamin-binding LIM protein 1 OS=Homo sapiens GN=FBLIM1 PE=1 SV=2;>sp|Q8WUP2-2|FBLI1_HUMAN Isoform 2 of Filamin-binding LIM protein 1 OS=Ho -0.08 -0.21 -0.28 -0.71 -0.40 -0.23 1.17 0.01 0.501771415 -0.458258772 biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of integrin activation;regulation of protein complex assembly binding;cation binding;cytoskeletal protein binding;filamin binding;ion binding;metal ion binding;protein binding;transition metal ion binding;zinc ion binding actin filament bundle;actomyosin;adherens junction;anchoring junction;cell cortex;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytosol;focal adhesion;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;organelle;organelle part;stress fiber 1.32E-16 10 5 5 24.3

Q13642-1;Q13642-5;Q13642-4;Q5JXI8;Q13642;Q5JXH9;Q13642-3;Q5JXH8;Q5JXH7;Q5JXI3;Q5JXI2;Q5JXI0 Four and a half LIM domains protein 1 FHL1 >sp|Q13642-1|FHL1_HUMAN Isoform 1 of Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1;>sp|Q13642-5|FHL1_HUMAN Isoform 5 of Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1;>sp|Q13642-4|FHL1_HUMAN Isoform 4 of Four and a half LIM d 0.39 0.08 -0.28 -0.21 -0.20 -0.35 0.51 -0.06 0.026486984 0.0194871 anatomical structure development;anatomical structure morphogenesis;biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell growth;negative regulation of cellular process;negative regulation of G1/S transition of mitotic cell cycle;negative regulation of G2/M transition of mitotic cell cycle;negative regulation of growth;negative regulation of mitotic cell cycle;organ development;organ morphogenesis;positive regulation of biological process;positive regulation of ion transport;positive regulation of potassium ion transport;positive regulation of transport;regulation of biological process;regulation of cell cycle;regulation of cell cycle process;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of G1/S transition of mitotic cell cycle;regulation of G2/M transition of mitotic cell cycle;regulation of growth;regulation of homeostatic process;regulation of interphase of mitotic cell cycle;regulation of ion homeostasis;regulation of ion transport;regulation of localization;regulation of membrane depolarization;regulation of metal ion transport;regulation of mitotic cell cycle;regulation of potassium ion transport;regulation of transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 4.43E-43 12 5 5 23.6

Q9C0B1;F8WCB8;Q9C0B1-4;Q9C0B1-2;B4DHN4 Alpha-ketoglutarate-dependent dioxygenase FTO FTO >sp|Q9C0B1|FTO_HUMAN Alpha-ketoglutarate-dependent dioxygenase FTO OS=Homo sapiens GN=FTO PE=1 SV=3 0.03 -0.14 -0.01 0.07 0.28 -0.25 -0.08 -0.56 0.309987596 0.142463971 "adipose tissue development;anatomical structure development;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;demethylation;developmental process;DNA dealkylation;DNA dealkylation involved in DNA repair;DNA demethylation;DNA metabolic process;DNA modification;homeostatic process;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal homeostasis;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;oxidation-reduction process;oxidative demethylation;oxidative DNA demethylation;oxidative RNA demethylation;oxidative single-stranded DNA demethylation;oxidative single-stranded RNA demethylation;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell proliferation;regulation of cellular process;regulation of fat cell proliferation;regulation of gene expression;regulation of gene expression, epigenetic;regulation of growth;regulation of lipid storage;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of respiratory gaseous exchange;regulation of respiratory system process;regulation of system process;regulation of white fat cell proliferation;RNA metabolic process;RNA modification;RNA repair;small molecule metabolic process;temperature homeostasis;tissue development" "binding;catalytic activity;cation binding;demethylase activity;dioxygenase activity;DNA demethylase activity;DNA-N1-methyladenine dioxygenase activity;ferrous iron binding;ion binding;iron ion binding;metal ion binding;oxidative DNA demethylase activity;oxidative RNA demethylase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;transition metal ion binding" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.34E-91 5 5 5 14.5

H7C3P4;B4DYH8;P15586;F6S8M0;H0YFA9;F5H4C6 N-acetylglucosamine-6-sulfatase GNS ">tr|H7C3P4|H7C3P4_HUMAN Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID), isoform CRA_b OS=Homo sapiens GN=GNS PE=2 SV=1;>tr|B4DYH8|B4DYH8_HUMAN N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=2 SV=1;>sp|P15586|GNS_HUMAN N-acetylgluco" -0.77 -0.07 -0.66 -0.04 0.57 1.37 0.15 0.04 1.080967693 -0.915360276 amine metabolic process;aminoglycan catabolic process;aminoglycan metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;keratan sulfate catabolic process;keratan sulfate metabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;sulfur compound catabolic process;sulfur compound metabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;N-acetylglucosamine-6-sulfatase activity;sulfuric ester hydrolase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;lysosome;lytic vacuole;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vacuolar lumen;vacuolar part;vacuole Glycosaminoglycan degradation;Lysosome 2.66E-23 6 5 5 11.1

Q9H8Y8-2;Q9H8Y8;B4DKT0 Golgi reassembly-stacking protein 2 GORASP2 >sp|Q9H8Y8-2|GORS2_HUMAN Isoform 2 of Golgi reassembly-stacking protein 2 OS=Homo sapiens GN=GORASP2;>sp|Q9H8Y8|GORS2_HUMAN Golgi reassembly-stacking protein 2 OS=Homo sapiens GN=GORASP2 PE=1 SV=3;>tr|B4DKT0|B4DKT0_HUMAN Golgi reassembly-stacking protein 2 0.06 0.17 -0.16 -0.07 0.18 0.13 -0.18 0.28 0.334125103 -0.103337615 cell cycle phase;cell cycle process;cellular process;M phase;M phase of mitotic cell cycle;mitotic prophase;prophase cell part;cytoplasmic part;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part 9.89E-29 3 5 5 23.4

G3V582;F8W7D6;Q9NQX3;Q9NQX3-2;F5H039;H0YJ30 Gephyrin;Molybdopterin adenylyltransferase;Molybdopterin molybdenumtransferase GPHN >tr|G3V582|G3V582_HUMAN Molybdopterin molybdenumtransferase OS=Homo sapiens GN=GPHN PE=2 SV=1;>tr|F8W7D6|F8W7D6_HUMAN Molybdopterin molybdenumtransferase OS=Homo sapiens GN=GPHN PE=2 SV=1;>sp|Q9NQX3|GEPH_HUMAN Gephyrin OS=Homo sapiens GN=GPHN PE=1 SV=1;>sp 0.07 -0.23 0.47 0.10 -0.42 -0.44 0.09 -0.65 0.912501011 0.457125667 aromatic compound biosynthetic process;biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;establishment of synaptic specificity at neuromuscular junction;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;molybdopterin cofactor biosynthetic process;molybdopterin cofactor metabolic process;Mo-molybdopterin cofactor biosynthetic process;Mo-molybdopterin cofactor metabolic process;nitrogen compound metabolic process;prosthetic group metabolic process;pteridine-containing compound biosynthetic process;pteridine-containing compound metabolic process;small molecule metabolic process;synapse organization;vitamin metabolic process;water-soluble vitamin metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity cell junction;cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;non-membrane-bounded organelle;organelle;plasma membrane;postsynaptic membrane;synapse part;synaptic membrane 1.60E-15 6 5 5 15.3

P07305;P07305-2 Histone H1.0 H1F0 >sp|P07305|H10_HUMAN Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3;>sp|P07305-2|H10_HUMAN Isoform 2 of Histone H1.0 OS=Homo sapiens GN=H1F0 -0.75

1.76 0.54 0.59 0.58 0.03 -1.98 -0.67 0.586640226 1.0471794 "catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization" binding;DNA binding;nucleic acid binding cell part;chromatin;chromosomal part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear part;nucleoplasm;nucleosome;organelle;organelle part;protein-DNA complex 3.81E-39 2 5 5 27.3

P98160;Q5SZJ1 Basement membrane-specific heparan sulfate proteoglycan core protein;Endorepellin;LG3 peptide HSPG2 >sp|P98160|PGBM_HUMAN Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4 -0.33 -0.08 -0.75 -0.14 0.21 0.20 0.35 1.41 1.111453866 -0.867752567 "amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;biological regulation;biosynthetic process;brain development;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;cardiac muscle tissue development;cartilage development;cartilage development involved in endochondral bone morphogenesis;catabolic process;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;chondrocyte differentiation;chondroitin sulfate metabolic process;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;diterpenoid metabolic process;embryonic morphogenesis;embryonic organ morphogenesis;embryonic skeletal system morphogenesis;endochondral ossification;extracellular matrix organization;extracellular structure organization;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;isoprenoid metabolic process;lipid metabolic process;lipoprotein metabolic process;localization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;metabolic process;multicellular organismal process;muscle tissue development;nitrogen compound metabolic process;organ development;organ morphogenesis;ossification;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;protein localization;regulation of biological process;regulation of cellular process;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;skeletal system morphogenesis;striated muscle tissue development;sulfur compound metabolic process;terpenoid metabolic process;tissue development" binding;cation binding;ion binding;metal ion binding basal lamina;cell part;cytoplasmic part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;Golgi apparatus part;Golgi lumen;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;vacuolar lumen;vacuolar part;vesicle ECM-receptor interaction 1.91E-11 2 5 5 2.1

Q7Z5L9-2;Q7Z5L9Interferon regulatory factor 2-binding protein 2 IRF2BP2 >sp|Q7Z5L9-2|I2BP2_HUMAN Isoform 2 of Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2;>sp|Q7Z5L9|I2BP2_HUMAN Interferon regulatory factor 2-binding protein 2 OS=Homo sapiens GN=IRF2BP2 PE=1 SV=2 0.19 -0.34 0.32 0.16 -0.37 -1.02 -0.87 -1.95 1.29326703 1.136376843 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cation binding;ion binding;metal ion binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.53E-19 2 5 5 13.8

Q6P597-2;Q6P597;Q6P597-3;K7EL76;K7ENJ3;K7ELP9;C9JZE5;C9J8T5;Q9NSK0-4;B4DME9;Q9NSK0;Q9NSK0-3 Kinesin light chain 3 KLC3 >sp|Q6P597-2|KLC3_HUMAN Isoform 2 of Kinesin light chain 3 OS=Homo sapiens GN=KLC3;>sp|Q6P597|KLC3_HUMAN Kinesin light chain 3 OS=Homo sapiens GN=KLC3 PE=1 SV=2;>sp|Q6P597-3|KLC3_HUMAN Isoform 3 of Kinesin light chain 3 OS=Homo sapiens GN=KLC3;>tr|K7EL76|K -0.14 0.36 0.05 0.34 -0.80 0.16 -0.15 -0.13 0.690764688 0.381425004 "cardiolipin synthase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;phosphatidyltransferase activity;phosphotransferase activity, for other substituted phosphate groups;pyrophosphatase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cell projection;cell projection part;ciliary rootlet;cilium part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;kinesin complex;macromolecular complex;microtubule;microtubule associated complex;neuron projection;organelle part;protein complex 1.60E-21 12 5 5 12.1

P11047 Laminin subunit gamma-1 LAMC1 >sp|P11047|LAMC1_HUMAN Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=30.08 0.46 -0.57 -0.14 1.09 0.76 -0.71 0.02 0.285768536 -0.332687335 anatomical structure development;anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;chemotaxis;developmental process;endoderm development;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of epithelial cell proliferation;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of epithelial cell proliferation;response to chemical stimulus;response to external stimulus;response to stimulus;substrate adhesion-dependent cell spreading;taxis;tissue development binding;extracellular matrix structural constituent;glycolipid binding;glycosphingolipid binding;lipid binding;sphingolipid binding;structural molecule activity extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;laminin complex;laminin-1 complex;laminin-10 complex;laminin-11 complex;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;organelle;protein complex;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Prion diseases;Small cell lung cancer;Toxoplasmosis 2.83E-71 1 5 5 5

Q15031;E9PHM2;C9JYR8 "Probable leucine--tRNA ligase, mitochondrial" LARS2 ">sp|Q15031|SYLM_HUMAN Probable leucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=LARS2 PE=1 SV=2;>tr|E9PHM2|E9PHM2_HUMAN Probable leucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=LARS2 PE=2 SV=1" 0.34 0.25 0.61 -0.55 -0.33 -0.33 0.32 0.40 0.17166313 0.149378411 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;leucyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;leucine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis" 1.84E-24 3 5 5 9.2

Q9Y2U8 Inner nuclear membrane protein Man1 LEMD3 >sp|Q9Y2U8|MAN1_HUMAN Inner nuclear membrane protein Man1 OS=Homo sapiens GN=LEMD3 PE=1 SV=2 -0.12 0.06 0.27 0.29 -0.33 -0.30 -0.68 -0.09 1.246127501 0.470089017 biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;muscle cell differentiation;negative regulation of activin receptor signaling pathway;negative regulation of biological process;negative regulation of BMP signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of activin receptor signaling pathway;regulation of biological process;regulation of BMP signaling pathway;regulation of cell communication;regulation of cell cycle;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;skeletal muscle cell differentiation;striated muscle cell differentiation binding;DNA binding;nucleic acid binding;nucleotide binding cell part;integral to membrane;integral to nuclear inner membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to nuclear inner membrane;intrinsic to organelle membrane;membrane part;nuclear membrane part;nuclear part;organelle part 5.09E-15 1 5 5 9.5

Q7Z434-4;Q7Z434 Mitochondrial antiviral-signaling protein MAVS >sp|Q7Z434-4|MAVS_HUMAN Isoform 4 of Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS;>sp|Q7Z434|MAVS_HUMAN Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2 -0.57 0.14 -0.05 0.15 0.61 0.78 -0.78 0.52 0.37260932 -0.364602292 "activation of immune response;activation of innate immune response;biological regulation;cellular process;cellular response to chemical stimulus;cellular response to dsRNA;cellular response to exogenous dsRNA;cellular response to organic substance;cellular response to stimulus;defense response;defense response to bacterium;defense response to virus;immune effector process;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of reproductive process;negative regulation of type I interferon production;negative regulation of viral genome replication;negative regulation of viral reproduction;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemokine (C-C motif) ligand 5 production;positive regulation of chemokine production;positive regulation of cytokine production;positive regulation of cytokine-mediated signaling pathway;positive regulation of defense response;positive regulation of defense response to virus by host;positive regulation of gene expression;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of interferon-alpha production;positive regulation of interferon-beta production;positive regulation of interleukin-8 production;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of IP-10 production;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein import into nucleus;positive regulation of protein import into nucleus, translocation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein transport;positive regulation of response to cytokine stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription factor import into nucleus;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of tumor necrosis factor production;positive regulation of type I interferon production;positive regulation of type I interferon-mediated signaling pathway;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemokine (C-C motif) ligand 5 production;regulation of chemokine production;regulation of cytokine production;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by host;regulation of establishment of protein localization;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-alpha production;regulation of interferon-beta production;regulation of interleukin-8 production;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of IP-10 production;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein transport;regulation of reproductive process;regulation of response to biotic stimulus;regulation of response to cytokine stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of tumor necrosis factor production;regulation of type I interferon production;regulation of type I interferon-mediated signaling pathway;regulation of viral genome replication;regulation of viral reproduction;reproductive process;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;viral reproductive process;virus-host interaction" molecular transducer activity;signal transducer activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;peroxisomal membrane;peroxisomal part Cytosolic DNA-sensing pathway;Hepatitis C;Measles;RIG-I-like receptor signaling pathway 2.78E-32 2 5 5 21.6

Q9NU22;Q5T795 Midasin MDN1 >sp|Q9NU22|MDN1_HUMAN Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2 0.25 -0.12 -0.42 -0.21 0.39 -0.27 -0.24 -0.12 0.109159979 -0.064252799 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;unfolded protein binding" cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part Ribosome biogenesis in eukaryotes 2.61E-13 2 5 5 1

C9JG87;Q9NYK5;Q9NYK5-2 "39S ribosomal protein L39, mitochondrial" MRPL39 ">tr|C9JG87|C9JG87_HUMAN 39S ribosomal protein L39, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL39 PE=2 SV=1;>sp|Q9NYK5|RM39_HUMAN 39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3;>sp|Q9NYK5-2|RM39_HUMAN Isoform 2 of 39S ribo" -0.34 0.29 -0.01 0.25 -0.01 -0.42 -1.08 -0.37 0.831321606 0.5174172 binding;nucleotide binding cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial ribosome;non-membrane-bounded organelle;organellar ribosome;organelle;organelle part;ribonucleoprotein complex;ribosome 2.21E-15 3 5 5 19.5

Q9Y676;B4DFG6 "28S ribosomal protein S18b, mitochondrial" MRPS18B ">sp|Q9Y676|RT18B_HUMAN 28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=1 SV=1" -0.27 0.21 0.38 0.32 -0.29 -0.37 -1.13 0.06 0.877997325 0.593675883 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial small ribosomal subunit;non-membrane-bounded organelle;organellar small ribosomal subunit;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit 2.57E-52 2 5 5 32.2

Q09161 Nuclear cap-binding protein subunit 1 NCBP1 >sp|Q09161|NCBP1_HUMAN Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 0.09 0.38 0.00 0.08 0.26 -0.23 -0.44 -0.24 0.753058958 0.300313734 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;gene silencing;gene silencing by RNA;histone mRNA metabolic process;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA capping;mRNA catabolic process;mRNA cleavage;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;ncRNA metabolic process;negative regulation of biological process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;nitrogen compound metabolic process;nuclear export;nuclear mRNA cis splicing, via spliceosome;nuclear mRNA splicing, via spliceosome;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA 3'-end processing;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of viral reproduction;positive regulation of viral transcription;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA 3'-end processing;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of translation;regulation of translational initiation;regulation of viral reproduction;regulation of viral transcription;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA capping;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;spliceosomal snRNP assembly;termination of RNA polymerase II transcription;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;transcription termination, DNA-dependent;transport;viral reproductive process" binding;DNA binding;nucleic acid binding;RNA binding;RNA cap binding cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;mRNA cap binding complex;nuclear cap binding complex;nuclear part;nucleoplasm;organelle part;protein complex;ribonucleoprotein complex;RNA cap binding complex mRNA surveillance pathway;RNA transport;Spliceosome 6.38E-21 1 5 5 7.6

Q6PIU2;Q6PIU2-2;J3KN69;F5H7K4;Q6PIU2-3;H7C046 Neutral cholesterol ester hydrolase 1 NCEH1 >sp|Q6PIU2|NCEH1_HUMAN Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3;>sp|Q6PIU2-2|NCEH1_HUMAN Isoform 2 of Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1;>tr|J3KN69|J3KN69_HUMAN Arylacetamide deacetylase-like 1 OS 0.76 -0.22 -0.30 -0.74 1.25 0.71 0.40 -0.03 0.72576911 -0.706717842 catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;dephosphorylation;lipid catabolic process;lipid metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;xenobiotic metabolic process "anion binding;binding;carboxylesterase activity;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;phosphate ion binding;serine hydrolase activity" cell part;cytoplasmic part;endoplasmic reticulum;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;organelle Bile secretion 2.31E-23 6 5 5 14.2

O95299;E7ESZ7;Q8WXC9;H7C2W5;H7C1Y7;H7C2X4;Q8N1B9;C9J6X0 "NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial" NDUFA10 ">sp|O95299|NDUAA_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1;>tr|E7ESZ7|E7ESZ7_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN" -0.42 0.89 -0.33 0.75 -0.19 0.37 -1.43 -0.12 0.451335016 0.56561007 "cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, NADH to ubiquinone;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;oxidation-reduction process;primary metabolic process;respiratory electron transport chain;response to chemical stimulus;response to drug;response to stimulus;small molecule metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle lumen;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 9.53E-13 8 5 5 18

Q8TD19;G3V459 Serine/threonine-protein kinase Nek9 NEK9 >sp|Q8TD19|NEK9_HUMAN Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=1 SV=2;>tr|G3V459|G3V459_HUMAN Serine/threonine-protein kinase Nek9 OS=Homo sapiens GN=NEK9 PE=2 SV=1 -0.21 -0.16 -0.04 -0.04 -0.11 0.14 0.07 -0.43 0.071281819 -0.027996756 cell cycle phase;cell cycle process;cell division;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;M phase;M phase of mitotic cell cycle;membrane disassembly;membrane organization;mitotic nuclear envelope disassembly;mitotic prophase;nuclear envelope disassembly;nuclear envelope organization;prophase "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle 4.58E-25 2 5 5 8

O15118;B4DET3;K7EQ23 Niemann-Pick C1 protein NPC1 >sp|O15118|NPC1_HUMAN Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=1 SV=2 -0.11 0.08 -0.54 0.23 0.48 -0.15 -0.75 -0.29 0.10796238 0.092975408 adult behavior;adult locomotory behavior;adult walking behavior;alcohol metabolic process;autophagy;behavior;bile acid metabolic process;biological regulation;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to lipoprotein particle stimulus;cellular response to low-density lipoprotein particle stimulus;cellular response to organic substance;cellular response to steroid hormone stimulus;cellular response to stimulus;chemical homeostasis;cholesterol efflux;cholesterol homeostasis;cholesterol metabolic process;cholesterol transport;endocytosis;establishment of localization;establishment of localization in cell;glycosylation;homeostatic process;intracellular transport;lipid homeostasis;lipid metabolic process;lipid transport;locomotory behavior;lysosomal transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;negative regulation of autophagy;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cell communication;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macroautophagy;negative regulation of metabolic process;negative regulation of response to external stimulus;negative regulation of response to extracellular stimulus;negative regulation of response to nutrient levels;negative regulation of response to stimulus;organic acid metabolic process;organic substance transport;oxoacid metabolic process;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;regulation of autophagy;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of macroautophagy;regulation of metabolic process;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress;response to chemical stimulus;response to drug;response to endogenous stimulus;response to hormone stimulus;response to lipoprotein stimulus;response to low-density lipoprotein particle stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus;small molecule metabolic process;steroid metabolic process;sterol homeostasis;sterol metabolic process;sterol transport;transport;vacuolar transport;vesicle-mediated transport binding;cholesterol binding;hedgehog receptor activity;lipid binding;lipid transporter activity;molecular transducer activity;receptor activity;signal transducer activity;signaling receptor activity;steroid binding;sterol binding;sterol transporter activity;substrate-specific transporter activity;transmembrane signaling receptor activity;transporter activity cell part;cytoplasmic part;endoplasmic reticulum;endosomal part;endosome membrane;envelope;extracellular region;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome membrane;lysosomal membrane;lysosome;lytic vacuole;membrane;membrane part;membrane raft;membrane-bounded organelle;nuclear envelope;nuclear part;organelle;organelle envelope;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;vacuolar membrane;vacuolar part;vacuole;vesicle Lysosome 1.87E-13 3 5 5 4.4

Q8IVD9 NudC domain-containing protein 3 NUDCD3 >sp|Q8IVD9|NUDC3_HUMAN NudC domain-containing protein 3 OS=Homo sapiens GN=NUDCD3 PE=1 SV=3 -0.04 0.00 0.12 0.03 -0.08 -0.34 0.10 0.30 0.080872322 0.032775222 4.58E-23 1 5 5 25.2

J3KMX1;Q99567 Nuclear pore complex protein Nup88 NUP88 >tr|J3KMX1|J3KMX1_HUMAN Nuclear pore complex protein Nup88 (Fragment) OS=Homo sapiens GN=NUP88 PE=4 SV=1;>sp|Q99567|NUP88_HUMAN Nuclear pore complex protein Nup88 OS=Homo sapiens GN=NUP88 PE=1 SV=2 -0.13 0.25 0.16 0.18 -0.01 0.06 -0.10 -0.22 0.771184159 0.18481862 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;metabolic process;monosaccharide transport;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;organic substance transport;primary metabolic process;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process transporter activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;organelle part;pore complex;protein complex RNA transport 2.55E-13 2 5 5 10.8

Q15102;M0R389;M0R1K3;M0QXS6;M0R323;M0QZT2 Platelet-activating factor acetylhydrolase IB subunit gamma PAFAH1B3 >sp|Q15102|PA1B3_HUMAN Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1;>tr|M0R389|M0R389_HUMAN Platelet-activating factor acetylhydrolase IB subunit gamma (Fragment) OS=Homo sapiens GN=PAFAH1B3 PE=4 SV=1 -0.04 -0.11 -0.23 -0.01 -0.92 -0.53 0.37 -0.06 0.248542571 0.183726588 anatomical structure development;brain development;catabolic process;developmental process;gamete generation;lipid catabolic process;lipid metabolic process;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;nervous system development;organ development;primary metabolic process;reproductive process;spermatogenesis;system development "1-alkyl-2-acetylglycerophosphocholine esterase activity;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds" cell part;cytoplasmic part;cytosol;intracellular part Ether lipid metabolism 5.24E-50 6 5 5 27.3

C9J050;P49585;C9JEJ2;H7BZN1;H7C1T3;C9J2E1;C9JVS0;C9JPY0;F8WAZ5;Q9Y5K3-2;Q9Y5K3-4;Q9Y5K3-3;Q9Y5K3;F8WBU2 Choline-phosphate cytidylyltransferase A PCYT1A >tr|C9J050|C9J050_HUMAN Choline-phosphate cytidylyltransferase A (Fragment) OS=Homo sapiens GN=PCYT1A PE=2 SV=1;>sp|P49585|PCY1A_HUMAN Choline-phosphate cytidylyltransferase A OS=Homo sapiens GN=PCYT1A PE=1 SV=2;>tr|C9JEJ2|C9JEJ2_HUMAN Choline-phosphate cy 0.34 0.35 0.06 -0.02 -0.13 0.41 -0.14 0.15 0.253750822 0.106985826 biosynthetic process;gamete generation;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;ovarian follicle development;ovulation cycle process;reproductive process;response to abiotic stimulus;response to stimulus;rhythmic process;spermatogenesis "binding;catalytic activity;choline-phosphate cytidylyltransferase activity;cytidylyltransferase activity;lipid binding;nucleotidyltransferase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;glycogen granule;intracellular organelle part;intracellular part;membrane;membrane part;organelle membrane;organelle part Glycerophospholipid metabolism;Phosphonate and phosphinate metabolism 3.56E-17 14 5 5 28.7

Q53EL6-2;Q53EL6;Q5VZS7 Programmed cell death protein 4 PDCD4 >sp|Q53EL6-2|PDCD4_HUMAN Isoform 2 of Programmed cell death protein 4 OS=Homo sapiens GN=PDCD4;>sp|Q53EL6|PDCD4_HUMAN Programmed cell death protein 4 OS=Homo sapiens GN=PDCD4 PE=1 SV=2 -0.45 -0.36 0.16 0.19 -1.23 -1.28 0.06 -0.92 0.880901339 0.729040411 "aging;apoptosis;biological regulation;cell aging;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;developmental process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of JUN kinase activity;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of gene expression;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transcription, DNA-dependent;regulation of transferase activity;RNA metabolic process"binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.48E-21 3 5 5 17.9

F6T1Q0;Q6L8Q7-2;Q6L8Q7 "2,5-phosphodiesterase 12" PDE12 ">tr|F6T1Q0|F6T1Q0_HUMAN 2,5-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=2 SV=1;>sp|Q6L8Q7-2|PDE12_HUMAN Isoform 2 of 2,5-phosphodiesterase 12 OS=Homo sapiens GN=PDE12;>sp|Q6L8Q7|PDE12_HUMAN 2,5-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1" 0.31 0.07 -0.09 -0.13 -0.04 -0.13 0.16 -0.02 0.14230217 0.046159694 catalytic activity;hydrolase activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 6.49E-35 3 5 5 17.4

A6NDG6;H3BV17 Phosphoglycolate phosphatase PGP >sp|A6NDG6|PGP_HUMAN Phosphoglycolate phosphatase OS=Homo sapiens GN=PGP PE=1 SV=1 -0.10 -0.33 0.34 0.07 0.31 0.07 0.49 -0.25 0.297045745 -0.162193039 carbohydrate metabolic process;cellular metabolic process;cellular process;dephosphorylation;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphoglycolate phosphatase activity;phosphoric ester hydrolase activity" Glyoxylate and dicarboxylate metabolism 2.33E-40 2 5 5 19.6

O15031;E2PU09;A6QRH1;H0Y6J7;A6QRG9 Plexin-B2 PLXNB2 >sp|O15031|PLXB2_HUMAN Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3 -0.08 -0.04 0.28 -0.08 0.14 0.15 0.16 -0.04 0.33898044 -0.084266122 anatomical structure development;anatomical structure formation involved in morphogenesis;biological regulation;brain development;cell proliferation;cellular process;cellular response to stimulus;developmental process;neural precursor cell proliferation;neural tube closure;neuroblast proliferation;organ development;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of neurogenesis;regulation of anatomical structure morphogenesis;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cell shape;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Rho GTPase activity;response to stimulus;signal transduction;tube closure;tube formation enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;molecular transducer activity;nucleoside-triphosphatase regulator activity;receptor activity;semaphorin receptor activity;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity cell part;integral to membrane;integral to plasma membrane;intracellular;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Axon guidance 5.57E-20 5 5 5 4.9

Q10713;B4DKL3 Mitochondrial-processing peptidase subunit alphaPMPCA >sp|Q10713|MPPA_HUMAN Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens GN=PMPCA PE=1 SV=2 -0.03 0.10 0.05 0.16 0.15 0.03 0.24 -0.14 0.008423139 -0.002425506 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;proteolysis;transport "binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part 3.34E-32 2 5 5 14.7

Q9H307-2;Q9H307Pinin PNN >sp|Q9H307-2|PININ_HUMAN Isoform 2 of Pinin OS=Homo sapiens GN=PNN;>sp|Q9H307|PININ_HUMAN Pinin OS=Homo sapiens GN=PNN PE=1 SV=4 -0.30 0.94 -0.05 0.92 -0.08 0.35 -1.28 0.25 0.475188208 0.568336371 "biological adhesion;biological regulation;biosynthetic process;cell adhesion;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;structural molecule activity anchoring junction;catalytic step 2 spliceosome;cell junction;cell part;cell-cell junction;cytoplasm;cytoskeletal part;desmosome;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;membrane;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;plasma membrane;protein complex;ribonucleoprotein complex;spliceosomal complex mRNA surveillance pathway;RNA transport 7.51E-18 2 5 5 10.3

Q06203;D6RE15;D6RCC8 Amidophosphoribosyltransferase PPAT >sp|Q06203|PUR1_HUMAN Amidophosphoribosyltransferase OS=Homo sapiens GN=PPAT PE=1 SV=1 0.25 -0.04 0.36 0.04 -0.30 -0.97 -0.02 -0.65 1.177022331 0.637884447 amine catabolic process;amine metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;body fluid secretion;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell cycle process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to drug;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;'de novo' IMP biosynthetic process;developmental process;establishment of localization;G1/S transition of mitotic cell cycle;glutamine catabolic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;kidney development;lactation;macromolecular complex assembly;macromolecular complex subunit organization;maternal process involved in female pregnancy;metabolic process;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organ development;organ morphogenesis;organ regeneration;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;pigment biosynthetic process;pigment metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;purine base biosynthetic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regeneration;regulation of biological quality;regulation of body fluid levels;reproductive process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;small molecule catabolic process;small molecule metabolic process;transport "4 iron, 4 sulfur cluster binding;amidophosphoribosyltransferase activity;binding;catalytic activity;cation binding;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasmic part;cytosol;intracellular part "Alanine, aspartate and glutamate metabolism;Purine metabolism" 1.56E-32 3 5 5 12

Q9HAB8;Q9HAB8-2;Q5VVM3 Phosphopantothenate--cysteine ligase PPCS >sp|Q9HAB8|PPCS_HUMAN Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS PE=1 SV=2;>sp|Q9HAB8-2|PPCS_HUMAN Isoform 2 of Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS 0.23 0.02 0.18 0.01 -0.07 0.00 0.34 -0.21 0.287432389 0.094968805 amine metabolic process;biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme A biosynthetic process;coenzyme A metabolic process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxoacid metabolic process;pantothenate metabolic process;primary metabolic process;purine nucleoside metabolic process;purine ribonucleoside metabolic process;purine-containing compound metabolic process;ribonucleoside metabolic process;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;phosphopantothenate--cysteine ligase activity" cell part;cytoplasmic part;cytosol;intracellular part Pantothenate and CoA biosynthesis 1.29E-20 3 5 5 15.8

H0YDU8;P53041;A8MU39 Serine/threonine-protein phosphatase;Serine/threonine-protein phosphatase 5 PPP5C >tr|H0YDU8|H0YDU8_HUMAN Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP5C PE=3 SV=1;>sp|P53041|PPP5_HUMAN Serine/threonine-protein phosphatase 5 OS=Homo sapiens GN=PPP5C PE=1 SV=1;>tr|A8MU39|A8MU39_HUMAN Serine/threonine-protein phos 0.32 -0.01 -0.13 0.10 0.03 0.10 0.17 -0.12 0.07699074 0.025618306 "biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;dephosphorylation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitosis;nitrogen compound metabolic process;nuclear division;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle fission;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein complex assembly;protein complex subunit organization;protein dephosphorylation;protein heterooligomerization;protein metabolic process;protein modification process;protein oligomerization;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to alkaloid;response to chemical stimulus;response to isoquinoline alkaloid;response to morphine;response to organic cyclic compound;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;molecular transducer activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity;signal transducer activity" cell body;cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;neuron projection;neuronal cell body;nucleus;organelle MAPK signaling pathway 2.19E-105 3 5 5 15.3

E9PH29;P30048 "Thioredoxin-dependent peroxide reductase, mitochondrial" PRDX3 ">tr|E9PH29|E9PH29_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=2 SV=1;>sp|P30048|PRDX3_HUMAN Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3" -0.03 -0.11 -0.26 -0.08 0.32 -0.01 -0.25 -0.25 0.186581269 -0.071625409 "anatomical structure development;biological regulation;catabolic process;cell differentiation;cellular catabolic process;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;chemical homeostasis;developmental process;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;ion homeostasis;maternal placenta development;metabolic process;mitochondrion organization;myeloid cell differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of kinase activity;negative regulation of molecular function;negative regulation of programmed cell death;negative regulation of transferase activity;organelle organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of mitochondrial membrane potential;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;regulation of transferase activity;response to biotic stimulus;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress" "alkyl hydroperoxide reductase activity;antioxidant activity;caspase inhibitor activity;caspase regulator activity;catalytic activity;cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peptidase inhibitor activity;peptidase regulator activity;peroxidase activity;peroxiredoxin activity" cell part;cytoplasmic part;early endosome;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 1.26E-17 2 5 5 20.2

F8W9D1;F8VYY9;P54619-2;P54619;P54619-3;H0YHF8;H0YIC9;F8VZX1;Q9UGJ0-2;G8JLM0;E9PGP6;Q9UGJ0-3;Q9UGJ0 5-AMP-activated protein kinase subunit gamma-1 PRKAG1 >tr|F8W9D1|F8W9D1_HUMAN 5-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=2 SV=1;>tr|F8VYY9|F8VYY9_HUMAN 5-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=2 SV=1;>sp|P54619-2|AAKG1_HUMAN Isoform 2 of 5 -0.22 -0.09 -0.12 -0.07 -0.39 -0.11 0.35 -0.11 0.136931334 -0.059893467 alcohol metabolic process;amine transport;amino acid transmembrane transport;amino acid transport;ATP biosynthetic process;ATP metabolic process;betaine transport;biological regulation;biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;carnitine shuttle;carnitine transport;cation transport;cell cycle arrest;cell cycle process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular glucan metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular polysaccharide metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;fatty acid biosynthetic process;fatty acid metabolic process;fatty acid transport;gamete generation;generation of precursor metabolites and energy;glucan metabolic process;glycogen metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;insulin receptor signaling pathway;intracellular lipid transport;intracellular protein kinase cascade;intracellular signal transduction;intracellular transport;ion transport;lipid biosynthetic process;lipid metabolic process;lipid transport;long-chain fatty acid transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;male gamete generation;membrane organization;metabolic process;mitochondrial transport;monocarboxylic acid metabolic process;monocarboxylic acid transport;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;nitrogen compound metabolic process;nitrogen compound transport;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic acid transport;organic cation transport;organic substance transport;oxidation-reduction process;oxoacid metabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of kinase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of peptidyl-threonine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of transferase activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;quaternary ammonium group transport;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of fatty acid oxidation;regulation of gene expression;regulation of generation of precursor metabolites and energy;regulation of glucose import;regulation of glucose metabolic process;regulation of glucose transport;regulation of glycolysis;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptidyl-threonine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;regulation of transport;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;signal transduction;small molecule biosynthetic process;small molecule metabolic process;spermatogenesis;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;AMP binding;AMP-activated protein kinase activity;ATP binding;binding;cAMP-dependent protein kinase activity;cAMP-dependent protein kinase inhibitor activity;cAMP-dependent protein kinase regulator activity;catalytic activity;cyclic nucleotide-dependent protein kinase activity;enzyme activator activity;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;kinase activator activity;kinase activity;kinase binding;kinase inhibitor activity;kinase regulator activity;nucleotide binding;phosphorylase kinase regulator activity;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activator activity;protein kinase activity;protein kinase binding;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase activity;protein serine/threonine kinase inhibitor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" AMP-activated protein kinase complex;cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex Adipocytokine signaling pathway;Hypertrophic cardiomyopathy (HCM);Insulin signaling pathway 2.50E-16 13 5 5 24.7

Q969G5;E9PIE3 Protein kinase C delta-binding protein PRKCDBP >sp|Q969G5|PRDBP_HUMAN Protein kinase C delta-binding protein OS=Homo sapiens GN=PRKCDBP PE=1 SV=3;>tr|E9PIE3|E9PIE3_HUMAN Protein kinase C delta-binding protein OS=Homo sapiens GN=PRKCDBP PE=2 SV=1 -0.19 0.21 -0.17 0.24 1.24 0.80 -0.95 0.35 0.269935163 -0.339391839 5.06E-46 2 5 5 23

P09417;B7Z415;D6RGG7;B3KW71;D6RHJ7;H0Y8F7 Dihydropteridine reductase QDPR >sp|P09417|DHPR_HUMAN Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2;>tr|B7Z415|B7Z415_HUMAN Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=2 SV=1;>tr|D6RGG7|D6RGG7_HUMAN Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=2 SV=1;>tr -0.20 -0.10 0.12 0.00 0.25 0.19 0.56 0.18 1.225095436 -0.337134669 amine catabolic process;amine metabolic process;anatomical structure development;aromatic amino acid family catabolic process;aromatic amino acid family metabolic process;aromatic compound biosynthetic process;aromatic compound catabolic process;biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to drug;cellular response to stimulus;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;developmental process;dihydrobiopterin metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;liver development;L-phenylalanine catabolic process;L-phenylalanine metabolic process;metabolic process;nitrogen compound metabolic process;organ development;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;pteridine-containing compound biosynthetic process;pteridine-containing compound metabolic process;response to aluminum ion;response to chemical stimulus;response to drug;response to endogenous stimulus;response to glucagon stimulus;response to hormone stimulus;response to inorganic substance;response to lead ion;response to metal ion;response to organic substance;response to peptide hormone stimulus;response to stimulus;small molecule catabolic process;small molecule metabolic process;tetrahydrobiopterin biosynthetic process;tetrahydrobiopterin metabolic process "6,7-dihydropteridine reductase activity;binding;catalytic activity;coenzyme binding;cofactor binding;electron carrier activity;NAD binding;NADH binding;NADP binding;NADPH binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH group of donors;oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor" cell part;cell projection;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;organelle Folate biosynthesis 3.86E-50 6 5 5 23

Q2TAL8 Glutamine-rich protein 1QRICH1 >sp|Q2TAL8|QRIC1_HUMAN Glutamine-rich protein 1 OS=Homo sapiens GN=QRICH1 PE=1 SV=1 0.19 -0.05 -0.06 -0.18 0.20 -0.42 -0.23 -0.52 0.509618401 0.216770783 6.41E-13 1 5 5 10.2

Q9NW13;Q9NW13-2;C9JE21;H7C5G8;C9JAA9RNA-binding protein 28 RBM28 >sp|Q9NW13|RBM28_HUMAN RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3;>sp|Q9NW13-2|RBM28_HUMAN Isoform 2 of RNA-binding protein 28 OS=Homo sapiens GN=RBM28 -0.21 0.69 -0.07 0.98 -0.90 0.19 -0.96 -0.23 0.881931262 0.82157214 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Ribosome biogenesis in eukaryotes 3.61E-25 5 5 5 9.4

Q96D71-2;H0YDT0;J3KP76;Q96D71-3;Q96D71;E9PMG1;H0YCR2;H0YE89;H7C225;H7C1V2 RalBP1-associated Eps domain-containing protein 1 REPS1 >sp|Q96D71-2|REPS1_HUMAN Isoform 2 of RalBP1-associated Eps domain-containing protein 1 OS=Homo sapiens GN=REPS1;>tr|H0YDT0|H0YDT0_HUMAN RalBP1-associated Eps domain-containing protein 1 (Fragment) OS=Homo sapiens GN=REPS1 PE=2 SV=1;>tr|J3KP76|J3KP76_HUMAN 0.27 -0.01 0.03 -0.04 0.34 0.09 -0.05 -0.17 0.025504204 0.010177111 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;membrane invagination;membrane organization;receptor-mediated endocytosis;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;coated pit;membrane;membrane part;plasma membrane 2.08E-13 10 5 5 10.6

Q5VTR2;C9J0A5;C9JXC9;O60308 E3 ubiquitin-protein ligase BRE1A RNF20 >sp|Q5VTR2|BRE1A_HUMAN E3 ubiquitin-protein ligase BRE1A OS=Homo sapiens GN=RNF20 PE=1 SV=2 0.06 0.13 0.02 -0.04 -0.04 -0.38 -0.66 0.13 0.660536082 0.278939204 "biological regulation;catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;histone H2B ubiquitination;histone modification;histone monoubiquitination;histone ubiquitination;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of histone methylation;positive regulation of histone modification;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of gene expression;regulation of histone methylation;regulation of histone modification;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;ubiquitin-dependent protein catabolic process" "acid-amino acid ligase activity;binding;catalytic activity;cation binding;chromatin binding;histone binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;p53 binding;protein binding;protein binding transcription factor activity;small conjugating protein ligase activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;centriole;chromosomal part;cytoplasmic part;cytoskeletal part;HULC complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule organizing center part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex;ubiquitin conjugating enzyme complex;ubiquitin ligase complex 6.99E-11 4 5 5 6.6

P05387;H0YDD8 60S acidic ribosomal protein P2 RPLP2 >sp|P05387|RLA2_HUMAN 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1 0.02 0.05 -0.13 0.12 0.47 -0.41 -0.22 -0.38 0.273626395 0.149992082 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 5.73E-141 2 5 5 76.5

Q9UBV2;Q9UBV2-2 Protein sel-1 homolog 1 SEL1L >sp|Q9UBV2|SE1L1_HUMAN Protein sel-1 homolog 1 OS=Homo sapiens GN=SEL1L PE=1 SV=3 -0.15 -0.01 -0.01 -0.21 0.50 0.43 -0.17 0.09 0.805964392 -0.305660259 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;cellular response to stress;Notch signaling pathway;regulation of biological process;regulation of cellular process;response to endoplasmic reticulum stress;response to stimulus;response to stress;signal transduction cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Protein processing in endoplasmic reticulum 1.51E-92 2 5 5 12.1

O95470;H0Y3V8;H7BXL7 Sphingosine-1-phosphate lyase 1 SGPL1 >sp|O95470|SGPL1_HUMAN Sphingosine-1-phosphate lyase 1 OS=Homo sapiens GN=SGPL1 PE=1 SV=3 0.07 0.03 0.05 -0.12 -0.07 -0.11 -0.03 0.03 0.393353563 0.051443994 ameboidal cell migration;anatomical structure development;anatomical structure morphogenesis;androgen metabolic process;apoptosis;biological regulation;biosynthetic process;carboxylic acid metabolic process;catabolic process;cell death;cell differentiation;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component movement;cellular developmental process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;ceramide metabolic process;death;developmental process;developmental process involved in reproduction;enzyme linked receptor protein signaling pathway;estrogen metabolic process;face morphogenesis;fibroblast migration;gamete generation;hemopoiesis;hemopoietic or lymphoid organ development;hormone metabolic process;kidney development;Leydig cell differentiation;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;locomotion;luteinization;male gamete generation;membrane lipid biosynthetic process;membrane lipid catabolic process;membrane lipid metabolic process;metabolic process;multicellular organismal process;multicellular organismal reproductive process;organ development;organ morphogenesis;organic acid metabolic process;ovulation cycle process;oxoacid metabolic process;palate development;platelet-derived growth factor receptor signaling pathway;post-embryonic development;primary metabolic process;programmed cell death;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of growth;regulation of hormone levels;regulation of multicellular organism growth;regulation of multicellular organismal process;reproductive process;response to stimulus;rhythmic process;signal transduction;skeletal system morphogenesis;small molecule metabolic process;spermatogenesis;sphingoid metabolic process;sphingolipid biosynthetic process;sphingolipid catabolic process;sphingolipid metabolic process;steroid metabolic process;transmembrane receptor protein tyrosine kinase signaling pathway;vasculogenesis aldehyde-lyase activity;binding;carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;cofactor binding;lyase activity;pyridoxal phosphate binding;sphinganine-1-phosphate aldolase activity;vitamin B6 binding;vitamin binding cell part;cytoplasmic part;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane part;organelle part Sphingolipid metabolism 2.82E-45 3 5 5 13.6

Q15758;M0QXM4;Q15758-3;Q15758-2;M0QX44 Neutral amino acid transporter B(0) SLC1A5 >sp|Q15758|AAAT_HUMAN Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2;>tr|M0QXM4|M0QXM4_HUMAN Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=4 SV=1;>sp|Q15758-3|AAAT_HUMAN Isoform 3 of Neutral amino acid transporte 0.21 0.14 -0.24 -0.07 -0.73 -0.84 -0.31 -0.26 1.261376772 0.544821894 active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;anion transmembrane transporter activity;anion:cation symporter activity;carboxylic acid transmembrane transporter activity;cation transmembrane transporter activity;dicarboxylic acid transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;L-amino acid transmembrane transporter activity;L-glutamine transmembrane transporter activity;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;neutral amino acid transmembrane transporter activity;organic acid transmembrane transporter activity;organic acid:sodium symporter activity;receptor activity;secondary active transmembrane transporter activity;sodium ion transmembrane transporter activity;sodium:dicarboxylate symporter activity;solute:cation symporter activity;solute:sodium symporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;plasma membrane part;vesicle Protein digestion and absorption 5.47E-62 5 5 5 12.9

Q9NWH9;H7BXE3;H0YLW7;H0YMW8;H0YKH2;H0YNF3;H0YMR6;H0YLE6;H0YL55;H7C3F4;A8K5V8 SAFB-like transcription modulatorSLTM >sp|Q9NWH9|SLTM_HUMAN SAFB-like transcription modulator OS=Homo sapiens GN=SLTM PE=1 SV=2;>tr|H7BXE3|H7BXE3_HUMAN SAFB-like transcription modulator (Fragment) OS=Homo sapiens GN=SLTM PE=2 SV=1 -0.14 1.11 0.15 1.07 -0.19 0.53 -1.15 0.40 0.548982201 0.650272787 "apoptosis;biological regulation;biosynthetic process;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.35E-37 11 5 5 5.9

P51532-5;P51532-2;P51532-3;P51532-4;P51532;Q9HBD4;H0YGM3;P51531-2;P51531;K7EP28;F6XE55;F6XDY1;F6UH26;B1ALG1;B1ALG2;F6XG14;B1ALF6 Transcription activator BRG1SMARCA4 >sp|P51532-5|SMCA4_HUMAN Isoform 5 of Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4;>sp|P51532-2|SMCA4_HUMAN Isoform 2 of Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4;>sp|P51532-3|SMCA4_HUMAN Isoform 3 of Transcription activator BRG1 O 0.12 0.36 0.16 0.39 0.08 -0.33 -0.91 0.00 1.00045461 0.549637306 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;aortic smooth muscle cell differentiation;appendage morphogenesis;biological regulation;blastocyst growth;blastocyst hatching;cell differentiation;cell fate determination;cell morphogenesis;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromatin remodeling;chromatin silencing;chromosome organization;covalent chromatin modification;definitive erythrocyte differentiation;developmental growth;developmental process;DNA alkylation;DNA metabolic process;DNA methylation;DNA methylation on cytosine;DNA methylation on cytosine within a CG sequence;DNA modification;embryonic appendage morphogenesis;embryonic hindlimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;epidermal cell differentiation;epidermis morphogenesis;epithelial cell differentiation;erythrocyte differentiation;extracellular matrix organization;extracellular structure organization;forebrain development;gene silencing;glial cell fate determination;growth;hatching;heart trabecula formation;hindbrain development;hindlimb morphogenesis;histone acetylation;histone H3 acetylation;histone modification;interaction with symbiont;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;interspecies interaction between organisms;keratinocyte differentiation;limb morphogenesis;liver development;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;methylation-dependent chromatin silencing;modification by host of symbiont morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by host of symbiont transcription;modulation by host of viral transcription;modulation of transcription in other organism involved in symbiotic interaction;multi-organism process;muscle cell differentiation;myeloid cell differentiation;negative regulation of androgen receptor signaling pathway;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of gene expression, epigenetic;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitotic cell cycle;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of S phase of mitotic cell cycle;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nervous system development;neural retina development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;one-carbon metabolic process;organ development;organ morphogenesis;organelle organization;organism emergence from protective structure;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;positive regulation by host of viral transcription;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA binding;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of androgen receptor signaling pathway;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell differentiation;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA binding;regulation of gene expression;regulation of gene expression, epigenetic;regulation of growth;regulation of interphase of mitotic cell cycle;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of S phase;regulation of S phase of mitotic cell cycle;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;small molecule metabolic process;smooth muscle cell differentiation;stem cell maintenance;system development;tissue morphogenesis;trabecula formation;vascular smooth muscle cell differentiation;vasculogenesis"   "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;chromatin binding;DNA binding;DNA-dependent ATPase activity;helicase activity;histone acetyl-lysine binding;histone binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;RNA polymerase II transcription coactivator activity;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;RNA polymerase II transcription factor binding transcription factor activity involved in positive regulation of transcription;sequence-specific DNA binding;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding"   cell part;chromatin;chromatin remodeling complex;chromosomal part;cytoskeleton;euchromatin;heterochromatin;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;nBAF complex;non-membrane-bounded organelle;npBAF complex;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleoplasm;organelle;organelle part;perichromatin fibrils;protein complex;SWI/SNF complex;SWI/SNF-type complex;WINAC complex   5.65E-28 17   5   5   3.8

F8WAN1;Q69YQ0-2;Q69YQ0;C9J8U1   Cytospin-A   SPECC1L   >tr|F8WAN1|F8WAN1_HUMAN Uncharacterized protein OS=Homo sapiens PE=2 SV=1;>sp|Q69YQ0-2|CYTSA_HUMAN Isoform 2 of Cytospin-A OS=Homo sapiens GN=SPECC1L;>sp|Q69YQ0|CYTSA_HUMAN Cytospin-A OS=Homo sapiens GN=SPECC1L PE=1 SV=2;>tr|C9J8U1|C9J8U1_HUMAN Cytospin-A   -0.09   0.28 0.20 -0.03   0.07 0.31 -0.26   0.19   0.025876107   0.011976282   cell cycle;cell division;cellular process   cell junction;cell part;cell-cell junction;cytoplasm;cytoskeletal part;gap junction;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;spindle   6.15E-25 4   5   5   7.7

C9J0K6;B4DKK2;P30626-2;P30626;B4DHQ6   Sorcin   SRI   >tr|C9J0K6|C9J0K6_HUMAN Sorcin OS=Homo sapiens GN=SRI PE=2 SV=1;>tr|B4DKK2|B4DKK2_HUMAN Sorcin OS=Homo sapiens GN=SRI PE=2 SV=1;>sp|P30626-2|SORCN_HUMAN Isoform 2 of Sorcin OS=Homo sapiens GN=SRI;>sp|P30626|SORCN_HUMAN Sorcin OS=Homo sapiens GN=SRI PE=1 SV   0.14 -0.14   -0.07   -0.29   0.26 -0.30   0.52   0.04   0.457397529   -0.21721418   anatomical structure development;biological regulation;calcium ion transport;cation transport;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;developmental process;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;heart development;homeostatic process;intracellular sequestering of iron ion;ion homeostasis;ion transport;maintenance of location;maintenance of location in cell;metal ion transport;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of heart contraction;negative regulation of heart rate;negative regulation of ion transmembrane transporter activity;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of ryanodine-sensitive calcium-release channel activity;negative regulation of transport;negative regulation of transporter activity;organ development;regulation of action potential;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cellular localization;regulation of cellular process;regulation of heart contraction;regulation of heart rate;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of membrane potential;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to stimulus;sequestering of metal ion;signal transduction;transport   binding;calcium channel regulator activity;calcium ion binding;cation binding;channel regulator activity;ion binding;ion channel binding;metal ion binding;protein binding;receptor binding   cell part;contractile fiber part;cytoplasmic part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part;sarcoplasmic reticulum;sarcoplasmic reticulum membrane;T-tubule;vesicle;Z disc   1.55E-34 5   5   5   24.5

O15400-2;O15400   Syntaxin-7   STX7   >sp|O15400-2|STX7_HUMAN Isoform 2 of Syntaxin-7 OS=Homo sapiens GN=STX7;>sp|O15400|STX7_HUMAN Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4   0.22   0.23 -0.13   0.09 0.37 0.41 -0.54   0.05   0.040151472   0.028264698   cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;Golgi vesicle transport;intracellular protein transport;intracellular transport;post-Golgi vesicle-mediated transport;protein transport;secretion;secretion by cell;synaptic vesicle exocytosis;synaptic vesicle transport;transport;vesicle-mediated transport   binding;protein binding;SNAP receptor activity;SNARE binding   cell part;cytoplasmic part;early endosome membrane;endosomal part;endosome membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;SNARE complex   Phagosome;SNARE interactions in vesicular transport   1.29E-85 2   5   5   35.1

P53597;H7C233   "Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial"   SUCLG1   ">sp|P53597|SUCA_HUMAN Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4"   -0.12   -0.09   -0.60   0.09 -0.39   -0.12   -0.09   -0.12   0.000594282   -0.000304678   acetyl-CoA catabolic process;acetyl-CoA metabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;metabolic process;organic acid metabolic process;oxoacid metabolic process;small molecule metabolic process;succinate metabolic process;succinyl-CoA metabolic process;tricarboxylic acid cycle   "acid-thiol ligase activity;ATP citrate synthase activity;binding;catalytic activity;CoA-ligase activity;cofactor binding;GDP binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ligase activity;ligase activity, forming carbon-sulfur bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;succinate-CoA ligase (ADP-forming) activity;succinate-CoA ligase (GDP-forming) activity;succinate-CoA ligase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer"   cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrial tricarboxylic acid cycle enzyme complex;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane;protein complex;succinate-CoA ligase complex;succinate-CoA ligase complex (GDP-forming);tricarboxylic acid cycle enzyme complex   Citrate cycle (TCA cycle);Propanoate metabolism   4.20E-37 2   5   5   19.7

Q969Z0;Q969Z0-2;C9J7P5;H7C4R5;C9IZN7   Protein TBRG4   TBRG4   >sp|Q969Z0|TBRG4_HUMAN Protein TBRG4 OS=Homo sapiens GN=TBRG4 PE=1 SV=1;>sp|Q969Z0-2|TBRG4_HUMAN Isoform 2 of Protein TBRG4 OS=Homo sapiens GN=TBRG4   0.19 -0.06   0.39 -0.05   -0.13   -0.62   -0.26   -0.69   1.278748246   0.538937203   biological regulation;cell cycle arrest;cell cycle phase;cell cycle process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular respiration;energy derivation by oxidation of organic compounds;G1 phase;G1 phase of mitotic cell cycle;generation of precursor metabolites and energy;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of cell cycle;regulation of cell proliferation;regulation of cellular process "catalytic activity;kinase activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 8.06E-17 5 5 5 14.3

Q9NXF1-2;Q9NXF1;B7Z9D5 Testis-expressed sequence 10 protein TEX10 >sp|Q9NXF1-2|TEX10_HUMAN Isoform 2 of Testis-expressed sequence 10 protein OS=Homo sapiens GN=TEX10;>sp|Q9NXF1|TEX10_HUMAN Testis-expressed sequence 10 protein OS=Homo sapiens GN=TEX10 PE=1 SV=2;>tr|B7Z9D5|B7Z9D5_HUMAN Testis-expressed sequence 10 protein -0.19 0.64 0.23 0.58 -0.46 0.01 -1.32 -0.27 1.01436869 0.824698389 cell part;cytoplasm;histone methyltransferase complex;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;methyltransferase complex;MLL1 complex;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;nucleoplasm part;organelle;organelle membrane;organelle part;protein complex 7.09E-40 3 5 5 8

Q9H3N1;G3V448 Thioredoxin-related transmembrane protein 1 TMX1 >sp|Q9H3N1|TMX1_HUMAN Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1 -0.12 -0.10 -0.10 0.02 0.42 0.03 -0.16 -0.19 0.265833703 -0.098725652 "biological regulation;biosynthetic process;cell activation;cell proliferation;cell redox homeostasis;cellular biosynthetic process;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;DNA metabolic process;DNA replication;electron transport chain;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;Golgi vesicle transport;homeostatic process;immune system process;intracellular transport;leukocyte activation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oxidation-reduction process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of growth;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;response to stress;signal transduction;transport;vesicle-mediated transport" "arsenate reductase (thioredoxin) activity;arsenate reductase activity;catalytic activity;disulfide oxidoreductase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part 1.80E-31 2 5 5 19.3

O96008-2;O96008;K7EKG4;K7EJ57 Mitochondrial import receptor subunit TOM40 homolog TOMM40 >sp|O96008-2|TOM40_HUMAN Isoform 2 of Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40;>sp|O96008|TOM40_HUMAN Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1;>tr|K7EKG4|K7EKG4_HUMAN Mitoc -0.04 0.96 -0.10 1.02 0.08 0.64 -1.18 0.44 0.365109697 0.463564049 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;ion transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transmembrane transport;transport channel activity;macromolecule transmembrane transporter activity;passive transmembrane transporter activity;porin activity;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;wide pore channel activity cell part;cytoplasmic part;integral to membrane;integral to mitochondrial membrane;integral to mitochondrial outer membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to mitochondrial outer membrane;intrinsic to organelle membrane;macromolecular complex;membrane;membrane part;mitochondrial membrane;mitochondrial membrane part;mitochondrial outer membrane;mitochondrial outer membrane translocase complex;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane;pore complex;protein complex Amyotrophic lateral sclerosis (ALS) 4.05E-15 4 5 5 15.5

Q13641 Trophoblast glycoprotein TPBG >sp|Q13641|TPBG_HUMAN Trophoblast glycoprotein OS=Homo sapiens GN=TPBG PE=1 SV=1-0.05 -0.07 0.23 0.07 1.59 0.75 -0.40 -0.01 0.400059762 -0.436714283 biological adhesion;cell adhesion;cellular process cell part;cytoplasmic part;endoplasmic reticulum;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;organelle;plasma membrane part 1.45E-52 1 5 5 15.2

Q9UJA5;B4DUV6;Q9UJA5-3;Q9UJA5-2 tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 TRMT6 ">sp|Q9UJA5|TRM6_HUMAN tRNA (adenine(58)-N(1))-methyltransferase non-catalytic subunit TRM6 OS=Homo sapiens GN=TRMT6 PE=1 SV=1;>tr|B4DUV6|B4DUV6_HUMAN cDNA FLJ51319, highly similar to tRNA (adenine-N(1)-)-methyltransferase non-catalytic subunit TRM6 OS=Homo" 0.29 -0.05 0.08 -0.09 0.10 -0.56 -0.52 -0.59 1.031929236 0.453829722 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;RNA metabolic process;RNA processing;tRNA metabolic process;tRNA processing "binding;catalytic activity;methyltransferase activity;nucleic acid binding;RNA binding;transferase activity;transferase activity, transferring one-carbon groups;translation factor activity, nucleic acid binding;translation initiation factor activity"cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 6.80E-54 4 5 5 16.3

Q99598;C4P0D6;C4P0D8;C4P0D4;Q5VVQ1;Q9NRI2 Translin-associated protein X TSNAX;DISC1 >sp|Q99598|TSNAX_HUMAN Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1;>tr|C4P0D6|C4P0D6_HUMAN Disrupted in schizophrenia 1 isoform 49 OS=Homo sapiens GN=DISC1 PE=2 SV=1;>tr|C4P0D8|C4P0D8_HUMAN Disrupted in schizophrenia 1 isoform 51 OS=Ho -0.26 -0.08 -0.11 -0.19 0.00 -0.06 0.15 0.01 1.246054382 -0.186763539 cell differentiation;cellular developmental process;cellular process;developmental process;gamete generation;male gamete generation;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;reproductive process;spermatogenesis binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;protein transporter activity;sequence-specific DNA binding;substrate-specific transporter activity;transporter activity cell part;cytoplasm;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm 2.90E-17 6 5 5 22.4

P15374;Q5TBK7 Ubiquitin carboxyl-terminal hydrolase isozyme L3 UCHL3 >sp|P15374|UCHL3_HUMAN Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1;>tr|Q5TBK7|Q5TBK7_HUMAN Ubiquitin carboxyl-terminal hydrolase isozyme L3 (Fragment) OS=Homo sapiens GN=UCHL3 PE=2 SV=1 0.00 -0.15 0.02 -0.05 -0.47 -0.18 0.58 0.25 0.141112875 -0.091664089 catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process "binding;catalytic activity;cysteine-type peptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;small conjugating protein binding;thiolester hydrolase activity;ubiquitin binding;ubiquitin thiolesterase activity" cell part;cytoplasmic part;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle 2.94E-67 2 5 5 31.3

B7WPF4;Q9UPU5 Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 24 USP24 >tr|B7WPF4|B7WPF4_HUMAN Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP24 PE=2 SV=2;>sp|Q9UPU5|UBP24_HUMAN Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3 0.15 -0.16 0.15 0.07 0.00 -0.21 0.30 -0.44 0.310399522 0.135949463 catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process "catalytic activity;cysteine-type peptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;peptidase activity;peptidase activity, acting on L-amino acid peptides;thiolester hydrolase activity;ubiquitin thiolesterase activity" 9.76E-16 2 5 5 2.9

P40818;B4DKA8;H0YLH2;H0YM47;H0YNL5;H0YKV1 Ubiquitin carboxyl-terminal hydrolase 8;Ubiquitin carboxyl-terminal hydrolase USP8 >sp|P40818|UBP8_HUMAN Ubiquitin carboxyl-terminal hydrolase 8 OS=Homo sapiens GN=USP8 PE=1 SV=1;>tr|B4DKA8|B4DKA8_HUMAN Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP8 PE=2 SV=1 0.05 0.06 0.01 -0.12 0.16 -0.04 0.28 -0.18 0.185433662 -0.054550151 biological regulation;catabolic process;cell cycle cytokinesis;cell cycle process;cell proliferation;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cytokinesis;cytokinesis after mitosis;endosome organization;intracellular signal transduction;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;organelle organization;primary metabolic process;protein deubiquitination;protein K48-linked deubiquitination;protein K63-linked deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;Ras protein signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;ubiquitin-dependent protein catabolic process "catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;peptidase activity;peptidase activity, acting on L-amino acid peptides;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" cell part;cytoplasmic part;cytosol;early endosome;endosomal part;endosome;endosome membrane;extrinsic to membrane;extrinsic to plasma membrane;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;midbody;nucleus;organelle;organelle membrane;organelle part;plasma membrane part Endocytosis 4.94E-27 6 5 5 6

Q9NP79;E7ETQ7;Q5TGM0 Vacuolar protein sorting-associated protein VTA1 homolog VTA1 >sp|Q9NP79|VTA1_HUMAN Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1 -0.12 -0.01 -0.03 0.02 0.05 0.19 0.27 0.03 1.085351228 -0.165875774 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;membrane organization;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic part;cytosol;endosomal part;endosome membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part Endocytosis 6.57E-116 3 5 5 19.5

Q9BZH6 WD repeat-containing protein 11 WDR11 >sp|Q9BZH6|WDR11_HUMAN WD repeat-containing protein 11 OS=Homo sapiens GN=WDR11 PE=1 SV=1 0.36 -0.19 -0.10 -0.30 -0.10 0.16 0.46 -0.35 0.158850558 -0.098311665 cell part;cell projection;cilium;cytoplasm;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;nucleus;organelle 6.92E-15 1 5 5 6.5

Q9UIA9;E7ESC6;E9PEN8;E5RIW1;H0YBE1 Exportin-7 XPO7 >sp|Q9UIA9|XPO7_HUMAN Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3;>tr|E7ESC6|E7ESC6_HUMAN Exportin-7 OS=Homo sapiens GN=XPO7 PE=2 SV=1;>tr|E9PEN8|E9PEN8_HUMAN Exportin-7 OS=Homo sapiens GN=XPO7 PE=2 SV=1 0.06 -0.11 0.04 0.12 -0.36 -0.28 0.11 -0.15 0.74566535 0.196728784 establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;intracellular protein transport;intracellular transport;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;protein transport;RNA transport;transport binding;nuclear export signal receptor activity;protein binding;protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;organelle part;pore complex;protein complex 4.65E-63 5 5 5 6.4

P49750-3;P49750;P49750-4;H0YIQ2;F8VU51 YLP motif-containing protein 1 YLPM1 >sp|P49750-3|YLPM1_HUMAN Isoform 3 of YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1;>sp|P49750|YLPM1_HUMAN YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3;>sp|P49750-4|YLPM1_HUMAN Isoform 4 of YLP motif-containing protein 1 OS=H-0.10 0.16 0.21 0.20 0.35 0.05 -0.71 -0.61 0.550388591 0.34957443 biological regulation;regulation of biological process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of chromosome organization;regulation of DNA metabolic process;regulation of homeostatic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of telomere maintenance nucleic acid binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part 6.59E-26 5 5 5 5.4

Q86VM9;E7ERS3;Q86VM9-2;H3BRH3;H3BRN6 Zinc finger CCCH domain-containing protein 18 ZC3H18 >sp|Q86VM9|ZCH18_HUMAN Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=1 SV=2;>tr|E7ERS3|E7ERS3_HUMAN Zinc finger CCCH domain-containing protein 18 OS=Homo sapiens GN=ZC3H18 PE=2 SV=1;>sp|Q86VM9-2|ZCH18_HUMAN Isoform 2 of Zinc fi -0.19 0.35 0.25 0.31 0.29 -0.30 -1.32 -0.48 0.764282299 0.634797495 binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.99E-42 5 5 5 8.6

O75844 CAAX prenyl protease 1 homolog ZMPSTE24 >sp|O75844|FACE1_HUMAN CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2 0.30 0.11 -0.50 -0.62 0.67 0.42 0.08 0.26 0.894960387 -0.536843725 CAAX-box protein processing;catabolic process;cellular catabolic process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;membrane organization;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nuclear envelope organization;prenylated protein catabolic process;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;proteolysis involved in cellular protein catabolic process "binding;catalytic activity;cation binding;endopeptidase activity;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part 3.13E-17 1 5 5 12.2

E9PG40;P05067-7;P05067-11;P05067-8;P05067-9;P05067;H7C0V9;P05067-10;E9PEV0;P05067-3;P05067-4;P05067-5;P05067-6;H7C104;P05067-2 Amyloid beta A4 protein;N-APP;Soluble APP-alpha;Soluble APP-beta;C99;Beta-amyloid protein 42;Beta-amyloid protein 40;C83;P3(42);P3(40);C80;Gamma-secretase C-terminal fragment 59;Gamma-secretase C-terminal fragment 57;Gamma-secretase C-terminal fragment 50;C31 APP >tr|E9PG40|E9PG40_HUMAN Gamma-secretase C-terminal fragment 59 OS=Homo sapiens GN=APP PE=2 SV=1;>sp|P05067-7|A4_HUMAN Isoform L-APP733 of Amyloid beta A4 protein OS=Homo sapiens GN=APP;>sp|P05067-11|A4_HUMAN Isoform 11 of Amyloid beta A4 protein OS=Homo sa -0.19 0.30 -0.99 -0.18 -0.15 0.26 0.36 0.94 0.755395196 -0.615146056 "adult behavior;adult locomotory behavior;alcohol metabolic process;anatomical structure development;apoptosis;associative learning;axon cargo transport;axon choice point recognition;axon midline choice point recognition;behavior;behavioral interaction between organisms;biological adhesion;biological regulation;calcium ion homeostasis;cation homeostasis;cell activation;cell adhesion;cell cycle phase;cell cycle process;cell death;cell growth;cell maturation;cell projection organization;cell recognition;cell surface receptor linked signaling pathway;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular copper ion homeostasis;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chemical homeostasis;cholesterol metabolic process;cognition;collateral sprouting;collateral sprouting in absence of injury;copper ion homeostasis;cytoskeleton-dependent intracellular transport;death;defense response;dendrite development;developmental cell growth;developmental growth;developmental growth involved in morphogenesis;developmental maturation;developmental process;divalent inorganic cation homeostasis;endocytosis;endoplasmic reticulum calcium ion homeostasis;establishment of localization;establishment of localization in cell;exocytosis;extracellular matrix organization;extracellular structure organization;feeding behavior;forebrain development;G2 phase;G2 phase of mitotic cell cycle;glutamate signaling pathway;growth;homeostatic process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;intracellular receptor mediated signaling pathway;intracellular transport;ion homeostasis;ionotropic glutamate receptor signaling pathway;learning;learning or memory;lipid metabolic process;locomotory behavior;macromolecule metabolic process;macromolecule modification;mating behavior;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;microtubule-based movement;microtubule-based process;microtubule-based transport;mRNA 3'-end processing;mRNA metabolic process;mRNA polyadenylation;mRNA processing;multicellular organismal process;multi-organism process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neuron differentiation;neurological system process;neuromuscular junction development;neuromuscular process;neuromuscular process controlling balance;neuron apoptosis;neuron death;neuron maturation;neuron projection development;neuron recognition;neuron remodeling;nitrogen compound metabolic process;Notch signaling pathway;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;platelet degranulation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell cycle;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitotic cell cycle;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein metabolic process;protein modification process;protein phosphorylation;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of epidermal growth factor receptor signaling pathway;regulation of epidermal growth factor-activated receptor activity;regulation of gene expression;regulation of growth;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of multicellular organism growth;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein binding;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein tyrosine kinase activity;regulation of receptor activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of synapse structure and activity;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;reproductive behavior;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to light stimulus;response to oxidative stress;response to radiation;response to stimulus;response to stress;RNA 3'-end processing;RNA metabolic process;RNA polyadenylation;RNA processing;secretion;secretion by cell;signal transduction;small molecule metabolic process;smooth endoplasmic reticulum calcium ion homeostasis;steroid metabolic process;sterol metabolic process;suckling behavior;synapse assembly;synapse organization;synaptic growth at neuromuscular junction;system process;transport;vesicle-mediated transport;visual behavior;visual learning" binding;carbohydrate binding;cation binding;DNA binding;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme activator activity;enzyme inhibitor activity;enzyme regulator activity;glycosaminoglycan binding;heparin binding;ion binding;metal ion binding;nucleic acid binding;pattern binding;peptidase activator activity;peptidase inhibitor activity;peptidase regulator activity;polysaccharide binding;serine-type endopeptidase inhibitor activity;transition metal ion binding apical part of cell;axon;cell part;cell projection;cell projection part;cell surface;ciliary rootlet;cilium part;coated pit;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;cytosol;dendritic shaft;dendritic spine;extracellular region;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;neuromuscular junction;neuron projection;neuron spine;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane part;platelet alpha granule lumen;secretory granule lumen;spindle midzone;synapse;vesicle lumen Alzheimer's disease 2.37E-20 15 6 5 9

G5E9L0;Q8N6H7;E9PQP3;B4DX29;B7Z9M7;H0YDN9;E9PIY6;E9PMU9;E9PM18;E9PMR9;E9PM63;E9PNY8;E9PJT7;E9PK28 ADP-ribosylation factor GTPase-activating protein 2 ARFGAP2 >tr|G5E9L0|G5E9L0_HUMAN ADP-ribosylation factor GTPase-activating protein 2 OS=Homo sapiens GN=ARFGAP2 PE=2 SV=1;>sp|Q8N6H7|ARFG2_HUMAN ADP-ribosylation factor GTPase-activating protein 2 OS=Homo sapiens GN=ARFGAP2 PE=1 SV=1;>tr|E9PQP3|E9PQP3_HUMAN ADP-rib 0.20 0.01 0.28 0.21 -0.56 -0.08 -0.05 -0.24 1.291769331 0.406974733 biological regulation;cellular process;establishment of localization;establishment of protein localization;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;protein transport;regulation of ARF GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;transport;vesicle-mediated transport ARF GTPase activator activity;binding;cation binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;small GTPase regulator activity;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle membrane;organelle part;plasma membrane Endocytosis 1.86E-70 14 6 5
22.3

E7ETZ4;Q9Y6E2;Q75MG1;B5MCE7;B5MCH7;E9PFD4;C9JF98;F8WDX8;E7EMS9 Basic leucine zipper and W2 domain-containing protein 2 BZW2 >tr|E7ETZ4|E7ETZ4_HUMAN Basic leucine zipper and W2 domain-containing protein 2 (Fragment) OS=Homo sapiens GN=BZW2 PE=2 SV=1;>sp|Q9Y6E2|BZW2_HUMAN Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens GN=BZW2 PE=1 SV=1;>tr|Q75MG1|Q75MG1_H -0.01 -0.04 -0.10 0.07 0.06 -0.39 0.25 -0.07 0.039140753 0.016250575 anatomical structure development;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule metabolic process;metabolic process;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;system development
1.82E-77 9 6 5 15.4

P63092-3;P63092-2;P63092;P63092-4;Q5JWF2-2;Q5JWF2;Q5JWE9;H0Y7F4 Guanine nucleotide-binding protein G(s) subunit alpha isoforms short;Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas GNAS >sp|P63092-3|GNAS2_HUMAN Isoform 3 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS;>sp|P63092-2|GNAS2_HUMAN Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapie -0.07 0.33 -0.05 0.29 -0.09 0.12 -0.55 -0.40 0.817161864 0.355394732 "activation of adenylate cyclase activity;activation of adenylate cyclase activity by dopamine receptor signaling pathway;activation of adenylate cyclase activity by G-protein signaling pathway;anatomical structure development;anatomical structure homeostasis;anatomical structure morphogenesis;appendage morphogenesis;behavior;biological regulation;blood coagulation;body morphogenesis;cAMP-mediated signaling;cartilage development;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to amine stimulus;cellular response to catecholamine stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to glucagon stimulus;cellular response to hormone stimulus;cellular response to lipid;cellular response to monoamine stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to prostaglandin E stimulus;cellular response to prostaglandin stimulus;cellular response to stimulus;coagulation;cyclic-nucleotide-mediated signaling;developmental process;DNA alkylation;DNA metabolic process;DNA methylation;DNA modification;dopamine receptor signaling pathway;embryonic appendage morphogenesis;embryonic cranial skeleton morphogenesis;embryonic hindlimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic organ morphogenesis;embryonic skeletal system morphogenesis;endochondral ossification;energy derivation by oxidation of organic compounds;energy reserve metabolic process;epidermis development;establishment of localization;establishment of localization in cell;fluid transport;generation of precursor metabolites and energy;genetic imprinting;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;growth;hemostasis;hindlimb morphogenesis;homeostatic process;intracellular signal transduction;intracellular transport;limb morphogenesis;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;multicellular organism growth;multicellular organismal process;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organ morphogenesis;ossification;oxidation-reduction process;positive regulation of adenylate cyclase activity;positive regulation of adenylate cyclase activity by G-protein signaling pathway;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of cyclase activity;positive regulation of developmental process;positive regulation of lyase activity;positive regulation of molecular function;positive regulation of myeloid cell differentiation;positive regulation of myeloid leukocyte differentiation;positive regulation of osteoblast differentiation;positive regulation of osteoclast differentiation;post-embryonic body morphogenesis;post-embryonic morphogenesis;primary metabolic process;regulation of adenylate cyclase activity;regulation of adenylate cyclase activity involved in G-protein signaling pathway;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of developmental process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of hormone secretion;regulation of immune system process;regulation of insulin secretion;regulation of localization;regulation of lyase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoclast differentiation;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of primary metabolic process;regulation of secretion;regulation of signaling;regulation of transport;response to amine stimulus;response to catecholamine stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to glucagon stimulus;response to hormone stimulus;response to lipid;response to monoamine stimulus;response to organic nitrogen;response to organic substance;response to peptide hormone stimulus;response to prostaglandin E stimulus;response to prostaglandin stimulus;response to stimulus;second-messenger-mediated signaling;sensory perception;sensory perception of chemical stimulus;sensory perception of smell;signal transduction;skeletal system morphogenesis;skin development;small molecule metabolic process;system process;tissue development;tissue homeostasis;transmembrane transport;transport;water transport""adenylate cyclase activity;binding;catalytic activity;cation binding;cyclase activity;glutamate receptor binding;G-protein beta/gamma-subunit complex binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;ionotropic glutamate receptor binding;lyase activity;metal ion binding;molecular transducer activity;mu-type opioid receptor binding;nucleoside-triphosphatase activity;nucleotide binding;opioid receptor binding;phosphorus-oxygen lyase activity;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;signal transducer activity" cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;dendrite;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;Golgi apparatus part;Golgi membrane;heterotrimeric G-protein complex;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;neuron projection;organelle membrane;organelle part;plasma membrane part;protein complex;trans-Golgi network membrane Amoebiasis;Bile secretion;Calcium signaling pathway;Chagas disease (American trypanosomiasis);Dilated cardiomyopathy;Endocrine and other factor-regulated calcium reabsorption;Gap junction;Gastric acid secretion;GnRH signaling pathway;Long-term depression;Melanogenesis;Pancreatic secretion;Salivary secretion;Taste transduction;Vascular smooth muscle contraction;Vasopressin-regulated water reabsorption;Vibrio cholerae infection 4.08E-25 8 6 5 17.9

C9JA97;E9PEE8;P18564 Integrin beta;Integrin beta-6 ITGB6 >tr|C9JA97|C9JA97_HUMAN Integrin beta OS=Homo sapiens GN=ITGB6 PE=2 SV=1;>tr|E9PEE8|E9PEE8_HUMAN Integrin beta OS=Homo sapiens GN=ITGB6 PE=2 SV=1;>sp|P18564|ITB6_HUMAN Integrin beta-6 OS=Homo sapiens GN=ITGB6 PE=1 SV=2 -0.94 -0.55 -0.21 0.04 -0.58 0.33 0.57 1.19 0.794377565 -0.78994849 biological adhesion;biological regulation;cell adhesion;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;defense response;developmental process;extracellular matrix organization;extracellular structure organization;inflammatory response;integrin-mediated signaling pathway;interaction with host;interspecies interaction between organisms;multicellular organismal development;multicellular organismal process;multi-organism process;regulation of biological process;regulation of cellular process;reproductive process;response to stimulus;response to stress;response to wounding;signal transduction;viral reproductive process;virus-host interaction receptor activity cell part;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Regulation of actin cytoskeleton 7.10E-22 3 6 5 9.3

O00139-2;O00139-1;O00139-5;O00139;O00139-4;D6R9M0;H0YB64;H0Y5Z9 Kinesin-like protein KIF2A KIF2A >sp|O00139-2|KIF2A_HUMAN Isoform 2 of Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A;>sp|O00139-1|KIF2A_HUMAN Isoform 1 of Kinesin-like protein KIF2A OS=Homo sapiens GN=KIF2A;>sp|O00139-5|KIF2A_HUMAN Isoform 5 of Kinesin-like protein KIF2A OS=Homo sap 0.23 0.03 0.09 0.10 0.41 0.06 -0.42 -0.08 0.264308617 0.121052234 anaphase;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;blood coagulation;cell cycle phase;cell cycle process;cell differentiation;cell division;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;coagulation;cytoskeleton organization;developmental process;hemostasis;immune system process;M phase;M phase of mitotic cell cycle;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;mitotic anaphase;mitotic prometaphase;mitotic spindle organization;multicellular organismal process;nervous system development;organelle organization;regulation of biological quality;regulation of body fluid levels;spindle organization;system development "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;spindle pole 9.65E-18 8 6 5 11.8

P27361;E9PJF0;P27361-2;E9PQW4;P27361-3;B3KR49;E9PBK7;H0YEX6;E9PRH7 Mitogen-activated protein kinase 3MAPK3 >sp|P27361|MK03_HUMAN Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 PE=1 SV=4;>tr|E9PJF0|E9PJF0_HUMAN Mitogen-activated protein kinase 3 OS=Homo sapiens GN=MAPK3 PE=2 SV=1;>sp|P27361-2|MK03_HUMAN Isoform 2 of Mitogen-activated protein kinase -0.48 0.28 -1.10 0.30 0.14 0.27 -0.14 -0.18 0.299148773 -0.269723587 "activation of immune response;activation of innate immune response;activation of MAPK activity;activation of MAPKK activity;activation of protein kinase activity;anatomical structure development;anatomical structure morphogenesis;apoptosis;axon guidance;biological regulation;biosynthetic process;BMP signaling pathway;cartilage development;caveolin-mediated endocytosis;cell activation;cell cycle;cell death;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to interleukin-1;cellular response to lipopolysaccharide;cellular response to mechanical stimulus;cellular response to molecule of bacterial origin;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chemotaxis;cytokine-mediated signaling pathway;death;defense response;developmental process;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;fibroblast growth factor receptor signaling pathway;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;insulin receptor signaling pathway;interaction with host;interleukin-1-mediated signaling pathway;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;lipopolysaccharide-mediated signaling pathway;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;membrane invagination;membrane organization;metabolic process;multicellular organismal process;multi-organism process;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of apolipoprotein binding;negative regulation of binding;negative regulation of molecular function;negative regulation of protein binding;nerve growth factor receptor signaling pathway;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ morphogenesis;pattern recognition receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of defense response;positive regulation of ERK1 and ERK2 cascade;positive regulation of gene expression;positive regulation of histone acetylation;positive regulation of histone modification;positive regulation of histone phosphorylation;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of peptidyl-lysine acetylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;primary metabolic process;programmed cell death;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;receptor-mediated endocytosis;regulation of apolipoprotein binding;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chromosome organization;regulation of cytoskeleton organization;regulation of defense response;regulation of early endosome to late endosome transport;regulation of ERK1 and ERK2 cascade;regulation of gene expression;regulation of Golgi inheritance;regulation of histone acetylation;regulation of histone modification;regulation of histone phosphorylation;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-lysine acetylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein binding;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to dsRNA;response to endogenous stimulus;response to epidermal growth factor stimulus;response to exogenous dsRNA;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to interleukin-1;response to lipopolysaccharide;response to mechanical stimulus;response to molecule of bacterial origin;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;sensory perception;sensory perception of pain;signal transduction;small GTPase mediated signal transduction;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;system process;taxis;tissue development;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transcription initiation from RNA polymerase I promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent;transmembrane receptor protein serine/threonine kinase signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;transport;TRIF-dependent toll-like receptor signaling pathway;vesicle-mediated transport;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;MAP kinase activity;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;caveola;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;early endosome;endosome;focal adhesion;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;membrane part;membrane raft;membrane-bounded organelle;microtubule cytoskeleton;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane part;pseudopodium Acute myeloid leukemia;Adherens junction;Aldosterone-regulated sodium reabsorption;Alzheimer's disease;Axon guidance;B cell receptor signaling pathway;Bladder cancer;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Chronic myeloid leukemia;Colorectal cancer;Dorso-ventral axis formation;Endometrial cancer;ErbB signaling pathway;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;Hepatitis C;Insulin signaling pathway;ko05152;Leishmaniasis;Long-term depression;Long-term potentiation;MAPK signaling pathway;MAPK signaling pathway - fly;Melanogenesis;Melanoma;mTOR signaling pathway;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;NOD-like receptor signaling pathway;Non-small cell lung cancer;Oocyte meiosis;Osteoclast differentiation;Pancreatic cancer;Pathways in cancer;Prion diseases;Progesterone-mediated oocyte maturation;Prostate cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;T cell receptor signaling pathway;TGF-beta signaling pathway;Thyroid cancer;Toll-like receptor signaling pathway;Toxoplasmosis;Type II diabetes mellitus;Vascular smooth muscle contraction;VEGF signaling pathway 9.97E-20 9 6 5 21.4

P51148;P51148-2;K7ERI8;K7ERQ8;F8VSF8;F8VWU4;F8VVK3;K7EIP6;F8WCY6;F8WD79;F8VPW9;F8VWZ7;F8VVZ0;F8VUA5;K7ENY4 Ras-related protein Rab-5C RAB5C >sp|P51148|RAB5C_HUMAN Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2;>sp|P51148-2|RAB5C_HUMAN Isoform 2 of Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C;>tr|K7ERI8|K7ERI8_HUMAN Uncharacterized protein OS=Homo sapiens PE=3 SV=1;>tr|K7E 0.04 0.11 -0.15 0.05 0.18 0.02 -0.16 0.00 0.014352906 0.003993715 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;endosome organization;establishment of localization;establishment of protein localization;histone acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of endocytosis;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of transport;regulation of vesicle-mediated transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport" "acetyltransferase activity;binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;histone acetyltransferase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lysine N-acetyltransferase activity;N-acetyltransferase activity;N-acyltransferase activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome membrane;endocytic vesicle;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;vesicle Amoebiasis;Endocytosis;ko05152;Phagosome;Vasopressin-regulated water reabsorption 2.55E-47 15 6 5 35.6

P11233;H7C3P7;C9JPE8;F8WEQ6;C9JYR1 Ras-related protein Ral-A RALA >sp|P11233|RALA_HUMAN Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1;>tr|H7C3P7|H7C3P7_HUMAN Ras-related protein Ral-A (Fragment) OS=Homo sapiens GN=RALA PE=4 SV=1 -0.10 0.07 -0.25 0.15 0.93 1.16 -0.25 0.56 0.8365761 -0.631819051 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;biological regulation;cell cycle;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;cytokinesis;cytoskeleton organization;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;interaction with host;interspecies interaction between organisms;intracellular signal transduction;localization;localization within membrane;locomotion;membrane organization;membrane raft localization;multi-organism process;nerve growth factor receptor signaling pathway;organelle organization;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of filopodium assembly;Ras protein signal transduction;regulation of biological process;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of filopodium assembly;regulation of localization;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;secretion;secretion by cell;signal transduction;small GTPase mediated signal transduction;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction "binding;catalytic activity;Edg-2 lysophosphatidic acid receptor binding;endothelial differentiation G-protein coupled receptor binding;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding" cell division site part;cell part;cell surface;cleavage furrow;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;intracellular organelle part;intracellular part;membrane;midbody;organelle membrane;organelle part;plasma membrane;vesicle membrane Pancreatic cancer;Pathways in cancer 4.72E-25 5 6 5 31.1

P62070;B7Z5Z2;E9PK85;P62070-3;P62070-2;E9PQ87 Ras-related protein R-Ras2 RRAS2 >sp|P62070|RRAS2_HUMAN Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=1 SV=1;>tr|B7Z5Z2|B7Z5Z2_HUMAN Ras-related protein R-Ras2 OS=Homo sapiens GN=RRAS2 PE=2 SV=1;>tr|E9PK85|E9PK85_HUMAN Ras-related protein R-Ras2 (Fragment) OS=Homo sapiens GN=RRAS -0.07 0.14 0.04 0.10 0.37 0.17 -0.50 -0.03 0.086141329 0.047953847 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;Ras protein signal transduction;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of locomotion;response to stimulus;signal transduction;small GTPase mediated signal transduction "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle;plasma membrane MAPK signaling pathway;Regulation of actin cytoskeleton;Tight junction 3.59E-82 6 6 5 26.5

O95486;O95486-2 Protein transport protein Sec24A SEC24A >sp|O95486|SC24A_HUMAN Protein transport protein Sec24A OS=Homo sapiens GN=SEC24A PE=1 SV=2 0.29 -0.09 0.07 -0.23 1.05 0.63 0.32 0.28 1.118353877 -0.557746813 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;small molecule metabolic process;transport;vesicle coating;vesicle organization binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;COPII vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;vesicle coat Protein processing in endoplasmic reticulum 1.67E-30 2 6 5 7.4

Q13242;H0YIB4 Serine/arginine-rich splicing factor 9 SRSF9 >sp|Q13242|SRSF9_HUMAN Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1;>tr|H0YIB4|H0YIB4_HUMAN Serine/arginine-rich-splicing factor 9 (Fragment) OS=Homo sapiens GN=SRSF9 PE=4 SV=1 0.12 0.23 0.24 0.55 0.21 -0.09 -0.90 -0.27 0.921885528 0.544948988 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA splice site selection;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part Spliceosome 2.40E-30 2 6 5 27.1

Q92783-2;Q92783;B4DZT2;C9J1E5;A6NMU3 Signal transducing adapter molecule 1 STAM >sp|Q92783-2|STAM1_HUMAN Isoform 2 of Signal transducing adapter molecule 1 OS=Homo sapiens GN=STAM;>sp|Q92783|STAM1_HUMAN Signal transducing adapter molecule 1 OS=Homo sapiens GN=STAM PE=1 SV=3;>tr|B4DZT2|B4DZT2_HUMAN Signal transducing adapter molecule 1 0.01 -0.03 -0.02 -0.12 0.09 -0.02 0.15 -0.09 0.506112044 -0.073868975 biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;endosome transport;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport "binding;binding, bridging;protein binding;protein binding, bridging;SH3/SH2 adaptor activity;signaling adaptor activity" cell part;cytoplasmic part;cytosol;early endosome membrane;endosomal part;endosome membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part Endocytosis;Jak-STAT signaling pathway 1.18E-31 5 6 5 18.6

P22681;C9JU85;C9JRB3;F5H4J9 E3 ubiquitin-protein ligase CBL CBL >sp|P22681|CBL_HUMAN E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=2 0.19 -0.25 0.24 -0.26 -0.28 -0.25 0.42 0.00 0.012136729 0.008011689 biological regulation;cell activation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway;immune response;immune system process;intracellular signal transduction;leukocyte activation;lymphocyte activation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of alpha-beta T cell activation;negative regulation of alpha-beta T cell proliferation;negative regulation of antigen receptor-mediated signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell activation;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of mononuclear cell proliferation;negative regulation of programmed cell death;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of T cell activation;negative regulation of T cell proliferation;negative regulation of T cell receptor signaling pathway;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of immune system process;positive regulation of lymphocyte anergy;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of receptor-mediated endocytosis;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of T cell anergy;positive regulation of T cell tolerance induction;positive regulation of tolerance induction;positive regulation of transport;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;regulation of alpha-beta T cell activation;regulation of alpha-beta T cell proliferation;regulation of antigen receptor-mediated signaling pathway;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of endocytosis;regulation of epidermal growth factor receptor signaling pathway;regulation of immune system process;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of localization;regulation of lymphocyte activation;regulation of lymphocyte anergy;regulation of lymphocyte proliferation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of phosphatidylinositol 3-kinase cascade;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein metabolic process;regulation of receptor-mediated endocytosis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell activation;regulation of T cell anergy;regulation of T cell proliferation;regulation of T cell receptor signaling pathway;regulation of T cell tolerance induction;regulation of tolerance induction;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;signal transduction;T cell activation;transmembrane receptor protein tyrosine kinase signaling pathway "acid-amino acid ligase activity;binding;calcium ion binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;molecular transducer activity;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity;signal transducer activity;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;cytoplasmic part;cytosol;flotillin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane;plasma membrane part;protein complex Bacterial invasion of epithelial cells;Chronic myeloid leukemia;Endocytosis;ErbB signaling pathway;Insulin signaling pathway;Jak-STAT signaling pathway;Pathways in cancer;T cell receptor signaling pathway;Ubiquitin mediated proteolysis 1.83E-31 4 7 5 12

P26583;D6R9A6 High mobility group protein B2 HMGB2 >sp|P26583|HMGB2_HUMAN High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 -0.02 0.14 0.08 0.19 0.26 -0.62 -0.54 -0.96 0.922604802 0.56606482 "anatomical structure development;base-excision repair, DNA ligation;biological regulation;catabolic process;cell chemotaxis;cell migration;cell motility;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to stimulus;chemotaxis;chromatin organization;chromosome organization;developmental process;developmental process involved in reproduction;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA conformation change;DNA fragmentation involved in apoptotic nuclear change;DNA ligation;DNA ligation involved in DNA repair;DNA metabolic process;DNA recombination;DNA topological change;gonad development;immune system process;inositol lipid-mediated signaling;intracellular signal transduction;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;male gonad development;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;nucleus organization;organ development;organelle organization;phosphatidylinositol-mediated signaling;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of DNA binding;positive regulation of endothelial cell proliferation;positive regulation of epithelial cell proliferation;positive regulation of erythrocyte differentiation;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of megakaryocyte differentiation;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of myeloid cell differentiation;positive regulation of nitrogen compound metabolic process;positive regulation of nuclease activity;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA binding;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of erythrocyte differentiation;regulation of gene expression;regulation of homeostatic process;regulation of hydrolase activity;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of megakaryocyte differentiation;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;reproductive structure development;response to biotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to hormone stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to steroid hormone stimulus;response to stimulus;signal transduction;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;spermatid nucleus differentiation;taxis;V(D)J recombination" binding;chemoattractant activity;damaged DNA binding;DNA bending activity;DNA binding;double-stranded DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;RAGE receptor binding;receptor binding;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;transcription regulatory region DNA binding cell part;chromosome;condensed chromosome;cytoplasmic part;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;perinuclear region of cytoplasm;protein complex 4.16E-32 2 7 5 23.9

Q70UQ0;Q70UQ0-2 Inhibitor of nuclear factor kappa-B kinase-interacting protein IKBIP >sp|Q70UQ0|IKIP_HUMAN Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP PE=1 SV=1;>sp|Q70UQ0-2|IKIP_HUMAN Isoform 2 of Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP -0.49 0.03 -0.34 0.12 0.99 0.55 -0.64 0.05 0.441836851 -0.407280634 biological regulation;induction of apoptosis;induction of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to abiotic stimulus;response to ionizing radiation;response to radiation;response to stimulus;response to X-ray cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 1.99E-62 2 7 5 24.3

P20839;E7EQS0;P20839-3;P20839-7;P20839-5;P20839-6;P20839-2;P20839-4;C9J381;C9K0R9 Inosine-5-monophosphate dehydrogenase 1;Inosine-5-monophosphate dehydrogenase IMPDH1 >sp|P20839|IMDH1_HUMAN Inosine-5-monophosphate dehydrogenase 1 OS=Homo sapiens GN=IMPDH1 PE=1 SV=2;>tr|E7EQS0|E7EQS0_HUMAN Inosine-5-monophosphate dehydrogenase OS=Homo sapiens GN=IMPDH1 PE=2 SV=1;>sp|P20839-3|IMDH1_HUMAN Isoform 3 of Inosine-5-monophos 0.18 -0.06 -0.15 -0.07 -0.08 -0.45 0.41 -0.18 0.092694143 0.051023346 biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;GMP biosynthetic process;GMP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;DNA binding;IMP dehydrogenase activity;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-

OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;RNA binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Drug metabolism - other enzymes;Purine metabolism 2.80E-35 10 7 5 19.3
O00264;B7Z1L3 Membrane-associated progesterone receptor component 1 PGRMC1 >sp|O00264|PGRC1_HUMAN Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3;>tr|B7Z1L3|B7Z1L3_HUMAN Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=2 SV=1 -0.30 -0.09 0.00 0.10 0.67 0.61 -0.46 -0.17 0.309337638 -0.231547217 axon guidance;chemotaxis;locomotion;response to chemical stimulus;response to external stimulus;response to stimulus;taxis binding;cation binding;heme binding;ion binding;iron ion binding;lipid binding;metal ion binding;steroid binding;tetrapyrrole binding;transition metal ion binding cell part;cell surface;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle membrane;organelle part 8.47E-21 2 7 5 37.4
Q9UMY4-2;Q9UMY4;Q9UMY4-3 Sorting nexin-12 SNX12 >sp|Q9UMY4-2|SNX12_HUMAN Isoform 2 of Sorting nexin-12 OS=Homo sapiens GN=SNX12;>sp|Q9UMY4|SNX12_HUMAN Sorting nexin-12 OS=Homo sapiens GN=SNX12 PE=1 SV=3;>sp|Q9UMY4-3|SNX12_HUMAN Isoform 3 of Sorting nexin-12 OS=Homo sapiens GN=SNX12 -0.05 -0.08 -0.03 0.13 0.10 0.23 0.71 0.10 0.814639161 -0.290979443 cell communication;cellular process;establishment of localization;establishment of protein localization;protein transport;transport binding;lipid binding;phosphatidylinositol binding;phospholipid binding cell part;membrane 2.98E-19 3 7 5 32.7
Q70UQ0-4 >sp|Q70UQ0-4|IKIP_HUMAN Isoform 4 of Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP -0.58 -0.06 -0.52 0.05 0.80 0.69 -0.64 0.57 0.730726812 -0.633896447 1.22E-80 1 7 5 20.7
O00629;H7C4F6 Importin subunit alpha-4 KPNA4 >sp|O00629|IMA3_HUMAN Importin subunit alpha-3 OS=Homo sapiens GN=KPNA4 PE=1 SV=1 0.01 -0.08 -0.19 0.07 0.02 0.21 0.41 -0.03 0.739720061 -0.199463784 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleocytoplasmic transport;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction;transport protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part 7.40E-68 2 8 5 20.9
Q8WXF1-2;Q8WXF1 Paraspeckle component 1 PSPC1 >sp|Q8WXF1-2|PSPC1_HUMAN Isoform 2 of Paraspeckle component 1 OS=Homo sapiens GN=PSPC1;>sp|Q8WXF1|PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1 -0.19 0.62 -0.05 0.71 0.46 0.47 -1.14 0.12 0.257752678 0.296160231 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;paraspeckles 3.44E-55 2 8 5 23.4
Q9UHD9 Ubiquilin-2 UBQLN2 >sp|Q9UHD9|UBQL2_HUMAN Ubiquilin-2 OS=Homo sapiens GN=UBQLN2 PE=1 SV=2 0.01 -0.11 -0.04 0.03 0.26 0.56 0.48 -0.06 1.01707176 -0.338939997 cell death;cellular process;death cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane Protein processing in endoplasmic reticulum 7.72E-132 1 8 5 19.4
Q9UN37;I3L4J1;Q6PIW4-2;Q6PIW4 Vacuolar protein sorting-associated protein 4A VPS4A >sp|Q9UN37|VPS4A_HUMAN Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1;>tr|I3L4J1|I3L4J1_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=2 0.27 0.02 -0.04 -0.10 0.24 -0.05 0.57 -0.32 0.121746137 -0.070340466 ATP metabolic process;biological regulation;cell cycle;cell differentiation;cell proliferation;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytokinesis;developmental process;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;heterocycle metabolic process;intracellular transport;membrane organization;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;osteoblast differentiation;osteoblast proliferation;primary metabolic process;protein transport;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell death;regulation of cellular process;regulation of programmed cell death;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;small molecule metabolic process;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;magnesium ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome membrane;membrane;membrane-bounded organelle;midbody;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm Endocytosis 4.21E-20 4 8 5 21.3
B3KRS5;Q92769;J3KPW7;E5RFI6;E5RJ04;E5RGV4;E5RHE7;E5RH52;E5RG37;E5RFP9;H3BM24;E5RK19 Histone deacetylase;Histone deacetylase 2 HDAC2 >tr|B3KRS5|B3KRS5_HUMAN Histone deacetylase OS=Homo sapiens GN=HDAC2 PE=2 SV=1;>sp|Q92769|HDAC2_HUMAN Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=1 SV=2;>tr|J3KPW7|J3KPW7_HUMAN Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=4 SV=1 0.05 0.45 -0.05 0.28 -0.05 -0.41 -0.96 -0.50 1.251101188 0.663534476 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;biosynthetic process;blood coagulation;cell differentiation;cell projection organization;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;coagulation;covalent chromatin modification;dendrite development;developmental process;ectodermal placode formation;embryonic digit morphogenesis;embryonic morphogenesis;enzyme linked receptor protein signaling pathway;epidermal cell differentiation;eyelid development in camera-type eye;fungiform papilla formation;hair follicle placode formation;hemostasis;hippocampus development;histone deacetylation;histone H3 deacetylation;histone H4 deacetylation;histone modification;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;maintenance of chromatin silencing;metabolic process;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell projection organization;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of MHC class II biosynthetic process;negative regulation of molecular function;negative regulation of neuron projection development;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of Wnt receptor signaling pathway;nerve growth factor receptor signaling pathway;neuron projection development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of collagen biosynthetic process;positive

regulation of collagen metabolic process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of glial cell differentiation;positive regulation of gliogenesis;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal metabolic process;positive regulation of multicellular organismal process;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of oligodendrocyte differentiation;positive regulation of protein metabolic process;positive regulation of proteolysis;positive regulation of receptor biosynthetic process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein deacetylation;protein deacylation;protein metabolic process;protein modification process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of collagen biosynthetic process;regulation of collagen metabolic process;regulation of developmental process;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of MHC class II biosynthetic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal metabolic process;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oligodendrocyte differentiation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein deacetylation;regulation of protein metabolic process;regulation of protein modification process;regulation of proteolysis;regulation of receptor biosynthetic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of Wnt receptor signaling pathway;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway" "binding;catalytic activity;chromatin binding;chromatin DNA binding;deacetylase activity;DNA binding;histone deacetylase activity;histone deacetylase activity (H3-K14 specific);histone deacetylase activity (H3-K9 specific);hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;NAD-dependent histone deacetylase activity;NAD-dependent histone deacetylase activity (H3-K14 specific);NAD-dependent histone deacetylase activity (H3-K9 specific);NAD-dependent histone deacetylase activity (H4-K16 specific);NAD-dependent protein deacetylase activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein deacetylase activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;structure-specific DNA binding" cell part;chromatin;chromatin remodeling complex;chromosomal part;cytoplasm;ESC/E(Z) complex;heterochromatin;histone deacetylase complex;histone methyltransferase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;methyltransferase complex;nuclear chromatin;nuclear chromosome part;nuclear part;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;PcG protein complex;protein complex;replication fork;Sin3 complex;Sin3-type complex;transcription factor complex;transcriptional repressor complex Cell cycle;Chronic myeloid leukemia;Huntington's disease;Notch signaling pathway;Pathways in cancer 3.80E-57 12 9 5 24.9

P61006;B4DEK7;H0YNE9;F5GY21;Q92930;H0YMN7 Ras-related protein Rab-8A;Ras-related protein Rab-8B RAB8A;RAB8B >sp|P61006|RAB8A_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1;>tr|B4DEK7|B4DEK7_HUMAN Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=2 SV=1;>tr|H0YNE9|H0YNE9_HUMAN Ras-related protein Rab-8B (Fragment) OS=Homo sapiens GN=RAB8 0.02 0.08 -0.64 -0.06 0.02 0.16 -0.22 -0.10 0.239329604 -0.1147224 adherens junction organization;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;axonogenesis;biological regulation;cell cycle process;cell junction organization;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane fusion;cellular membrane organization;cellular process;cellular response to stimulus;cilium assembly;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to peroxisome;G2/M transition of mitotic cell cycle;Golgi vesicle fusion to target membrane;intracellular protein transport;intracellular signal transduction;intracellular transport;membrane docking;membrane fusion;membrane organization;neuron projection morphogenesis;organelle fusion;organelle organization;peroxisomal transport;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of corticotropin secretion;positive regulation of hormone secretion;positive regulation of secretion;positive regulation of transport;protein import;protein import into peroxisome membrane;protein targeting;protein targeting to membrane;protein targeting to peroxisome;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of corticotropin secretion;regulation of endocrine process;regulation of establishment of protein localization;regulation of hormone secretion;regulation of localization;regulation of long-term neuronal synaptic plasticity;regulation of multicellular organismal process;regulation of neurological system process;regulation of neuronal synaptic plasticity;regulation of protein localization;regulation of protein transport;regulation of secretion;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle fusion;vesicle organization "binding;catalytic activity;enzyme binding;GDP binding;GTP binding;GTPase activity;GTPase binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;Rab GTPase binding;Ras GTPase binding;ribonucleotide binding;small GTPase binding" cell body;cell part;cell pole;cell projection;cell projection part;cell tip;cilium;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;endocytic vesicle;endocytic vesicle membrane;endosome;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;microbody;microbody membrane;microbody part;microtubule basal body;microtubule organizing center;mitochondrion;neuronal cell body;nonmotile primary cilium;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;peroxisomal membrane;peroxisomal part;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;postsynaptic density;primary cilium;recycling endosome;synapse part;vesicle;vesicle membrane Pancreatic secretion 9.33E-85 6 9 5 41.5

P29034;R4GN49 Protein S100-A2 S100A2 >sp|P29034|S10A2_HUMAN Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=1 SV=3;>tr|R4GN49|R4GN49_HUMAN Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=4 SV=1 -0.21 -0.21 -0.62 -0.08 -1.21 -0.90 0.64 0.01 0.064118938 0.082610919 cell migration;cell motility;cellular component movement;cellular process;endothelial cell migration;locomotion binding;calcium ion binding;cation binding;ion binding;metal ion binding 7.94E-45 2 9 5 39.8

O75746;B3KR64;F8W9J0;H0YFB2;B4DGK6 Calcium-binding mitochondrial carrier protein Aralar1 SLC25A12 >sp|O75746|CMC1_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2;>tr|B3KR64|B3KR64_HUMAN Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=2 SV=1 -0.33 0.71 0.22 0.84 0.51 1.23 -1.27 0.99 0.002170883 -0.004245687 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;establishment of localization;establishment of localization in cell;gluconeogenesis;glucose metabolic process;hexose biosynthetic process;hexose metabolic process;intracellular transport;malate-aspartate shuttle;metabolic process;mitochondrial transport;monosaccharide biosynthetic process;monosaccharide metabolic process;primary metabolic process;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;small molecule biosynthetic process;small molecule metabolic process;transmembrane transport;transport acidic amino acid transmembrane transporter activity;active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;binding;calcium ion binding;carboxylic acid transmembrane transporter activity;cation binding;ion binding;L-amino acid transmembrane transporter activity;L-aspartate transmembrane transporter activity;L-glutamate transmembrane transporter activity;metal ion binding;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 1.61E-51 5 9 5 17.6

P62879;C9JIS1;C9JXA5;C9JZN1;E7EP32;Q9HAV0;C9JD14;B3KPU1 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2;Guanine nucleotide-binding protein subunit beta-4 GNB2;GNB4 >sp|P62879|GBB2_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3;>tr|C9JIS1|C9JIS1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 (Fragment) OS=Homo sapiens GN=GNB2 PE=2 SV=1;> -0.01 0.20 0.15 0.38 0.24 0.15 -0.84 -0.20 0.561327581 0.34459739 biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to glucagon stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;G-protein coupled receptor protein signaling pathway;metabolic process;oxidation-reduction process;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to glucagon stimulus;response to hormone stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;signaling;small molecule metabolic process;synaptic transmission "calcium channel regulator activity;catalytic activity;channel regulator activity;GTPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;molecular transducer activity;nucleoside-triphosphatase activity;pyrophosphatase activity;signal transducer activity" cell body;cell part;cytoplasmic part;intracellular part;macromolecular complex;membrane;perinuclear region of cytoplasm;plasma membrane;protein complex Chemokine signaling pathway 1.55E-72 8 10 5 27.9

F5H4G7;O60684;F5GYL8;Q5TFJ7;O15131 Importin subunit alpha;Importin subunit alpha-7;Importin subunit alpha-6 KPNA6;KPNA5 >tr|F5H4G7|F5H4G7_HUMAN Importin subunit alpha OS=Homo sapiens GN=KPNA6 PE=2 SV=1;>sp|O60684|IMA7_HUMAN Importin subunit alpha-7 OS=Homo sapiens GN=KPNA6 PE=1 SV=1;>tr|F5GYL8|F5GYL8_HUMAN Importin subunit alpha OS=Homo sapiens GN=KPNA6 PE=2 SV=1;>tr|Q5TFJ7 0.21 0.01 -0.06 0.22 -0.08 0.12 0.21 -0.05 0.170422953 0.045642311 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleocytoplasmic transport;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction;transport protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part 1.84E-86 5 10 5 24.2

P49023-2;P49023;P49023-3;F5GZ78;F5H836 Paxillin PXN >sp|P49023-2|PAXI_HUMAN Isoform Alpha of Paxillin OS=Homo sapiens GN=PXN;>sp|P49023|PAXI_HUMAN Paxillin OS=Homo sapiens GN=PXN PE=1 SV=3;>sp|P49023-3|PAXI_HUMAN Isoform Gamma of Paxillin OS=Homo sapiens GN=PXN;>tr|F5GZ78|F5GZ78_HUMAN Paxillin OS=Homo sapie0.10 -0.09 -0.39 -0.26 -0.28 -0.29 0.33 0.23 0.324281091 -0.160261478 activation of MAPK activity;anatomical structure morphogenesis;biological adhesion;biological regulation;branching morphogenesis of a tube;cell adhesion;cell junction assembly;cell junction organization;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to growth hormone stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to oxidative stress;cellular response to peptide hormone stimulus;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cytoskeleton organization;developmental process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;focal adhesion assembly;growth hormone receptor signaling pathway;integrin-mediated signaling pathway;lamellipodium assembly;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of a branching structure;multicellular organismal process;muscle contraction;muscle system process;organelle organization;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transferase activity;response to chemical stimulus;response to endogenous stimulus;response to growth hormone stimulus;response to hormone stimulus;response to inorganic substance;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to reactive oxygen species;response to stimulus;response to stress;signal complex assembly;signal transduction;system process;transmembrane receptor protein tyrosine kinase signaling pathway;tube morphogenesis binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding adherens junction;anchoring junction;cell cortex;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane;microtubule associated complex;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex Bacterial invasion of epithelial cells;Chemokine signaling pathway;Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;VEGF signaling pathway 2.41E-124 5 10 5 30.9

Q02880-2;Q02880;E9PCY5;B4DLV2 DNA topoisomerase 2-beta;DNA topoisomerase 2 TOP2B >sp|Q02880-2|TOP2B_HUMAN Isoform Beta-1 of DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B;>sp|Q02880|TOP2B_HUMAN DNA topoisomerase 2-beta OS=Homo sapiens GN=TOP2B PE=1 SV=3;>tr|E9PCY5|E9PCY5_HUMAN DNA topoisomerase 2 (Fragment) OS=Homo sapiens GN=TOP2B -0.01 1.19 -0.43 1.02 -0.33 0.18 -0.93 0.65 0.432214769 0.546014549 anatomical structure development;anatomical structure morphogenesis;axonogenesis;biosynthetic process;cell cycle process;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome organization;chromosome segregation;chromosome separation;developmental process;DNA conformation change;DNA metabolic process;DNA recombination;DNA replication;DNA topological change;DNA-dependent DNA replication;forebrain development;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;meiotic chromosome separation;metabolic process;mitotic recombination;neuron migration;neuron projection morphogenesis;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;resolution of meiotic recombination intermediates;sister chromatid segregation "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cation binding;chromatin binding;DNA binding;DNA topoisomerase (ATP-hydrolyzing) activity;DNA topoisomerase activity;DNA-dependent ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;isomerase activity;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromatin remodeling complex;chromosomal part;chromosome;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;SWI/SNF-type complex;synaptonemal complex;WINAC complex 1.92E-51 4 10 5 8.5

E7ENQ1;H7C360;O95819;E7EN19;O95819-4;G3XAA2;O95819-2;O95819-5;E7ESS2;O95819-3;G5E948;E7EX83;C9J840;H7C0P6;F6V107;H7C3Z6;Q9NRD5 Mitogen-activated protein kinase kinase kinase kinase 4 MAP4K4 >tr|E7ENQ1|E7ENQ1_HUMAN Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=2 SV=1;>tr|H7C360|H7C360_HUMAN Mitogen-activated protein kinase kinase kinase kinase 4 (Fragment) OS=Homo sapiens GN=MAP4K4 PE=2 SV=1;>sp|O95819|M4 0.36 -0.15 -0.24 -0.57 1.75 1.03 0.63 -0.09 0.973112003 -0.982778849 "activation of protein kinase activity;activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway;amine transport;biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein localization;cellular protein metabolic process;cellular response to stimulus;DNA alkylation;DNA metabolic process;DNA methylation;DNA methylation involved in embryo development;DNA methylation involved in gamete generation;DNA modification;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;G-protein coupled receptor protein signaling pathway;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;localization;macromolecule localization;macromolecule metabolic process;macromolecule methylation;macromolecule modification;membrane organization;metabolic process;methylation;monoamine transport;neuronal ion channel clustering;nitrogen compound metabolic process;nitrogen compound transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organic substance transport;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein localization;protein localization in membrane;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein transport;receptor clustering;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of gene expression;regulation of gene expression, epigenetic;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;reproductive process;response to stimulus;response to stress;retrograde vesicle-mediated transport, Golgi to ER;signal transduction;signaling;small molecule metabolic process;synaptic transmission;transport;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cation binding;enzyme binding;enzyme regulator activity;GTPase regulator activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;kinase activity;kinase binding;metal ion binding;nucleoside-triphosphatase activity;nucleoside-triphosphatase regulator activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein kinase binding;protein kinase C binding;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;small GTPase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell junction;cell part;cytoplasm;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;presynaptic membrane;synapse part;synaptic membrane;vesicle membrane MAPK signaling pathway 1.62E-41 17 12 5 12.1

P62136;P62136-2;E9PMD7;P62136-3;F5H1L6;F5H037 Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;Serine/threonine-protein phosphatase PPP1CA >sp|P62136|PP1A_HUMAN Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1;>sp|P62136-2|PP1A_HUMAN Isoform 2 of Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA;>tr|E 0.01 0.25 -0.04 0.27 0.26 0.07 -0.33 0.06 0.278637686 0.10501181 acylglycerol catabolic process;acylglycerol metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;branching morphogenesis of a tube;carbohydrate metabolic process;catabolic process;cell cycle;cell division;cell surface receptor linked signaling pathway;cellular carbohydrate metabolic process;cellular catabolic process;cellular glucan metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;dephosphorylation;developmental process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;generation of precursor metabolites and energy;glucan metabolic process;glycerol ether catabolic process;glycerol ether metabolic process;glycerolipid catabolic process;glycerolipid metabolic process;glycogen metabolic process;lipid catabolic process;lipid metabolic process;lung development;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of a branching structure;multicellular organismal process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;neutral lipid catabolic process;neutral lipid metabolic process;organ development;organic ether metabolic process;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;polysaccharide metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen biosynthetic process;regulation of glycogen catabolic process;regulation of glycogen metabolic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to stimulus;signal transduction;small molecule metabolic process;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;triglyceride catabolic process;triglyceride metabolic process;tube morphogenesis "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity;ribonucleoprotein binding" cell part;cell projection;cell projection part;cytoplasmic part;cytosol;dendritic spine;glycogen granule;histone methyltransferase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL5-L complex;neuron projection;neuron spine;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;organelle;organelle part;perikaryon;protein complex;protein phosphatase type 1 complex;protein serine/threonine phosphatase complex;PTW/PP1 phosphatase complex Focal adhesion;Insulin signaling pathway;Long-term potentiation;Meiosis - yeast;Oocyte meiosis;Regulation of actin cytoskeleton;Vascular smooth muscle contraction 2.33E-95 6 12 5 40.3

P42167;G5E972;P42167-2;H0YJH7 "Lamina-associated polypeptide 2, isoforms beta/gamma;Thymopoietin;Thymopentin" TMPO ">sp|P42167|LAP2B_HUMAN Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2;>tr|G5E972|G5E972_HUMAN Thymopentin OS=Homo sapiens GN=TMPO PE=2 SV=1;>sp|P42167-2|LAP2B_HUMAN Isoform Gamma of Lamina-associated polypeptide 2, i" 0.05 0.19 0.03 0.17 0.16 -0.58 -1.01 -1.13 1.07154712 0.747376648 binding;DNA binding;lamin binding;nucleic acid binding;protein binding cell part;envelope;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;nuclear envelope;nuclear inner membrane;nuclear membrane;nuclear part;organelle envelope;organelle inner membrane;organelle membrane;organelle part 7.51E-99 4 13 5 46.7

Q13838;Q13838-2;F8VQ10;Q5STU3;F6WLT2;B4DP52;F6UN21;F6TRA5;F6S4E6;F6UJC5;H0Y400;F6R6M7;B4DIJ6;F6QYI9;K7EPJ3;F6QWI5;F6U6E2;F6S2B7;E7EMX2;H0YCC6;F6SXL5 Spliceosome RNA helicase DDX39B DDX39B >sp|Q13838|DX39B_HUMAN Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1;>sp|Q13838-2|DX39B_HUMAN Isoform 2 of Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B;>tr|F8VQ10|F8VQ10_HUMAN Spliceosome RNA helicase DDX39B OS=Homo sapie -0.06 0.54 -0.01 0.61 -0.18 -0.13 -0.95 -0.22 1.028947116 0.637937746 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;intronless viral mRNA export from host nucleus;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA export from nucleus;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA export from nucleus;RNA metabolic process;RNA secondary structure unwinding;RNA transport;spliceosome assembly;transport;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent protein binding;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;snRNA binding;U4 snRNA binding;U6 snRNA binding" cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex;transcription export complex mRNA surveillance pathway;RNA transport;Spliceosome 5.60E-106 21 14 5 40

P05141;Q9H0C2 ADP/ATP translocase 2 SLC25A5 >sp|P05141|ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 0.11 0.40 0.23 1.23 -0.10 -0.81 -1.02 0.22 1.009169089 0.916668069 biological regulation;cellular metabolic process;cellular process;chromosome segregation;energy derivation by oxidation of organic compounds;energy reserve metabolic process;establishment of localization;generation of precursor metabolites and energy;interaction with host;interspecies interaction between organisms;metabolic process;multi-organism process;oxidation-reduction process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;regulation of biological process;regulation of cell communication;regulation of cell proliferation;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;reproductive process;small molecule metabolic process;transmembrane transport;transport;viral reproduction;viral reproductive process;virus-host interaction adenine transmembrane transporter activity;nucleobase transmembrane transporter activity;nucleobase-containing compound transmembrane transporter activity;purine base transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cell projection;cilium;cytoplasmic part;cytoskeletal part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;mitochondrion;MMXD complex;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane part;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease 7.36E-106 2 18 5 42.6

P12236;I7HJJ0 ADP/ATP translocase 3 SLC25A6 >sp|P12236|ADT3_HUMAN ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4;>tr|I7HJJ0|I7HJJ0_HUMAN ADP/ATP translocase 3 (Fragment) OS=Homo sapiens GN=SLC25A6 PE=4 SV=1 -1.12 0.54 0.00 1.00 -0.68 -0.93 -1.17 -0.07 0.674395053 0.814227388 active induction of host immune response by virus;apoptosis;biological regulation;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;energy derivation by oxidation of organic compounds;energy reserve metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;generation of precursor metabolites and energy;induction by organism of defense response of other organism involved in symbiotic interaction;induction by symbiont of host defense response;induction of host immune response by virus;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;modification by symbiont of host morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by organism of defense response of other organism involved in symbiotic interaction;modulation by symbiont of host defense response;multi-organism process;oxidation-reduction process;positive regulation by organism of defense response of other organism involved in symbiotic interaction;positive regulation by symbiont of host defense response;positive regulation of biological process;positive regulation of defense response;positive regulation of response to stimulus;primary metabolic process;programmed cell death;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of defense response;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of signaling;regulation of transport;reproductive process;response to biotic stimulus;response to defenses of other organism involved in symbiotic interaction;response to host;response to host defenses;response to other organism;response to stimulus;small molecule metabolic process;transmembrane transport;transport;viral infectious cycle;viral reproductive process;virus-host interaction active transmembrane transporter activity;antiporter activity;ATP:ADP antiporter activity;secondary active transmembrane transporter activity;solute:solute antiporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial inner membrane presequence translocase complex;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease 6.39E-97 2 19 5 44.6

P05388;F8VWS0;Q3B7A4;F8VU65;G3V210;F8VQY6;F8VPE8;F8VRK7;F8VZS0;Q8NHW5;F8VWV4;F8VS58;F8W1K8;F8VYN4;REV__B4DYD8;REV__E7ENZ3;REV__B7ZAR1;REV__E9PCA1;REV__P48643 60S acidic ribosomal protein P0;60S acidic ribosomal protein P0-likeRPLP0;RPLP0P6 >sp|P05388|RLA0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1;>tr|F8VWS0|F8VWS0_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=2 SV=1;>tr|Q3B7A4|Q3B7A4_HUMAN 60S acidic ribosomal protein P0 OS=Homo sapiens GN=R-0.06 0.04 0.01 0.01 -0.04 -0.38 -0.34 -0.23 1.280761918 0.2472579 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral reproductive process;viral transcription;virus-host interaction" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.73E-229 19 21 5 60.6

A8MUB1;P68366;C9JEV8;C9JQ00;C9JJQ8;C9JDL2 Tubulin alpha-4A chain TUBA4A>tr|A8MUB1|A8MUB1_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=2 SV=1;>sp|P68366|TBA4A_HUMAN Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 0.07 0.14 -0.32 -0.03 0.05 0.49 0.39 0.32 1.071513155 -0.34826976 cell activation;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;exocytosis;G2/M transition of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;platelet activation;platelet degranulation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;secretion;secretion by cell;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 6 26 5 59.6

P07437;Q5JP53;Q5ST81;E9PBJ4;F5H0I4;Q5SQY0;I3L2F9;A6NNZ2;A6NKZ8;Q9H4B7;G3V4U2;G3V3J6;G3V3W7;M0R2T4 Tubulin beta chain TUBB >sp|P07437|TBB5_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2;>tr|Q5JP53|Q5JP53_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=2 SV=1;>tr|Q5ST81|Q5ST81_HUMAN Tubulin beta chain OS=Homo sapiens GN=TUBB PE=2 SV=1 0.09 -0.03 -0.25 -0.11 0.13 -0.01 0.21 0.12 0.944033039 -0.186062266 axon guidance;biological regulation;cell cycle phase;cell cycle process;cell division;cell killing;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chemotaxis;cytoskeleton organization;cytoskeleton-dependent intracellular transport;'de novo' posttranslational protein folding;'de novo' protein folding;defense response;establishment of localization;establishment of localization in cell;G2/M transition of mitotic cell cycle;immune effector process;immune response;immune system process;induction of apoptosis;induction of programmed cell death;innate immune response;intracellular transport;leukocyte mediated cytotoxicity;leukocyte mediated immunity;locomotion;lymphocyte mediated immunity;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitosis;natural killer cell mediated cytotoxicity;natural killer cell mediated immunity;nuclear division;organelle assembly;organelle fission;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;spindle assembly;spindle organization;taxis;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;MHC class I protein binding;MHC protein binding;nucleoside-triphosphatase activity;nucleotide binding;peptide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" axon;cell body;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microtubule;microtubule cytoskeleton;neuron projection;non-membrane-bounded organelle;nuclear envelope lumen;nuclear part;nucleus;organelle;organelle envelope lumen;organelle part;plasma membrane;protein complex;vesicle Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 14 32 5 75.9

Q14247;H7C314;B4E358;H0YCD9;H0YEV2;E9PKG3;E9PP90 Src substrate cortactin CTTN >sp|Q14247|SRC8_HUMAN Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 -0.09 -0.03 0.03 -0.01 0.02 0.29 0.47 0.30 1.257235012 -0.293331762 cell cortex;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeleton;dendritic spine;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;neuron projection;neuron spine;non-membrane-bounded organelle;organelle;ruffle Bacterial invasion of epithelial cells;Pathogenic Escherichia coli infection;Shigellosis;Tight junction 0 7 38 5 60.9

P14618;P14618-3;H3BQ34;H3BUW1;H3BTJ2;H3BT25;H3BU13;H3BN34;H3BQZ3 Pyruvate kinase isozymes M1/M2;Pyruvate kinase PKM >sp|P14618|KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4;>sp|P14618-3|KPYM_HUMAN Isoform 3 of Pyruvate kinase PKM OS=Homo sapiens GN=PKM;>tr|H3BQ34|H3BQ34_HUMAN Pyruvate kinase OS=Homo sapiens GN=PKM PE=2 SV=1 -0.05 -0.11 -0.28 0.07 -0.58 -0.17 0.41 0.09 0.048407688 -0.032029588 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell death;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;death;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;primary metabolic process;programmed cell death;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;alkali metal ion binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;potassium ion binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyruvate kinase activity;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups"cell part;cytoplasmic part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;nucleus;organelle;plasma membrane;vesicle Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis;Purine metabolism;Pyruvate metabolism;Type II diabetes mellitus 0 9 60 5 86.3

Q01082 "Spectrin beta chain, non-erythrocytic 1" SPTBN1 ">sp|Q01082|SPTB2_HUMAN Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2" -0.06 -0.08 0.18 -0.01 0.09 0.03 0.00 -0.25 0.154195566 0.040184707 actin filament capping;axon guidance;biological regulation;cell cycle cytokinesis;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;common-partner SMAD protein phosphorylation;cytokinesis;cytokinesis after mitosis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;intracellular protein transport;intracellular transport;locomotion;macromolecule metabolic process;macromolecule modification;membrane assembly;membrane organization;metabolic process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;nuclear import;nuclear transport;nucleocytoplasmic transport;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;post-Golgi vesicle-mediated transport;primary metabolic process;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein targeting to plasma membrane;protein transport;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;SMAD protein import into nucleus;taxis;transport;vesicle-mediated transport actin binding;ankyrin binding;binding;cytoskeletal protein binding;lipid binding;phospholipid binding;protein binding;structural constituent of cytoskeleton;structural molecule activityaxolemma;axon part;cell cortex part;cell part;cell projection membrane;cell projection part;contractile fiber part;cuticular plate;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;M band;membrane part;neuron projection membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane part;spectrin;spectrin-associated cytoskeleton 0 1 109 5 56.5

Q15149 Plectin PLEC >sp|Q15149|PLEC_HUMAN Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 -0.03 0.15 0.03 0.09 -0.09 0.09 0.07 0.23 0.058010947 -0.012818716 cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly structural constituent of muscle;structural molecule activity adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;costamere;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;focal adhesion;hemidesmosome;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;sarcolemma;sarcoplasm 0 1 465 5 76.6

Q8IZP0-10;Q8IZP0-8;F5H1G9;Q8IZP0-7;F8WA55;Q8IZP0-2;Q8IZP0-4;Q8IZP0-3;Q8IZP0-5;Q8IZP0-6;Q8IZP0-9;F8WA56;Q8IZP0-12;Q8IZP0;A6NFN2;Q8IZP0-11;H0Y6B5;F8WAL6;Q9NYB9-3;E9PEZ7;Q9NYB9-2;E7EW77;E7EP65;Q9NYB9-4;Q9NYB9;J3KNB2 Abl interactor 1 ABI1 >sp|Q8IZP0-10|ABI1_HUMAN Isoform 10 of Abl interactor 1 OS=Homo sapiens GN=ABI1;>sp|Q8IZP0-8|ABI1_HUMAN Isoform 8 of Abl interactor 1 OS=Homo sapiens GN=ABI1;>tr|F5H1G9|F5H1G9_HUMAN Abl interactor 1 OS=Homo sapiens GN=ABI1 PE=2 SV=1;>sp|Q8IZP0-7|ABI1_HUMAN -0.12 -0.09 0.08 -0.08 -0.11 -0.09 0.02 -0.02 0.009890779 -0.001644285 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin polymerization or depolymerization;anatomical structure development;anatomical structure formation involved in morphogenesis;anterior/posterior pattern specification;behavior;biological regulation;camera-type eye development;cell migration;cell motility;cell projection organization;cell surface receptor linked signaling pathway;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cognition;cytoskeleton organization;defense response;dendrite development;developmental process;enzyme linked receptor protein signaling pathway;eye development;immune response;immune system process;innate immune response;learning or memory;locomotion;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;neurological system process;neuron projection development;organ development;organelle organization;pattern specification process;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regionalization;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to stimulus;response to stress;segmentation;sensory organ development;signal transduction;somitogenesis;system process;transmembrane receptor protein tyrosine kinase signaling pathway "binding;binding, bridging;cytoskeletal adaptor activity;cytoskeletal protein binding;DNA binding;enzyme activator activity;enzyme binding;enzyme regulator activity;kinase activator activity;kinase binding;kinase regulator activity;nucleic acid binding;protein binding;protein binding, bridging;protein domain specific binding;protein kinase activator activity;protein kinase regulator activity;protein tyrosine kinase activator activity;SH3 domain binding" adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection part;cell-cell adherens junction;cell-cell junction;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;dendrite;endoplasmic reticulum;filopodium;growth cone;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nucleus;organelle;site of polarized growth;synapse Regulation of actin cytoskeleton 7.83E-51 26 6 6 23.2

P35611-2;E7EV99;A2A3N8;E7ENY0;P35611;P35611-3;H0Y9H2;Q86XM2;D6RJE2;D6RAH3;D6RF25;P35612-2;P35612-8;P35612-4;P35612-3;P35612 Alpha-adducinADD1 >sp|P35611-2|ADDA_HUMAN Isoform 2 of Alpha-adducin OS=Homo sapiens GN=ADD1;>tr|E7EV99|E7EV99_HUMAN Alpha-adducin OS=Homo sapiens GN=ADD1 PE=2 SV=1;>tr|A2A3N8|A2A3N8_HUMAN Adducin 1 (Alpha) OS=Homo sapiens GN=ADD1 PE=2 SV=1;>tr|E7ENY0|E7ENY0_HUMAN Alpha-add -0.03 0.22 -0.42 0.09 0.36 0.24 -0.23 0.14 0.336797899 -0.158978805 actin cytoskeleton organization;actin filament bundle assembly;actin filament capping;actin filament organization;actin filament-based process;activation of signaling protein activity involved in unfolded protein response;anatomical structure development;anatomical structure homeostasis;anatomical structure morphogenesis;barbed-end actin filament capping;biological regulation;cell communication;cell differentiation;cell morphogenesis;cell volume homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;chordate embryonic development;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;erythrocyte differentiation;growth;hemoglobin metabolic process;hemopoiesis;hemopoietic or lymphoid organ development;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;in utero embryonic development;macromolecule metabolic process;metabolic process;multicellular organism growth;multicellular organismal process;myeloid cell differentiation;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organ development;organelle organization;positive regulation of angiogenesis;positive regulation of binding;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of endocytosis;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein binding;positive regulation of protein kinase activity;positive regulation of transferase activity;positive regulation of transport;primary metabolic process;protein metabolic process;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of angiogenesis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of developmental process;regulation of endocytosis;regulation of hydrolase activity;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nuclease activity;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein binding;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to retinoic acid;response to stimulus;response to vitamin;response to vitamin A;tissue homeostasis actin binding;actin filament binding;binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding;spectrin binding;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;F-actin capping protein complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;postsynaptic density;protein complex;synapse part 2.65E-21 16 6 6 13.2

E9PC15;Q53H12;E9PG39 "Acylglycerol kinase, mitochondrial" AGK ">tr|E9PC15|E9PC15_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=2 SV=1;>sp|Q53H12|AGK_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=1 SV=2;>tr|E9PG39|E9PG39_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens" -0.44 0.45 0.24 0.32 0.04 0.33 -1.31 1.36 0.02189977 0.039143014 activation of protein kinase activity;activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway;biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;ceramide biosynthetic process;ceramide metabolic process;glycerolipid metabolic process;G-protein coupled receptor protein signaling pathway;lipid biosynthetic process;lipid metabolic process;membrane lipid biosynthetic process;membrane lipid metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;signal transduction;sphingoid biosynthetic process;sphingoid metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process "acylglycerol kinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ceramide kinase activity;diacylglycerol kinase activity;kinase activity;lipid kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial membrane;mitochondrial part;organelle membrane;organelle part Glycerolipid metabolism8.49E-18 3 6 6 20.8

H3BLU7;O43488;Q8NHP1;H7C5H7 Aflatoxin B1 aldehyde reductase member 2;Aflatoxin B1 aldehyde reductase member 4 AKR7A2;AKR7L >tr|H3BLU7|H3BLU7_HUMAN Aflatoxin B1 aldehyde reductase member 2 (Fragment) OS=Homo sapiens GN=AKR7A2 PE=2 SV=1;>sp|O43488|ARK72_HUMAN Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3;>sp|Q8NHP1|ARK74_HUMAN Aflatoxin B1 aldehyde 0.20 -0.04 0.11 -0.11 0.60 0.17 0.06 -0.29 0.174324677 -0.092797827 carbohydrate metabolic process;cellular aldehyde metabolic process;cellular metabolic process;cellular process;metabolic process;primary metabolic process "alcohol dehydrogenase (NADP+) activity;alditol:NADP+ 1-oxidoreductase activity;aldo-keto reductase (NADP) activity;catalytic activity;electron carrier activity;epoxide hydrolase activity;ether hydrolase activity;hydrolase activity;hydrolase activity, acting on ether bonds;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;phenanthrene-9,10-epoxide hydrolase activity;phenanthrene-epoxide hydrolase activity" cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 1.47E-63 4 6 6 25.5

F5H2H5;Q86XL3;Q86XL3-2;F5H417;Q86XL3-3;F5H6J0;F5H1D4 Ankyrin repeat and LEM domain-containing protein 2 ANKLE2 >tr|F5H2H5|F5H2H5_HUMAN Ankyrin repeat and LEM domain-containing protein 2 OS=Homo sapiens GN=ANKLE2 PE=2 SV=1;>sp|Q86XL3|ANKL2_HUMAN Ankyrin repeat and LEM domain-containing protein 2 OS=Homo sapiens GN=ANKLE2 PE=1 SV=4;>sp|Q86XL3-2|ANKL2_HUMAN Isoform 2 0.07 0.27 0.06 -0.06 0.17 0.09 -0.21 0.25 0.024850966 0.00926799 anaphase;biological regulation;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;M phase;M phase of mitotic cell cycle;membrane organization;mitotic anaphase;mitotic nuclear envelope reassembly;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;nuclear envelope organization;nuclear envelope reassembly;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of dephosphorylation;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process binding;enzyme binding;enzyme regulator activity;phosphatase binding;phosphatase regulator activity;protein binding;protein phosphatase 2A binding;protein phosphatase binding;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane part;organelle part 9.46E-26 7 6 6 13

Q96P48-3;Q96P48;Q96P48-7;E7EU13;Q96P48-2;Q96P48-4;Q96P48-1;Q96P48-5;H0YGD1;F5GWQ2;F5GWN4;F8WBT0 "Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1" ARAP1 ">sp|Q96P48-3|ARAP1_HUMAN Isoform 3 of Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1;>sp|Q96P48|ARAP1_HUMAN Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=A" 0.60 0.05 0.33 -0.29 -0.32 -0.58 0.03 -0.78 0.961426615 0.58458579 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament organization;actin filament reorganization involved in cell cycle;actin filament-based process;biological regulation;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;cytoskeleton organization;intracellular signal transduction;negative regulation of actin filament bundle assembly;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of stress fiber assembly;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of Cdc42 GTPase activity;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of filopodium assembly;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of ARF GTPase activity;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of Cdc42 GTPase activity;regulation of cell morphogenesis;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell shape;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of filopodium assembly;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Rho GTPase activity;regulation of stress fiber assembly;response to stimulus;signal transduction;small GTPase mediated signal transduction "ARF GTPase activator activity;binding;cation binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;lipid binding;metal ion binding;nucleoside-triphosphatase regulator activity;phosphatidylinositol binding;phosphatidylinositol-3,4,5-trisphosphate binding;phospholipid binding;Ras GTPase activator activity;Rho GTPase activator activity;small GTPase regulator activity;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane Endocytosis 6.91E-39 12 6 6 5.5

O15145;C9JZD1;F8VR50 Actin-related protein 2/3 complex subunit 3 ARPC3 >sp|O15145|ARPC3_HUMAN Actin-related protein 2/3 complex subunit 3 OS=Homo sapiens GN=ARPC3 PE=1 SV=3;>tr|C9JZD1|C9JZD1_HUMAN Actin-related protein 2/3 complex subunit 3 (Fragment) OS=Homo sapiens GN=ARPC3 PE=2 SV=1 -0.31 0.13 -1.40 0.28 -0.79 0.46 0.32 0.31 0.335349263 -0.401436049 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin nucleation;Arp2/3 complex-mediated actin nucleation;biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;defense response;immune response;immune system process;innate immune response;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stressstructural constituent of cytoskeleton;structural molecule activity Arp2/3 protein complex;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;organelle part;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis 4.33E-51 3 6 6 33.1

Q9H1I8-3;Q9H1I8;Q9H1I8-2;H7C3Y4;B1AH59;B1AH60 Activating signal cointegrator 1 complex subunit 2 ASCC2 >sp|Q9H1I8-3|ASCC2_HUMAN Isoform 3 of Activating signal cointegrator 1 complex subunit 2 OS=Homo sapiens GN=ASCC2;>sp|Q9H1I8|ASCC2_HUMAN Activating signal cointegrator 1 complex subunit 2 OS=Homo sapiens GN=ASCC2 PE=1 SV=3;>sp|Q9H1I8-2|ASCC2_HUMAN Isoform 0.23 -0.24 0.20 -0.13 -0.19 0.14 0.29 0.29 0.290323935 -0.120641548 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" 3.22E-19 6 6 6 10.4

O95352-3;O95352;O95352-2;C9JE55;C9J415;C9JFF4;C9JGL2;F8WDY9;C9JNU2;C9JKA3;H7C2R3;H7BZ92;H7C059;H7C2J8 Ubiquitin-like modifier-activating enzyme ATG7 ATG7 >sp|O95352-3|ATG7_HUMAN Isoform 3 of Ubiquitin-like modifier-activating enzyme ATG7 OS=Homo sapiens GN=ATG7;>sp|O95352|ATG7_HUMAN Ubiquitin-like modifier-activating enzyme ATG7 OS=Homo sapiens GN=ATG7 PE=1 SV=1;>sp|O95352-2|ATG7_HUMAN Isoform 2 of Ubiquiti 0.12 -0.11 0.02 -0.04 0.48 0.12 0.25 -0.46 0.17405652 -0.097149153 adult behavior;adult locomotory behavior;adult walking behavior;amine metabolic process;anatomical structure development;anatomical structure morphogenesis;autophagy;axonogenesis;behavior;biological regulation;carboxylic acid metabolic process;cardiac cell development;cardiac muscle cell development;catabolic process;cell development;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular amine metabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;central nervous system neuron axonogenesis;central nervous system neuron development;cerebellar Purkinje cell layer development;cerebral cortex development;developmental process;establishment of localization;establishment of protein localization;forebrain neuron development;liver development;locomotory behavior;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane fusion;membrane organization;metabolic process;multicellular organismal process;muscle cell development;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;neurological system process;neuron development;neuron projection morphogenesis;nitrogen compound metabolic process;organ development;organelle organization;organic acid metabolic process;oxoacid metabolic process;positive regulation of autophagy;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macroautophagy;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of response to external stimulus;positive regulation of response to extracellular stimulus;positive regulation of response to nutrient levels;positive regulation of response to stimulus;post-embryonic development;primary metabolic process;protein catabolic process;protein lipidation;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein transport;pyramidal neuron development;regulation of apoptosis;regulation of autophagy;regulation of biological process;regulation of catabolic process;regulation of cell communication;regulation of cell death;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of macroautophagy;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress;response to external stimulus;response to extracellular stimulus;response to nutrient levels;response to starvation;response to stimulus;response to stress;small molecule metabolic process;system process;transport APG12 activating enzyme activity;binding;catalytic activity;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity;small protein activating enzyme activity;ubiquitin activating enzyme activity cell part;cytoplasm;intracellular part Regulation of autophagy 6.37E-27 14 6 6 10.9

Q9UI12-2;Q9UI12;G3V126;E5RK31;E5RJG1;E5RG49;E5RHH0 V-type proton ATPase subunit H ATP6V1H ">sp|Q9UI12-2|VATH_HUMAN Isoform 2 of V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H;>sp|Q9UI12|VATH_HUMAN V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1;>tr|G3V126|G3V126_HUMAN ATPase, H+ transporting, lysosomal 50/57kDa, V1"0.08 0.46 -0.46 0.33 -0.14 0.39 0.16 0.13 0.051730343 -0.035561007 "ATP catabolic process;ATP hydrolysis coupled proton transport;ATP metabolic process;biological regulation;catabolic process;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular monovalent inorganic cation homeostasis;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;endocytosis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;intracellular pH reduction;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;pH reduction;phagosome maturation;primary metabolic process;protein transport;proton transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular pH;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune system process;regulation of intracellular pH;regulation of multi-organism process;regulation of pH;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport;vacuolar acidification;vesicle-mediated transport;viral reproduction;viral reproductive process;virus-host interaction" "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;enzyme regulator activity;hydrogen ion transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;organelle part;plasma membrane;protein complex;proton-transporting two-sector ATPase complex, catalytic domain;proton-transporting V-type ATPase, V1 domain;vacuolar part;vacuolar proton-transporting V-type ATPase, V1 domain" Epithelial cell signaling in Helicobacter pylori infection;ko05152;Lysosome;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection 7.28E-43 7 6 6 20.9

P56945-5;P56945-8;P56945;P56945-7;P56945-3;P56945-2;P56945-6;P56945-4;F5H855;H3BVF0;H3BSY4;H3BQJ7;H3BSB2 Breast cancer anti-estrogen resistance protein 1 BCAR1 >sp|P56945-5|BCAR1_HUMAN Isoform 5 of Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens GN=BCAR1;>sp|P56945-8|BCAR1_HUMAN Isoform 8 of Breast cancer anti-estrogen resistance protein 1 OS=Homo sapiens GN=BCAR1;>sp|P56945|BCAR1_HUMAN Breast ca 0.23 -0.03 -0.55 -0.34 -0.09 0.21 0.29 0.34 0.791922025 -0.360964886 actin cytoskeleton organization;actin filament organization;actin filament-based process;activation of immune response;antigen receptor-mediated signaling pathway;B cell receptor signaling pathway;biological adhesion;biological regulation;cell activation;cell adhesion;cell chemotaxis;cell division;cell migration;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to growth factor stimulus;cellular response to hepatocyte growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to vascular endothelial growth factor stimulus;chemotaxis;cytoskeleton organization;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;G-protein coupled receptor protein signaling pathway;hepatocyte growth factor receptor signaling pathway;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;insulin receptor signaling pathway;integrin-mediated signaling pathway;locomotion;nerve growth factor receptor signaling pathway;organelle organization;platelet activation;platelet-derived growth factor receptor signaling pathway;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of endothelial cell migration;positive regulation of immune response;positive regulation of immune system process;positive regulation of locomotion;positive regulation of response to stimulus;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell growth;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of endothelial cell migration;regulation of growth;regulation of immune response;regulation of immune system process;regulation of localization;regulation of locomotion;regulation of programmed cell death;regulation of response to stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to growth factor stimulus;response to hepatocyte growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;T cell receptor signaling pathway;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;vascular endothelial growth factor receptor signaling pathway molecular transducer activity;signal transducer activityadherens junction;anchoring junction;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytosol;focal adhesion;intracellular part;lamellipodium;ruffle Bacterial invasion of epithelial cells;Chemokine signaling pathway;Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton 4.67E-42 13 6 6 12.8

E9PIF8;Q96Q25;Q14137;E9PRN9 Ribosome biogenesis protein BOP1 BOP1;KM-PA-2 >tr|E9PIF8|E9PIF8_HUMAN Ribosome biogenesis protein BOP1 (Fragment) OS=Homo sapiens GN=BOP1 PE=2 SV=1;>tr|Q96Q25|Q96Q25_HUMAN KM-PA-2 protein OS=Homo sapiens GN=KM-PA-2 PE=2 SV=1;>sp|Q14137|BOP1_HUMAN Ribosome biogenesis protein BOP1 OS=Homo sapiens GN=BOP 0.10 0.83 -0.04 0.67 -0.37 -0.22 -0.96 0.18 0.979881547 0.732719251 "biological regulation;cell proliferation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;maturation of LSU-rRNA;maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cellular process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleolar part;nucleoplasm;nucleus;organelle;organelle part;PeBoW complex;protein complex 1.18E-62 4 6 6 26

P35613-2;P35613;P35613-3;P35613-4;I3L192;R4GMX5;R4GN83 Basigin BSG>sp|P35613-2|BASI_HUMAN Isoform 2 of Basigin OS=Homo sapiens GN=BSG;>sp|P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2;>sp|P35613-3|BASI_HUMAN Isoform 3 of Basigin OS=Homo sapiens GN=BSG;>sp|P35613-4|BASI_HUMAN Isoform 4 of Basigin OS=Homo sapi -0.28 0.03 0.09 0.26 -0.45 -0.03 -0.46 -0.08 0.738453805 0.277767302 anatomical structure development;anatomical structure morphogenesis;biological regulation;blood coagulation;carboxylic acid metabolic process;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component movement;cellular ketone metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;coagulation;decidualization;developmental process;developmental process involved in reproduction;embryo implantation;hemostasis;immune system process;leukocyte migration;locomotion;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;organic acid metabolic process;oxoacid metabolic process;pyruvate metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;reproductive process;response to cAMP;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to inorganic substance;response to mercury ion;response to metal ion;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;small molecule metabolic process;tissue development binding;carbohydrate binding;mannose binding;monosaccharide binding;sugar binding acrosomal membrane;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;sarcolemma;secretory granule membrane;vesicle;vesicle membrane 5.94E-45 7 6 6 30.1

Q96CT7;M0R2F5 Coiled-coil domain-containing protein 124 CCDC124 >sp|Q96CT7|CC124_HUMAN Coiled-coil domain-containing protein 124 OS=Homo sapiens GN=CCDC124 PE=1 SV=1;>tr|M0R2F5|M0R2F5_HUMAN Coiled-coil domain-containing protein 124 (Fragment) OS=Homo sapiens GN=CCDC124 PE=4 SV=1 0.09 -0.01 0.39 0.06 0.28 0.14 0.05 -0.12 0.127821141 0.043575452 3.02E-29 2 6 6 25.1

O60826 Coiled-coil domain-containing protein 22 CCDC22 >sp|O60826|CCD22_HUMAN Coiled-coil domain-containing protein 22 OS=Homo sapiens GN=CCDC22 PE=1 SV=1 0.14 -0.03 0.10 0.21 0.11 0.31 0.28 0.03 0.380613256 -0.078812662 8.28E-32 1 6 6 16.7

Q16204 Coiled-coil domain-containing protein 6 CCDC6 >sp|Q16204|CCDC6_HUMAN Coiled-coil domain-containing protein 6 OS=Homo sapiens GN=CCDC6 PE=1 SV=2 0.02 -0.11 0.21 -0.18 -0.17 0.02 0.41 -0.44 0.049737698 0.029250262 structural constituent of cytoskeleton;structural molecule activity cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle Pathways in cancer;Thyroid cancer 4.81E-32 1 6 6 15.4

Q9NX63;C9JRZ6;F8WAR4;G3V1K1;F8WD73 "Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial" CHCHD3 ">sp|Q9NX63|CHCH3_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens GN=CHCHD3 PE=1 SV=1;>tr|C9JRZ6|C9JRZ6_HUMAN Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Homo sapiens" -0.37 0.93 -0.11 0.87 0.10 0.62 -0.32 0.59 0.071542188 0.083770365 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular process;inner mitochondrial membrane organization;membrane fusion;membrane organization;mitochondrial fusion;mitochondrial membrane organization;mitochondrion organization;organelle fusion;organelle organization binding;enzyme binding;phosphatase binding;protein binding;protein complex scaffold;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part 3.94E-49 5 6 6 22

Q8IWX8;J3QK89 Calcium homeostasis endoplasmic reticulum protein CHERP >sp|Q8IWX8|CHERP_HUMAN Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=3;>tr|J3QK89|J3QK89_HUMAN Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=4 SV=1 0.01 0.10 0.32 0.30 -0.09 -0.26 -0.77 -0.25 1.29312477 0.522383226 anatomical structure development;biological regulation;calcium ion homeostasis;calcium ion transport;calcium ion transport into cytosol;cation homeostasis;cation transport;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;cytosolic calcium ion homeostasis;cytosolic calcium ion transport;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of cytosolic calcium ion concentration;establishment of localization;homeostatic process;ion homeostasis;ion transport;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of sequestering of calcium ion;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of NFAT protein import into nucleus;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of transcription factor import into nucleus;positive regulation of transmembrane transport;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell proliferation;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of homeostatic process;regulation of intracellular protein transport;regulation of intracellular transport;regulation of ion homeostasis;regulation of localization;regulation of NFAT protein import into nucleus;regulation of nucleocytoplasmic transport;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of sequestering of calcium ion;regulation of transcription factor import into nucleus;regulation of transmembrane transport;regulation of transport;release of sequestered calcium ion into cytosol;RNA metabolic process;RNA processing;system development;transport binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;membrane;membrane part;organelle membrane;organelle part;perinuclear region of cytoplasm;sarcoplasmic reticulum membrane Spliceosome 1.78E-13 2 6 6 7.3

P31327-2;P31327;P31327-3 "Carbamoyl-phosphate synthase [ammonia], mitochondrial" CPS1 ">sp|P31327-2|CPSM_HUMAN Isoform 2 of Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1;>sp|P31327|CPSM_HUMAN Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2;>sp|P31327-3|CPSM_HUMAN Isoform" -0.64 -0.24 0.45 0.12 -0.20 -0.26 0.28 -0.25 0.031030865 0.025100885 acylglycerol catabolic process;acylglycerol metabolic process;amide biosynthetic process;amine biosynthetic process;amine catabolic process;amine metabolic process;biological regulation;biosynthetic process;carbamoyl phosphate biosynthetic process;carbamoyl phosphate metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amide metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular glucan metabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;citrulline biosynthetic process;citrulline metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan catabolic process;glucan metabolic process;glutamine catabolic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;glycerol ether catabolic process;glycerol ether metabolic process;glycerolipid catabolic process;glycerolipid metabolic process;glycogen catabolic process;glycogen metabolic process;homocysteine metabolic process;lipid catabolic process;lipid metabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;neutral lipid catabolic process;neutral lipid metabolic process;nitric oxide metabolic process;nitrogen compound metabolic process;nitrogen cycle metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of multicellular organismal process;positive regulation of vasodilation;primary metabolic process;regulation of biological process;regulation of multicellular organismal process;regulation of system process;regulation of vasodilation;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound metabolic process;triglyceride catabolic process;triglyceride metabolic process;urea cycle;urea metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;ATP binding;binding;carbamoyl-phosphate synthase (ammonia) activity;carboxylic acid binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;modified amino acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding"cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nuclear part;nucleoid;nucleolus;organelle;organelle part "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;Nitrogen metabolism" 4.43E-23 3 6 6 8

Q9UJW0-2;Q9UJW0;Q9UJW0-3;E5RGG1;H9KVE0;E5RK21 Dynactin subunit 4 DCTN4 >sp|Q9UJW0-2|DCTN4_HUMAN Isoform 2 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4;>sp|Q9UJW0|DCTN4_HUMAN Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1;>sp|Q9UJW0-3|DCTN4_HUMAN Isoform 3 of Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 -0.12 -0.11 -0.26 0.12 0.39 0.23 0.06 -0.04 0.874501729 -0.252521602 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;immune system process cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part Huntington's disease;Vasopressin-regulated water reabsorption 1.38E-25 6 6 6 22.8

Q9UHI6;E9PJ60;B4DWV7 Probable ATP-dependent RNA helicase DDX20 DDX20 >sp|Q9UHI6|DDX20_HUMAN Probable ATP-dependent RNA helicase DDX20 OS=Homo sapiens GN=DDX20 PE=1 SV=2 0.18 0.04 -0.18 -0.09 -0.07 -0.38 -0.08 -0.25 0.716704554 0.182442986 "assembly of spliceosomal tri-snRNP;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;induction of apoptosis;induction of programmed cell death;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA helicase activity;RNA-dependent ATPase activity" Cajal body;cell part;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm;nucleoplasm part;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex;transcriptional repressor complex RNA transport 4.49E-35 3 6 6 13

G3V529;Q9GZR7;F5GYL3 ATP-dependent RNA helicase DDX24 DDX24 >tr|G3V529|G3V529_HUMAN ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=2 SV=1;>sp|Q9GZR7|DDX24_HUMAN ATP-dependent RNA helicase DDX24 OS=Homo sapiens GN=DDX24 PE=1 SV=1;>tr|F5GYL3|F5GYL3_HUMAN ATP-dependent RNA helicase DDX24 OS=Homo sapiens -0.03 0.79 -0.01 0.57 -0.02 0.61 -1.14 0.05 0.444613661 0.455120056 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 1.08E-59 3 6 6 12.6

Q8TDD1;Q8TDD1-2;F8VRX4 ATP-dependent RNA helicase DDX54 DDX54 >sp|Q8TDD1|DDX54_HUMAN ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 PE=1 SV=2;>sp|Q8TDD1-2|DDX54_HUMAN Isoform 2 of ATP-dependent RNA helicase DDX54 OS=Homo sapiens GN=DDX54 -0.13 0.81 0.00 0.91 -0.75 0.13 -0.99 0.24 0.774795799 0.742433292 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;estrogen receptor signaling pathway;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;signal transduction;steroid hormone receptor signaling pathway;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;estrogen receptor binding;helicase activity;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;steroid hormone receptor binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 6.73E-39 3 6 6 9.4

O60832;O60832-2;C9IYT0;H7C0M1;H7BZF2;H7C2Q9;H7C2Q2 H/ACA ribonucleoprotein complex subunit 4 DKC1 >sp|O60832|DKC1_HUMAN H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3;>sp|O60832-2|DKC1_HUMAN Isoform 3 of H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1;>tr|C9IYT0|C9IYT0_HUMAN H/ACA ribonucleoprotein complex -0.23 0.71 0.02 0.59 -0.02 0.50 -1.20 -0.06 0.455594966 0.467048979 anatomical structure homeostasis;biological regulation;biosynthetic process;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome organization;DNA metabolic process;DNA replication;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;pseudouridine synthesis;regulation of biological quality;RNA metabolic process;RNA modification;RNA processing;RNA-dependent DNA replication;rRNA metabolic process;rRNA processing;telomere maintenance;telomere maintenance via telomerase;telomere maintenance via telomere lengthening;telomere organization "binding;catalytic activity;DNA polymerase activity;intramolecular transferase activity;isomerase activity;nucleic acid binding;nucleotidyltransferase activity;pseudouridine synthase activity;RNA binding;RNA-directed DNA polymerase activity;telomerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" Cajal body;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleolus;nucleoplasm;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;telomerase holoenzyme complex Ribosome biogenesis in eukaryotes 3.54E-39 7 6 6 15.6

P47813;O14602;A6NJH9 "Eukaryotic translation initiation factor 1A, X-chromosomal;Eukaryotic translation initiation factor 1A, Y-chromosomal" EIF1AX;EIF1AY ">sp|P47813|IF1AX_HUMAN Eukaryotic translation initiation factor 1A, X-chromosomal OS=Homo sapiens GN=EIF1AX PE=1 SV=2;>sp|O14602|IF1AY_HUMAN Eukaryotic translation initiation factor 1A, Y-chromosomal OS=Homo sapiens GN=EIF1AY PE=1 SV=4;>tr|A6NJH9|A6NJH9_HU" -0.04 -0.03 -0.29 -0.12 0.11 0.00 0.34 -0.02 0.958284428 -0.228089489 cellular process;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;intracellular part RNA transport 3.41E-34 3 6 6 55.6

P06730;P06730-2;P06730-3;D6RBW1;H0Y8J7;D6RFJ3 Eukaryotic translation initiation factor 4E EIF4E >sp|P06730|IF4E_HUMAN Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E PE=1 SV=2;>sp|P06730-2|IF4E_HUMAN Isoform 2 of Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E;>sp|P06730-3|IF4E_HUMAN Isoform 3 of Eukaryotic t -0.07 0.00 -0.02 -0.08 0.02 -0.13 0.08 -0.12 0.020615111 -0.00349159 anatomical structure development;biological regulation;catabolic process;cell cycle process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of RNA localization;G1/S transition of mitotic cell cycle;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;intracellular transport;lung development;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;organ development;positive regulation of biological process;positive regulation of cell cycle;positive regulation of cellular process;positive regulation of mitotic cell cycle;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;signal transduction;translational initiation;transmembrane receptor protein tyrosine kinase signaling pathway;transport;viral reproductive process;virus-host interaction "binding;nucleic acid binding;RNA binding;RNA cap binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;mRNA cap binding complex;non-membrane-bounded organelle;organelle;protein complex;ribonucleoprotein complex;RNA cap binding complex;RNA granule;RNAi effector complex;RNA-induced silencing complex;stress granule Insulin signaling pathway;mTOR signaling pathway;RNA transport 6.95E-41 6 6 6 39.2

P56537;P56537-2;B7ZBH1;F8WD20;F8WDS6 Eukaryotic translation initiation factor 6 EIF6 >sp|P56537|IF6_HUMAN Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1;>sp|P56537-2|IF6_HUMAN Isoform 2 of Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6;>tr|B7ZBH1|B7ZBH1_HUMAN Eukaryotic translation initiati 0.15 -0.02 -0.27 0.08 -0.56 -0.19 0.18 -0.09 0.334869525 0.148827549 cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of ribosome localization;intracellular transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;mature ribosome assembly;nuclear export;nuclear transport;nucleocytoplasmic transport;organelle assembly;ribonucleoprotein complex assembly;ribonucleoprotein complex biogenesis;ribonucleoprotein complex export from nucleus;ribonucleoprotein complex localization;ribonucleoprotein complex subunit organization;ribosomal large subunit biogenesis;ribosomal subunit export from nucleus;ribosome assembly;rRNA-containing ribonucleoprotein complex export from nucleus;transport "binding;nucleic acid binding;ribonucleoprotein binding;ribosomal large subunit binding;ribosome binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;protein complex Ribosome biogenesis in eukaryotes 1.58E-93 5 6 6 29

Q9UBC2-4;Q9UBC2-3;M0R165;Q9UBC2;Q9UBC2-2;M0R2S2;K7EJR2;M0R330;M0QX30;M0R1V5;M0R3I1 Epidermal growth factor receptor substrate 15-like 1 EPS15L1 >sp|Q9UBC2-4|EP15R_HUMAN Isoform 4 of Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens GN=EPS15L1;>sp|Q9UBC2-3|EP15R_HUMAN Isoform 3 of Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens GN=EPS15L1;>tr|M0R165|M0R165_HU -0.02 -0.22 0.39 0.21 0.07 0.17 -0.23 -0.10 0.269402421 0.110647846 biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;coated pit;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane 7.23E-46 11 6 6 12

Q01844-6;B0QYK0;Q01844-3;Q01844;Q01844-5;Q01844-2;C9JGE3;H7BY36;F8WC90;Q01844-4 RNA-binding protein EWS EWSR1 >sp|Q01844-6|EWS_HUMAN Isoform 6 of RNA-binding protein EWS OS=Homo sapiens GN=EWSR1;>tr|B0QYK0|B0QYK0_HUMAN RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=2 SV=1;>sp|Q01844-3|EWS_HUMAN Isoform 3 of RNA-binding protein EWS OS=Homo sapiens GN=EWSR1;>sp 0.07 0.04 -0.14 -0.06 0.19 -0.17 -0.78 -0.28 0.472754066 0.236172626 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 2.85E-86 10 6 6 17.5

Q96CS3 FAS-associated factor 2 FAF2 >sp|Q96CS3|FAF2_HUMAN FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2 -0.02 -0.11 -0.03 0.08 0.41 0.35 -0.42 1.67 0.499852877 -0.521451089 response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein binding;enzyme binding;protein binding;small conjugating protein binding;ubiquitin binding;ubiquitin protein ligase binding Cdc48p-Npl4p-Ufd1p AAA ATPase complex;cell part;cytoplasmic part;endoplasmic reticulum part;intracellular organelle part;intracellular part;lipid particle;macromolecular complex;membrane part;organelle part;protein complex 2.15E-20 1 6 6 22.5

Q96ME1-4;Q96ME1-2;H0Y6I6;F5H4Z4;Q96ME1;Q96ME1-3 F-box/LRR-repeat protein 18 FBXL18 >sp|Q96ME1-4|FXL18_HUMAN Isoform 4 of F-box/LRR-repeat protein 18 OS=Homo sapiens GN=FBXL18;>sp|Q96ME1-2|FXL18_HUMAN Isoform 2 of F-box/LRR-repeat protein 18 OS=Homo sapiens GN=FBXL18;>tr|H0Y6I6|H0Y6I6_HUMAN F-box/LRR-repeat protein 18 (Fragment) OS=Homo s -0.19 -0.17 0.21 0.08 -0.37 -0.19 0.34 -0.02 0.079823952 0.041591018 3.31E-16 6 6 6 11.1

P22570-6;P22570-5;P22570;P22570-2;P22570-7;P22570-3;P22570-4;J3QQX3;G3V0F2;J3KS64;J3QKZ8;J3QQW7 "NADPH:adrenodoxin oxidoreductase, mitochondrial"FDXR ">sp|P22570-6|ADRO_HUMAN Isoform 6 of NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR;>sp|P22570-5|ADRO_HUMAN Isoform 5 of NADPH:adrenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR;>sp|P22570|ADRO_HUMAN NADPH:adrenodoxi" 0.34 -0.48 -0.01 0.06 0.69 -0.05 0.29 -0.83 0.044770272 -0.048769847 alcohol metabolic process;biosynthetic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cholesterol metabolic process;coenzyme metabolic process;cofactor metabolic process;electron transport chain;generation of precursor metabolites and energy;heterocycle metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;NADP metabolic process;NADPH oxidation;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;ferredoxin-NADP+ reductase activity;NADP binding;NADPH binding;NADPH-adrenodoxin reductase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on iron-sulfur proteins as donors;oxidoreductase activity, acting on iron-sulfur proteins as donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part 3.59E-25 12 6 6 20.2

P39748;P39748-2;I3L3E9;F5H1Y3 Flap endonuclease 1 FEN1 >sp|P39748|FEN1_HUMAN Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1;>sp|P39748-2|FEN1_HUMAN Isoform FENMIT of Flap endonuclease 1 OS=Homo sapiens GN=FEN1;>tr|I3L3E9|I3L3E9_HUMAN Flap endonuclease 1 (Fragment) OS=Homo sapiens GN=FEN1 PE=4 SV=1;>tr|F 0.31 0.10 -0.07 -0.10 0.08 -0.80 -0.55 -1.21 1.013466984 0.684037387 "anatomical structure homeostasis;base-excision repair;behavior;biological regulation;biosynthetic process;catabolic process;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;cognition;DNA metabolic process;DNA recombination;DNA repair;DNA replication;DNA replication, removal of RNA primer;DNA-dependent DNA replication;double-strand break repair;homeostatic process;inositol lipid-mediated signaling;intracellular signal transduction;learning or memory;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;memory;metabolic process;mitotic recombination;multicellular organismal process;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;organelle organization;phosphatidylinositol-mediated signaling;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;RNA catabolic process;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;system process;telomere maintenance;telomere maintenance via recombination;telomere maintenance via semi-conservative replication;telomere maintenance via telomere lengthening;telomere organization;UV protection" "5'-3' exonuclease activity;5'-flap endonuclease activity;binding;catalytic activity;cation binding;damaged DNA binding;deoxyribonuclease activity;DNA binding;double-stranded DNA binding;double-stranded DNA specific exodeoxyribonuclease activity;endodeoxyribonuclease activity;endodeoxyribonuclease activity, producing 5'-phosphomonoesters;endonuclease activity;endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;endoribonuclease activity;endoribonuclease activity, producing 5'-phosphomonoesters;exodeoxyribonuclease activity;exodeoxyribonuclease activity, producing 5'-phosphomonoesters;exonuclease activity;exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;flap endonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;magnesium ion binding;manganese ion binding;metal ion binding;nuclease activity;nucleic acid binding;ribonuclease activity;ribonuclease H activity;structure-specific DNA binding;transition metal ion binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part Base excision repair;DNA replication;Non-homologous end-joining 9.23E-73 4 6 6 15.8

Q14192;J3KNW4 Four and a half LIM domains protein 2 FHL2 >sp|Q14192|FHL2_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=1 SV=3;>tr|J3KNW4|J3KNW4_HUMAN Four and a half LIM domains protein 2 OS=Homo sapiens GN=FHL2 PE=4 SV=1 -0.14 -0.19 -0.80 -0.07 -0.16 0.47 0.70 0.83 1.152056843 -0.763388641 "anatomical structure development;anatomical structure formation involved in morphogenesis;androgen receptor signaling pathway;atrial cardiac muscle cell development;biological regulation;biosynthetic process;cardiac cell development;cardiac muscle cell development;cell development;cell differentiation;cellular biosynthetic process;cellular developmental process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;developmental process;heart trabecula formation;intracellular receptor mediated signaling pathway;lipid metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;muscle cell development;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;osteoblast differentiation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;small molecule metabolic process;steroid hormone receptor signaling pathway;trabecula formation;transcription, DNA-dependent;ventricular cardiac muscle cell development" androgen receptor binding;binding;cation binding;hormone receptor binding;ion binding;metal ion binding;nuclear hormone receptor binding;protein binding;protein binding transcription factor activity;receptor binding;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasmic part;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;M band;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;Z disc Osteoclast differentiation 1.62E-15 2 6 6 24.7

Q6UN15-3;Q6UN15-5;Q6UN15;Q6UN15-4;H0Y8P7 Pre-mRNA 3-end-processing factor FIP1 FIP1L1 >sp|Q6UN15-3|FIP1_HUMAN Isoform 3 of Pre-mRNA 3-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1;>sp|Q6UN15-5|FIP1_HUMAN Isoform 5 of Pre-mRNA 3-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1;>sp|Q6UN15|FIP1_HUMAN Pre-mRNA 3-end-processing fac -0.07 0.34 0.20 0.31 0.08 -0.25 -1.20 -0.70 1.029278179 0.713012189 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing binding;nucleic acid binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mRNA cleavage and polyadenylation specificity factor complex;mRNA cleavage factor complex;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex mRNA surveillance pathway 1.44E-49 5 6 6 19.4

Q9NZU0 Leucine-rich repeat transmembrane protein FLRT3 FLRT3 >sp|Q9NZU0|FLRT3_HUMAN Leucine-rich repeat transmembrane protein FLRT3 OS=Homo sapiens GN=FLRT3 PE=1 SV=1 0.03 -0.01 0.49 0.12 -1.34 -0.50 -0.22 -0.32 1.123691581 0.752208937 biological adhesion;cell adhesion;cellular process "binding;binding, bridging;molecular transducer activity;protein binding;protein binding, bridging;receptor signaling protein activity;signal transducer activity" cell part;extracellular matrix;extracellular region part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part;proteinaceous extracellular matrix 8.83E-31 1 6 6 12.3

Q92820 Gamma-glutamyl hydrolase GGH >sp|Q92820|GGH_HUMAN Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 -0.38 -0.18 -0.19 0.00 1.96 1.46 0.35 0.14 1.109644319 -1.165858719 amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;glutamine family amino acid metabolic process;glutamine metabolic process;metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to hormone stimulus;response to inorganic substance;response to insulin stimulus;response to metal ion;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to zinc ion;small molecule metabolic process "catalytic activity;exopeptidase activity;gamma-glutamyl-peptidase activity;hydrolase activity;omega peptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;melanosome;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;vacuole;vesicle Folate biosynthesis 2.41E-22 1 6 6 22.6

F5H0U5;Q9NZD2;H0YFS9;F5GZ49 Glycolipid transfer protein GLTP >tr|F5H0U5|F5H0U5_HUMAN Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=2 SV=1;>sp|Q9NZD2|GLTP_HUMAN Glycolipid transfer protein OS=Homo sapiens GN=GLTP PE=1 SV=3 0.03 0.28 0.00 -0.10 0.82 1.06 0.76 -0.67 0.45584614 -0.44272152 establishment of localization;glycolipid transport;lipid transport;organic substance transport;transport binding;glycolipid binding;glycolipid transporter activity;lipid binding;lipid transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular part;membrane 1.10E-23 4 6 6 35.3

Q9Y5P6;Q9Y5P6-2 Mannose-1-phosphate guanyltransferase beta GMPPB >sp|Q9Y5P6|GMPPB_HUMAN Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2;>sp|Q9Y5P6-2|GMPPB_HUMAN Isoform 2 of Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB 0.24 -0.10 -0.70 -0.09 -0.31 -0.31 0.20 -0.43 0.072938028 0.051373366 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;dolichol-linked oligosaccharide biosynthetic process;GDP-mannose biosynthetic process;GDP-mannose metabolic process;glycosylation;hexose biosynthetic process;hexose metabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;mannose biosynthetic process;mannose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar biosynthetic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;small molecule biosynthetic process;small molecule metabolic process "binding;catalytic activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;guanylyltransferase activity;mannose-1-phosphate guanylyltransferase activity;mannose-phosphate guanylyltransferase activity;nucleotide binding;nucleotidyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Amino sugar and nucleotide sugar metabolism;Fructose and mannose metabolism 5.25E-42 2 6 6 22.5

P07203;P07203-2 Glutathione peroxidase 1 GPX1 >sp|P07203|GPX1_HUMAN Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4 0.02 -0.11 -0.19 -0.01 -0.01 -0.01 0.21 -0.06

0.571189162 -0.103253637 "acylglycerol metabolic process;amine metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;angiogenesis involved in wound healing;apoptotic mitochondrial changes;arachidonic acid metabolic process;biological regulation;blood vessel endothelial cell migration;carboxylic acid metabolic process;catabolic process;cell development;cell differentiation;cell migration;cell motility;cell proliferation;cell redox homeostasis;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;circulatory system process;developmental growth;developmental process;endothelial cell development;endothelial cell migration;epithelial cell development;fat cell differentiation;fatty acid metabolic process;glutathione metabolic process;glycerol ether metabolic process;glycerolipid metabolic process;growth;heart contraction;heart process;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;icosanoid metabolic process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of apoptosis by oxidative stress;induction of programmed cell death;interaction with symbiont;interspecies interaction between organisms;lipid metabolic process;lipoxygenase pathway;locomotion;macromolecule metabolic process;macromolecule modification;metabolic process;mitochondrion organization;monocarboxylic acid metabolic process;multicellular organismal homeostasis;multicellular organismal process;multi-organism process;muscle cell development;muscle cell differentiation;muscle fiber development;myoblast proliferation;myotube differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of defense response;negative regulation of hydrolase activity;negative regulation of immune response;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of inflammatory response to antigenic stimulus;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of response to external stimulus;negative regulation of response to stimulus;neurological system process;neutral lipid metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;peptide metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cellular process;positive regulation of intracellular protein kinase cascade;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein metabolic process;protein modification process;protein oxidation;purine base metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;reactive oxygen species metabolic process;regeneration;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of blood vessel size;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of defense response;regulation of developmental process;regulation of endopeptidase activity;regulation of epithelial cell proliferation;regulation of gene expression;regulation of gene expression, epigenetic;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of inflammatory response to antigenic stimulus;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of mammary gland epithelial cell proliferation;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of neuron apoptosis;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of protein catabolic process;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of proteolysis;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of tube size;release of cytochrome c from mitochondria;response to abiotic stimulus;response to bacterium;response to biotic stimulus;response to chemical stimulus;response to gamma radiation;response to hydrogen peroxide;response to hydroperoxide;response to inorganic substance;response to ionizing radiation;response to light stimulus;response to metal ion;response to other organism;response to oxidative stress;response to radiation;response to reactive oxygen species;response to selenium ion;response to stimulus;response to stress;response to symbiont;response to symbiotic bacterium;response to toxin;response to UV;response to xenobiotic stimulus;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;skeletal muscle cell differentiation;skeletal muscle fiber development;skeletal muscle tissue regeneration;small molecule metabolic process;striated muscle cell development;striated muscle cell differentiation;sulfur compound metabolic process;system process;temperature homeostasis;tissue development;tissue regeneration;triglyceride metabolic process;unsaturated fatty acid metabolic process;UV protection;vascular process in circulatory system;vasodilation;very long-chain fatty acid metabolic process" "antioxidant activity;catalytic activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;glutathione peroxidase activity;oxidoreductase activity;oxidoreductase activity, acting on peroxide as acceptor;peptidase inhibitor activity;peptidase regulator activity;peroxidase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Arachidonic acid metabolism;Glutathione metabolism 1.01E-43 2 6 6 34

P00390-2;P00390-3;P00390;P00390-5;P00390-4;E5RI06;H0YBD4;H0YC68 "Glutathione reductase, mitochondrial" GSR">sp|P00390-2|GSHR_HUMAN Isoform Cytoplasmic of Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR;>sp|P00390-3|GSHR_HUMAN Isoform 2 of Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR;>sp|P00390|GSHR_HUMAN Glutathione reductase, mitocho" 0.20 -0.12 0.33 0.23 0.23 -0.63 -0.62 -0.83 1.032850153 0.622817801 amine metabolic process;biological regulation;carboxylic acid metabolic process;cell redox homeostasis;cellular amine metabolic process;cellular amino acid metabolic process;cellular homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;glutathione metabolic process;homeostatic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;organic acid metabolic process;oxoacid metabolic process;peptide metabolic process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process;sulfur compound metabolic process "antioxidant activity;binding;catalytic activity;coenzyme binding;cofactor binding;disulfide oxidoreductase activity;electron carrier activity;flavin adenine dinucleotide binding;glutathione disulfide oxidoreductase activity;glutathione-disulfide reductase activity;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on NADH or NADPH;peptide disulfide oxidoreductase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Glutathione metabolism 7.30E-54 8 6 6 18.4

O00178;F5H716;F5H257;B0QY59 GTP-binding protein 1 GTPBP1 >sp|O00178|GTPB1_HUMAN GTP-binding protein 1 OS=Homo sapiens GN=GTPBP1 PE=1 SV=3;>tr|F5H716|F5H716_HUMAN GTP-binding protein 1 (Fragment) OS=Homo sapiens GN=GTPBP1 PE=2 SV=1 0.31 -0.07 0.06 0.05 0.12 -0.08 0.09 -0.12 0.33809823 0.085170176 biological regulation;cellular process;cellular response to stimulus;immune response;immune system process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA catabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA catabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;response to stimulus;signal transduction "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic exosome (RNase complex);cytoplasmic part;cytosol;exosome (RNase complex);intracellular part;macromolecular complex;protein complex 2.52E-26 4 6 6 12

D3DR31;P09914 Interferon-induced protein with tetratricopeptide repeats 1 IFIT1 >tr|D3DR31|D3DR31_HUMAN Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=2 SV=1;>sp|P09914|IFIT1_HUMAN Interferon-induced protein with tetratricopeptide repeats 1 OS=Homo sapiens GN=IFIT1 PE=1 SV=2 0.46 0.27 -0.43 -0.24 -1.04 -1.40 -0.17 -0.21 0.826721224 0.719955284 biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to dsRNA;cellular response to exogenous dsRNA;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;establishment of localization;establishment of localization in cell;establishment of protein localization;immune effector process;immune system process;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular protein transport in other organism involved in symbiotic interaction;intracellular transport;intracellular transport of viral proteins in host cell;multi-organism process;negative regulation of binding;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of defense response;negative regulation of defense response to virus;negative regulation of defense response to virus by host;negative regulation of helicase activity;negative regulation of hydrolase activity;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of molecular function;negative regulation of multi-organism process;negative regulation of protein binding;negative regulation of reproductive process;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of viral genome replication;negative regulation of viral reproduction;positive regulation of biological process;positive regulation of reproductive process;positive regulation of viral genome replication;positive regulation of viral reproduction;protein transport;regulation of binding;regulation of biological process;regulation of catalytic activity;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by host;regulation of helicase activity;regulation of hydrolase activity;regulation of immune effector process;regulation of immune system process;regulation of metabolic process;regulation of molecular function;regulation of multi-organism process;regulation of protein binding;regulation of reproductive process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of viral genome replication;regulation of viral reproduction;reproductive process;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;signal transduction;symbiont intracellular protein transport in host;transport;type I interferon-mediated signaling pathway;viral reproductive process binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular part Hepatitis C 6.06E-68 2 6 6 18.3

P29218;P29218-3;E5RG13;E5RIP7;H0YBL1;E5RG94;E5RIF4;E5RHE9;E5RI82;P29218-2;E5RGY4 Inositol monophosphatase 1 IMPA1 >sp|P29218|IMPA1_HUMAN Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1 PE=1 SV=1;>sp|P29218-3|IMPA1_HUMAN Isoform 3 of Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1;>tr|E5RG13|E5RG13_HUMAN Inositol monophosphatase 1 (Fragment) OS=Homo sapiens GN= 0.30 0.06 -0.03 -0.19 0.19 0.25 0.37 0.12 0.733128458 -0.198708988 alcohol biosynthetic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;dephosphorylation;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;inositol biosynthetic process;inositol metabolic process;inositol phosphate catabolic process;inositol phosphate dephosphorylation;inositol phosphate metabolic process;lipid biosynthetic process;lipid metabolic process;lipid modification;lipid phosphorylation;metabolic process;organophosphate catabolic process;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phosphatidylinositol phosphorylation;phospholipid biosynthetic process;phospholipid metabolic process;phosphorus metabolic process;phosphorylated carbohydrate dephosphorylation;phosphorylation;polyol biosynthetic process;polyol metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small molecule biosynthetic process;small molecule metabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;inositol monophosphate phosphatase activity;inositol or phosphatidylinositol phosphatase activity;inositol phosphate phosphatase activity;ion binding;metal ion binding;phosphatase activity;phosphoric ester hydrolase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle Inositol phosphate metabolism;Phosphatidylinositol signaling system;Streptomycin biosynthesis 1.25E-64 11 6 6 21.3

Q8WZA9;M0QZP8 Immunity-related GTPase family Q protein IRGQ >sp|Q8WZA9|IRGQ_HUMAN Immunity-related GTPase family Q protein OS=Homo sapiens GN=IRGQ PE=1 SV=1 0.14 0.16 -0.14 -0.14 -0.17 0.18 0.77 0.69 0.648740989 -0.361298654 1.80E-19 2 6 6 13.3

Q96EK5 KIF1-binding protein KIAA1279 >sp|Q96EK5|KBP_HUMAN KIF1-binding protein OS=Homo sapiens GN=KIAA1279 PE=1 SV=1 0.31 0.09 0.03 0.07 -0.16 -0.06 0.12 -0.09 0.841487757 0.173681839 anatomical structure development;cell differentiation;cellular developmental process;cellular process;developmental process;establishment of localization;establishment of localization in cell;intracellular transport;mitochondrial transport;nervous system development;system development;transport cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 2.76E-36 1 6 6 19.8

Q92615;H0Y641;H0Y4V9 La-related protein 4B LARP4B >sp|Q92615|LAR4B_HUMAN La-related protein 4B OS=Homo sapiens GN=LARP4B PE=1 SV=3;>tr|H0Y641|H0Y641_HUMAN La-related protein 4B (Fragment) OS=Homo sapiens GN=LARP4B PE=4 SV=1;>tr|H0Y4V9|H0Y4V9_HUMAN La-related protein 4B (Fragment) OS=Homo sapiens GN=LARP4B 0.14 0.13 0.13 0.01 0.10 -0.11 -0.12 -0.36 0.994254257 0.229158821 biological regulation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;polysomal ribosome;ribonucleoprotein complex;ribosome;RNA granule;stress granule 2.59E-37 3 6 6 10.6

P30533;D6REW6 Alpha-2-macroglobulin receptor-associated protein LRPAP1 >sp|P30533|AMRP_HUMAN Alpha-2-macroglobulin receptor-associated protein OS=Homo sapiens GN=LRPAP1 PE=1 SV=1 0.19 0.05 -0.07 -0.04 0.17 -0.15 0.26 0.00 0.13409517 -0.040177944 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;negative regulation of binding;negative regulation of biological process;negative regulation of lipoprotein particle clearance;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of protein binding;negative regulation of very-low-density lipoprotein particle clearance;primary metabolic process;protein folding;protein metabolic process;regulation of binding;regulation of biological process;regulation of lipoprotein particle clearance;regulation of molecular function;regulation of multicellular organismal process;regulation of protein binding;regulation of very-low-density lipoprotein particle clearance asialoglycoprotein receptor activity;binding;carbohydrate binding;cargo receptor activity;glycosaminoglycan binding;heparin binding;lipoprotein particle receptor binding;low-density lipoprotein particle receptor binding;pattern binding;polysaccharide binding;protein binding;receptor activity;receptor antagonist activity;receptor binding;receptor inhibitor activity;receptor regulator activity;unfolded protein binding cell part;cell surface;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular region;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;plasma membrane;rough endoplasmic reticulum lumen;vesicle 7.76E-28 2 6 6 21

P21397;P21397-2 Amine oxidase [flavin-containing] A MAOA >sp|P21397|AOFA_HUMAN Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1;>sp|P21397-2|AOFA_HUMAN Isoform 2 of Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA -0.05 0.46 -0.24 0.25 0.64 1.38 -0.77 0.82 0.340608165 -0.412553513 alcohol catabolic process;alcohol metabolic process;amine catabolic process;amine metabolic process;behavior;benzene-containing compound metabolic process;biological regulation;biosynthetic process;catabolic process;catecholamine catabolic process;catecholamine metabolic process;catechol-containing compound catabolic process;catechol-containing compound metabolic process;cellular amine metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;diol catabolic process;diol metabolic process;dopamine catabolic process;dopamine metabolic process;establishment of localization;establishment of localization in cell;metabolic process;neurotransmitter biosynthetic process;neurotransmitter catabolic process;neurotransmitter metabolic process;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;phenol-containing compound metabolic process;regulation of biological quality;regulation of neurotransmitter levels;response to stimulus;secretion;secretion by cell;signal release;small molecule catabolic process;small molecule metabolic process;transport;xenobiotic metabolic process "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH2 group of donors;oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor;primary amine oxidase activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane "Arginine and proline metabolism;Drug metabolism - cytochrome P450;Glycine, serine and threonine metabolism;Histidine metabolism;Isoquinoline alkaloid biosynthesis;Phenylalanine metabolism;Tryptophan metabolism;Tyrosine metabolism" 5.75E-23 2 6 6 14.6

Q99797 Mitochondrial intermediate peptidase MIPEP >sp|Q99797|MIPEP_HUMAN Mitochondrial intermediate peptidase OS=Homo sapiens GN=MIPEP PE=1 SV=2 -0.03 0.13 -0.29 0.24 -0.79 -0.88 -0.14 -0.32 1.089477296 0.548428681 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;mitochondrial protein processing;primary metabolic process;protein maturation;protein metabolic process;protein processing;protein processing involved in protein targeting to mitochondrion;proteolysis "binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part 5.92E-25 1 6 6 11.6

Q14165;F5H1S8;H0YG07;F5GX14 Malectin MLEC >sp|Q14165|MLEC_HUMAN Malectin OS=Homo sapiens GN=MLEC PE=1 SV=1;>tr|F5H1S8|F5H1S8_HUMAN Malectin (Fragment) OS=Homo sapiens GN=MLEC PE=2 SV=1;>tr|H0YG07|H0YG07_HUMAN Malectin (Fragment) OS=Homo sapiens GN=MLEC PE=4 SV=1 -0.22 0.14 -0.11 0.02 1.05 0.79 -0.61 0.35 0.484565289 -0.435937482 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine binding;carbohydrate binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part 9.28E-91 4 6 6 27.1

C9JX83;O00566 U3 small nucleolar ribonucleoprotein protein MPP10 MPHOSPH10 >tr|C9JX83|C9JX83_HUMAN U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=2 SV=1;>sp|O00566|MPP10_HUMAN U3 small nucleolar ribonucleoprotein protein MPP10 OS=Homo sapiens GN=MPHOSPH10 PE=1 SV=2 -0.54 1.16 -0.03 1.19 -0.64 0.25 -1.27 0.38 0.552951156 0.768047468 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;rRNA metabolic process;rRNA processing" cell part;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes 1.35E-28 2 6 6 20.5

P41227;P41227-2;F8W808;A8MWP7;C9JN83;C9JW55;Q9BSU3;H0Y8T0 N-alpha-acetyltransferase 10 NAA10 >sp|P41227|NAA10_HUMAN N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1;>sp|P41227-2|NAA10_HUMAN Isoform 2 of N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10;>tr|F8W808|F8W808_HUMAN N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 0.06 -0.01 -0.05 0.08 -0.39 -0.22 0.01 -0.34 1.143726222 0.255030025 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;DNA conformation change;DNA metabolic process;DNA packaging;internal protein amino acid acetylation;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;N-terminal protein amino acid acetylation;N-terminal protein amino acid modification;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process"acetyltransferase activity;catalytic activity;N-acetyltransferase activity;N-acyltransferase activity;peptide alpha-N-acetyltransferase activity;peptide N-acetyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part 8.71E-26 8 6 6 36.2

E7ENA9;Q92542-2;Q92542;H0Y6T7;F6Y097;Q5T205;H0Y3Z4;Q5T209 Nicastrin NCSTN >tr|E7ENA9|E7ENA9_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=2 SV=2;>sp|Q92542-2|NICA_HUMAN Isoform 2 of Nicastrin OS=Homo sapiens GN=NCSTN;>sp|Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2;>tr|H0Y6T7|H0Y6T7_HUMAN Nicastrin (Fragment) OS= -0.15 0.05 -0.04 0.04 0.34 0.18 -0.34 -0.20 0.043286132 -0.021538781 amyloid precursor protein catabolic process;amyloid precursor protein metabolic process;beta-amyloid metabolic process;biological regulation;catabolic process;cell activation;cell proliferation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;epithelial cell proliferation;glycoprotein catabolic process;glycoprotein metabolic process;homeostasis of number of cells;homeostatic process;immune system process;leukocyte activation;leukocyte proliferation;lymphocyte activation;lymphocyte proliferation;macromolecule catabolic process;macromolecule metabolic process;membrane protein ectodomain proteolysis;membrane protein intracellular domain proteolysis;membrane protein proteolysis;metabolic process;mononuclear cell proliferation;myeloid cell homeostasis;nerve growth factor receptor signaling pathway;Notch receptor processing;Notch signaling pathway;positive regulation of catalytic activity;positive regulation of molecular function;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular process;regulation of metabolic process;regulation of molecular function;response to stimulus;signal transduction;T cell activation;T cell proliferation;transmembrane receptor protein tyrosine kinase signaling pathway "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;plasma membrane part;vacuolar membrane;vacuolar part;vesicle Alzheimer's disease;Notch signaling pathway 9.76E-46 8 6 6 16.2

B4DYB4;Q8NFH5;C9IYQ7;F8WCF5;F8WEL4;B4DP57;C9JIY9;C9JWU7 Nucleoporin NUP53 NUP35 >tr|B4DYB4|B4DYB4_HUMAN Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=2 SV=1;>sp|Q8NFH5|NUP53_HUMAN Nucleoporin NUP53 OS=Homo sapiens GN=NUP35 PE=1 SV=1;>tr|C9IYQ7|C9IYQ7_HUMAN Nucleoporin NUP53 (Fragment) OS=Homo sapiens GN=NUP35 PE=2 SV=1;>tr|F8WCF5|F8WC -0.14 0.84 0.11 0.78 -0.03 0.08 -1.51 0.07 0.691693847 0.742583039 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;metabolic process;monosaccharide transport;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;organic substance transport;primary metabolic process;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process cell part;cytoskeleton;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;nuclear pore;organelle;organelle membrane;organelle part;plasma membrane;pore complex;protein complex RNA transport 2.03E-53 8 6 6 29.1

Q9NX40;D6RDK6;D6RBN5;D6RG39;D6RIT9;Q9NX40-3;Q9NX40-2;Q9NX40-4;D6RI08;D6RDK1;D6RIV2;D6R9T5;D6R918;D6RBC5;D6RDI5;D6RA54;D6RC55 OCIA domain-containing protein 1 OCIAD1 >sp|Q9NX40|OCAD1_HUMAN OCIA domain-containing protein 1 OS=Homo sapiens GN=OCIAD1 PE=1 SV=1;>tr|D6RDK6|D6RDK6_HUMAN OCIA domain-containing protein 1 (Fragment) OS=Homo sapiens GN=OCIAD1 PE=2 SV=1;>tr|D6RBN5|D6RBN5_HUMAN OCIA domain-containing protein 1 OS= -0.45 0.52 -0.15 0.63 0.18 0.44 -1.35 0.51 0.139000721 0.195999596 cell part;cytoplasmic part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 3.91E-60 17 6 6 22.9

Q9NZT2-2;Q9NZT2;Q4VXW4 Opioid growth factor receptor OGFR >sp|Q9NZT2-2|OGFR_HUMAN Isoform 2 of Opioid growth factor receptor OS=Homo sapiens GN=OGFR;>sp|Q9NZT2|OGFR_HUMAN Opioid growth factor receptor OS=Homo sapiens GN=OGFR PE=1 SV=3;>tr|Q4VXW4|Q4VXW4_HUMAN Opioid growth factor receptor OS=Homo sapiens GN=OGFR P 0.28 0.17 0.01 -0.13 0.30 0.03 0.09 -0.05 0.026640781 -0.009559996 biological regulation;regulation of biological process;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of growth "binding;G-protein coupled receptor activity;molecular transducer activity;opioid receptor activity;peptide binding;peptide receptor activity;peptide receptor activity, G-protein coupled;receptor activity;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle 1.83E-63 3 6 6 14.5

H7C487;Q9BXB5-2;Q9BXB5;Q9BXB4;H7C199 Oxysterol-binding protein;Oxysterol-binding protein-related protein 10 OSBPL10 >tr|H7C487|H7C487_HUMAN Oxysterol-binding protein (Fragment) OS=Homo sapiens GN=OSBPL10 PE=3 SV=1;>sp|Q9BXB5-2|OSB10_HUMAN Isoform 2 of Oxysterol-binding protein-related protein 10 OS=Homo sapiens GN=OSBPL10;>sp|Q9BXB5|OSB10_HUMAN Oxysterol-binding protein 0.22 0.07 0.11 -0.12 -0.33 -0.48 0.32 0.01 0.406357422 0.191100904 biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;establishment of localization;fat cell differentiation;lipid transport;organic substance transport;positive regulation of biological process;positive regulation of lipid storage;positive regulation of sequestering of triglyceride;regulation of biological process;regulation of lipid storage;regulation of localization;regulation of sequestering of triglyceride;transport binding;cholesterol binding;lipid binding;phospholipid binding;steroid binding;sterol binding 1.06E-12 5 6 6 14.3

Q9BVG4;A6NDF3 Protein PBDC1 PBDC1 >sp|Q9BVG4|PBDC1_HUMAN Protein PBDC1 OS=Homo sapiens GN=PBDC1 PE=1 SV=1;>tr|A6NDF3|A6NDF3_HUMAN Protein PBDC1 OS=Homo sapiens GN=PBDC1 PE=2 SV=2 0.12 0.00 0.07 0.09 -0.61 -0.34 0.18 -0.10 0.725236735 0.291394799 2.62E-39 2 6 6 29.6

Q96JY6;Q96JY6-3;Q96JY6-5;C9JS55;Q96JY6-4;C9J0X3;C9K0F0;C9JSR2;E5RGS7;H0YBP7;C9J760;Q96JY6-2;F8WFB8;H7C1D1 PDZ and LIM domain protein 2 PDLIM2 >sp|Q96JY6|PDLI2_HUMAN PDZ and LIM domain protein 2 OS=Homo sapiens GN=PDLIM2 PE=1 SV=1;>sp|Q96JY6-3|PDLI2_HUMAN Isoform 3 of PDZ and LIM domain protein 2 OS=Homo sapiens GN=PDLIM2;>sp|Q96JY6-5|PDLI2_HUMAN Isoform 5 of PDZ and LIM domain protein 2 OS=Homo 0.47 0.05 0.22 0.01 -1.90 -0.91 -0.20 0.00 0.910199436 0.940324582 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell surface;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeleton;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 3.46E-76 14 6 6 26.7

Q9BTU6;E9PAM4 Phosphatidylinositol 4-kinase type 2-alpha PI4K2A >sp|Q9BTU6|P4K2A_HUMAN Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=1 SV=1;>tr|E9PAM4|E9PAM4_HUMAN Phosphatidylinositol 4-kinase type 2-alpha OS=Homo sapiens GN=PI4K2A PE=4 SV=1 -0.08 0.16 -0.08 -0.12 0.39 0.45 -0.13 0.13 0.697284084 -0.24056592 basophil activation;basophil activation involved in immune response;basophil degranulation;biosynthetic process;cell activation;cell activation involved in immune response;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;establishment of localization;establishment of localization in cell;exocytosis;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;leukocyte degranulation;lipid biosynthetic process;lipid metabolic process;metabolic process;myeloid cell activation involved in immune response;myeloid leukocyte activation;organophosphate metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;regulated secretory pathway;secretion;secretion by cell;small molecule metabolic process;transport;vesicle-mediated transport "1-phosphatidylinositol 4-kinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;AP-3 adaptor complex binding;ATP binding;binding;catalytic activity;cation binding;inositol or phosphatidylinositol kinase activity;ion binding;kinase activity;lipid kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphatidylinositol kinase activity;phosphotransferase activity, alcohol group as acceptor;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell body;cell junction;cell part;cell pole;cell projection;cell tip;clathrin coated vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;dendrite;early endosome membrane;endosomal part;endosome;endosome membrane;exocytic vesicle;extracellular region part;growing cell tip;host cell membrane;host cell part;host cell presynaptic membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;neuron projection;neuronal cell body;organelle;organelle membrane;organelle part;other organism cell membrane;other organism membrane;other organism part;other organism presynaptic membrane;perikaryon;plasma membrane part;presynaptic membrane;protein complex;site of polarized growth;synapse part;synaptic membrane;synaptic vesicle membrane;transport vesicle;vesicle;vesicle membrane Inositol phosphate metabolism;Phosphatidylinositol signaling system 1.84E-34 2 6 6 19.6

Q8TBX8-3;Q8TBX8;Q8TBX8-2;H0YIJ6;F8VNT5;F8VU68 Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma PIP4K2C >sp|Q8TBX8-3|PI42C_HUMAN Isoform 3 of Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens GN=PIP4K2C;>sp|Q8TBX8|PI42C_HUMAN Phosphatidylinositol 5-phosphate 4-kinase type-2 gamma OS=Homo sapiens GN=PIP4K2C PE=1 SV=3;>sp|Q8TBX8-2|PI42C_HU -0.19 -0.08 0.00 -0.07 -0.52 0.32 0.75 0.34 0.480019665 -0.311986219 cellular lipid metabolic process;cellular metabolic process;cellular process;glycerolipid metabolic process;glycerophospholipid metabolic process;lipid metabolic process;lipid modification;lipid phosphorylation;metabolic process;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphatidylinositol metabolic process;phosphatidylinositol phosphorylation;phospholipid metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process "1-phosphatidylinositol-5-phosphate 4-kinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;inositol or phosphatidylinositol kinase activity;kinase activity;lipid kinase activity;nucleotide binding;phosphatidylinositol phosphate kinase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle Inositol phosphate metabolism;Phosphatidylinositol signaling system;Regulation of actin cytoskeleton 1.69E-28 6 6 6 15.6

O75038-3;O75038;O75038-2;O75038-4;B9DI82;B9DI81;O75038-5;A6NGX9 "1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2" PLCH2 ">sp|O75038-3|PLCH2_HUMAN Isoform 3 of 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2 OS=Homo sapiens GN=PLCH2;>sp|O75038|PLCH2_HUMAN 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase eta-2 OS=Homo sapiens GN=PLCH2 PE=2 SV=3;>sp|O75" 0.10 0.21 0.23 0.09 -2.03 -1.34 -0.15 -0.11 0.960527903 1.066181628 biological regulation;catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;glycerolipid metabolic process;glycerophospholipid metabolic process;inositol phosphate metabolic process;intracellular signal transduction;lipid catabolic process;lipid metabolic process;metabolic process;organophosphate metabolic process;phosphatidylinositol metabolic process;phospholipid metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction "binding;calcium ion binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lipase activity;lipid binding;metal ion binding;molecular transducer activity;phosphatidylinositol phospholipase C activity;phospholipase activity;phospholipase C activity;phospholipid binding;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;signal transducer activity" cell part;cytoplasm;intracellular part;membrane;plasma membrane 1.72E-29 8 6 6 7.5

Q8IY17-5;Q8IY17-2;Q8IY17-3;Q8IY17;Q8IY17-4;M0R2H4;M0R2K2 Neuropathy target esterase PNPLA6 >sp|Q8IY17-5|PLPL6_HUMAN Isoform 5 of Neuropathy target esterase OS=Homo sapiens GN=PNPLA6;>sp|Q8IY17-2|PLPL6_HUMAN Isoform 2 of Neuropathy target esterase OS=Homo sapiens GN=PNPLA6;>sp|Q8IY17-3|PLPL6_HUMAN Isoform 3 of Neuropathy target esterase OS=Homo s -0.06 -0.01 -0.12 0.14 0.69 0.83 -0.08 0.47 0.996068867 -0.48573012 alcohol metabolic process;amine metabolic process;catabolic process;cell death;cellular amine metabolic process;cellular biogenic amine metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;ethanolamine-containing compound metabolic process;glycerolipid metabolic process;glycerophospholipid metabolic process;lipid catabolic process;lipid metabolic process;metabolic process;nitrogen compound metabolic process;organophosphate metabolic process;phosphatidylcholine metabolic process;phospholipid metabolic process;primary metabolic process;small molecule metabolic process "carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;lysophospholipase activity;phospholipase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Glycerophospholipid metabolism 5.35E-25 7 6 6 10

P49593;B7Z2C3;A8MX49;B5MCT7;C9J2F3;C9JL74 Protein phosphatase 1F PPM1F >sp|P49593|PPM1F_HUMAN Protein phosphatase 1F OS=Homo sapiens GN=PPM1F PE=1 SV=3;>tr|B7Z2C3|B7Z2C3_HUMAN Protein phosphatase 1F OS=Homo sapiens GN=PPM1F PE=2 SV=1;>tr|A8MX49|A8MX49_HUMAN Protein phosphatase 1F OS=Homo sapiens GN=PPM1F PE=2 SV=2;>tr|B5MCT7| 0.37 0.22 0.57 -0.03 0.51 0.24 0.24 -0.11 0.130017262 0.064443898 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to drug;cellular response to stimulus;dephosphorylation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of peptidyl-serine phosphorylation;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;peptidyl-threonine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of actin filament bundle assembly;positive regulation of behavior;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of cytoskeleton organization;positive regulation of epithelial cell migration;positive regulation of focal adhesion assembly;positive regulation of gene expression;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of peptidase activity;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of stress fiber assembly;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of behavior;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytoskeleton organization;regulation of endopeptidase activity;regulation of epithelial cell migration;regulation of focal adhesion assembly;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidase activity;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to external stimulus;regulation of response to stimulus;regulation of RNA metabolic process;regulation of stress fiber assembly;regulation of transcription, DNA-dependent;response to chemical stimulus;response to drug;response to stimulus" "binding;calcium-dependent protein serine/threonine phosphatase activity;calmodulin-dependent protein phosphatase activity;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;kinase activity;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;perinuclear region of cytoplasm;protein complex 1.93E-32 6 6 6 22.9

P63151;P63151-2;E5RIY1;E5RFR9;Q00005-6;Q00005;Q00005-2;Q00005-3;Q66LE6;Q00005-4;Q00005-5;Q00005-7;F5GXJ6;Q9Y2T4-3;Q9Y2T4-4;Q9Y2T4-2;Q9Y2T4 Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoformPPP2R2A >sp|P63151|2ABA_HUMAN Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1;>sp|P63151-2|2ABA_HUMAN Isoform 2 of Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isof 0.21 0.06 -0.14 -0.10 -0.16 0.04 0.38 -0.06 0.108454095 -0.043230678 "anaphase;anatomical structure development;apoptotic mitochondrial changes;biological regulation;brain development;catabolic process;cell cycle phase;cell cycle process;cell development;cell differentiation;cell division;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;dephosphorylation;developmental process;developmental process involved in reproduction;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;exit from mitosis;gene expression;germ cell development;intracellular protein transport;intracellular transport;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane organization;metabolic process;mitochondrial fission;mitochondrial fragmentation involved in apoptosis;mitochondrial transport;mitochondrion organization;mitotic anaphase;mitotic nuclear envelope reassembly;mitotic prophase;mRNA catabolic process;mRNA metabolic process;neuron differentiation;nitrogen compound metabolic process;nuclear envelope organization;nuclear envelope reassembly;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle fission;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of neuron apoptosis;positive regulation of programmed cell death;primary metabolic process;prophase;protein dephosphorylation;protein import;protein metabolic process;protein modification process;protein targeting;protein targeting to mitochondrion;protein transport;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of programmed cell death;regulation of protein phosphatase type 2A activity;reproductive process;response to alkaloid;response to chemical stimulus;response to isoquinoline alkaloid;response to morphine;response to organic cyclic compound;response to organic substance;response to stimulus;response to stress;RNA catabolic process;RNA metabolic process;signal transduction;spermatid development;transport" "catalytic activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphatase regulator activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein serine/threonine phosphatase activity" cell part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;non-membrane-bounded organelle;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex Cell cycle - yeast;Chagas disease (American trypanosomiasis);Hepatitis C;mRNA surveillance pathway;Tight junction 4.04E-93 17 6 6 18.8

Q13131;Q13131-2;Q96E92;P54646 5-AMP-activated protein kinase catalytic subunit alpha-1;5-AMP-activated protein kinase catalytic subunit alpha-2 PRKAA1;PRKAA2 >sp|Q13131|AAPK1_HUMAN 5-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1 PE=1 SV=4;>sp|Q13131-2|AAPK1_HUMAN Isoform 2 of 5-AMP-activated protein kinase catalytic subunit alpha-1 OS=Homo sapiens GN=PRKAA1;>tr|Q96E92|Q96E92 -0.08 0.10 -0.18 0.24 -0.27 0.09 0.20 -0.22 0.166140976 0.067423329 "activation of MAPK activity;alcohol metabolic process;amine transport;amino acid transmembrane transport;amino acid transport;autophagy;betaine transport;biological regulation;biosynthetic process;carbohydrate homeostasis;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;carnitine shuttle;carnitine transport;catabolic process;cation transport;cell communication;cell cycle arrest;cell cycle process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to ethanol;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to hormone stimulus;cellular response to hydrogen peroxide;cellular response to hypoxia;cellular response to insulin stimulus;cellular response to nutrient levels;cellular response to organic substance;cellular response to oxidative stress;cellular response to oxygen levels;cellular response to peptide hormone stimulus;cellular response to reactive oxygen species;cellular response to starvation;cellular response to stimulus;cellular response to stress;chemical homeostasis;cholesterol biosynthetic process;cholesterol metabolic process;cold acclimation;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;fatty acid biosynthetic process;fatty acid homeostasis;fatty acid metabolic process;fatty acid oxidation;fatty acid transport;generation of precursor metabolites and energy;glucose homeostasis;glucose metabolic process;hexose metabolic process;homeostatic process;insulin receptor signaling pathway;intracellular lipid transport;intracellular transport;ion transport;lipid biosynthetic process;lipid homeostasis;lipid metabolic process;lipid modification;lipid oxidation;lipid transport;long-chain fatty acid transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;membrane organization;metabolic process;mitochondrial transport;monocarboxylic acid metabolic process;monocarboxylic acid transport;monosaccharide metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catabolic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of glucosylceramide biosynthetic process;negative regulation of lipid biosynthetic process;negative regulation of lipid catabolic process;negative regulation of lipid metabolic process;negative regulation of metabolic process;negative regulation of programmed cell death;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of sphingolipid biosynthetic process;negative regulation of TOR signaling cascade;nitrogen compound metabolic process;nitrogen compound transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic acid transport;organic cation transport;organic substance transport;oxidation-reduction process;oxoacid metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of autophagy;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of carbohydrate metabolic process;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular carbohydrate metabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cholesterol biosynthetic process;positive regulation of cholesterol metabolic process;positive regulation of gene expression;positive regulation of glucose metabolic process;positive regulation of glycolysis;positive regulation of kinase activity;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of steroid biosynthetic process;positive regulation of steroid metabolic process;positive regulation of transferase activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein metabolic process;protein modification process;protein oligomerization;protein phosphorylation;quaternary ammonium group transport;regulation of apoptosis;regulation of autophagy;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular ketone metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ceramide biosynthetic process;regulation of cholesterol biosynthetic process;regulation of cholesterol metabolic process;regulation of circadian rhythm;regulation of energy homeostasis;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of gene expression;regulation of generation of precursor metabolites and energy;regulation of glucose metabolic process;regulation of glucosylceramide biosynthetic process;regulation of glycolysis;regulation of homeostatic process;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid catabolic process;regulation of lipid metabolic process;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of sphingolipid biosynthetic process;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of TOR signaling cascade;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transport;regulation of vesicle-mediated transport;response to abiotic stimulus;response to activity;response to alkaloid;response to caffeine;response to chemical stimulus;response to cold;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to hydrogen peroxide;response to hypoxia;response to inorganic substance;response to insulin stimulus;response to nutrient levels;response to organic cyclic compound;response to organic substance;response to oxidative stress;response to oxygen levels;response to peptide hormone stimulus;response to purine-containing compound;response to reactive oxygen species;response to starvation;response to stimulus;response to stress;response to temperature stimulus;rhythmic process;RNA biosynthetic process;RNA metabolic process;signal transduction;small molecule biosynthetic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport;Wnt receptor signaling pathway" "[acetyl-CoA carboxylase] kinase activity;[hydroxymethylglutaryl-CoA reductase (NADPH)] kinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;AMP-activated protein kinase activity;ATP binding;binding;cAMP-dependent protein kinase activity;catalytic activity;cation binding;chromatin binding;cyclic nucleotide-dependent protein kinase activity;histone kinase activity;histone serine kinase activity;ion binding;kinase activity;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;tau-protein kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" AMP-activated protein kinase complex;apical plasma membrane;cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane part;protein complex Adipocytokine signaling pathway;Hypertrophic cardiomyopathy (HCM);Insulin signaling pathway;mTOR signaling pathway;Regulation of autophagy 7.61E-35 4 6 6 13.6

O94903;E5RG77;E5RFZ4;E5RFX7;H0YBG2 Proline synthase co-transcribed bacterial homolog protein PROSC >sp|O94903|PROSC_HUMAN Proline synthase co-transcribed bacterial homolog protein OS=Homo sapiens GN=PROSC PE=1 SV=1;>tr|E5RG77|E5RG77_HUMAN Proline synthase co-transcribed bacterial homolog protein (Fragment) OS=Homo sapiens GN=PROSC PE=2 SV=1 -0.09 -0.28 -0.18 0.11 -0.71 -0.43 0.33 -0.18 0.223120109 0.137961537 binding;cofactor binding;pyridoxal phosphate binding;vitamin B6 binding;vitamin binding cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 2.21E-43 5 6 6 26.2

P28066;P28066-2 Proteasome subunit alpha type-5 PSMA5 >sp|P28066|PSA5_HUMAN Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3;>sp|P28066-2|PSA5_HUMAN Isoform 2 of Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 -0.02 0.05 0.01 -0.05 -0.08 -0.12 -0.07 -0.01 0.827594683 0.060648956 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex" Proteasome 9.26E-80 2 6 6 24.9

P28070 Proteasome subunit beta type-4 PSMB4 >sp|P28070|PSB4_HUMAN Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4 0.08 0.04 -0.59 0.00 -0.29 -0.12 -0.18 -0.08 0.109815511 0.051072017 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of defense response;negative regulation of immune response;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of inflammatory response to antigenic stimulus;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of inflammatory response to antigenic stimulus;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "binding;catalytic activity;endopeptidase activity;hydrolase activity;lipopolysaccharide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome core complex;protein complex Proteasome 2.58E-66 1 6 6 30.7

P28072;I3L3X7 Proteasome subunit beta type-6 PSMB6 >sp|P28072|PSB6_HUMAN Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 0.15 0.06 0.04 -0.03 0.03 -0.01 -0.01 -0.01 0.61909842 0.056587561 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome core complex;protein complexProteasome 1.76E-25 2 6 6 23.8

Q05397-2;Q8IYN9;H0YBP1;Q05397;Q05397-5;J3QT16;E7ESA6;E9PEI4;Q8N9D7;H0YB16;H0YBZ1;E5RHD8;Q05397-6;B4DWJ1;E5RI03;Q05397-3;H0YB99;Q05397-4 Focal adhesion kinase 1 PTK2 >sp|Q05397-2|FAK1_HUMAN Isoform 2 of Focal adhesion kinase 1 OS=Homo sapiens GN=PTK2;>tr|Q8IYN9|Q8IYN9_HUMAN Focal adhesion kinase 1 OS=Homo sapiens GN=PTK2 PE=2 SV=1;>tr|H0YBP1|H0YBP1_HUMAN Focal adhesion kinase 1 (Fragment) OS=Homo sapiens GN=PTK2 PE=4 S 0.19 -0.08 -0.01 0.02 -0.20 0.05 0.35 0.21 0.200053107 -0.069949034 anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;anion homeostasis;axon guidance;axonogenesis;biological regulation;cell activation;cell differentiation;cell migration;cell motility;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell surface receptor linked signaling pathway;cellular anion homeostasis;cellular chemical homeostasis;cellular chloride ion homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular monovalent inorganic anion homeostasis;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to growth hormone stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;central nervous system neuron axonogenesis;chemical homeostasis;chemotaxis;chloride ion homeostasis;cytoskeleton organization;defense response;developmental process;embryo development;endothelial cell migration;enzyme linked receptor protein signaling pathway;ephrin receptor signaling pathway;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of nucleus localization;establishment of organelle localization;establishment or maintenance of cell polarity;extracellular matrix organization;extracellular structure organization;fat cell differentiation;growth hormone receptor signaling pathway;heart morphogenesis;homeostatic process;immune response;immune system process;innate immune response;integrin-mediated signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;ion homeostasis;JNK cascade;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;microtubule cytoskeleton organization;microtubule-based process;monovalent inorganic anion homeostasis;negative regulation of anoikis;negative regulation of apoptosis;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell projection organization;negative regulation of cell-cell adhesion;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of growth;negative regulation of locomotion;negative regulation of nervous system development;negative regulation of neurogenesis;negative regulation of organ growth;negative regulation of programmed cell death;negative regulation of synapse assembly;netrin-activated signaling pathway;neuron migration;neuron projection morphogenesis;organ development;organ morphogenesis;organelle organization;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;placenta development;platelet activation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of endocytosis;positive regulation of glial cell proliferation;positive regulation of gliogenesis;positive regulation of growth;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of neurogenesis;positive regulation of neurological system process;positive regulation of phagocytosis;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phosphatidylinositol 3-kinase cascade;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smooth muscle cell migration;positive regulation of smooth muscle cell proliferation;positive regulation of synaptic transmission;positive regulation of transferase activity;positive regulation of transmission of nerve impulse;positive regulation of transport;positive regulation of vasodilation;primary metabolic process;protein autophosphorylation;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification process;protein phosphorylation;regulation of anatomical structure morphogenesis;regulation of anoikis;regulation of apoptosis;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cell proliferation;regulation of cell shape;regulation of cell-cell adhesion;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of developmental process;regulation of endocytosis;regulation of endothelial cell migration;regulation of focal adhesion assembly;regulation of glial cell proliferation;regulation of gliogenesis;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organ growth;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphatidylinositol 3-kinase cascade;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein ubiquitination;regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process;regulation of proteolysis;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of Rho GTPase activity;regulation of signal transduction;regulation of signaling;regulation of smooth muscle cell migration;regulation of smooth muscle cell proliferation;regulation of synapse assembly;regulation of synapse organization;regulation of synaptic transmission;regulation of system process;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of transport;regulation of vasodilation;regulation of vesicle-mediated transport;response to abiotic stimulus;response to arsenic-containing substance;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to external stimulus;response to glucose stimulus;response to growth hormone stimulus;response to hexose stimulus;response to hormone stimulus;response to inorganic substance;response to mechanical stimulus;response to monosaccharide stimulus;response to organic nitrogen;response to organic substance;response to peptide hormone stimulus;response to steroid hormone stimulus;response to stimulus;response to stress;signal complex assembly;signal transduction;stress-activated protein kinase signaling cascade;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;vasculogenesis "actin binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cytoskeletal protein binding;enzyme binding;JUN kinase binding;kinase activity;kinase binding;molecular transducer activity;non-membrane spanning protein tyrosine kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein kinase binding;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups"adherens junction;anchoring junction;apical plasma membrane;basolateral plasma membrane;cell cortex;cell junction;cell part;cell projection;cell-cell contact zone;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;focal adhesion;intercalated disc;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear body;nuclear part;nucleolus;nucleoplasm part;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;sarcolemma Amoebiasis;Axon guidance;Bacterial invasion of epithelial cells;Chemokine signaling pathway;ErbB signaling pathway;Focal adhesion;Leukocyte transendothelial migration;Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer;VEGF signaling pathway 1.84E-21 18 6 6 8.8

P43487;C9JXG8;C9JJ34;C9JDM3;C9JGV6;C9JIC6;H7C137;B3KUP2 Ran-specific GTPase-activating protein RANBP1 >sp|P43487|RANG_HUMAN Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1;>tr|C9JXG8|C9JXG8_HUMAN Ran-specific GTPase-activating protein (Fragment) OS=Homo sapiens GN=RANBP1 PE=2 SV=2;>tr|C9JJ34|C9JJ34_HUMAN Ran-specific GTPase-activ 0.09 0.05 0.01 0.00 0.06 -0.41 0.04 -0.21 0.624405079 0.168940642 biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;cytoskeleton organization;establishment of localization;establishment of localization in cell;intracellular transport;microtubule cytoskeleton organization;microtubule-based process;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of centrosome cycle;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of mitotic centrosome separation;positive regulation of molecular function;positive regulation of organelle organization;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of centrosome cycle;regulation of cytoskeleton organization;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic centrosome separation;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;reproductive process;response to stimulus;signal transduction;spindle organization;transport;viral reproductive process binding;enzyme activator activity;enzyme binding;enzyme regulator activity;GDP-dissociation inhibitor activity;GTPase activator activity;GTPase binding;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;Ran GTPase binding;Ras GTPase binding;small GTPase binding;small GTPase regulator activity cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;envelope;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;microtubule organizing center;non-membrane-bounded organelle;nuclear envelope;nuclear part;organelle;organelle envelope;organelle part 2.12E-61 8 6 6 38.8

Q6NUM9;Q6NUM9-2;G5E9N3;H7BZ81;H7C3J0;H7BZ16;H0YGU3 "All-trans-retinol 13,14-reductase"RETSAT ">sp|Q6NUM9|RETST_HUMAN All-trans-retinol 13,14-reductase OS=Homo sapiens GN=RETSAT PE=1 SV=2;>sp|Q6NUM9-2|RETST_HUMAN Isoform 2 of All-trans-retinol 13,14-reductase OS=Homo sapiens GN=RETSAT;>tr|G5E9N3|G5E9N3_HUMAN All-trans-13,14-dihydroretinol saturase," -0.44 -0.23 0.08

0.22 -0.04 0.17 0.20 0.12 0.540187581 -0.202666025 biological regulation;cellular hormone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;diterpenoid metabolic process;fat-soluble vitamin metabolic process;hormone metabolic process;isoprenoid metabolic process;lipid metabolic process;metabolic process;primary metabolic process;regulation of biological quality;regulation of hormone levels;retinoid metabolic process;retinol metabolic process;small molecule metabolic process;terpenoid metabolic process;vitamin A metabolic process;vitamin metabolic process "all-trans-retinol 13,14-reductase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;membrane;membrane part;nuclear membrane;nuclear outer membrane;nuclear part;organelle membrane;organelle outer membrane;organelle part;outer membrane Retinol metabolism 2.81E-71 7 6 6 15.2

H0YGR4;F5GYG5;Q9Y3B8;F5GX07;H0YG83;H0YG54;Q9Y3B8-2;H0YH58;F5H7P1;Q9BTR4;F5H6P8;H0YG37;F5H784 "Oligoribonuclease, mitochondrial" REXO2 ">tr|H0YGR4|H0YGR4_HUMAN Oligoribonuclease, mitochondrial (Fragment) OS=Homo sapiens GN=REXO2 PE=4 SV=1;>tr|F5GYG5|F5GYG5_HUMAN Oligoribonuclease, mitochondrial OS=Homo sapiens GN=REXO2 PE=2 SV=1;>sp|Q9Y3B8|ORN_HUMAN Oligoribonuclease, mitochondrial OS=Homo" 0.11 -0.05 -0.72 -0.11 -0.37 0.11 0.53 0.21 0.497476763 -0.3114722 cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;primary metabolic process;small molecule metabolic process "3'-5' exonuclease activity;binding;catalytic activity;exonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane Ribosome biogenesis in eukaryotes 4.94E-20 13 6 6 32.8

M0R1A7;M0R117;Q02543;M0R0P7;M0R3D6 60S ribosomal protein L18a RPL18A >tr|M0R1A7|M0R1A7_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=3 SV=1;>tr|M0R117|M0R117_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=3 SV=1;>sp|Q02543|RL18A_HUMAN 60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 S -0.20 0.04 -0.41 0.10 -0.55 -0.47 -0.45 -0.27 1.02233734 0.316218602 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.99E-44 5 6 6 40.1

P47914;F8WF43;C9IYI4 60S ribosomal protein L29 RPL29 >sp|P47914|RL29_HUMAN 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2 -0.32 0.21 0.15 0.04 0.02 -0.52 -0.50 -0.49 0.948522173 0.394596887 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;embryo implantation;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;nucleic acid binding;pattern binding;polysaccharide binding;RNA binding;structural constituent of ribosome;structural molecule activitycell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 3.61E-40 3 6 6 28.3

P49207 60S ribosomal protein L34 RPL34 >sp|P49207|RL34_HUMAN 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3 -0.18 0.01 -0.02 -0.08 0.13 -0.41 -0.36 -0.43 0.60169869 0.199844811 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome 2.48E-28 1 6 6 36.8

P62263;H0YB22;E5RH77 40S ribosomal protein S14 RPS14 >sp|P62263|RS14_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3;>tr|H0YB22|H0YB22_HUMAN 40S ribosomal protein S14 (Fragment) OS=Homo sapiens GN=RPS14 PE=4 SV=1;>tr|E5RH77|E5RH77_HUMAN 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE -0.02 -0.03 0.20 0.06 -1.03 -1.21 -0.04 -0.35 1.0681922 0.71177434 "biological regulation;biosynthetic process;catabolic process;cell differentiation;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;erythrocyte differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maturation of SSU-rRNA;metabolic process;mRNA catabolic process;mRNA metabolic process;myeloid cell differentiation;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity;translation regulator activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 2.84E-62 3 6 6 31.8

E9PGZ4;B4DK71;Q9NTJ5;F8WDN7;C9JV50;C9J3E3;F8WD07 Phosphatidylinositide phosphatase SAC1 SACM1L >tr|E9PGZ4|E9PGZ4_HUMAN Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=2 SV=1;>tr|B4DK71|B4DK71_HUMAN Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=2 SV=1;>sp|Q9NTJ5|SAC1_HUMAN Phosphatidylinositide phosphatase SA 0.51 -0.23 -0.36 -0.41 0.71 0.49 0.15 -0.04 0.710083097 -0.451988951 biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;dephosphorylation;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid metabolic process;lipid modification;metabolic process;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphatidylinositol biosynthetic process;phosphatidylinositol dephosphorylation;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid dephosphorylation;phospholipid metabolic process;phosphorus metabolic process;primary metabolic process;small molecule metabolic process "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;inositol or phosphatidylinositol phosphatase activity;lipid phosphatase activity;phosphatase activity;phosphatidylinositol bisphosphate phosphatase activity;phosphatidylinositol monophosphate phosphatase activity;phosphatidylinositol-3-phosphatase activity;phosphatidylinositol-4-phosphate phosphatase activity;phosphoric ester hydrolase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;organelle membrane;organelle part 6.93E-34 7 6 6 14.7

O75396 Vesicle-trafficking protein SEC22b SEC22B >sp|O75396|SC22B_HUMAN Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 -0.32 0.06 -0.12 0.05 1.29 1.00 -0.24 0.43 0.861222619 -0.700869393 cellular process;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;protein transport;transport;vesicle-mediated transport cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;pigment granule;vesicle Phagosome;SNARE interactions in vesicular transport 2.73E-105 1 6 6 33

Q9UP95-2;Q9UP95;Q9UP95-4;Q9UP95-3;Q9UP95-5;Q9UP95-6;B3KXX3;I3L4N6;Q9UHW9-6;Q9UP95-7;Q9UHW9-5;Q9UHW9-2;Q9UHW9-3;Q9UHW9-4;Q9UHW9;I3L1N8;H0YMQ9;H0YKQ8;J3QSF2;Q9H2X9-2;Q9H2X9 Solute carrier family 12 member 4;Solute carrier family 12 member 6 SLC12A4;SLC12A6 >sp|Q9UP95-2|S12A4_HUMAN Isoform 2 of Solute carrier family 12 member 4 OS=Homo sapiens GN=SLC12A4;>sp|Q9UP95|S12A4_HUMAN Solute carrier family 12 member 4 OS=Homo sapiens GN=SLC12A4 PE=1 SV=2;>sp|Q9UP95-4|S12A4_HUMAN Isoform 4 of Solute carrier family 12 0.52 0.20 -0.72 -0.78 0.34 0.82 0.21 0.38 0.759085748 -0.629535094 anatomical structure formation involved in morphogenesis;angiogenesis;behavior;biological regulation;cation transport;cell communication;cell volume homeostasis;cell-cell signaling;cellular chemical homeostasis;cellular homeostasis;cellular hypotonic response;cellular hypotonic salinity response;cellular ion homeostasis;cellular process;cellular response to abiotic stimulus;cellular response to osmotic stress;cellular response to salt stress;cellular response to stimulus;cellular response to stress;chemical homeostasis;cognition;developmental process;establishment of localization;growth;homeostatic process;hypotonic response;hypotonic salinity response;ion homeostasis;ion transport;learning;learning or memory;metal ion transport;monovalent inorganic cation transport;multicellular organism growth;multicellular organismal process;neurological system process;potassium ion transport;regulation of biological quality;response to abiotic stimulus;response to chemical stimulus;response to drug;response to osmotic stress;response to salt stress;response to stimulus;response to stress;response to temperature stimulus;signaling;synaptic transmission;system process;thermosensory behavior;transport active transmembrane transporter activity;anion transmembrane transporter activity;anion:cation symporter activity;cation transmembrane transporter activity;cation:chloride symporter activity;chloride transmembrane transporter activity;inorganic anion transmembrane transporter activity;ion transmembrane transporter activity;potassium:chloride symporter activity;secondary active transmembrane transporter activity;solute:cation symporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity basolateral plasma membrane;cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane;plasma membrane part 8.65E-17 21 6 6 6.7

P53007;B4DP62 "Tricarboxylate transport protein, mitochondrial" SLC25A1 ">sp|P53007|TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2;>tr|B4DP62|B4DP62_HUMAN Solute carrier family 25 (Mitochondrial carrier;citrate transporter), member 1, isoform CRA_b OS=Homo sapiens GN=SLC25A1 PE="-0.70 0.52 0.05 0.75 0.41 1.05 -1.42 0.42 0.020266287 0.038643856 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;alcohol biosynthetic process;alcohol metabolic process;anion transport;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid transport;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;citrate transport;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;establishment of localization;establishment of localization in cell;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;gluconeogenesis;glucose metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;hexose biosynthetic process;hexose metabolic process;intracellular transport;ion transport;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;mitochondrial citrate transport;mitochondrial transport;monosaccharide biosynthetic process;monosaccharide metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid transport;organic anion transport;organic ether metabolic process;organic substance transport;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;transport;tricarboxylic acid transport;triglyceride biosynthetic process;triglyceride metabolic process carboxylic acid transmembrane transporter activity;citrate transmembrane transporter activity;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;tricarboxylic acid transmembrane transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 3.40E-32 2 6 6 20.3

P18583-2;P18583-5;P18583-10;P18583-3;P18583-4;P18583-7;P18583;P18583-9;H7C1M2;P18583-6;J3QSZ5;P18583-8;H7C2G8 Protein SON SON >sp|P18583-2|SON_HUMAN Isoform A of Protein SON OS=Homo sapiens GN=SON;>sp|P18583-5|SON_HUMAN Isoform D of Protein SON OS=Homo sapiens GN=SON;>sp|P18583-10|SON_HUMAN Isoform J of Protein SON OS=Homo sapiens GN=SON;>sp|P18583-3|SON_HUMAN Isoform B of Protei 0.07 0.62 0.11 0.59 -0.12 -0.29 -1.20 -0.03 1.036995588 0.754947867 biological regulation;cell cycle;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytokinesis;cytoskeleton organization;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mRNA metabolic process;mRNA processing;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing binding;DNA binding;double-stranded RNA binding;nucleic acid binding;RNA binding cell part;intracellular organelle part;intracellular part;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part 8.92E-27 13 6 6 5.2

P22532;P35325;P35326;P22531;Q9BYE4;Q96RM1 Small proline-rich protein 2D;Small proline-rich protein 2B;Small proline-rich protein 2A;Small proline-rich protein 2E;Small proline-rich protein 2G SPRR2D;SPRR2B;SPRR2A;SPRR2E;SPRR2G >sp|P22532|SPR2D_HUMAN Small proline-rich protein 2D OS=Homo sapiens GN=SPRR2D PE=2 SV=2;>sp|P35325|SPR2B_HUMAN Small proline-rich protein 2B OS=Homo sapiens GN=SPRR2B PE=2 SV=1;>sp|P35326|SPR2A_HUMAN Small proline-rich protein 2A OS=Homo sapiens GN=SPRR2A -1.26 -0.90 0.56 0.37 1.05 0.70 1.17 -0.26 0.746417951 -0.974189319 cell differentiation;cellular developmental process;cellular process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation structural molecule activity cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 1.52E-27 6 6 6 90.3

Q86Y82;B1AJQ6 Syntaxin-12 STX12 >sp|Q86Y82|STX12_HUMAN Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1;>tr|B1AJQ6|B1AJQ6_HUMAN Syntaxin-12 (Fragment) OS=Homo sapiens GN=STX12 PE=2 SV=2 -0.45 0.16 0.05 0.34 0.71 0.95 -0.35 0.44 0.525893626 -0.413147797 biological regulation;cellular process;cholesterol efflux;cholesterol transport;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;intracellular protein transport;intracellular transport;lipid transport;organic substance transport;posttranscriptional regulation of gene expression;protein stabilization;protein transport;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability;secretion;secretion by cell;sterol transport;synaptic vesicle exocytosis;synaptic vesicle transport;transport;vesicle-mediated transport binding;protein binding;SNAP receptor activity;SNARE binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endocytic vesicle;endosomal part;endosome membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;phagocytic vesicle;protein complex;SNARE complex;vesicle Phagosome 3.32E-91 2 6 6 29.7

Q9Y2Z0-2;Q9Y2Z0;F5H5A9 Suppressor of G2 allele of SKP1 homolog SUGT1 >sp|Q9Y2Z0-2|SUGT1_HUMAN Isoform 2 of Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1;>sp|Q9Y2Z0|SUGT1_HUMAN Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3;>tr|F5H5A9|F5H5A9_HUMAN Suppressor of G2 allele of SKP1 0.21 -0.03 0.05 0.01 0.21 0.00 0.07 -0.16 0.111289483 0.028970094 "biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;defense response;immune response;immune system process;innate immune response;intracellular receptor mediated signaling pathway;mitosis;nuclear division;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;organelle fission;organelle organization;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;signal transduction" cell part;chromosomal part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;ubiquitin ligase complex NOD-like receptor signaling pathway;Plant-pathogen interaction 2.54E-33 3 6 6 23.1

Q8NBJ7;J3KQJ1;E9PBT8;C9JL30;A8MXB9;C9J660;Q8NBJ7-2;Q8NBJ7-5;J3QT17;H7C3B2;Q8NBJ7-3;F8WA42;F8WEX5;E9PG02;F8WEV7;F8WES7;Q8NBJ7-4 Sulfatase-modifying factor 2 SUMF2 >sp|Q8NBJ7|SUMF2_HUMAN Sulfatase-modifying factor 2 OS=Homo sapiens GN=SUMF2 PE=1 SV=2;>tr|J3KQJ1|J3KQJ1_HUMAN Sulfatase-modifying factor 2 OS=Homo sapiens GN=SUMF2 PE=4 SV=1;>tr|E9PBT8|E9PBT8_HUMAN Sulfatase-modifying factor 2 OS=Homo sapiens GN=SUMF2 PE= 0.12 -0.03 0.34 0.00 -0.11 -0.20 0.33 0.11 0.193533072 0.074793252 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;post-translational protein modification;primary metabolic process;protein metabolic process;protein modification process binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part 6.12E-38 17 6 6 26.6

O60343-2;O60343-3;O60343;Q5JU47;O60343-4;O60343-5 TBC1 domain family member 4 TBC1D4 >sp|O60343-2|TBCD4_HUMAN Isoform 2 of TBC1 domain family member 4 OS=Homo sapiens GN=TBC1D4;>sp|O60343-3|TBCD4_HUMAN Isoform 3 of TBC1 domain family member 4 OS=Homo sapiens GN=TBC1D4;>sp|O60343|TBCD4_HUMAN TBC1 domain family member 4 OS=Homo sapiens GN=TB 0.04 -0.12 0.26 0.03 -0.65 -0.55 0.30 -0.26 0.647439936 0.343953642 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;establishment of localization;membrane organization;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Rab GTPase activity;positive regulation of Ras GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Rab GTPase activity;regulation of Ras GTPase activity;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;transport;vesicle-mediated transport enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Rab GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;vesicle membrane 3.75E-70 6 6 6 6.6

Q92609;Q92609-2;C9J3F6 TBC1 domain family member 5 TBC1D5 >sp|Q92609|TBCD5_HUMAN TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5 PE=1 SV=1;>sp|Q92609-2|TBCD5_HUMAN Isoform 2 of TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5;>tr|C9J3F6|C9J3F6_HUMAN TBC1 domain family member 5 OS=Homo sapiens GN=TBC1D5 0.23 -0.05 0.25 -0.06 0.27 -0.16 0.00 -0.18 0.340721763 0.114486159 biological regulation;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Rab GTPase activity;positive regulation of Ras GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Rab GTPase activity;regulation of Ras GTPase activity enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Rab GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;intracellular;macromolecular complex;membrane part;protein complex;retromer complex 2.08E-22 3 6 6 9.7

Q66K14-2;Q66K14;E5RIN2;H0YB08;H0YB58;F5H6M5;G3V133 TBC1 domain family member 9B TBC1D9B >sp|Q66K14-2|TBC9B_HUMAN Isoform 2 of TBC1 domain family member 9B OS=Homo sapiens GN=TBC1D9B;>sp|Q66K14|TBC9B_HUMAN TBC1 domain family member 9B OS=Homo sapiens GN=TBC1D9B PE=1 SV=3 0.22 0.07 -0.15 -0.20 0.54 0.42 0.67 0.12 1.214626098 -0.451371925 biological regulation;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Rab GTPase activity;positive regulation of Ras GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Rab GTPase activity;regulation of Ras GTPase activity binding;calcium ion binding;cation binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;Rab GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;integral to membrane;intracellular;intrinsic to membrane;membrane part 4.00E-62 7 6 6 6.7

O75962-5;O75962-2;O75962;E7EWP2;O75962-4;E7EPJ7;F5H228 Triple functional domain protein TRIO >sp|O75962-5|TRIO_HUMAN Isoform 5 of Triple functional domain protein OS=Homo sapiens GN=TRIO;>sp|O75962-2|TRIO_HUMAN Isoform 2 of Triple functional domain protein OS=Homo sapiens GN=TRIO;>sp|O75962|TRIO_HUMAN Triple functional domain protein OS=Homo sapie 0.09 -0.26 -0.03 -0.12 0.76 1.75 0.18 0.31 0.972039856 -0.829265269 axon guidance;biological regulation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;chemotaxis;enzyme linked receptor protein signaling pathway;intracellular signal transduction;locomotion;nerve growth factor receptor signaling pathway;regulation of biological process;regulation of cellular process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;small GTPase mediated signal transduction;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane receptor protein tyrosine phosphatase signaling pathway"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;kinase activity;lipid binding;nucleoside-triphosphatase regulator activity;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;Ras guanyl-nucleotide exchange factor activity;Rho guanyl-nucleotide exchange factor activity;ribonucleotide binding;small GTPase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular;intracellular part 1.02E-17 7 6 6 3.3

Q15654;H7BZE2 Thyroid receptor-interacting protein 6 TRIP6 >sp|Q15654|TRIP6_HUMAN Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3 -0.07 -0.06 -0.58 0.17 -0.43 -0.23 -0.05 -0.24 0.222586597 0.103626037 "biological regulation;biosynthetic process;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;focal adhesion assembly;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of locomotion;positive regulation of NF-kappaB import into nucleus;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of transcription factor import into nucleus;positive regulation of transmembrane transport;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of establishment of protein localization;regulation of gene expression;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of NF-kappaB import into nucleus;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of RNA metabolic process;regulation of transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;release of cytoplasmic sequestered NF-kappaB;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;cation binding;cytokine receptor binding;growth factor receptor binding;hormone receptor binding;interleukin-1 receptor binding;ion binding;metal ion binding;nuclear hormone receptor binding;protein binding;receptor binding;thyroid hormone receptor binding;transcription factor binding;transition metal ion binding;zinc ion binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeleton;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle NOD-like receptor signaling pathway 2.65E-33 2 6 6 29

F5H442;Q99816;Q99816-2;J3QRU6;J3QKS4 Tumor susceptibility gene 101 protein TSG101 >tr|F5H442|F5H442_HUMAN Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=2 SV=1;>sp|Q99816|TS101_HUMAN Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2;>sp|Q99816-2|TS101_HUMAN Isoform 2 of Tumor susceptibility ge 0.28 0.08 -0.04 0.07 -0.04 -0.07 0.40 -0.08 0.116180582 0.04351021 "biological regulation;catabolic process;cell cycle arrest;cell cycle process;cell differentiation;cell division;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;developmental process;egress of virus within host cell;endosome transport;epidermal cell differentiation;epithelial cell differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;keratinocyte differentiation;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane organization;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;non-lytic viral release;non-lytic virus budding;primary metabolic process;protein maturation;protein metabolic process;protein modification process;protein processing;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;release of virus from host;reproductive process;transport;ubiquitin-dependent protein catabolic process;ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway;vesicle-mediated transport;viral protein processing;viral reproductive process;virion assembly"binding;DNA binding;nucleic acid binding;protein binding;protein binding transcription factor activity;small conjugating protein binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;ubiquitin bindingcell part;cytoplasm;cytoplasmic part;early endosome;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;late endosome membrane;membrane;membrane-bounded organelle;multivesicular body;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle membrane;organelle part;plasma membrane Endocytosis 7.85E-22 5 6 6 19.7

Q13630;E9PKL9;E9PLH9;E9PP14;E9PP60;H0YCP7 GDP-L-fucose synthase TSTA3 >sp|Q13630|FCL_HUMAN GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1;>tr|E9PKL9|E9PKL9_HUMAN GDP-L-fucose synthase (Fragment) OS=Homo sapiens GN=TSTA3 PE=2 SV=1;>tr|E9PLH9|E9PLH9_HUMAN GDP-L-fucose synthase (Fragment) OS=Homo sapiens GN=TSTA3 PE=2 0.03 -0.20 0.04 0.04 -0.56 -0.37 0.47 0.12 0.093384151 0.064740057 alcohol biosynthetic process;alcohol metabolic process;biological adhesion;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cell adhesion;cell death;cell-cell adhesion;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytolysis;'de novo' GDP-L-fucose biosynthetic process;death;fucose biosynthetic process;fucose metabolic process;GDP-L-fucose biosynthetic process;GDP-L-fucose metabolic process;GDP-mannose metabolic process;hexose biosynthetic process;hexose metabolic process;leukocyte cell-cell adhesion;L-fucose biosynthetic process;L-fucose metabolic process;mannose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar biosynthetic process;nucleotide-sugar metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;electron carrier activity;GDP-4-dehydro-D-rhamnose reductase activity;GDP-L-fucose synthase activity;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasm;intracellular part Amino sugar and nucleotide sugar metabolism;Fructose and mannose metabolism 1.65E-69 6 6 6 25.5

Q9BZX2;B4DGD3;Q9BZX2-2;Q9HA47-3;Q9HA47;Q5JT09 Uridine-cytidine kinase 2 UCK2 >sp|Q9BZX2|UCK2_HUMAN Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=1 SV=1;>tr|B4DGD3|B4DGD3_HUMAN Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=2 SV=1 0.67 -0.02 -0.30 -0.24 -0.12 -0.32 0.29 -0.38 0.228619252 0.161452121 behavior;biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to oxygen levels;cellular response to stimulus;CTP biosynthetic process;CTP metabolic process;CTP salvage;feeding behavior;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside salvage;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;nucleotide salvage;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;pyrimidine base metabolic process;pyrimidine nucleoside biosynthetic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside monophosphate biosynthetic process;pyrimidine nucleoside monophosphate metabolic process;pyrimidine nucleoside salvage;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine nucleotide salvage;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside monophosphate biosynthetic process;pyrimidine ribonucleoside monophosphate metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine ribonucleotide salvage;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;pyrimidine-containing compound salvage;response to axon injury;response to chemical stimulus;response to oxygen levels;response to stimulus;response to stress;response to wounding;ribonucleoside metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;UMP biosynthetic process;UMP metabolic process;UMP salvage "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleobase-containing compound kinase activity;nucleoside kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups;uridine kinase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle Drug metabolism - other enzymes;Pyrimidine metabolism 1.63E-23 6 6 6 36.4

P46939;Q5SYY1;Q5T097 Utrophin UTRN >sp|P46939|UTRO_HUMAN Utrophin OS=Homo sapiens GN=UTRN PE=1 SV=2 -0.14 0.26 -0.42 -0.19 1.18 0.15 -0.06 0.56 0.80843261 -0.582393912 anatomical structure development;biological regulation;developmental process;multicellular organismal process;muscle contraction;muscle organ development;muscle structure development;muscle system process;organ development;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-matrix adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;regulation of biological process;regulation of cell adhesion;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cellular process;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of molecular function;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;system process actin binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding;transition metal ion binding;zinc ion binding cell junction;cell part;cell projection;cytoplasm;cytoskeleton;dystrophin-associated glycoprotein complex;filopodium;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuromuscular junction;non-membrane-bounded organelle;nucleus;organelle;plasma membrane;plasma membrane part;postsynaptic membrane;protein complex;synapse;synapse part;synaptic membrane 1.28E-21 3 6 6 2.4

Q5VIR6-4;F6VX93;Q5VIR6-3;Q5VIR6;G3V0H8;Q5VIR6-2;I3L184;I3L0S6 Vacuolar protein sorting-associated protein 53 homolog VPS53 >sp|Q5VIR6-4|VPS53_HUMAN Isoform 4 of Vacuolar protein sorting-associated protein 53 homolog OS=Homo sapiens GN=VPS53;>tr|F6VX93|F6VX93_HUMAN Vacuolar protein sorting-associated protein 53 homolog OS=Homo sapiens GN=VPS53 PE=2 SV=1;>sp|Q5VIR6-3|VPS53_HUMAN -0.04 0.00 0.14 -0.14 -0.09 -0.14 0.12 0.17 0.101384888 -0.027605127 establishment of localization;establishment of protein localization;protein transport;transport cell part;cytoplasmic part;cytoplasmic vesicle part;endosomal part;endosome membrane;GARP complex;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane;organelle membrane;organelle part;protein complex 5.78E-21 8 6 6 9.1

O15498;B4DR94;H7C3K7 Synaptobrevin homolog YKT6 YKT6 >sp|O15498|YKT6_HUMAN Synaptobrevin homolog YKT6 OS=Homo sapiens GN=YKT6 PE=1 SV=1;>tr|B4DR94|B4DR94_HUMAN Synaptobrevin homolog YKT6 OS=Homo sapiens GN=YKT6 PE=2 SV=1 0.04 -0.15 -0.05 -0.51 0.10 0.11 0.89 0.54 1.083510027 -0.577803399 "cellular process;endosome transport;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular transport;membrane docking;protein transport;retrograde transport, endosome to Golgi;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle targeting;vesicle-mediated transport" "binding;catalytic activity;palmitoyltransferase activity;protein binding;protein-cysteine S-acyltransferase activity;protein-cysteine S-palmitoleyltransferase activity;S-acyltransferase activity;SNAP receptor activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endoplasmic reticulum;endosome;Golgi apparatus;Golgi apparatus part;Golgi membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part;plasma membrane part;protein complex;SNARE complex;vesicle membrane SNARE interactions in vesicular transport 2.23E-23 3 6 6 28.8

H7C0E5;O75312;H7BZM7 Zinc finger protein ZPR1 ZNF259 >tr|H7C0E5|H7C0E5_HUMAN Zinc finger protein ZPR1 (Fragment) OS=Homo sapiens GN=ZNF259 PE=4 SV=1;>sp|O75312|ZPR1_HUMAN Zinc finger protein ZPR1 OS=Homo sapiens GN=ZNF259 PE=1 SV=1;>tr|H7BZM7|H7BZM7_HUMAN Zinc finger protein ZPR1 (Fragment) OS=Homo sapiens G 0.28 0.05 0.04 -0.17 0.29 0.16 0.38 -0.08 0.40652876 -0.135580475 biological regulation;cell proliferation;cellular process;cellular response to stimulus;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 2.39E-79 3 6 6 23.1

A8MYT4;Q8NEB9;M0R0U1;M0R0G8;M0R308;M0R2C5;K7ENH3;K7EIV6;K7EKH3 Phosphatidylinositol 3-kinase catalytic subunit type 3 PIK3C3 >tr|A8MYT4|A8MYT4_HUMAN Phosphatidylinositol 3-kinase catalytic subunit type 3 OS=Homo sapiens GN=PIK3C3 PE=2 SV=2;>sp|Q8NEB9|PK3C3_HUMAN Phosphatidylinositol 3-kinase catalytic subunit type 3 OS=Homo sapiens GN=PIK3C3 PE=1 SV=1;>tr|M0R0U1|M0R0U1_HUMAN Pho 0.24 0.00 0.00 -0.03 0.07 -0.09 0.41 0.01 0.134495759 -0.04696533 activation of immune response;activation of innate immune response;autophagic vacuole assembly;biological regulation;cell cycle;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytokinesis;defense response;early endosome to late endosome transport;endosome organization;endosome transport;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;glycerolipid metabolic process;glycerophospholipid metabolic process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;inositol lipid-mediated signaling;insulin receptor signaling pathway;intracellular signal transduction;intracellular transport;lipid metabolic process;lipid modification;lipid phosphorylation;macromolecule metabolic process;metabolic process;organelle assembly;organelle organization;organophosphate metabolic process;pattern recognition receptor signaling pathway;phosphate-containing compound metabolic process;phosphatidylinositol metabolic process;phosphatidylinositol phosphorylation;phosphatidylinositol-mediated signaling;phospholipid metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of response to stimulus;primary metabolic process;protein maturation;protein metabolic process;protein processing;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of defense response;regulation of establishment of protein localization;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of localization;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of transport;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to leucine;response to organic nitrogen;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;small molecule metabolic process;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vacuole organization;vesicle-mediated transport "1-phosphatidylinositol-3-kinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;inositol or phosphatidylinositol kinase activity;kinase activity;lipid kinase activity;nucleotide binding;phosphatidylinositol 3-kinase activity;phosphatidylinositol kinase activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosolic part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;late endosome;macromolecular complex;membrane-bounded organelle;midbody;organelle;phosphatidylinositol 3-kinase complex;protein complex Inositol phosphate metabolism;ko05152;Phagosome;Phosphatidylinositol signaling system;Regulation of autophagy 3.14E-14 9 7 6 9.7

P28340;M0R2B7;M0QZR8;M0QXE6;M0QXQ2;M0QZB4;M0R3H8 DNA polymerase delta catalytic subunit;DNA polymerase POLD1 >sp|P28340|DPOD1_HUMAN DNA polymerase delta catalytic subunit OS=Homo sapiens GN=POLD1 PE=1 SV=2;>tr|M0R2B7|M0R2B7_HUMAN DNA polymerase OS=Homo sapiens GN=POLD1 PE=3 SV=1;>tr|M0QZR8|M0QZR8_HUMAN DNA polymerase OS=Homo sapiens GN=POLD1 PE=3 SV=1;>tr|M0QXE6| 0.28 -0.07 0.28 0.12 0.01 -0.89 -0.19 -0.82 1.089135038 0.624217579 "anatomical structure homeostasis;base-excision repair, gap-filling;biological regulation;biosynthetic process;catabolic process;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;DNA biosynthetic process;DNA metabolic process;DNA recombination;DNA repair;DNA replication;DNA replication proofreading;DNA replication, removal of RNA primer;DNA synthesis involved in DNA repair;DNA-dependent DNA replication;homeostatic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maintenance of fidelity involved in DNA-dependent DNA replication;metabolic process;mitotic recombination;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;nucleotide-excision repair, DNA gap filling;organelle organization;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell cycle;regulation of cellular process;regulation of mitotic cell cycle;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;RNA catabolic process;RNA metabolic process;S phase;S phase of mitotic cell cycle;small molecule metabolic process;telomere maintenance;telomere maintenance via recombination;telomere maintenance via semi-conservative replication;telomere maintenance via telomere lengthening;telomere organization;transcription-coupled nucleotide-excision repair" "3'-5' exonuclease activity;4 iron, 4 sulfur cluster binding;binding;catalytic activity;cation binding;chromatin binding;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;exonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;nuclease activity;nucleic acid binding;nucleic acid binding transcription factor activity;nucleotide binding;nucleotidyltransferase activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;chromosomal part;delta DNA polymerase complex;DNA polymerase complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear chromosome part;nuclear part;nucleoplasm;nucleotide-excision repair complex;organelle part;protein complex Base excision repair;DNA replication;Homologous recombination;Mismatch repair;Nucleotide excision repair;Purine metabolism;Pyrimidine metabolism 1.92E-20 7 7 6 6.3

P42766;H0Y3A0;F2Z388;REV__B4E0P7;REV__Q4G0S7 60S ribosomal protein L35 RPL35 >sp|P42766|RL35_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2;>tr|H0Y3A0|H0Y3A0_HUMAN 60S ribosomal protein L35 (Fragment) OS=Homo sapiens GN=RPL35 PE=3 SV=1;>tr|F2Z388|F2Z388_HUMAN 60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE -0.10 0.03 0.07 0.01 -0.10 -0.61 -0.29 -0.29 1.220131365 0.326564207 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;mRNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.15E-57 5 7 6 39

Q5R363;B4DS61;Q96SB4;H3BLV9;Q96SB4-3;D6RBF8;H0Y932;H7C2I2;H7C521;Q9UPE1-2;A8MPP7;Q9UPE1-3;A8MPY5;Q9UPE1-4;Q9UPE1;E7ETV6 SRSF protein kinase 1 SRPK1 ">tr|Q5R363|Q5R363_HUMAN SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=2 SV=1;>tr|B4DS61|B4DS61_HUMAN SFRS protein kinase 1, isoform CRA_f OS=Homo sapiens GN=SRPK1 PE=2 SV=1;>sp|Q96SB4|SRPK1_HUMAN SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1 PE=1 SV=2" -0.05 0.31 -0.14 0.10 -0.23 -0.31 -0.22 0.40 0.295775736 0.14359162 "anatomical structure development;biological regulation;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;chromatin organization;chromosome organization;chromosome segregation;defense response;developmental process;DNA conformation change;DNA metabolic process;DNA packaging;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;muscle tissue development;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of reproductive process;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of viral genome replication;regulation of viral reproduction;reproductive process;response to stimulus;response to stress;RNA metabolic process;RNA processing;RNA splicing;signal transduction;skeletal muscle tissue development;sperm chromatin condensation;striated muscle tissue development;tissue development;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear matrix;nuclear part;nucleus;organelle;organelle part 2.38E-32 16 7 6 18.3

Q16629-3;Q16629-2;Q16629-4;C9JAB2;Q16629 Serine/arginine-rich splicing factor 7 SRSF7 >sp|Q16629-3|SRSF7_HUMAN Isoform 3 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7;>sp|Q16629-2|SRSF7_HUMAN Isoform 2 of Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7;>sp|Q16629-4|SRSF7_HUMAN Isoform 4 of Serine/arginin -0.09 0.36 0.16 0.42 -0.14 -0.34 -1.35 -0.11 0.944097239 0.694254413 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part Spliceosome 6.27E-50 5 7 6 43.9

Q9Y4E8-2;Q9Y4E8-3;E9PCQ3;Q9Y4E8;F8W0H4;Q9Y4E8-4;H0YI31;G5E9A6;P51784 Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 15 USP15 >sp|Q9Y4E8-2|UBP15_HUMAN Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15;>sp|Q9Y4E8-3|UBP15_HUMAN Isoform 3 of Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15;>tr|E9PCQ3|E9PCQ3_HUMAN Ubiquitin carboxyl-termi 0.12 -0.08 0.32 0.03 0.13 -0.06 0.43 -0.52 0.175043133 0.102137443 biological regulation;BMP signaling pathway;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;monoubiquitinated protein deubiquitination;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;pathway-restricted SMAD protein phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;protein phosphorylation;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to stimulus;signal transduction;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;ubiquitin-dependent protein catabolic process "catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;peptidase activity;peptidase activity, acting on L-amino acid peptides;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.98E-20 9 7 6 7.6

Q6NXG1-2;Q6NXG1-5;Q6NXG1-4;Q6NXG1-3;Q6NXG1;H0YBR2;H0YBB3;E5RI26 Epithelial splicing regulatory protein 1 ESRP1 >sp|Q6NXG1-2|ESRP1_HUMAN Isoform 2 of Epithelial splicing regulatory protein 1 OS=Homo sapiens GN=ESRP1;>sp|Q6NXG1-5|ESRP1_HUMAN Isoform 5 of Epithelial splicing regulatory protein 1 OS=Homo sapiens GN=ESRP1;>sp|Q6NXG1-4|ESRP1_HUMAN Isoform 4 of Epithelial 0.07 0.14 0.29 0.15 -1.68 -0.68 -0.21 0.12 0.841190937 0.776493197 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 8.18E-62 8 8 6 19.1

Q9BQL6;Q9BQL6-4;Q9BQL6-2;G3V1L6;Q9BQL6-3 Fermitin family homolog 1 FERMT1 >sp|Q9BQL6|FERM1_HUMAN Fermitin family homolog 1 OS=Homo sapiens GN=FERMT1 PE=1 SV=1;>sp|Q9BQL6-4|FERM1_HUMAN Isoform 4 of Fermitin family homolog 1 OS=Homo sapiens GN=FERMT1;>sp|Q9BQL6-2|FERM1_HUMAN Isoform 2 of Fermitin family homolog 1 OS=Homo sapiens G 0.96 -0.07 -0.13 -0.97 0.12 0.57 0.92 0.47 0.559717378 -0.56912302 biological adhesion;cell adhesion;cell migration;cell motility;cell proliferation;cellular component movement;cellular process;establishment of cell polarity;establishment of epithelial cell polarity;establishment or maintenance of cell polarity;keratinocyte migration;keratinocyte proliferation;locomotion binding;lipid binding;phospholipid binding adherens junction;anchoring junction;cell junction;cell part;cell projection membrane;cell projection part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytosol;filamentous actin;focal adhesion;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;organelle part;plasma membrane part;protein complex;ruffle membrane 5.72E-94 5 8 6 13.6

P32455;P32456 Interferon-induced guanylate-binding protein 1 GBP1 >sp|P32455|GBP1_HUMAN Interferon-induced guanylate-binding protein 1 OS=Homo sapiens GN=GBP1 PE=1 SV=2 -0.59 -0.18 -0.10 -0.04 0.18 -0.14 0.41 -0.10 0.746853344 -0.313284838 biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;immune effector process;immune system process;interferon-gamma-mediated signaling pathway;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of cellular process;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;type I interferon-mediated signaling pathway "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;extracellular region;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part 4.78E-42 2 8 6 16.7

P09012;M0QZG7;M0R268;M0R221;M0R2B8;M0QXK2;M0R0G9 U1 small nuclear ribonucleoprotein A SNRPA >sp|P09012|SNRPA_HUMAN U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3;>tr|M0QZG7|M0QZG7_HUMAN U1 small nuclear ribonucleoprotein A (Fragment) OS=Homo sapiens GN=SNRPA PE=4 SV=1;>tr|M0R268|M0R268_HUMAN U1 small nuclear ribonucleopro -0.06 0.15 0.04 0.14 -0.05 -0.55 -0.96 -0.57 1.278568903 0.599615196 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding;snRNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 4.36E-54 7 8 6 33.7

O60493;O60493-2;O60493-4;O60493-3 Sorting nexin-3 SNX3 >sp|O60493|SNX3_HUMAN Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1 SV=3;>sp|O60493-2|SNX3_HUMAN Isoform 2 of Sorting nexin-3 OS=Homo sapiens GN=SNX3;>sp|O60493-4|SNX3_HUMAN Isoform 4 of Sorting nexin-3 OS=Homo sapiens GN=SNX3;>sp|O60493-3|SNX3_HUMAN Isofor -0.09 -0.07 0.02 -0.02 0.07 0.22 0.57 0.29 1.253875585 -0.328300496 cell communication;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;establishment of protein localization;membrane invagination;membrane organization;protein transport;transport;vesicle-mediated transport binding;lipid binding;phosphatidylinositol binding;phosphatidylinositol-3-phosphate binding;phospholipid binding cell part;cytoplasmic part;early endosome;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part 6.38E-24 4 8 6 40.7

P04632;K7EIV0;K7ELJ7;K7EKD8;K7ES82;K7EP80;K7EM73;K7EK10;K7EMQ1;K7ES78 Calpain small subunit 1 CAPNS1 >sp|P04632|CPNS1_HUMAN Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1;>tr|K7EIV0|K7EIV0_HUMAN Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=4 SV=1;>tr|K7ELJ7|K7ELJ7_HUMAN Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=4 SV=1;>tr|K -0.05 -0.16 -0.10 0.03 0.23 0.01 0.26 -0.07 0.830768323 -0.176291595 biological regulation;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;regulation of biological process;regulation of cell proliferation;regulation of cellular process "binding;calcium ion binding;calcium-dependent cysteine-type endopeptidase activity;catalytic activity;cation binding;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasm;intracellular part;membrane;plasma membrane 4.74E-175 10 9 6 36.2

J3KTE9;P22223;P22223-2;J3QR60;J3QL41 Cadherin-3 CDH3 >tr|J3KTE9|J3KTE9_HUMAN Cadherin-3 OS=Homo sapiens GN=CDH3 PE=3 SV=1;>sp|P22223|CADH3_HUMAN Cadherin-3 OS=Homo sapiens GN=CDH3 PE=1 SV=2;>sp|P22223-2|CADH3_HUMAN Isoform 2 of Cadherin-3 OS=Homo sapiens GN=CDH3 -0.12 0.14 0.06 0.35 -2.24 -1.01 -0.20 0.18 0.730531793 0.929377109 adherens junction organization;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion;multicellular organismal process;neurological system process;response to stimulus;sensory perception;sensory perception of light stimulus;system process;visual perception binding;calcium ion binding;cation binding;ion binding;metal ion binding adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane Cell adhesion molecules (CAMs) 3.14E-58 5 9 6 14

O00505;H0Y4S9 Importin subunit alpha-3KPNA3 >sp|O00505|IMA4_HUMAN Importin subunit alpha-4 OS=Homo sapiens GN=KPNA3 PE=1 SV=2 0.23 0.26 -0.05 0.00 0.22 0.29 0.15 -0.15 0.041465499 -0.015611155 biological regulation;cell surface receptor linked signaling pathway;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of virus into host cell;establishment of localization;establishment of localization in cell;establishment of protein localization;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multi-organism process;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleocytoplasmic transport;protein complex assembly;protein complex subunit organization;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction;transport binding;nuclear localization sequence binding;peptide binding;protein transporter activity;signal sequence binding;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;nucleoplasm;organelle part;pore complex;protein complex 7.41E-72 2 9 6 23.6

Q02750;Q02750-2 Dual specificity mitogen-activated protein kinase kinase 1 MAP2K1>sp|Q02750|MP2K1_HUMAN Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 PE=1 SV=2;>sp|Q02750-2|MP2K1_HUMAN Isoform 2 of Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens GN=MAP2K1 0.21 -0.03 0.01 -0.08 -0.26 -0.37 0.16 -0.40 0.7288695 0.245845512 "activation of immune response;activation of innate immune response;activation of MAPKK activity;activation of protein kinase activity;aging;anatomical structure development;axon guidance;biological regulation;blood vessel development;cell aging;cell cycle arrest;cell cycle phase;cell cycle process;cell differentiation;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;cellular senescence;chemotaxis;cytoskeleton-dependent intracellular transport;defense response;developmental process;enzyme linked receptor protein signaling pathway;epidermal cell differentiation;epidermal growth factor receptor signaling pathway;epithelial cell differentiation;establishment of localization;establishment of localization in cell;establishment of melanosome localization;establishment of organelle localization;establishment of pigment granule localization;establishment of vesicle localization;fibroblast growth factor receptor signaling pathway;Golgi inheritance;Golgi organization;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;insulin receptor signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;intracellular transport;keratinocyte differentiation;labyrinthine layer development;localization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;melanosome transport;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;mitosis;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell cycle;negative regulation of cell proliferation;negative regulation of cell-cell adhesion;negative regulation of cellular process;negative regulation of homotypic cell-cell adhesion;nerve growth factor receptor signaling pathway;nuclear division;organelle fission;organelle inheritance;organelle localization;organelle organization;organelle transport along microtubule;pattern recognition receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;pigment granule transport;placenta blood vessel development;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of defense response;positive regulation of developmental process;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein kinase activity;positive regulation of Ras GTPase activity;positive regulation of Ras protein signal transduction;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of small GTPase mediated signal transduction;positive regulation of transcription elongation from RNA polymerase II promoter;positive regulation of transcription elongation, DNA-dependent;positive regulation of transferase activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein metabolic process;protein modification process;protein oligomerization;protein phosphorylation;Ras protein signal transduction;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cell-cell adhesion;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of defense response;regulation of developmental process;regulation of early endosome to late endosome transport;regulation of gene expression;regulation of Golgi inheritance;regulation of GTP catabolic process;regulation of GTPase activity;regulation of homotypic cell-cell adhesion;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of smooth muscle contraction;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of system process;regulation of transcription elongation from RNA polymerase II promoter;regulation of transcription elongation, DNA-dependent;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transport;regulation of vascular smooth muscle contraction;regulation of vasoconstriction;regulation of vesicle-mediated transport;response to axon injury;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to glucocorticoid stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;signal transduction;small GTPase mediated signal transduction;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;taxis;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;transport;TRIF-dependent toll-like receptor signaling pathway;vesicle localization;vesicle transport along microtubule" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on ester bonds;kinase activator activity;kinase activity;kinase regulator activity;MAP kinase kinase activity;molecular transducer activity;nucleotide binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activator activity;protein kinase activity;protein kinase regulator activity;protein serine/threonine kinase activator activity;protein serine/threonine kinase activity;protein serine/threonine/tyrosine kinase activity;protein tyrosine kinase activity;protein tyrosine phosphatase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein activity;receptor signaling protein tyrosine phosphatase activity;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;axon part;cell cortex;cell junction;cell part;cell projection cytoplasm;cell projection part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytosol;dendrite cytoplasm;early endosome;endosome;focal adhesion;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;membrane;membrane-bounded organelle;microtubule organizing center;mitochondrion;nucleus;organelle;organelle part;perikaryon;perinuclear region of cytoplasm;plasma membrane;spindle pole body Acute myeloid leukemia;B cell receptor signaling pathway;Bladder cancer;Chemokine signaling pathway;Chronic myeloid leukemia;Colorectal cancer;Dorso-ventral axis formation;Endometrial cancer;ErbB signaling pathway;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;Insulin signaling pathway;Long-term depression;Long-term potentiation;MAPK signaling pathway;MAPK signaling pathway - fly;Melanogenesis;Melanoma;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Non-small cell lung cancer;Oocyte meiosis;Osteoclast differentiation;Pancreatic cancer;Pathways in cancer;Plant-pathogen interaction;Prion diseases;Progesterone-mediated oocyte maturation;Prostate cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;T cell receptor signaling pathway;Thyroid cancer;Toll-like receptor signaling pathway;Vascular smooth muscle contraction;VEGF signaling pathway 6.54E-48 2 9 6 21.6

P61026;P59190-2;P59190;H0YLJ8;H0YL94;E9PI18;E9PJQ5;Q6MZX6;E9PRF7;Q6PIK3;E9PNB9;E9PS06;J3QSF4;G3V562;Q6MZH2;G3V196;H0YDK7;E9PMJ1;A8MSP2;Q96AX2-4;A8MTC6;A8MZI4;B7Z3L0;Q15771;Q96DA2;Q96AX2-2;Q14964;Q96AX2;Q96AX2-3 Ras-related protein Rab-10 RAB10 >sp|P61026|RAB10_HUMAN Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1 -0.16 0.12 0.23 -0.12 0.24 0.58 -0.04 -0.09 0.342808562 -0.153609352 anatomical structure morphogenesis;axonogenesis;biological regulation;cation homeostasis;cell differentiation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular cation homeostasis;cellular chemical homeostasis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular monovalent inorganic cation homeostasis;cellular process;cellular protein localization;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;developmental process;endoplasmic reticulum organization;endoplasmic reticulum tubular network organization;endosome transport;epithelial cell differentiation;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of neuroblast polarity;establishment of protein localization;establishment of protein localization in endoplasmic reticulum membrane;establishment of protein localization in membrane;establishment or maintenance of cell polarity;establishment or maintenance of neuroblast polarity;Golgi organization;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;homeostatic process;intracellular pH reduction;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;localization;macromolecule localization;membrane organization;monovalent inorganic cation homeostasis;neuron projection morphogenesis;organelle fusion;organelle organization;pH reduction;phagosome acidification;phagosome-lysosome fusion;plasma membrane organization;polarized epithelial cell differentiation;post-Golgi vesicle-mediated transport;protein localization;protein localization in membrane;protein localization in plasma membrane;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular pH;regulation of cellular process;regulation of intracellular pH;regulation of pH;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;small GTPase mediated signal transduction;synapse organization;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cell projection;cilium;cis-Golgi network;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum tubular network;endoplasmic reticulum-Golgi intermediate compartment;endosomal part;endosome;endosome membrane;Golgi apparatus;Golgi apparatus part;Golgi cisterna;insulin-responsive compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;organelle subcompartment;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;primary cilium;recycling endosome;recycling endosome membrane;stored secretory granule;trans-Golgi network;vesicle;vesicle membrane

2.92E-71 29 9 6 49

P04899;P04899-4;B4E2X5;P04899-3;P04899-2;B3KTZ0;F5GZL8;P11488;P09471-2;P09471;P19087;A8MTJ3;A2A2R6;Q5JWD1;H0Y7E8;H3BTM2;P38405-3;Q03113;P38405;P38405-2 Guanine nucleotide-binding protein G(i) subunit alpha-2 GNAI2 >sp|P04899|GNAI2_HUMAN Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3;>sp|P04899-4|GNAI2_HUMAN Isoform sGi2 of Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2;>tr|B4E2X5|B4E2X5_HU -0.10 0.24 -0.33 0.23 0.38 0.32 -0.59 0.01 0.023917681 -0.019098487 "activation of adenylate cyclase activity;activation of adenylate cyclase activity by dopamine receptor signaling pathway;activation of adenylate cyclase activity by G-protein signaling pathway;activation of MAPKK activity;activation of protein kinase activity;adenosine receptor signaling pathway;aging;anatomical structure development;anatomical structure morphogenesis;behavior;biological regulation;calcium ion homeostasis;cAMP-mediated signaling;catabolic process;cation homeostasis;cell activation;cell communication;cell cycle;cell development;cell differentiation;cell division;cell projection organization;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to electrical stimulus;cellular response to stimulus;chemical homeostasis;chordate embryonic development;cyclic-nucleotide-mediated signaling;cytosolic calcium ion homeostasis;detection of abiotic stimulus;detection of chemical stimulus;detection of chemical stimulus involved in sensory perception;detection of chemical stimulus involved in sensory perception of bitter taste;detection of chemical stimulus involved in sensory perception of taste;detection of external stimulus;detection of light stimulus;detection of light stimulus involved in sensory perception;detection of light stimulus involved in visual perception;detection of stimulus;detection of stimulus involved in sensory perception;detection of visible light;developmental process;divalent inorganic cation homeostasis;dopamine receptor signaling pathway;elevation of cytosolic calcium ion concentration;embryo development;embryo development ending in birth or egg hatching;embryonic digit morphogenesis;embryonic morphogenesis;eye photoreceptor cell development;forebrain development;gamma-aminobutyric acid signaling pathway;G-protein coupled purinergic receptor signaling pathway;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;in utero embryonic development;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;ion homeostasis;locomotory behavior;macromolecule metabolic process;macromolecule modification;metabolic process;metal ion homeostasis;multicellular organismal process;muscarinic acetylcholine receptor signaling pathway;muscle contraction;muscle system process;negative regulation of adenylate cyclase activity;negative regulation of biological process;negative regulation of calcium ion transport;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cellular process;negative regulation of cyclase activity;negative regulation of cyclic-nucleotide phosphodiesterase activity;negative regulation of hydrolase activity;negative regulation of ion transport;negative regulation of lyase activity;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of neurological system process;negative regulation of signaling;negative regulation of synaptic transmission;negative regulation of transmission of nerve impulse;negative regulation of transport;neurological system process;neuron development;neuron projection development;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;photoreceptor cell development;phototransduction;phototransduction, visible light;platelet activation;positive regulation of adenylate cyclase activity;positive regulation of adenylate cyclase activity by G-protein signaling pathway;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of cyclase activity;positive regulation of cyclic-nucleotide phosphodiesterase activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of lyase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;purinergic receptor signaling pathway;Ras protein signal transduction;regulation of adenylate cyclase activity;regulation of adenylate cyclase activity involved in G-protein signaling pathway;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of calcium ion transport;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell morphogenesis;regulation of cell proliferation;regulation of cell shape;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of cyclic-nucleotide phosphodiesterase activity;regulation of developmental process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of heart contraction;regulation of hydrolase activity;regulation of ion transport;regulation of kinase activity;regulation of localization;regulation of lyase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of signaling;regulation of synaptic transmission;regulation of system process;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of transport;response to abiotic stimulus;response to alkaloid;response to amine stimulus;response to amphetamine;response to caffeine;response to chemical stimulus;response to cytokine stimulus;response to drug;response to electrical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hydrogen peroxide;response to inorganic substance;response to isoquinoline alkaloid;response to light intensity;response to light stimulus;response to morphine;response to nicotine;response to nutrient;response to nutrient levels;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to oxidative stress;response to purine-containing compound;response to radiation;response to reactive oxygen species;response to stimulus;response to stress;retina development in camera-type eye;retinal cone cell development;Rho protein signal transduction;rhodopsin mediated signaling pathway;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;second-messenger-mediated signaling;sensory perception;sensory perception of chemical stimulus;sensory perception of smell;sensory perception of sweet taste;sensory perception of taste;sensory perception of umami taste;signal transduction;signaling;small GTPase mediated signal transduction;small molecule metabolic process;synaptic transmission;system process" "acyl binding;binding;catalytic activity;cation binding;D5 dopamine receptor binding;dopamine receptor binding;enzyme binding;GDP binding;G-protein beta/gamma-subunit complex binding;G-protein coupled photoreceptor activity;G-protein coupled receptor activity;G-protein-coupled receptor binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;kinase binding;metabotropic serotonin receptor binding;metal ion binding;molecular transducer activity;nucleoside-triphosphatase activity;nucleotide binding;photoreceptor activity;protein binding;protein complex binding;protein kinase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor activity;receptor binding;ribonucleotide binding;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity" apical plasma membrane;brush border membrane;cell body;cell part;cell projection;cell projection membrane;cell projection part;centrosome;cilium;cilium part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;microtubule organizing center;midbody;neuron projection;neuronal cell body;non-membrane-bounded organelle;nonmotile primary cilium;nucleus;organelle;organelle part;photoreceptor connecting cilium;photoreceptor inner segment;photoreceptor outer segment;photoreceptor outer segment membrane;plasma membrane;plasma membrane part;primary cilium;protein complex Amoebiasis;Axon guidance;Calcium signaling pathway;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Gap junction;Gastric acid secretion;Leukocyte transendothelial migration;Long-term depression;MAPK signaling pathway;Melanogenesis;Olfactory transduction;Phototransduction;Progesterone-mediated oocyte maturation;Regulation of actin cytoskeleton;Tight junction;Toxoplasmosis;Vascular smooth muscle contraction 4.93E-59 20 10 6 37.2

Q14651;C9JAM8 Plastin-1 PLS1 >sp|Q14651|PLSI_HUMAN Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2;>tr|C9JAM8|C9JAM8_HUMAN Plastin-1 (Fragment) OS=Homo sapiens GN=PLS1 PE=2 SV=1 0.57 0.22 0.04 -0.10 -2.05 -1.20 -0.15 -0.50 1.098152323 1.158507255 actin binding;actin filament binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding;structural constituent of cytoskeleton;structural molecule activity cell part;cytoplasm;intracellular part 7.18E-98 2 10 6 22.1

P62873;B1AKQ8;F6UT28;F6X3N5;F5H100;F5H8J8;F5H0S8;E9PCP0;P16520 Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 GNB1 >sp|P62873|GBB1_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3;>tr|B1AKQ8|B1AKQ8_HUMAN Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 (Fragment) OS=Homo sapiens GN=GNB1 PE=2 SV=1;> 0.03 0.24 -0.21 0.23 0.11 0.16 -0.61 0.50 0.044005717 0.033700071 "activation of adenylate cyclase activity;activation of adenylate cyclase activity by dopamine receptor signaling pathway;activation of adenylate cyclase activity by G-protein signaling pathway;activation of phospholipase C activity;activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger;anatomical structure development;apoptosis;biological regulation;calcium ion homeostasis;cAMP-mediated signaling;cardiac muscle cell apoptosis;cation homeostasis;cell activation;cell communication;cell death;cell proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to amine stimulus;cellular response to catecholamine stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to glucagon stimulus;cellular response to hormone stimulus;cellular response to hypoxia;cellular response to lipid;cellular response to monoamine stimulus;cellular response to organic nitrogen;cellular response to organic substance;cellular response to oxygen levels;cellular response to peptide hormone stimulus;cellular response to prostaglandin E stimulus;cellular response to prostaglandin stimulus;cellular response to stimulus;cellular response to stress;chemical homeostasis;cyclic-nucleotide-mediated signaling;cytosolic calcium ion homeostasis;death;developmental process;divalent inorganic cation homeostasis;dopamine receptor signaling pathway;elevation of cytosolic calcium ion concentration;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;homeostatic process;inositol phosphate-mediated signaling;intracellular signal transduction;ion homeostasis;metabolic process;metal ion homeostasis;multicellular organismal process;muscarinic acetylcholine receptor signaling pathway;muscle cell apoptosis;neurological system process;oxidation-reduction process;platelet activation;positive regulation of adenylate cyclase activity;positive regulation of adenylate cyclase activity by G-protein signaling pathway;positive regulation of catalytic activity;positive regulation of cyclase activity;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of lyase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;programmed cell death;Ras protein signal transduction;regulation of adenylate cyclase activity;regulation of adenylate cyclase activity involved in G-protein signaling pathway;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of hydrolase activity;regulation of lipase activity;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of phospholipase activity;regulation of primary metabolic process;response to amine stimulus;response to catecholamine stimulus;response to chemical stimulus;response to endogenous stimulus;response to glucagon stimulus;response to hormone stimulus;response to hypoxia;response to lipid;response to monoamine stimulus;response to organic nitrogen;response to organic substance;response to oxygen levels;response to peptide hormone stimulus;response to prostaglandin E stimulus;response to prostaglandin stimulus;response to stimulus;response to stress;retina development in camera-type eye;second-messenger-mediated signaling;sensory perception;sensory perception of chemical stimulus;sensory perception of taste;signal transduction;signaling;small GTPase mediated signal transduction;striated muscle cell apoptosis;synaptic transmission;system process" "catalytic activity;GTPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;molecular transducer activity;nucleoside-triphosphatase activity;pyrophosphatase activity;signal transducer activity" cell body;cell part;cell projection;cell projection part;cilium part;dendrite;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;heterotrimeric G-protein complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;neuron projection;organelle part;photoreceptor inner segment;photoreceptor outer segment membrane;plasma membrane;plasma membrane part;protein complex Chemokine signaling pathway;Phototransduction;Taste transduction 4.17E-102 9 11 6 29.1

P22392-2;Q32Q12;P22392;J3KPD9;F6XY72;O60361;E7ERL0;E5RHP0;C9K028 Nucleoside diphosphate kinase;Nucleoside diphosphate kinase BNME1-NME2;NME2 >sp|P22392-2|NDKB_HUMAN Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2;>tr|Q32Q12|Q32Q12_HUMAN Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=2 SV=1;>sp|P22392|NDKB_HUMAN Nucleoside diphosphate kinase B OS=Homo sapiens 0.09 -0.12 -0.26 -0.07 -0.27 -0.25 0.50 -0.12 0.095589912 -0.052788209 "anatomical structure development;biological adhesion;biological regulation;biosynthetic process;carbohydrate homeostasis;cell adhesion;cellular biosynthetic process;cellular chemical homeostasis;cellular glucose homeostasis;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to drug;cellular response to fatty acid;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to lipid;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;CTP biosynthetic process;CTP metabolic process;developmental process;glucose homeostasis;GTP biosynthetic process;GTP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;hippocampus development;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte differentiation;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of epidermal cell differentiation;positive regulation of epidermis development;positive regulation of epithelial cell differentiation;positive regulation of epithelial cell proliferation;positive regulation of keratinocyte differentiation;positive regulation of neuron projection development;primary metabolic process;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of gene expression;regulation of immune system process;regulation of keratinocyte differentiation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;response to amine stimulus;response to cAMP;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to fatty acid;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to lipid;response to monosaccharide stimulus;response to organic nitrogen;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to testosterone stimulus;ribonucleoside metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;transcription, DNA-dependent;UTP biosynthetic process;UTP metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;DNA binding;ion binding;kinase activity;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;nucleobase-containing compound kinase activity;nucleoside diphosphate kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;phosphotransferase activity, nitrogenous group as acceptor;phosphotransferase activity, phosphate group as acceptor;protein histidine kinase activity;protein kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cell projection;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;membrane;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;ruffle Purine metabolism;Pyrimidine metabolism 1.29E-67 9 11 6 58.8

Q92688-2;Q92688;Q5T6W8 Acidic leucine-rich nuclear phosphoprotein 32 family member B ANP32B >sp|Q92688-2|AN32B_HUMAN Isoform 2 of Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B;>sp|Q92688|AN32B_HUMAN Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1;>tr|Q5T6W -0.01 -0.02 -0.14 0.11 -0.12 -0.62 -0.25 -0.72 1.133487917 0.410400084 cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.54E-116 3 13 6 47.2

P20340-2;P20340;H0YGL6;P20340-4;H7BYW1;P20340-3;F5H3K7;F5GX61;B7Z337;J3KR73;C9JU14;C9JB90 Ras-related protein Rab-6A RAB6A >sp|P20340-2|RAB6A_HUMAN Isoform 2 of Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A;>sp|P20340|RAB6A_HUMAN Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3;>tr|H0YGL6|H0YGL6_HUMAN Ras-related protein Rab-6A (Fragment) OS=Homo sapiens GN= -0.22 0.08 -0.59 0.17 -0.32 0.26 -0.06 0.18 0.278157915 -0.153387078 "biological regulation;cellular component movement;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cytoskeleton-dependent intracellular transport;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;Golgi vesicle transport;intracellular protein transport;intracellular signal transduction;intracellular transport;intra-Golgi vesicle-mediated transport;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;microtubule-based movement;microtubule-based process;microtubule-based transport;minus-end-directed organelle transport along microtubule;one-carbon metabolic process;organelle transport along microtubule;peptidyl-amino acid modification;peptidyl-cysteine methylation;peptidyl-cysteine modification;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;protein targeting;protein targeting to Golgi;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;retrograde transport, vesicle recycling within Golgi;retrograde vesicle-mediated transport, Golgi to ER;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process;transport;vesicle-mediated transport" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;trans-Golgi network;vesicle 1.04E-71 12 13 6 59.6

Q9H845;H0Y8Z9;D6RCD8 "Acyl-CoA dehydrogenase family member 9, mitochondrial" ACAD9 ">sp|Q9H845|ACAD9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1;>tr|H0Y8Z9|H0Y8Z9_HUMAN Acyl-CoA dehydrogenase family member 9, mitochondrial (Fragment) OS=Homo sapiens GN=ACAD9 PE=2 SV=1" -0.43 0.15 -0.32 0.12 0.02 0.15 -0.36 -0.11 0.085889079 -0.045407807 "acyl-CoA dehydrogenase activity;binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors" cell part;cell projection;cytoplasmic part;dendrite;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;nucleus;organelle Geraniol degradation;Naphthalene degradation 1.68E-42 3 7 7 14.5

B7Z9I1;P11310;P11310-2;Q5T4U5;B4DJE7;E9PJM9;H0YDT5;E9PRX4 "Medium-chain specific acyl-CoA dehydrogenase, mitochondrial" ACADM ">tr|B7Z9I1|B7Z9I1_HUMAN Medium-chain-specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=2 SV=1;>sp|P11310|ACADM_HUMAN Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1;>sp|P11310-2|ACADM_" 0.07 -0.05 0.16 -0.07 -0.49 -0.70 -0.06 -0.33 1.199571212 0.422001028 "amine biosynthetic process;amine metabolic process;anatomical structure development;betaine biosynthetic process;betaine metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;cardiac cell differentiation;cardiac muscle cell differentiation;carnitine biosynthetic process;carnitine metabolic process;carnitine metabolic process, CoA-linked;catabolic process;cell differentiation;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular developmental process;cellular glucan metabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;developmental process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;fatty acid beta-oxidation;fatty acid beta-oxidation using acyl-CoA dehydrogenase;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;generation of precursor metabolites and energy;glucan biosynthetic process;glucan metabolic process;glycogen biosynthetic process;glycogen metabolic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;liver development;macromolecule biosynthetic process;macromolecule metabolic process;medium-chain fatty acid catabolic process;medium-chain fatty acid metabolic process;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;muscle cell differentiation;nitrogen compound metabolic process;organ development;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;polysaccharide biosynthetic process;polysaccharide metabolic process;post-embryonic development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate metabolic process;regulation of cellular biosynthetic process;regulation of cellular carbohydrate metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gluconeogenesis;regulation of glucose metabolic process;regulation of metabolic process;regulation of primary metabolic process;response to abiotic stimulus;response to cold;response to external stimulus;response to extracellular stimulus;response to nutrient levels;response to starvation;response to stimulus;response to stress;response to temperature stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;striated muscle cell differentiation" "acyl-CoA dehydrogenase activity;binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;identical protein binding;medium-chain-acyl-CoA dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;protein binding" axon;cell part;cell projection;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;neuron projection;organelle;organelle lumen;organelle part "beta-Alanine metabolism;Fatty acid metabolism;PPAR signaling pathway;Propanoate metabolism;Valine, leucine and isoleucine degradation" 2.56E-48 8 7 7 24.2

Q8N3C0;Q8N3C0-4 Activating signal cointegrator 1 complex subunit 3 ASCC3 >sp|Q8N3C0|ASCC3_HUMAN Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens GN=ASCC3 PE=1 SV=3 0.30 0.09 -0.04 -0.37 0.31 -0.20 0.41 -0.11 0.200499713 -0.109663812 "biological regulation;biosynthetic process;cell proliferation;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA dealkylation;DNA dealkylation involved in DNA repair;DNA metabolic process;DNA modification;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "3'-5' DNA helicase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent 3'-5' DNA helicase activity;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 6.01E-18 2 7 7 3.9

Q9UBB4-2;Q9UBB4;B1AHE4;B1AHE3;H0Y7N2 Ataxin-10 ATXN10 >sp|Q9UBB4-2|ATX10_HUMAN Isoform 2 of Ataxin-10 OS=Homo sapiens GN=ATXN10;>sp|Q9UBB4|ATX10_HUMAN Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1 0.18 0.09 -0.22 -0.09 -0.21 -0.73 -0.11 -0.56 0.98958302 0.392972529 cell death;cell projection organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;death;neuron projection development cell body;cell part;cell projection;cytoplasmic part;cytosol;dendrite;intracellular part;neuron projection;neuronal cell body;perinuclear region of cytoplasm 2.18E-39 5 7 7 21.9

H0YH87;Q99700-2;Q24JQ7;F8WB06;F8VQP2;Q99700-4;Q99700;F8VRK6;F8VQS0;F8W0B5;F8VZQ7;F8VVY6 Ataxin-2 ATXN2 >tr|H0YH87|H0YH87_HUMAN Ataxin-2 (Fragment) OS=Homo sapiens GN=ATXN2 PE=4 SV=1;>sp|Q99700-2|ATX2_HUMAN Isoform 2 of Ataxin-2 OS=Homo sapiens GN=ATXN2;>tr|Q24JQ7|Q24JQ7_HUMAN ATXN2 protein OS=Homo sapiens GN=ATXN2 PE=2 SV=1;>tr|F8WB06|F8WB06_HUMAN Ataxin-2 0.08 0.05 -0.15 -0.25 0.10 0.12 0.05 -0.06 0.561362085 -0.119025194 anatomical structure morphogenesis;biological regulation;cell death;cell differentiation;cell differentiation in hindbrain;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;central nervous system neuron differentiation;cerebellar Purkinje cell differentiation;cytoplasmic mRNA processing body assembly;death;developmental process;establishment of localization;establishment of RNA localization;homeostasis of number of cells;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of endocytosis;negative regulation of growth;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of multicellular organism growth;negative regulation of multicellular organismal process;negative regulation of receptor internalization;negative regulation of receptor-mediated endocytosis;negative regulation of transport;neurological system process;neuromuscular process;neuron differentiation;neuron projection morphogenesis;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of endocytosis;regulation of gene expression;regulation of growth;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of receptor internalization;regulation of receptor-mediated endocytosis;regulation of translation;regulation of transport;regulation of vesicle-mediated transport;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA transport;stress granule assembly;system process;transport binding;nucleic acid binding;RNA binding cell part;cytoplasm;cytoplasmic part;Golgi apparatus;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;polysome;ribonucleoprotein complex;RNA granule;stress granule;trans-Golgi network 2.38E-69 12 7 7 12.3

P11274-2;P11274;H0Y554;A9UF05;I3L1U8;I3L2P5;B7Z683;Q12979-4;Q12979-2;Q12979 Breakpoint cluster region protein BCR >sp|P11274-2|BCR_HUMAN Isoform 2 of Breakpoint cluster region protein OS=Homo sapiens GN=BCR;>sp|P11274|BCR_HUMAN Breakpoint cluster region protein OS=Homo sapiens GN=BCR PE=1 SV=2;>tr|H0Y554|H0Y554_HUMAN Breakpoint cluster region protein (Fragment) OS=Hom 0.11 -0.07 0.08 -0.06 -0.52 -0.33 0.55 0.12 0.086125186 0.060327593 actin cytoskeleton organization;actin filament-based process;anatomical structure development;anatomical structure morphogenesis;biological regulation;brain development;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cytoskeleton organization;developmental process;embryonic morphogenesis;enzyme linked receptor protein signaling pathway;inner ear morphogenesis;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cell activation;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of defense response;negative regulation of exocytosis;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of leukocyte activation;negative regulation of leukocyte degranulation;negative regulation of locomotion;negative regulation of neutrophil degranulation;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of transport;nerve growth factor receptor signaling pathway;neurological system process;neuromuscular process;neuromuscular process controlling balance;organ development;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet-derived growth factor receptor signaling pathway;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of phagocytosis;positive regulation of transport;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell cycle;regulation of cell migration;regulation of cell motility;regulation of cellular catabolic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of defense response;regulation of endocytosis;regulation of exocytosis;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of leukocyte activation;regulation of leukocyte degranulation;regulation of leukocyte mediated immunity;regulation of localization;regulation of locomotion;regulation of metabolic process;regulation of molecular function;regulation of myeloid leukocyte mediated immunity;regulation of neutrophil degranulation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of phagocytosis;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras protein signal transduction;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho protein signal transduction;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transport;regulation of vesicle-mediated transport;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;signal transduction;small GTPase mediated signal transduction;system process;transmembrane receptor protein tyrosine kinase signaling pathway "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;kinase activity;lipid binding;nucleoside-triphosphatase regulator activity;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;Rac GTPase activator activity;Ras GTPase activator activity;Ras guanyl-nucleotide exchange factor activity;Rho GTPase activator activity;Rho guanyl-nucleotide exchange factor activity;ribonucleotide binding;small GTPase regulator activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular;intracellular part;membrane;plasma membrane Chronic myeloid leukemia;Pathways in cancer 1.04E-25 10 7 7 7.9

Q9UQ88-4;P21127-8;J3QR29;Q9UQ88-3;Q5QPR3;Q9UQ88-2;P21127-3;P21127-2;Q9UQ88;J3QKR5;J3QR44;P21127;Q9UQ88-5;Q9UQ88-10;P21127-12;P21127-4;P21127-5;P21127-10;J3QL65;P21127-6;J3KTL7;Q5QPR4;P21127-9;Q9UQ88-8;Q9UQ88-9;Q5QPQ9;E9PFJ2;G8JLH1;J3KS35;E7ESP2Cyclin-dependent kinase 11A;Cyclin-dependent kinase 11BCDK11B;CDK11A >sp|Q9UQ88-4|CD11A_HUMAN Isoform SV3 of Cyclin-dependent kinase 11A OS=Homo sapiens GN=CDK11A;>sp|P21127-8|CD11B_HUMAN Isoform 8 of Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B;>tr|J3QR29|J3QR29_HUMAN Cyclin-dependent kinase 11B OS=Homo sapiens GN0.00 0.15 0.28 -0.03 0.05 -0.50 -0.57 -0.19 1.061474937 0.400893073 "apoptosis;biological regulation;cell cycle phase;cell cycle process;cell death;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;death;mitosis;nuclear division;organelle fission;organelle organization;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent""adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cyclin-dependent protein kinase activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 5.53E-33 30 7 7 10.9

Q9UHD1-2;Q9UHD1;E9PPQ5;E9PIZ4;E9PSD5;E9PHZ2;E9PL00;E9PIF7 Cysteine and histidine-rich domain-containing protein 1 CHORDC1 >sp|Q9UHD1-2|CHRD1_HUMAN Isoform 2 of Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1;>sp|Q9UHD1|CHRD1_HUMAN Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=2;>tr|E9PPQ5|E9PPQ5_H 0.35 0.01 -0.31 -0.07 -0.53 -0.31 0.45 -0.31 0.258378696 0.171042735 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone-mediated protein folding;macromolecule metabolic process;metabolic process;negative regulation of catalytic activity;negative regulation of kinase activity;negative regulation of molecular function;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of Rho-dependent protein serine/threonine kinase activity;negative regulation of transferase activity;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of centrosome cycle;regulation of centrosome duplication;regulation of cytoskeleton organization;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of molecular function;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of Rho-dependent protein serine/threonine kinase activity;regulation of transferase activity;response to stimulus;response to stress binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding 1.52E-66 8 7 7 39.3

Q13057;Q13057-2;K7EP09;K7EPT0;K7ESK6;K7ES73;K7EN91;K7EQ60 Bifunctional coenzyme A synthase;Phosphopantetheine adenylyltransferase;Dephospho-CoA kinase COASY >sp|Q13057|COASY_HUMAN Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4;>sp|Q13057-2|COASY_HUMAN Isoform 2 of Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY 0.12 -0.15 0.20 0.22 0.10 0.03 0.27 -0.41 0.228520161 0.101738786 amine metabolic process;biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme A biosynthetic process;coenzyme A metabolic process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxoacid metabolic process;pantothenate metabolic process;primary metabolic process;purine nucleoside metabolic process;purine ribonucleoside metabolic process;purine-containing compound metabolic process;ribonucleoside metabolic process;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;adenylyltransferase activity;ATP binding;binding;catalytic activity;dephospho-CoA kinase activity;kinase activity;nucleotide binding;nucleotidyltransferase activity;pantetheine-phosphate adenylyltransferase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;nucleus;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane Pantothenate and CoA biosynthesis 1.62E-40 8 7 7 17.6

Q53SF7-4;Q53SF7-3;Q53SF7-2;Q53SF7;G8JL86;H7C1G2;C9JWZ0;C9JAU3;C9J5Y6;C9JK90;C9J8C4 Cordon-bleu protein-like 1 COBLL1 >sp|Q53SF7-4|COBL1_HUMAN Isoform 4 of Cordon-bleu protein-like 1 OS=Homo sapiens GN=COBLL1;>sp|Q53SF7-3|COBL1_HUMAN Isoform 3 of Cordon-bleu protein-like 1 OS=Homo sapiens GN=COBLL1;>sp|Q53SF7-2|COBL1_HUMAN Isoform 2 of Cordon-bleu protein-like 1 OS=Homo s -0.16 0.06 0.46 0.08 -1.50 -0.51 -0.09 -0.05 0.76315349 0.646340989 6.56E-50 11 7 7 10.1

P21964-2;P21964;E7EMS6;E7EUU8;H7BZ45;F8WBW9 Catechol O-methyltransferaseCOMT >sp|P21964-2|COMT_HUMAN Isoform Soluble of Catechol O-methyltransferase OS=Homo sapiens GN=COMT;>sp|P21964|COMT_HUMAN Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2;>tr|E7EMS6|E7EMS6_HUMAN Catechol O-methyltransferase (Fragment) OS=Homo sap -0.06 0.00 -0.19 0.04 0.05 0.11 0.46 0.09 0.933465405 -0.23204635 alcohol catabolic process;alcohol metabolic process;amine catabolic process;amine metabolic process;behavior;benzene-containing compound metabolic process;biological regulation;biosynthetic process;catabolic process;catecholamine catabolic process;catecholamine metabolic process;catechol-containing compound catabolic process;catechol-containing compound metabolic process;cellular amine metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular hormone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cognition;diol catabolic process;diol metabolic process;dopamine catabolic process;dopamine metabolic process;estrogen metabolic process;female pregnancy;hormone metabolic process;learning;learning or memory;lipid metabolic process;metabolic process;multicellular organismal process;multicellular organismal reproductive process;multicellular organismal response to stress;multi-organism process;negative regulation of biological process;negative regulation of catecholamine metabolic process;negative regulation of cell proliferation;negative regulation of cellular amine metabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of dopamine metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of smooth muscle cell proliferation;neurological system process;neurotransmitter biosynthetic process;neurotransmitter catabolic process;neurotransmitter metabolic process;nitrogen compound metabolic process;phenol-containing compound metabolic process;positive regulation of biological process;positive regulation of cellular amine metabolic process;positive regulation of cellular amino acid metabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of homocysteine metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of sulfur amino acid metabolic process;positive regulation of sulfur metabolic process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of catecholamine metabolic process;regulation of cell proliferation;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of dopamine metabolic process;regulation of homocysteine metabolic process;regulation of hormone levels;regulation of metabolic process;regulation of neurotransmitter levels;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of smooth muscle cell proliferation;regulation of sulfur amino acid metabolic process;regulation of sulfur metabolic process;reproductive process;response to biotic stimulus;response to chemical stimulus;response to drug;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic cyclic compound;response to organic substance;response to pain;response to stimulus;response to stress;small molecule catabolic process;small molecule metabolic process;steroid metabolic process;system process;xenobiotic metabolic process "binding;catalytic activity;catechol O-methyltransferase activity;cation binding;ion binding;magnesium ion binding;metal ion binding;methyltransferase activity;O-methyltransferase activity;S-adenosylmethionine-dependent methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasmic part;cytosol;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;plasma membrane Betalain biosynthesis;Steroid hormone biosynthesis;Tyrosine metabolism 6.06E-36 6 7 7 31.2

Q9UNS2;Q9UNS2-2;H7C3P9;J3QL22;J3QS85;J3KTQ1;J3QKR0;C9JLV5 COP9 signalosome complex subunit 3 COPS3 >sp|Q9UNS2|CSN3_HUMAN COP9 signalosome complex subunit 3 OS=Homo sapiens

GN=COPS3 PE=1 SV=3;>sp|Q9UNS2-2|CSN3_HUMAN Isoform 2 of COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3;>tr|H7C3P9|H7C3P9_HUMAN COP9 signalosome complex subunit 3 OS=Homo 0.16 -0.17 -0.09 -0.02 -0.08 -0.20 -0.03 -0.34 0.562655897 0.132959632 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chordate embryonic development;cullin deneddylation;developmental process;embryo development;embryo development ending in birth or egg hatching;in utero embryonic development;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein deneddylation;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;regulation of biological process;regulation of cellular process;response to abiotic stimulus;response to light stimulus;response to radiation;response to stimulus;signal transduction cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;protein complex;signalosome 2.44E-98 8 7 7 25.8

Q96GQ7 Probable ATP-dependent RNA helicase DDX27 DDX27 >sp|Q96GQ7|DDX27_HUMAN Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2 -0.06 1.02 0.16 0.92 -0.46 0.11 -1.15 0.13 0.901699476 0.853545336 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.74E-36 1 7 7 10.3

O43583;F8VVL1 Density-regulated protein DENR >sp|O43583|DENR_HUMAN Density-regulated protein OS=Homo sapiens GN=DENR PE=1 SV=2;>tr|F8VVL1|F8VVL1_HUMAN Density-regulated protein OS=Homo sapiens GN=DENR PE=2 SV=1 0.02 -0.04 0.03 -0.07 0.01 0.04 0.37 0.17 0.831685639 -0.165018671 "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" 1.44E-56 2 7 7 35.4

Q9Y394-2;Q9Y394;H0YJ66;H0YJE4;H0YJR8 Dehydrogenase/reductase SDR family member 7 DHRS7 >sp|Q9Y394-2|DHRS7_HUMAN Isoform 2 of Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7;>sp|Q9Y394|DHRS7_HUMAN Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens GN=DHRS7 PE=1 SV=1;>tr|H0YJ66|H0YJ66_HUMAN Dehydrogenase/reductase 0.12 0.08 0.02 -0.20 0.16 0.07 0.17 0.11 0.686390099 -0.119250522 metabolic process;oxidation-reduction process catalytic activity;oxidoreductase activity 5.06E-52 5 7 7 24.6

Q9UBS4;H7C2Y5 DnaJ homolog subfamily B member 11 DNAJB11 >sp|Q9UBS4|DJB11_HUMAN DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=10.02 0.14 -0.59 -0.19 0.12 -0.13 0.19 0.19 0.591987925 -0.248144528 activation of signaling protein activity involved in unfolded protein response;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA metabolic process;mRNA modification;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;RNA metabolic process;RNA modification cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;nucleus;organelle;organelle lumen;organelle part Protein processing in endoplasmic reticulum 2.35E-101 2 7 7 18.4

Q5QJE6;J3KP30;E9PRB3 Deoxynucleotidyltransferase terminal-interacting protein 2 DNTTIP2 >sp|Q5QJE6|TDIF2_HUMAN Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens GN=DNTTIP2 PE=1 SV=2;>tr|J3KP30|J3KP30_HUMAN Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens GN=DNTTIP2 PE=4 SV=1 -0.33 1.52 0.14 1.12 -0.85 -0.02 -1.42 0.92 0.607964327 0.955774646 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 1.70E-36 3 7 7 14.7

P23919;H7BZ20;H7C312;G5E9E9;H7C3A4 Thymidylate kinase DTYMK >sp|P23919|KTHY_HUMAN Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4;>tr|H7BZ20|H7BZ20_HUMAN Thymidylate kinase (Fragment) OS=Homo sapiens GN=DTYMK PE=4 SV=1;>tr|H7C312|H7C312_HUMAN Thymidylate kinase (Fragment) OS=Homo sapiens GN=DTYMK PE=4 SV=1 0.35 -0.10 -0.54 -0.08 0.03 -0.19 0.00 -0.44 0.097668796 0.059152566 2'-deoxyribonucleotide biosynthetic process;2'-deoxyribonucleotide metabolic process;biosynthetic process;cell cycle;cell differentiation;cell proliferation;cellular biosynthetic process;cellular developmental process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;deoxyribonucleoside diphosphate biosynthetic process;deoxyribonucleoside diphosphate metabolic process;deoxyribonucleoside triphosphate biosynthetic process;deoxyribonucleoside triphosphate metabolic process;deoxyribonucleotide biosynthetic process;deoxyribonucleotide metabolic process;developmental process;dTDP biosynthetic process;dTDP metabolic process;dTTP biosynthetic process;dTTP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;muscle cell differentiation;myoblast differentiation;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside diphosphate biosynthetic process;nucleoside diphosphate metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;pyrimidine deoxyribonucleoside diphosphate biosynthetic process;pyrimidine deoxyribonucleoside diphosphate metabolic process;pyrimidine deoxyribonucleoside triphosphate biosynthetic process;pyrimidine deoxyribonucleoside triphosphate metabolic process;pyrimidine deoxyribonucleotide biosynthetic process;pyrimidine deoxyribonucleotide metabolic process;pyrimidine nucleoside diphosphate biosynthetic process;pyrimidine nucleoside diphosphate metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;response to cadmium ion;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to growth factor stimulus;response to hormone stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to steroid hormone stimulus;response to stimulus;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleobase-containing compound kinase activity;nucleoside phosphate kinase activity;nucleotide binding;nucleotide kinase activity;phosphotransferase activity, phosphate group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;thymidylate kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial intermembrane space;mitochondrial matrix;mitochondrial part;organelle envelope lumen;organelle lumen;organelle part Pyrimidine metabolism 2.39E-24 5 7 7 31.1

Q13144;E9PC74;H7C2X0;C9JRD9 Translation initiation factor eIF-2B subunit epsilon EIF2B5 >sp|Q13144|EI2BE_HUMAN Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=1 SV=3;>tr|E9PC74|E9PC74_HUMAN Translation initiation factor eIF-2B subunit epsilon OS=Homo sapiens GN=EIF2B5 PE=2 SV=1 -0.04 0.07 0.04 0.03 0.09 -0.12 -0.04 -0.13 0.539733104 0.072078365 anatomical structure development;astrocyte development;axon ensheathment;biological regulation;cell development;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;developmental process;ensheathment of neurons;glial cell development;macromolecule metabolic process;metabolic process;myelination;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;negative regulation of translation in response to stress;negative regulation of translational initiation;negative regulation of translational initiation in response to stress;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oligodendrocyte development;ovarian follicle development;ovulation cycle process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;positive regulation of translational initiation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translation in response to stress;regulation of translational initiation;regulation of translational initiation in response to stress;response to abiotic stimulus;response to carbohydrate stimulus;response to chemical stimulus;response to endogenous stimulus;response to glucose stimulus;response to heat;response to hexose stimulus;response to hormone stimulus;response to monosaccharide stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;rhythmic process;RNA metabolic process "binding;catalytic activity;enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleic acid binding;nucleoside-triphosphatase regulator activity;protein binding;RNA binding;transferase activity;translation factor activity, nucleic acid binding;translation initiation factor activity;translation initiation factor binding" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 2B complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex RNA transport 4.35E-30 4 7 7 14

O15372;B3KS98;E5RJT0;E5RGU4;E5RHC7;E5RH59;E5RFW7;E5RFH0 Eukaryotic translation initiation factor 3 subunit H EIF3H >sp|O15372|EIF3H_HUMAN Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1;>tr|B3KS98|B3KS98_HUMAN Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3S3 PE=2 SV=1 -0.11 0.17 -0.19 -0.21 -0.08 -0.24 -0.14 -0.47 0.512274062 0.14873196 biological regulation;cellular process;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex Measles;RNA transport 7.85E-50 8 7 7 28.7

Q9H9T3;Q9H9T3-2;B4DXV1;B4DE19;B4DIG1;B4DKA4;E5RG26;E5RHY2;E5RIC0;E5RIZ7;E5RHR2 Elongator complex protein 3 ELP3 >sp|Q9H9T3|ELP3_HUMAN Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=1 SV=2;>sp|Q9H9T3-2|ELP3_HUMAN Isoform 2 of Elongator complex protein 3 OS=Homo sapiens GN=ELP3;>tr|B4DXV1|B4DXV1_HUMAN Elongator complex protein 3 OS=Homo sapiens GN=ELP3 PE=2 SV 0.06 -0.11 0.54 0.08 -0.25 -0.51 0.02 -0.86 0.98955979 0.542015167 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;histone acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent" "acetyltransferase activity;binding;catalytic activity;cation binding;enzyme regulator activity;histone acetyltransferase activity;ion binding;iron-sulfur cluster binding;kinase regulator activity;lysine N-acetyltransferase activity;metal cluster binding;metal ion binding;N-acetyltransferase activity;N-acyltransferase activity;phosphorylase kinase regulator activity;protein kinase regulator activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" "cell part;cytoplasm;DNA-directed RNA polymerase II, holoenzyme;Elongator holoenzyme complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;organelle;organelle part;protein complex;transcription elongation factor complex" 4.44E-22 11 7 7 18.1

B5MDQ0;Q2NKX8 DNA excision repair protein ERCC-6-like ERCC6L >tr|B5MDQ0|B5MDQ0_HUMAN DNA excision repair protein ERCC-6-like OS=Homo sapiens GN=ERCC6L PE=2 SV=1;>sp|Q2NKX8|ERC6L_HUMAN DNA excision repair protein ERCC-6-like OS=Homo sapiens GN=ERCC6L PE=1 SV=1 0.71 0.08 0.21 0.14 -0.34 -0.77 -0.20 0.52 0.676262408 0.484252285 anaphase;cell cycle phase;cell cycle process;cell division;cellular process;M phase;M phase of mitotic cell cycle;mitotic anaphase;mitotic prometaphase "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;protein complex 4.32E-57 2 7 7 11.1

O95571;M0QXB5;M0QY80;M0QX80 "Protein ETHE1, mitochondrial" ETHE1 ">sp|O95571|ETHE1_HUMAN Persulfide dioxygenase ETHE1, mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2;>tr|M0QXB5|M0QXB5_HUMAN Protein ETHE1, mitochondrial OS=Homo sapiens GN=ETHE1 PE=4 SV=1" 0.13 0.00 -0.08 -0.10 -0.31 -0.14 0.26 -0.14 0.199226249 0.069477891 "amine catabolic process;amine metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;sulfide oxidation;sulfide oxidation, using sulfide:quinone oxidoreductase;sulfur amino acid catabolic process;sulfur amino acid metabolic process;sulfur compound catabolic process;sulfur compound metabolic process" "binding;catalytic activity;cation binding;dioxygenase activity;hydrolase activity;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;sulfur dioxygenase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nucleus;organelle;organelle lumen;organelle part 3.60E-44 4 7 7 30.7

Q96A65;B7Z321;Q96A65-2;F5GZT1;B7Z4J9 Exocyst complex component 4 EXOC4 >sp|Q96A65|EXOC4_HUMAN Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=1 SV=1;>tr|B7Z321|B7Z321_HUMAN Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=2 SV=1 -0.17 0.02 0.12 -0.23 -0.34 -0.05 0.16 0.07 0.064693571 -0.025772645 cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of protein localization;macromolecule metabolic process;membrane docking;membrane organization;metabolic process;primary metabolic process;protein metabolic process;protein transport;transport;vesicle docking;vesicle docking involved in exocytosis cell cortex part;cell part;cell projection part;cytoplasm;cytoplasmic part;exocyst;growth cone membrane;intracellular part;macromolecular complex;membrane;membrane part;myelin sheath abaxonal region;plasma membrane;plasma membrane part;protein complex Tight junction 1.58E-37 5 7 7 10.1

Q9Y2D4;Q9Y2D4-2;J3QT38 Exocyst complex component 6B EXOC6B >sp|Q9Y2D4|EXC6B_HUMAN Exocyst complex component 6B OS=Homo sapiens GN=EXOC6B PE=1 SV=3;>sp|Q9Y2D4-2|EXC6B_HUMAN Isoform 2 of Exocyst complex component 6B OS=Homo sapiens GN=EXOC6B;>tr|J3QT38|J3QT38_HUMAN Exocyst complex component 6B OS=Homo sapiens GN=EXO -0.15 -0.05 0.19 0.04 -0.14 0.23 0.40 0.21 0.503668491 -0.162829996 cellular process;establishment of localization;establishment of protein localization;membrane docking;protein transport;transport;vesicle docking;vesicle docking involved in exocytosis cell cortex part;cell part;cytoplasmic part;exocyst;intracellular part;macromolecular complex;protein complex 3.52E-22 3 7 7 8.6

Q5T1M5;Q5T1M5-2;Q5T1M5-3 FK506-binding protein 15 FKBP15 >sp|Q5T1M5|FKB15_HUMAN FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 PE=1 SV=2;>sp|Q5T1M5-2|FKB15_HUMAN Isoform 2 of FK506-binding protein 15 OS=Homo sapiens GN=FKBP15 0.21 -0.13 0.13 -0.14 0.10 0.06 0.22 0.06 0.389379277 -0.092630113 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;endocytosis;establishment of localization;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;transport;vesicle-mediated transport actin filament;axon;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;early endosome;endosome;growth cone;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;neuron projection;organelle;organelle part;protein complex;site of polarized growth 7.61E-40 3 7 7 8.6

E9PGR2;O14976;D6RF16;D6RAQ7;D6RE78;D6RAW3;H0Y8H5 Cyclin-G-associated kinase GAK >tr|E9PGR2|E9PGR2_HUMAN Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=2 SV=1;>sp|O14976|GAK_HUMAN Cyclin-G-associated kinase OS=Homo sapiens GN=GAK PE=1 SV=2 0.44 -0.18 0.12 -0.62 0.62 0.28 0.93 0.07 0.772420606 -0.535219606 cell cycle;cellular process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;focal adhesion;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle;perinuclear region of cytoplasm 3.34E-102 7 7 7 9.1

G3V1S6;Q10471;B7Z8V8 Polypeptide N-acetylgalactosaminyltransferase 2;Polypeptide N-acetylgalactosaminyltransferase 2 soluble form GALNT2 >tr|G3V1S6|G3V1S6_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 soluble form OS=Homo sapiens GN=GALNT2 PE=2 SV=1;>sp|Q10471|GALT2_HUMAN Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1 -0.18 0.01 -0.17 0.18 0.30 0.65 -0.28 0.32 0.576688631 -0.288280606 biosynthetic process;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;immunoglobulin biosynthetic process;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;O-glycan processing;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-threonine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein O-linked glycosylation;protein O-linked glycosylation via serine;protein O-linked glycosylation via threonine "acetylgalactosaminyltransferase activity;binding;catalytic activity;cation binding;ion binding;manganese ion binding;metal ion binding;polypeptide N-acetylgalactosaminyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;transition metal ion binding;UDP-glycosyltransferase activity" cell part;cytoplasmic part;extracellular region;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi stack;integral to Golgi membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to Golgi membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm Mucin type O-Glycan biosynthesis4.01E-56 3 7 7 18.8

O14908;K7EM11;O14908-2;K7ELJ2;Q8TF64 PDZ domain-containing protein GIPC1 GIPC1 >sp|O14908|GIPC1_HUMAN PDZ domain-containing protein GIPC1 OS=Homo sapiens GN=GIPC1 PE=1 SV=2;>tr|K7EM11|K7EM11_HUMAN PDZ domain-containing protein GIPC1 (Fragment) OS=Homo sapiens GN=GIPC1 PE=4 SV=1;>sp|O14908-2|GIPC1_HUMAN Isoform 2 of PDZ domain-contain 0.20 0.13 -0.05 0.11 -0.28 0.07 0.37 0.19 0.030393685 0.013487541 biological regulation;cell communication;cell migration;cell motility;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component movement;cellular process;cellular response to stimulus;endothelial cell migration;establishment of localization;establishment of localization in cell;establishment of protein localization;glutamate secretion;G-protein coupled receptor protein signaling pathway;intracellular protein transport;intracellular transport;locomotion;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of proteasomal ubiquitin-dependent protein catabolic process;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transforming growth factor beta receptor signaling pathway;positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;posttranscriptional regulation of gene expression;protein targeting;protein transport;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein stability;regulation of proteolysis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmission of nerve impulse;response to stimulus;secretion;secretion by cell;signal release;signal transduction;signaling;synaptic transmission;transport actin binding;binding;cytoskeletal protein binding;identical protein binding;myosin binding;protein binding;protein dimerization activity;protein homodimerization activity brush border;cell cortex;cell part;cell projection;cell projection part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;cytosolic part;dendritic shaft;dendritic spine;endocytic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;neuron projection;neuron spine;organelle;organelle membrane;organelle part;synapse part;synaptic vesicle;vesicle;vesicle membrane 6.07E-62 5 7 7 30.3

P16278-2;E7EQ29;P16278-3;P16278;C9J4G9 Beta-galactosidase GLB1 >sp|P16278-2|BGAL_HUMAN Isoform 2 of Beta-galactosidase OS=Homo sapiens GN=GLB1;>tr|E7EQ29|E7EQ29_HUMAN Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=2 SV=1;>sp|P16278-3|BGAL_HUMAN Isoform 3 of Beta-galactosidase OS=Homo sapiens GN=GLB1;>sp|P16278|BGAL_HUM -0.01 0.15 -0.41 0.07 -0.14 -0.02 -0.21 0.13 0.023722096 0.010499481 alcohol catabolic process;alcohol metabolic process;amine metabolic process;aminoglycan catabolic process;aminoglycan metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;galactose catabolic process;galactose metabolic process;glycolipid metabolic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;glycosphingolipid metabolic process;hexose catabolic process;hexose metabolic process;keratan sulfate catabolic process;keratan sulfate metabolic process;lipid metabolic process;macromolecule catabolic process;macromolecule metabolic process;membrane lipid metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;nitrogen compound metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;sphingolipid metabolic process;sulfur compound catabolic process;sulfur compound metabolic process "beta-galactosidase activity;binding;carbohydrate binding;catalytic activity;galactosidase activity;galactoside binding;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;monosaccharide binding;sugar binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-enclosed lumen;organelle lumen;organelle part;perinuclear region of cytoplasm;vacuolar lumen;vacuolar part Galactose metabolism;Glycosaminoglycan degradation;Glycosphingolipid biosynthesis - ganglio series;Lysosome;Other glycan degradation;Sphingolipid metabolism 2.85E-21 5 7 7 19

P15104 Glutamine synthetase GLUL >sp|P15104|GLNA_HUMAN Glutamine synthetase OS=Homo sapiens GN=GLUL PE=1 SV=4 -0.23 -0.29 0.14 0.56 -0.23 -1.13 -1.07 -0.98 1.280807697 0.896069556 "amine biosynthetic process;amine catabolic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell proliferation;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;glutamate catabolic process;glutamate metabolic process;glutamine biosynthetic process;glutamine family amino acid biosynthetic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;neurotransmitter transport;neurotransmitter uptake;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of epithelial cell proliferation;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of multicellular organismal process;positive regulation of neurological system process;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of secretion;positive regulation of signaling;positive regulation of synaptic transmission;positive regulation of synaptic transmission, glutamatergic;positive regulation of transmission of nerve impulse;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell proliferation;regulation of cellular localization;regulation of cellular process;regulation of epithelial cell proliferation;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of multicellular organismal process;regulation of neurological system process;regulation of neurotransmitter levels;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of synaptic transmission;regulation of synaptic transmission, glutamatergic;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;response to carbohydrate stimulus;response to chemical stimulus;response to glucose stimulus;response to hexose stimulus;response to monosaccharide stimulus;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;transport" "acid-ammonia (or amide) ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;ammonia ligase activity;ATP binding;binding;carbon-carbon lyase activity;carboxylic acid binding;carboxy-lyase activity;catalytic activity;cation binding;glutamate binding;glutamate decarboxylase activity;glutamate-ammonia ligase activity;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;lyase activity;magnesium ion binding;manganese ion binding;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transition metal ion binding" axon part;axon terminus;cell part;cell projection part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;neuron projection terminus;organelle;perikaryon;protein complex;rough endoplasmic reticulum "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;Nitrogen metabolism;Two-component system" 2.94E-39 1 7 7 22.3

Q96IJ6;Q96IJ6-2;F8WD54;C9J255;C9JAH0 Mannose-1-phosphate guanyltransferase alpha GMPPA >sp|Q96IJ6|GMPPA_HUMAN Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1;>sp|Q96IJ6-2|GMPPA_HUMAN Isoform 2 of Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA 0.09 -0.02 -1.21 0.00 -0.44 -0.14 0.27 0.25 0.302284297 -0.269889964 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;dolichol-linked oligosaccharide biosynthetic process;GDP-mannose biosynthetic process;GDP-mannose metabolic process;glycosylation;hexose biosynthetic process;hexose metabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;mannose biosynthetic process;mannose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar biosynthetic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;small molecule biosynthetic process;small molecule metabolic process "binding;catalytic activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;guanylyltransferase activity;mannose-1-phosphate guanylyltransferase activity;mannose-phosphate guanylyltransferase activity;nucleotide binding;nucleotidyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" Amino sugar and nucleotide sugar metabolism;Fructose and mannose metabolism 1.09E-35 5 7 7 21.2

P36915;B0V0L0;P36915-2;A2AB27 Guanine nucleotide-binding protein-like 1 GNL1 >sp|P36915|GNL1_HUMAN Guanine nucleotide-binding protein-like 1 OS=Homo sapiens GN=GNL1 PE=1 SV=2;>tr|B0V0L0|B0V0L0_HUMAN Guanine nucleotide-binding protein-like 1 (Fragment) OS=Homo sapiens GN=GNL1 PE=2 SV=1;>sp|P36915-2|GNL1_HUMAN Isoform 2 of Guanine nu0.18 -0.12 0.15 0.23 0.17 0.06 0.43 -0.04 0.131945942 -0.046760711 adaptive immune response;adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;biological regulation;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;cellular response to stress;immune effector process;immune response;immune system process;leukocyte mediated immunity;lymphocyte mediated immunity;regulation of biological process;regulation of cellular process;response to DNA damage stimulus;response to stimulus;response to stress;ribonucleoprotein complex biogenesis;ribosome biogenesis;signal transduction;T cell mediated immunity "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural molecule activity" cell part;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular part 5.43E-31 4 7 7 14.7

C9JFE4;Q13098-5;Q13098;Q13098-7;J3QQX0;Q13098-6;J3QS88;J3KTB0;J3QLT0;J3KSA5;J3KRJ4;J3QS84;J3QLE8;J3QL53;J3KRE8 COP9 signalosome complex subunit 1 GPS1 >tr|C9JFE4|C9JFE4_HUMAN COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=4 SV=2;>sp|Q13098-5|CSN1_HUMAN Isoform 4 of COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1;>sp|Q13098|CSN1_HUMAN COP9 signalosome complex subunit 1 OS=Homo sa 0.19 0.10 -0.07 0.10 -0.06 -0.05 0.13 -0.32 0.618942365 0.156868406 biological regulation;cell cycle;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;cullin deneddylation;inactivation of MAPK activity;intracellular protein kinase cascade;intracellular signal transduction;JNK cascade;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;negative regulation of catalytic activity;negative regulation of kinase activity;negative regulation of MAP kinase activity;negative regulation of molecular function;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of transferase activity;primary metabolic process;protein deneddylation;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transferase activity;response to stimulus;response to stress;signal transduction;stress-activated protein kinase signaling cascade enzyme inhibitor activity;enzyme regulator activity;GTPase inhibitor activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;protein complex;signalosome 1.92E-27 15 7 7 19.5

Q9Y5Z4;Q9Y5Z4-2;Q5THN1;C9IZA0 Heme-binding protein 2 HEBP2 >sp|Q9Y5Z4|HEBP2_HUMAN Heme-binding protein 2 OS=Homo sapiens GN=HEBP2 PE=1 SV=1;>sp|Q9Y5Z4-2|HEBP2_HUMAN Isoform 2 of Heme-binding protein 2 OS=Homo sapiens GN=HEBP2 0.11 0.01 0.05 -0.05 0.05 0.09 0.44 -0.01 0.430440342 -0.11186311 cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 3.67E-110 4 7 7 44.9

Q5GLZ8-6;Q5GLZ8-3;Q5GLZ8-2;Q5GLZ8;H0Y6K7 Probable E3 ubiquitin-protein ligase HERC4 HERC4 >sp|Q5GLZ8-6|HERC4_HUMAN Isoform 6 of Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens GN=HERC4;>sp|Q5GLZ8-3|HERC4_HUMAN Isoform 3 of Probable E3 ubiquitin-protein ligase HERC4 OS=Homo sapiens GN=HERC4;>sp|Q5GLZ8-2|HERC4_HUMAN Isoform 2 of Probab 0.14 -0.14 0.11 0.06 0.10 0.32 0.45 0.14 0.869685712 -0.208611432 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;gamete generation;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;reproductive process;spermatogenesis "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;ubiquitin-protein ligase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Ubiquitin mediated proteolysis 3.26E-21 5 7 7 11.1

Q71DI3;Q16695;P68431;K7EK07;P84243;K7EMV3;B4DEB1;Q6NXT2;K7ES00;K7EP01 Histone H3.2;Histone H3.1t;Histone H3.1;Histone H3;Histone H3.3;Histone H3.3C HIST2H3A;HIST3H3;HIST1H3A;H3F3B;H3F3A;H3F3C >sp|Q71DI3|H32_HUMAN Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3;>sp|Q16695|H31T_HUMAN Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3;>sp|P68431|H31_HUMAN Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2;>tr|K7EK07|K7EK07_HUMAN Histone H3 (Fra -0.41 1.31 0.03 1.35 -0.44 -0.04 -1.86 0.05 0.780900322 1.148018455 anatomical structure homeostasis;biological regulation;blood coagulation;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;coagulation;DNA metabolic process;hemostasis;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular process;regulation of gene silencing;S phase;telomere maintenance;telomere organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleosome;nucleus;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus 9.46E-18 10 7 7 36.8

Q9H910;B4DLH4;Q9H910-2;A6NGP5;H3BU16;H3BMV3;H3BMT0;H3BTV5;H3BMM8;B4E1P3;H3BS08 Hematological and neurological expressed 1-like protein HN1L >sp|Q9H910|HN1L_HUMAN Hematological and neurological expressed 1-like protein OS=Homo sapiens GN=HN1L PE=1 SV=1;>tr|B4DLH4|B4DLH4_HUMAN Hematological and neurological-expressed 1-like protein OS=Homo sapiens GN=HN1L PE=2 SV=1;>sp|Q9H910-2|HN1L_HUMAN Isofor 0.16 -0.05 0.19 -0.24 -0.48 -0.35 0.30 0.16 0.189253408 0.108763337 cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 1.47E-125 11 7 7 46.8

Q96J02-3;Q96J02-2;Q96J02;H0YBA4;Q9H0M0-6;Q9H0M0-3;Q9H0M0 E3 ubiquitin-protein ligase Itchy homolog ITCH >sp|Q96J02-3|ITCH_HUMAN Isoform 3 of E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens GN=ITCH;>sp|Q96J02-2|ITCH_HUMAN Isoform 2 of E3 ubiquitin-protein ligase Itchy homolog OS=Homo sapiens GN=ITCH;>sp|Q96J02|ITCH_HUMAN E3 ubiquitin-protein ligase 0.22 -0.08 -0.08 -0.11 -0.20 -0.28 0.23 -0.26 0.306281332 0.111966299 "activation of immune response;activation of innate immune response;anatomical structure development;apoptosis;biological regulation;catabolic process;cell death;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;central nervous system development;cytoplasmic pattern recognition receptor signaling pathway;death;defense response;defense response to virus;developmental process;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of virus into host cell;establishment of localization;immune effector process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;inflammatory response;innate immune response;innate immune response-activating signal transduction;interaction with host;interspecies interaction between organisms;intracellular receptor mediated signaling pathway;ion transmembrane transport;ion transport;locomotion;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multi-organism process;negative regulation of alpha-beta T cell activation;negative regulation of alpha-beta T cell proliferation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell activation;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of defense response;negative regulation of defense response to virus;negative regulation of gene expression;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of intracellular protein kinase cascade;negative regulation of JNK cascade;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAPKKK cascade;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of mononuclear cell proliferation;negative regulation of multicellular organismal process;negative regulation of multi-organism process;negative regulation of NF-kappaB transcription factor activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of stress-activated protein kinase signaling cascade;negative regulation of T cell activation;negative regulation of T cell proliferation;negative regulation of transcription, DNA-dependent;negative regulation of type I interferon production;Notch signaling pathway;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;nucleotide-binding oligomerization domain containing signaling pathway;pattern recognition receptor signaling pathway;positive regulation of biological process;positive regulation of catabolic process;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of lymphocyte anergy;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of response to stimulus;positive regulation of T cell anergy;positive regulation of T cell tolerance induction;positive regulation of tolerance induction;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein K29-linked ubiquitination;protein K48-linked ubiquitination;protein K63-linked ubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of alpha-beta T cell activation;regulation of alpha-beta T cell proliferation;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cell activation;regulation of cell communication;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of developmental process;regulation of gene expression;regulation of growth;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte anergy;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein deubiquitination;regulation of protein metabolic process;regulation of protein modification process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of T cell activation;regulation of T cell anergy;regulation of T cell proliferation;regulation of T cell tolerance induction;regulation of tolerance induction;regulation of transcription, DNA-dependent;regulation of type I interferon production;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus;response to wounding;signal transduction;system development;transmembrane transport;transport;ubiquitin-dependent protein catabolic process" "acid-amino acid ligase activity;binding;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;ribonucleoprotein binding;small conjugating protein ligase activity;ubiquitin-protein ligase activity" cell cortex;cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane;protein complex;ubiquitin ligase complex;vesicle Endocytosis;Ubiquitin mediated proteolysis 2.55E-32 7 7 7 12

Q15397 Pumilio domain-containing protein KIAA0020 KIAA0020 >sp|Q15397|K0020_HUMAN Pumilio domain-containing protein KIAA0020 OS=Homo sapiens GN=KIAA0020 PE=1 SV=3 -0.01 1.13 -0.04 0.28 -0.54 -0.37 -1.05 1.01 0.460525393 0.578091754 binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 7.14E-29 1 7 7 16

Q9Y383;Q9Y383-3;Q9Y383-2;Q96HJ9-2;B8ZZ10;A8MYV2;Q9NQ29-2;Q9NQ29-3;Q9NQ29;F8WB41;F8WEU3;B8ZZ09;C9JWT3 Putative RNA-binding protein Luc7-like 2 LUC7L2 >sp|Q9Y383|LC7L2_HUMAN Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2;>sp|Q9Y383-3|LC7L2_HUMAN Isoform 3 of Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2;>sp|Q9Y383-2|LC7L2_HUMAN Isoform 2 of Putative RNA- -0.10 -0.07 0.01 -0.01 -0.11 -0.60 -0.16 -0.62 0.989010464 0.325711956 biological regulation;negative regulation of biological process;negative regulation of developmental process;negative regulation of muscle organ development;negative regulation of striated muscle tissue development;regulation of biological process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of striated muscle tissue development cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part 4.57E-73 13 7 7 20.2

B4DH53;Q66K74;M0R1M7;M0QXQ9;M0R1J2;M0QY41 Microtubule-associated protein 1S;MAP1S heavy chain;MAP1S light chain MAP1S >tr|B4DH53|B4DH53_HUMAN MAP1S light chain OS=Homo sapiens GN=MAP1S PE=2 SV=1;>sp|Q66K74|MAP1S_HUMAN Microtubule-associated protein 1S OS=Homo sapiens GN=MAP1S PE=1 SV=2 -0.24 -0.01 -0.09 -0.20 1.06 0.51 0.07 0.14 1.052788098 -0.579849578 "anatomical structure development;anatomical structure morphogenesis;apoptosis;brain development;cell death;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;death;developmental process;establishment of localization;establishment of localization in cell;establishment of mitochondrion localization;establishment of mitochondrion localization, microtubule-mediated;establishment of organelle localization;intracellular transport;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrion transport along microtubule;neuron projection morphogenesis;organ development;organelle organization;organelle transport along microtubule;programmed cell death;transport" actin binding;actin filament binding;beta-tubulin binding;binding;catalytic activity;cytoskeletal protein binding;DNA binding;hydrolase activity;microtubule binding;nucleic acid binding;protein binding;tubulin binding cell body;cell part;cell projection;cytoplasmic part;cytoskeletal part;cytosol;dendrite;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;neuron projection;neuronal cell body;non-membrane-bounded organelle;nucleus;organelle;organelle part;perinuclear region of cytoplasm;protein complex;spindle;synapse 6.86E-40 6 7 7 10.8

Q9BYD6;H0Y8N7;H0YAB5 "39S ribosomal protein L1, mitochondrial" MRPL1 ">sp|Q9BYD6|RM01_HUMAN 39S ribosomal protein L1, mitochondrial OS=Homo sapiens GN=MRPL1 PE=1 SV=2;>tr|H0Y8N7|H0Y8N7_HUMAN 39S ribosomal protein L1, mitochondrial (Fragment) OS=Homo sapiens GN=MRPL1 PE=4 SV=1" -0.01 0.32 -0.08 -0.11 -0.10 -0.64 -0.78 -0.38 1.174664658 0.506856131 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;translation binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;mitochondrion;organelle;organelle part;ribonucleoprotein complex 2.20E-26 3 7 7 28

Q9UKD2 mRNA turnover protein 4 homolog MRTO4 >sp|Q9UKD2|MRT4_HUMAN mRNA turnover protein 4 homolog OS=Homo sapiens GN=MRTO4 PE=1 SV=2 -0.13 0.44 -0.20 0.09 -0.25 -0.66 -1.01 -0.10 0.942308299 0.555141097 cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;organelle;organelle membrane;organelle part 2.79E-27 1 7 7 36.8

P19105;O14950;J3QRS3;P24844;P24844-2;J3KTJ1 Myosin regulatory light chain 12A;Myosin regulatory light chain 12B;Myosin regulatory light polypeptide 9 MYL12A;MYL12B;MYL9 >sp|P19105|ML12A_HUMAN Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2;>sp|O14950|ML12B_HUMAN Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2;>tr|J3QRS3|J3QRS3_HUMAN Myosin regulatory light chain 12A OS=Homo sapi -0.16 0.65 -0.05 0.63 -0.12 0.60 -0.30 0.90 0.00432583 -0.004821485 axon guidance;biological regulation;chemotaxis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;intracellular protein transport;intracellular transport;locomotion;multicellular organismal process;muscle contraction;muscle system process;protein targeting;protein targeting to plasma membrane;protein transport;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of system process;response to chemical stimulus;response to external stimulus;response to stimulus;system process;taxis;transportbinding;calcium ion binding;cation binding;ion binding;metal ion binding;structural constituent of muscle;structural molecule activity actin filament bundle;actomyosin;apical part of cell;cell part;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;muscle myosin complex;myosin complex;myosin II complex;organelle part;protein complex;stress fiber;Z disc Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Tight junction;Vascular smooth muscle contraction 7.36E-86 6 7 7 44.4

Q9NR45;Q5TBR0;Q5TBR1 Sialic acid synthase NANS >sp|Q9NR45|SIAS_HUMAN Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 0.17 0.02 -0.39 -0.05 -0.04 -0.19 0.32 0.53 0.441744734 -0.216379046 biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;lipid biosynthetic process;lipid metabolic process;lipopolysaccharide biosynthetic process;lipopolysaccharide metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process "catalytic activity;cytidylyltransferase activity;N-acetylneuraminate synthase activity;N-acylneuraminate cytidylyltransferase activity;N-acylneuraminate-9-phosphate synthase activity;nucleotidyltransferase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Amino sugar and nucleotide sugar metabolism 8.83E-52 3 7 7 26.2

Q6ZVX7 F-box only protein 50 NCCRP1 >sp|Q6ZVX7|FBX50_HUMAN F-box only protein 50 OS=Homo sapiens GN=NCCRP1 PE=1 SV=1 -0.18 0.73 -0.01 -0.26 1.59 2.30 0.99 0.40 1.127619194 -1.250986614 biological regulation;catabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein catabolic process;protein metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process cell part;cytoplasm;intracellular part 9.36E-28 1 7 7 35.6

O60524-4;O60524-5;O60524-3;O60524;G3V5V3;G3V4D9;O60524-2 Nuclear export mediator factor NEMF NEMF >sp|O60524-4|NEMF_HUMAN Isoform 4 of Nuclear export mediator factor NEMF OS=Homo sapiens GN=NEMF;>sp|O60524-5|NEMF_HUMAN Isoform 5 of Nuclear export mediator factor NEMF OS=Homo sapiens GN=NEMF;>sp|O60524-3|NEMF_HUMAN Isoform 3 of Nuclear export mediator f 0.25 0.06 -0.11 -0.22 0.36 0.02 0.41 -0.20 0.343753406 -0.153115469 establishment of localization;establishment of localization in cell;intracellular transport;nuclear export;nuclear transport;nucleocytoplasmic transport;transport cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.79E-16 7 7 7 8.1

Q13423;D6RAI5;E9PCX7;D6RHU2;D6RCR6 "NAD(P) transhydrogenase, mitochondrial" NNT ">sp|Q13423|NNTM_HUMAN NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3;>tr|D6RAI5|D6RAI5_HUMAN NAD(P) transhydrogenase, mitochondrial (Fragment) OS=Homo sapiens GN=NNT PE=2 SV=1;>tr|E9PCX7|E9PCX7_HUMAN NAD(P) transhydrogenase, mitoch" -0.15 0.09 -0.29 -0.07 0.89 0.79 0.29 -0.24 0.848444181 -0.53840662 acetyl-CoA catabolic process;acetyl-CoA metabolic process;catabolic process;cation transport;cellular catabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;establishment of localization;hydrogen transport;ion transport;metabolic process;monovalent inorganic cation transport;proton transport;reactive oxygen species metabolic process;small molecule metabolic process;transport;tricarboxylic acid cycle "binding;catalytic activity;cation transmembrane transporter activity;coenzyme binding;cofactor binding;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;NAD binding;NAD(P)+ transhydrogenase (AB-specific) activity;NAD(P)+ transhydrogenase (B-specific) activity;NAD(P)+ transhydrogenase activity;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, NAD or NADP as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain;organelle inner membrane;organelle membrane;organelle part;respiratory chain Nicotinate and nicotinamide metabolism 1.09E-27 5 7 7 9.9

Q9H6R4-4;Q9H6R4;Q9H6R4-2;G8JLK7;Q9H6R4-3 Nucleolar protein 6 NOL6 >sp|Q9H6R4-4|NOL6_HUMAN Isoform 4 of Nucleolar protein 6 OS=Homo sapiens GN=NOL6;>sp|Q9H6R4|NOL6_HUMAN Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2;>sp|Q9H6R4-2|NOL6_HUMAN Isoform 2 of Nucleolar protein 6 OS=Homo sapiens GN=NOL6;>tr|G8JLK7|G8JLK7_ -0.07 1.07 0.12 1.01 -0.95 -0.09 -0.99 0.47 0.853133764 0.920784505 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing binding;nucleic acid binding;RNA binding cell part;chromosome;condensed chromosome;condensed nuclear chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes 1.21E-47 5 7 7 10

Q9UKX7-2;Q9UKX7;B4E2D3;B0QY21 Nuclear pore complex protein Nup50 NUP50 >sp|Q9UKX7-2|NUP50_HUMAN Isoform 2 of Nuclear pore complex protein Nup50 OS=Homo sapiens GN=NUP50;>sp|Q9UKX7|NUP50_HUMAN Nuclear pore complex protein Nup50 OS=Homo sapiens GN=NUP50 PE=1 SV=2 -0.57 0.17 0.24 0.74 0.36 0.29 -0.89 -0.16 0.239392522 0.245381705 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular transport;metabolic process;monosaccharide transport;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;organic substance transport;primary metabolic process;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process cell part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear pore;nucleoplasm;organelle membrane;organelle part;pore complex;protein complex RNA transport 1.05E-36 4 7 7 24.5

Q6DKJ4;Q6DKJ4-3;Q6DKJ4-2;I3L4V6 Nucleoredoxin NXN >sp|Q6DKJ4|NXN_HUMAN Nucleoredoxin OS=Homo sapiens GN=NXN PE=1 SV=2 0.29 0.04 -0.23 0.01 -0.45 -0.23 0.72 -0.44 0.157829226 0.127947369 anatomical structure development;biological regulation;cardiovascular system development;cell differentiation;cell surface receptor linked signaling pathway;cellular developmental process;cellular process;cellular response to stimulus;developmental process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;regulation of biological process;regulation of cell communication;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of Wnt receptor signaling pathway;response to stimulus;signal transduction;system development;Wnt receptor signaling pathway "antioxidant activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on NADH or NADPH;protein-disulfide reductase activity;thioredoxin-disulfide reductase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.89E-39 4 7 7 25.1

Q9BZF1-3;Q9BZF1-2;Q9BZF1;F8VUA7;F8VQX7;F8VVD3;F8VVE7;F8VZ43 Oxysterol-binding protein-related protein 8;Oxysterol-binding protein OSBPL8 >sp|Q9BZF1-3|OSBL8_HUMAN Isoform 3 of Oxysterol-binding protein-related protein 8 OS=Homo sapiens GN=OSBPL8;>sp|Q9BZF1-2|OSBL8_HUMAN Isoform 2 of Oxysterol-binding protein-related protein 8 OS=Homo sapiens GN=OSBPL8;>sp|Q9BZF1|OSBL8_HUMAN Oxysterol-binding -0.03 0.05 0.02 -0.16 0.14 -0.19 -0.17 0.14 0.038372354 -0.011990821 biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;establishment of localization;fat cell differentiation;lipid transport;negative regulation of biological process;negative regulation of lipid storage;negative regulation of sequestering of triglyceride;organic substance transport;regulation of biological process;regulation of lipid storage;regulation of localization;regulation of sequestering of triglyceride;transport binding;cholesterol binding;lipid binding;phospholipid binding;steroid binding;sterol binding 2.51E-34 8 7 7 12.2

P30086 Phosphatidylethanolamine-binding protein 1;Hippocampal cholinergic neurostimulating peptide PEBP1 >sp|P30086|PEBP1_HUMAN Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3 0.05 -0.10 -0.29 -0.08 0.07 0.15 0.59 0.19 1.095391839 -0.354164869 adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;lipid binding;nucleotide binding;peptidase inhibitor activity;peptidase regulator activity;phosphatidylethanolamine binding;phospholipid binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;serine-type endopeptidase inhibitor activity cell part;cytoplasm;intracellular part 2.94E-138 1 7 7 49.2

P12955-2;P12955;P12955-3;K7ES25 Xaa-Pro dipeptidase PEPD >sp|P12955-2|PEPD_HUMAN Isoform 2 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD;>sp|P12955|PEPD_HUMAN Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD PE=1 SV=3;>sp|P12955-3|PEPD_HUMAN Isoform 3 of Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD 0.19 0.08 0.16 -0.02 0.21 0.07 0.39 -0.41 0.06431583 0.033476369 amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;collagen catabolic process;collagen metabolic process;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein metabolic process;proteolysis;small molecule metabolic process "aminopeptidase activity;binding;carboxypeptidase activity;catalytic activity;cation binding;dipeptidase activity;exopeptidase activity;hydrolase activity;ion binding;manganese ion binding;metal ion binding;metallocarboxypeptidase activity;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding" 9.37E-70 4 7 7 18.8

O95394;O95394-3;O95394-4;J3KN95;H0Y8I3;H0Y987;D6RCD1;D6RC77;D6RCQ8;D6RF77;D6RIS6 Phosphoacetylglucosamine mutase PGM3 >sp|O95394|AGM1_HUMAN Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1;>sp|O95394-3|AGM1_HUMAN Isoform 2 of Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3;>sp|O95394-4|AGM1_HUMAN Isoform 3 of Phosphoacetylglucosamine mutase OS=Hom 0.22 -0.08 -0.23 -0.15 0.58 0.60 0.45 0.07 1.277420301 -0.487429766 alcohol biosynthetic process;alcohol metabolic process;amino sugar biosynthetic process;amino sugar metabolic process;anatomical structure development;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;developmental process;dolichol-linked oligosaccharide biosynthetic process;embryo development;gamete generation;glucosamine biosynthetic process;glucosamine metabolic process;glucose 1-phosphate metabolic process;glucose metabolic process;glycosylation;hemopoiesis;hemopoietic or lymphoid organ development;hexose metabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;multicellular organismal process;multicellular organismal reproductive process;N-acetylglucosamine biosynthetic process;N-acetylglucosamine metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;organ development;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;reproductive process;small molecule biosynthetic process;small molecule metabolic process;spermatogenesis;UDP-N-acetylglucosamine biosynthetic process;UDP-N-acetylglucosamine metabolic process "binding;catalytic activity;cation binding;intramolecular transferase activity;intramolecular transferase activity, phosphotransferases;ion binding;isomerase activity;magnesium ion binding;metal ion binding;phosphoacetylglucosamine mutase activity;phosphoglucomutase activity" cell part;cytoplasmic part;cytosol;intracellular part Amino sugar and nucleotide sugar metabolism 3.17E-54 11 7 7 17

Q99570;D6RJ98;D6RAC3;D6RBB7 Phosphoinositide 3-kinase regulatory subunit 4 PIK3R4 >sp|Q99570|PI3R4_HUMAN Phosphoinositide 3-kinase regulatory subunit 4 OS=Homo sapiens GN=PIK3R4 PE=1 SV=3 0.16 0.02 -0.14 -0.17 0.30 -0.11 0.45 -0.09 0.436139563 -0.169291778 activation of immune response;activation of innate immune response;biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;defense response;enzyme linked receptor protein signaling pathway;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;insulin receptor signaling pathway;lipid biosynthetic process;lipid metabolic process;metabolic process;organophosphate metabolic process;pattern recognition receptor signaling pathway;phosphatidylinositol biosynthetic process;phosphatidylinositol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;positive regulation of biological process;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of response to stimulus;primary metabolic process;regulation of biological process;regulation of cellular process;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of response to stimulus;regulation of response to stress;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;small molecule metabolic process;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;late endosome;membrane-bounded organelle;organelle Regulation of autophagy 6.22E-29 4 7 7 6.8

P24928;Q6NX41 DNA-directed RNA polymerase II subunit RPB1 POLR2A >sp|P24928|RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens GN=POLR2A PE=1 SV=2 0.22 0.69 0.23 0.47 0.04 -0.08 -0.86 0.07 1.042947656 0.610245164 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA capping;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA capping;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent;transcription-coupled nucleotide-excision repair;viral reproductive process" "binding;catalytic activity;cation binding;DNA binding;DNA-directed RNA polymerase activity;ion binding;metal ion binding;nucleic acid binding;nucleotidyltransferase activity;RNA polymerase activity;RNA-directed RNA polymerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" "cell part;DNA-directed RNA polymerase complex;DNA-directed RNA polymerase II, core complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear DNA-directed RNA polymerase complex;nuclear part;nucleoplasm part;organelle part;protein complex;RNA polymerase complex" Huntington's disease;Purine metabolism;Pyrimidine metabolism;RNA polymerase 2.70E-43 2 7 7 5.3

Q15257-3;Q15257-2;A6PVN5;Q15257;B4DZF8;Q68CR8;Q5T949;Q5T948;A6PVN9;Q15257-4;B7ZBQ0;A6PVN8;C9IZ76;A6PVN6;A6PVN7;B7ZBP9;B7ZBP7;B4DDQ6;H0Y6E5 Serine/threonine-protein phosphatase 2A activator PPP2R4;DKFZp781M17165 >sp|Q15257-3|PTPA_HUMAN Isoform 3 of Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4;>sp|Q15257-2|PTPA_HUMAN Isoform 1 of Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4;>tr|A6PVN5|A6PVN5_HUMAN Serine 0.00 -0.12 0.31 0.10 0.13 0.26 0.44 -0.17 0.221709496 -0.091329301 ATP catabolic process;ATP metabolic process;biological regulation;catabolic process;cell cycle process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cytoskeleton organization;heterocycle catabolic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic spindle organization;mitotic spindle organization in nucleus;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of dephosphorylation;negative regulation of hydrolase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of phosphatase activity;negative regulation of phosphate metabolic process;negative regulation of phosphoprotein phosphatase activity;negative regulation of phosphorus metabolic process;negative regulation of protein dephosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of dephosphorylation;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of phosphatase activity;positive regulation of phosphate metabolic process;positive regulation of phosphoprotein phosphatase activity;positive regulation of phosphorus metabolic process;positive regulation of programmed cell death;positive regulation of protein dephosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;primary metabolic process;protein folding;protein metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of lipase activity;regulation of lipoprotein lipase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;spindle organization adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cis-trans isomerase activity;enzyme activator activity;enzyme binding;enzyme regulator activity;identical protein binding;isomerase activity;nucleotide binding;peptidyl-prolyl cis-trans isomerase activity;phosphatase activator activity;phosphatase binding;phosphatase regulator activity;protein binding;protein dimerization activity;protein heterodimerization activity;protein homodimerization activity;protein phosphatase 2A binding;protein phosphatase activator activity;protein phosphatase binding;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein tyrosine phosphatase activator activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding calcium channel complex;cation channel complex;cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;ion channel complex;macromolecular complex;membrane part;membrane-bounded organelle;nucleus;organelle;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex 3.28E-39 19 7 7 39.5

Q9BUB1;P13861;H7C1L0;H7C330;C9J830;P31323 cAMP-dependent protein kinase type II-alpha regulatory subunit PRKAR2A >tr|Q9BUB1|Q9BUB1_HUMAN PRKAR2A protein OS=Homo sapiens GN=PRKAR2A PE=2 SV=1;>sp|P13861|KAP2_HUMAN cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2 -0.25 0.07 0.08 0.04 0.10 0.04 -0.21 -0.23 0.182580932 0.05660921 activation of phospholipase C activity;activation of protein kinase A activity;activation of protein kinase activity;behavior;biological regulation;blood coagulation;carboxylic acid metabolic process;cell cycle process;cell surface receptor linked signaling pathway;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to glucagon stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;coagulation;cognition;defense response;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;fatty acid metabolic process;fibroblast growth factor receptor signaling pathway;fluid transport;G2/M transition of mitotic cell cycle;generation of precursor metabolites and energy;hemostasis;immune response;immune system process;innate immune response;intracellular signal transduction;learning;learning or memory;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;nerve growth factor receptor signaling pathway;neurological system process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of lipase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of catalytic activity;regulation of cell communication;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of kinase activity;regulation of lipase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of secretion;regulation of signaling;regulation of transferase activity;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to glucagon stimulus;response to growth factor stimulus;response to hormone stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;small molecule metabolic process;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport;water transport "adenyl nucleotide binding;adenyl ribonucleotide binding;AMP binding;binding;cAMP binding;cAMP-dependent protein kinase regulator activity;catalytic activity;cyclic nucleotide binding;enzyme binding;enzyme regulator activity;kinase activity;kinase regulator activity;nucleotide binding;protein binding;protein kinase regulator activity;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups;ubiquitin protein ligase binding" cAMP-dependent protein kinase complex;cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane raft;microtubule organizing center;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;organelle;organelle inner membrane;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex Apoptosis;Insulin signaling pathway 2.21E-43 6 7 7 25.7

J3KN29;O00233;F5H5V4;F5GX23;F8W7V8;O00233-2;F5H7X1;F5H169;F5H182;O00233-3 26S proteasome non-ATPase regulatory subunit 9 PSMD9 >tr|J3KN29|J3KN29_HUMAN 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=4 SV=1;>sp|O00233|PSMD9_HUMAN 26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3;>tr|F5H5V4|F5H5V4_HUMAN 26S proteasome non-AT 0.18 -0.04 0.04 -0.10 0.11 -0.11 0.26 0.29 0.44217533 -0.118193611 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of secretion;negative regulation of transport;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of ligase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of RNA metabolic process;positive regulation of secretion;positive regulation of transcription, DNA-dependent;positive regulation of transport;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;proteasome assembly;proteasome regulatory particle assembly;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of hormone secretion;regulation of insulin secretion;regulation of ligase activity;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of RNA metabolic process;regulation of secretion;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transport;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" bHLH transcription factor binding;binding;protein binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome regulatory particle;protein complex 2.16E-37 10 7 7 36.5

C9JW69;P18754;P18754-2;H7C497;C9JRH2;C9JMJ4;C9J3R0;C9JQZ4 Regulator of chromosome condensationRCC1 >tr|C9JW69|C9JW69_HUMAN Regulator of chromosome condensation (Fragment) OS=Homo sapiens GN=RCC1 PE=2 SV=1;>sp|P18754|RCC1_HUMAN Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1;>sp|P18754-2|RCC1_HUMAN Isoform 2 of Regulator of chromos 0.09 0.69 0.06 0.74 -0.25 -0.19 -1.02 -0.13 1.18197671 0.792076695 biological regulation;cell cycle phase;cell cycle process;cell division;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chromosome segregation;cytoskeleton organization;G1/S transition of mitotic cell cycle;microtubule cytoskeleton organization;microtubule-based process;mitosis;mitotic spindle organization;nuclear division;organelle assembly;organelle fission;organelle organization;regulation of biological process;regulation of cell cycle;regulation of cell cycle process;regulation of cellular component organization;regulation of cellular process;regulation of mitosis;regulation of mitotic cell cycle;regulation of nuclear division;regulation of organelle organization;reproductive process;spindle assembly;spindle organization;viral reproductive process binding;chromatin binding;chromatin DNA binding;DNA binding;enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;histone binding;nucleic acid binding;nucleoside-triphosphatase regulator activity;nucleosomal DNA binding;nucleosome binding;protein binding;Ran guanyl-nucleotide exchange factor activity;Ras guanyl-nucleotide exchange factor activity;small GTPase regulator activity;structure-specific DNA binding cell part;chromatin;chromosomal part;chromosome;condensed chromosome;condensed nuclear chromosome;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome;nuclear chromosome part;nuclear membrane;nuclear part;nucleoplasm;nucleus;organelle;organelle membrane;organelle part 3.18E-34 8 7 7 25.8

Q8TC12;Q8TC12-2;G3V2G6;G3V234;Q8TC12-3;H0YIZ8;H0YJ10;H0YJ46 Retinol dehydrogenase 11 RDH11 >sp|Q8TC12|RDH11_HUMAN Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2;>sp|Q8TC12-2|RDH11_HUMAN Isoform 2 of Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11;>tr|G3V2G6|G3V2G6_HUMAN Retinol dehydrogenase 11 (Fragment) OS=Homo sapiens GN=RDH11 0.08 -0.03 0.08 0.03 0.22 0.26 -0.03 0.22 0.763627539 -0.126997053 "adaptation of rhodopsin mediated signaling;adaptation of signaling pathway;apocarotenoid metabolic process;biological regulation;cellular aldehyde metabolic process;cellular hormone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;diterpenoid metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;fat-soluble vitamin metabolic process;hormone metabolic process;intracellular protein transport;intracellular transport;isoprenoid metabolic process;lipid metabolic process;metabolic process;oxidation-reduction process;phototransduction;phototransduction, visible light;primary metabolic process;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of hormone levels;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to abiotic stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinal metabolic process;retinoid metabolic process;retinol metabolic process;signal transduction;small molecule metabolic process;terpenoid metabolic process;transport;vesicle-mediated transport;vitamin A metabolic process;vitamin metabolic process" "alcohol dehydrogenase (NADP+) activity;aldo-keto reductase (NADP) activity;catalytic activity;NADP-retinol dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;retinol dehydrogenase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part;photoreceptor inner segmentRetinol metabolism 1.34E-92 8 7 7 30.8

E9PNR2;Q13671-2;Q13671;E7EM96 Ras and Rab interactor 1 RIN1 >tr|E9PNR2|E9PNR2_HUMAN Ras and Rab interactor 1 OS=Homo sapiens GN=RIN1 PE=2 SV=1;>sp|Q13671-2|RIN1_HUMAN Isoform RIN1-delta of Ras and Rab interactor 1 OS=Homo sapiens GN=RIN1;>sp|Q13671|RIN1_HUMAN Ras and Rab interactor 1 OS=Homo sapiens GN=RIN1 PE=1 SV 0.31 -0.07 0.27 -0.21 -0.13 -0.50 0.46 -0.38 0.343054126 0.214776641 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;endocytosis;establishment of localization;membrane invagination;membrane organization;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;response to stimulus;signal transduction;transport;vesicle-mediated transport enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;non-membrane-bounded organelle;organelle;plasma membrane 1.42E-26 4 7 7 16.7

Q9H6T3-2;Q9H6T3;Q9H6T3-3 RNA polymerase II-associated protein 3 RPAP3 >sp|Q9H6T3-2|RPAP3_HUMAN Isoform 2 of RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3;>sp|Q9H6T3|RPAP3_HUMAN RNA polymerase II-associated protein 3 OS=Homo sapiens GN=RPAP3 PE=1 SV=2;>sp|Q9H6T3-3|RPAP3_HUMAN Isoform 3 of RNA polymerase II-a 0.10 0.11 0.02 -0.08 -0.22 -0.35 -0.02 -0.34 1.241120172 0.268854307 2.08E-23 3 7 7 13.3

P62851;E9PQK3;E9PK60;E9PPT4 40S ribosomal protein S25 RPS25 >sp|P62851|RS25_HUMAN 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1 0.05 -0.04 -0.04 0.04 -0.61 -0.86 -0.09 -0.31 1.158179209 0.473142286 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome 2.64E-48 4 7 7 46.4

P23921;F5H861;E9PL69;E9PD78 Ribonucleoside-diphosphate reductase large subunit;Ribonucleoside-diphosphate reductase RRM1 >sp|P23921|RIR1_HUMAN Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1;>tr|F5H861|F5H861_HUMAN Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=2 SV=1;>tr|E9PL69|E9PL69_HUMAN Ribonucleoside-d 0.31 0.03 0.38 -0.06 0.19 -0.59 -0.38 -0.88 0.990059702 0.579803408 biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;deoxyribonucleotide biosynthetic process;deoxyribonucleotide metabolic process;DNA metabolic process;DNA replication;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotetramerization;protein oligomerization;protein tetramerization;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH or CH2 groups;oxidoreductase activity, acting on CH or CH2 groups, disulfide as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleoside-diphosphate reductase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;protein complex;ribonucleoside-diphosphate reductase complex Glutathione metabolism;Purine metabolism;Pyrimidine metabolism 4.74E-30 4 7 7 12

P14678-2;P14678;P14678-3;J3QLE5;P63162;B3KVR1;J3KRY3;A8MT02 Small nuclear ribonucleoprotein-associated proteins B and B;Small nuclear ribonucleoprotein-associated protein N;Small nuclear ribonucleoprotein-associated protein SNRPB;SNRPN >sp|P14678-2|RSMB_HUMAN Isoform SM-B of Small nuclear ribonucleoprotein-associated proteins B and B OS=Homo sapiens GN=SNRPB;>sp|P14678|RSMB_HUMAN Small nuclear ribonucleoprotein-associated proteins B and B OS=Homo sapiens GN=SNRPB PE=1 SV=2;>sp|P14678-3 -0.24 0.28 -0.18 0.20 -0.11 -0.24 -1.09 -0.15 0.657192868 0.412349971 "biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;histone mRNA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA metabolic process;mRNA processing;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA 3'-end processing;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;spliceosomal snRNP assembly;termination of RNA polymerase II transcription;transcription termination, DNA-dependent" binding;histone pre-mRNA DCP binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;histone pre-mRNA 3'end processing complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U1 snRNP;U12-type spliceosomal complex;U2 snRNP;U7 snRNP Spliceosome;Systemic lupus erythematosus 3.63E-28 8 7 7 28.1

P37108;H0YLA2;H0YLW0 Signal recognition particle 14 kDa protein SRP14 >sp|P37108|SRP14_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2;>tr|H0YLA2|H0YLA2_HUMAN Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=2 SV=1 -0.02 0.07 -0.11 -0.22 -0.12 -0.69 -0.37 -0.38 1.01891063 0.317820529 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to drug;response to stimulus;SRP-dependent cotranslational protein targeting to membrane;translation;transport 7S RNA binding;binding;endoplasmic reticulum signal peptide binding;nucleic acid binding;peptide binding;RNA binding;signal sequence binding "cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;ribonucleoprotein complex;signal recognition particle;signal recognition particle, endoplasmic reticulum targeting" Protein export 5.48E-51 3 7 7 55.1

B4E2V5;P27105;P27105-2;Q8TAV4-2;Q8TAV4Erythrocyte band 7 integral membrane protein STOM >tr|B4E2V5|B4E2V5_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=2 SV=1;>sp|P27105|STOM_HUMAN Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3 -0.41 0.43 -0.32 0.33 -0.09 0.27 -0.41 0.80 0.144114443 -0.134782737 biological regulation;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular process;cellular response to stimulus;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;melanosome;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;pigment granule;plasma membrane;plasma membrane part;vesicle 2.50E-175 5 7 7 36.3

Q15833-2;Q15833;E7EQD5;M0R0M7;M0QZ54;M0R118;M0R1A1;M0R376;REV__Q9Y3P9-3;REV__Q9Y3P9-2;REV__Q9Y3P9 Syntaxin-binding protein 2 STXBP2 >sp|Q15833-2|STXB2_HUMAN Isoform 2 of

Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2;>sp|Q15833|STXB2_HUMAN Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE=1 SV=2;>tr|E7EQD5|E7EQD5_HUMAN Syntaxin-binding protein 2 OS=Homo sapiens GN=STXBP2 PE -0.11 0.05 -0.03 0.05 -1.06 -0.09 0.29 0.05 0.244537636 0.190229561 biological regulation;cell activation;cell activation involved in immune response;cell killing;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;leukocyte degranulation;leukocyte mediated cytotoxicity;membrane docking;myeloid cell activation involved in immune response;myeloid leukocyte activation;neutrophil activation;neutrophil activation involved in immune response;neutrophil degranulation;positive regulation of biological process;positive regulation of immune effector process;positive regulation of immune system process;protein transport;regulated secretory pathway;regulation of biological process;regulation of cell activation;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of leukocyte activation;regulation of leukocyte degranulation;regulation of leukocyte mediated immunity;regulation of localization;regulation of mast cell activation;regulation of mast cell activation involved in immune response;regulation of mast cell degranulation;regulation of myeloid leukocyte mediated immunity;regulation of response to stimulus;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;secretion;secretion by cell;transport;vesicle docking;vesicle docking involved in exocytosis;vesicle-mediated transport apical plasma membrane;azurophil granule;cell part;cytolytic granule;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;plasma membrane part;primary lysosome;specific granule;stored secretory granule;tertiary granule;vacuole;vesicle 1.30E-56 11 7 7 15.8

P09758 Tumor-associated calcium signal transducer 2 TACSTD2 >sp|P09758|TACD2_HUMAN Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3 -0.07 0.26 -0.07 0.30 -0.57 0.23 -0.06 -0.08 0.480221193 0.225600771 anatomical structure morphogenesis;biological regulation;cell proliferation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;developmental process;epithelial tube morphogenesis;morphogenesis of an epithelium;multicellular organismal process;negative regulation of actin filament bundle assembly;negative regulation of biological process;negative regulation of branching involved in ureteric bud morphogenesis;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of developmental process;negative regulation of epithelial cell migration;negative regulation of locomotion;negative regulation of multicellular organismal process;negative regulation of organelle organization;negative regulation of stress fiber assembly;neurological system process;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of branching involved in ureteric bud morphogenesis;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of epithelial cell migration;regulation of epithelial cell proliferation;regulation of kidney development;regulation of localization;regulation of locomotion;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of organ morphogenesis;regulation of organelle organization;regulation of stress fiber assembly;response to stimulus;sensory perception;sensory perception of light stimulus;signal transduction;system process;tissue morphogenesis;tube morphogenesis;ureteric bud morphogenesis;visual perception receptor activity basal plasma membrane;cell part;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lateral plasma membrane;membrane part;plasma membrane part 2.99E-66 1 7 7 33.4

Q01085;Q01085-2;E7ETJ9;E7ETC0;A6NKZ9;Q49AS9;C9JTN7;P31483-2;F8W8I6;P31483;F8WE16;E5RGV5;H7BY49;E5RG67;Q96B58 Nucleolysin TIAR TIAL1 >sp|Q01085|TIAR_HUMAN Nucleolysin TIAR OS=Homo sapiens GN=TIAL1 PE=1 SV=1;>sp|Q01085-2|TIAR_HUMAN Isoform 2 of Nucleolysin TIAR OS=Homo sapiens GN=TIAL1;>tr|E7ETJ9|E7ETJ9_HUMAN Nucleolysin TIAR (Fragment) OS=Homo sapiens GN=TIAL1 PE=2 SV=1;>tr|E7ETC0|E7ETC 0.28 -0.04 0.06 -0.04 0.11 -0.39 0.14 -0.26 0.436102644 0.163543183 "anatomical structure development;apoptosis;biological regulation;cell death;cell development;cell division;cellular developmental process;cellular process;cellular process involved in reproduction;death;defense response;developmental process;developmental process involved in reproduction;germ cell development;induction of apoptosis;induction of programmed cell death;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cytokine biosynthetic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of programmed cell death;posttranscriptional regulation of gene expression;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;response to stimulus;response to stress;stem cell division"AU-rich element binding;binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;RNA binding;single-stranded RNA binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex;RNA granule;stress granule;vacuole 1.68E-36 15 7 7 22.9

O43615;M0QXU7;M0QXM9;M0R301 Mitochondrial import inner membrane translocase subunit TIM44 TIMM44 >sp|O43615|TIM44_HUMAN Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2;>tr|M0QXU7|M0QXU7_HUMAN Mitochondrial import inner membrane translocase subunit TIM44 (Fragment) OS=Homo sapiens GN=TIMM44 PE=4 SV=1 0.10 0.12 -0.10 -0.15 -0.23 -0.54 0.06 0.04 0.416884325 0.15954073 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transport active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;macromolecule transmembrane transporter activity;nucleotide binding;P-P-bond-hydrolysis-driven protein transmembrane transporter activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein transmembrane transporter activity;protein transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part 1.85E-39 4 7 7 20.1

Q15785 Mitochondrial import receptor subunit TOM34 TOMM34 >sp|Q15785|TOM34_HUMAN Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2 0.49 0.02 0.06 -0.12 0.32 -0.26 0.05 -0.31 0.339463455 0.166639002 establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;mitochondrial transport;protein import;protein targeting;protein targeting to mitochondrion;protein transport;transport cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane 4.42E-109 1 7 7 32.7

C9J502;P55327-2;P55327-4;P55327;D0UFD3;D0UFD1;P55327-3;F5H0B0;E5RFR7;H0YC44;D0UFD5 Tumor protein D52 TPD52;PrLZ >tr|C9J502|C9J502_HUMAN Prostate leucine zipper variant 2 OS=Homo sapiens GN=TPD52 PE=2 SV=2;>sp|P55327-2|TPD52_HUMAN Isoform 2 of Tumor protein D52 OS=Homo sapiens GN=TPD52;>sp|P55327-4|TPD52_HUMAN Isoform 4 of Tumor protein D52 OS=Homo sapiens GN=TPD52;> 0.11 -0.03 -0.56 0.04 0.39 -0.95 -0.42 -0.69 0.379713093 0.307541018 anatomical structure morphogenesis;B cell activation;B cell differentiation;cell activation;cell differentiation;cellular developmental process;cellular process;developmental process;establishment of localization;immune system process;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;secretion;transport binding;calcium ion binding;cation binding;identical protein binding;ion binding;metal ion binding;protein binding;protein dimerization activity;protein heterodimerization activity;protein homodimerization activity cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle;perinuclear region of cytoplasm 1.25E-67 11 7 7 29.4

F2Z2B9;Q9BSJ2;Q9BSJ2-4;Q9BSJ2-3;R4GMM4;B3KTU7 Gamma-tubulin complex component 2 TUBGCP2 >tr|F2Z2B9|F2Z2B9_HUMAN Gamma-tubulin complex component 2 OS=Homo sapiens GN=TUBGCP2 PE=2 SV=1;>sp|Q9BSJ2|GCP2_HUMAN Gamma-tubulin complex component 2 OS=Homo sapiens GN=TUBGCP2 PE=1 SV=2;>sp|Q9BSJ2-4|GCP2_HUMAN Isoform 3 of Gamma-tubulin complex component 0.29 0.07

-0.15 -0.19 -0.23 -0.39 -0.11 -0.45 0.958835234 0.300630864 cell cycle process;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;G2/M transition of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule nucleation;microtubule-based process;organelle organization;protein complex assembly;protein complex subunit organization cell part;centrosome;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;spindle pole 5.73E-35 6 7 7 12.8

P10599-2;P10599 Thioredoxin TXN >sp|P10599-2|THIO_HUMAN Isoform 2 of Thioredoxin OS=Homo sapiens GN=TXN;>sp|P10599|THIO_HUMAN Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 -0.02 -0.12 -0.06 -0.32 -0.17 0.15 0.83 0.26 0.778217322 -0.400352994 "antibiotic metabolic process;biological regulation;biosynthetic process;carbohydrate homeostasis;cell communication;cell proliferation;cell redox homeostasis;cell-cell signaling;cellular biosynthetic process;cellular chemical homeostasis;cellular component movement;cellular glucose homeostasis;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to drug;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to hyperoxia;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;chemical homeostasis;defense response;drug metabolic process;electron transport chain;generation of precursor metabolites and energy;glucose homeostasis;glycerol ether metabolic process;homeostatic process;immune response;immune system process;innate immune response;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of protein export from nucleus;negative regulation of protein transport;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;organic ether metabolic process;oxidation-reduction process;positive regulation of binding;positive regulation of DNA binding;positive regulation of molecular function;primary metabolic process;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA binding;regulation of establishment of protein localization;regulation of gene expression;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein localization;regulation of protein transport;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;response to abiotic stimulus;response to activity;response to axon injury;response to carbohydrate stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to dexamethasone stimulus;response to drug;response to endogenous stimulus;response to glucocorticoid stimulus;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to hyperoxia;response to inorganic substance;response to metal ion;response to monosaccharide stimulus;response to organic substance;response to oxygen levels;response to radiation;response to selenium ion;response to steroid hormone stimulus;response to stimulus;response to stress;response to thyroid hormone stimulus;response to thyroxine stimulus;response to wounding;RNA biosynthetic process;RNA metabolic process;signal transduction;signaling;small molecule metabolic process;transcription, DNA-dependent" "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;peptide disulfide oxidoreductase activity;protein disulfide oxidoreductase activity" axon;cell body;cell part;cell projection;cytoplasmic part;cytosol;dendrite;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;neuronal cell body;nuclear part;nucleoplasm;organelle;organelle part 1.51E-29 2 7 7 57.6

Q15386;REV__H0YG41;REV__Q6ZVT0-3;Q15386-3;REV__Q6ZVT0-2;Q15386-2;REV__Q6ZVT0 Ubiquitin-protein ligase E3C UBE3C >sp|Q15386|UBE3C_HUMAN Ubiquitin-protein ligase E3C OS=Homo sapiens GN=UBE3C PE=1 SV=3 0.12 -0.09 -0.15 0.06 0.16 0.15 0.43 -0.16 0.483892377 -0.158240832 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;ubiquitin-protein ligase activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;proteasome complex;protein complex Ubiquitin mediated proteolysis 5.25E-26 7 7 7 7.6

Q16831;F8WD51;C9J486;C9JIP2;B4DND0;Q86Y75;C9K0J2 Uridine phosphorylase 1 UPP1 >sp|Q16831|UPP1_HUMAN Uridine phosphorylase 1 OS=Homo sapiens GN=UPP1 PE=1 SV=1;>tr|F8WD51|F8WD51_HUMAN Uridine phosphorylase 1 OS=Homo sapiens GN=UPP1 PE=2 SV=1;>tr|C9J486|C9J486_HUMAN Uridine phosphorylase 1 (Fragment) OS=Homo sapiens GN=UPP1 PE=2 SV=1;> 0.57 0.09 0.13 -0.19 -0.11 -0.07 -0.10 -0.52 0.79060823 0.351372283 biosynthetic process;catabolic process;cell communication;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside catabolic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside salvage;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;nucleotide salvage;primary metabolic process;pyrimidine base metabolic process;pyrimidine nucleoside biosynthetic process;pyrimidine nucleoside catabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside monophosphate biosynthetic process;pyrimidine nucleoside monophosphate metabolic process;pyrimidine nucleoside salvage;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine nucleotide salvage;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside monophosphate biosynthetic process;pyrimidine ribonucleoside monophosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine ribonucleotide salvage;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;pyrimidine-containing compound salvage;response to external stimulus;response to extracellular stimulus;response to nutrient levels;response to starvation;response to stimulus;response to stress;ribonucleoside metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;UMP biosynthetic process;UMP metabolic process;UMP salvage;uridine metabolic process "catalytic activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups;uridine phosphorylase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Drug metabolism - other enzymes;Pyrimidine metabolism 2.82E-19 7 7 7 24.8

P06132;H0Y5R6;Q5T446 Uroporphyrinogen decarboxylase UROD >sp|P06132|DCUP_HUMAN Uroporphyrinogen decarboxylase OS=Homo sapiens GN=UROD PE=1 SV=2;>tr|H0Y5R6|H0Y5R6_HUMAN Uroporphyrinogen decarboxylase (Fragment) OS=Homo sapiens GN=UROD PE=4 SV=1;>tr|Q5T446|Q5T446_HUMAN Uroporphyrinogen decarboxylase (Fragment) OS= 0.18 -0.04 -0.20 -0.06 -0.29 -0.37 0.43 -0.37 0.217638013 0.120352005 biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cofactor biosynthetic process;cofactor metabolic process;heme biosynthetic process;heme metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;pigment biosynthetic process;pigment metabolic process;porphyrin-containing compound biosynthetic process;porphyrin-containing compound metabolic process;protoporphyrinogen IX biosynthetic process;protoporphyrinogen IX metabolic process;small molecule metabolic process;tetrapyrrole biosynthetic process;tetrapyrrole metabolic process carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;lyase activity;uroporphyrinogen decarboxylase activity cell part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-bounded organelle;nucleus;organelle Porphyrin and chlorophyll metabolism 1.43E-20 3 7 7 23.4

P52735-3;P52735-2;P52735 Guanine nucleotide exchange factor VAV2 VAV2 >sp|P52735-3|VAV2_HUMAN Isoform 3 of Guanine nucleotide exchange factor VAV2 OS=Homo sapiens GN=VAV2;>sp|P52735-2|VAV2_HUMAN Isoform 2 of Guanine nucleotide exchange factor VAV2 OS=Homo sapiens GN=VAV2;>sp|P52735|VAV2_HUMAN Guanine nucleotide exchange fact -0.04 -0.12 -0.13 0.10 -0.77 -0.33 0.45 -0.07 0.193733614 0.134173955 anatomical structure formation involved in morphogenesis;angiogenesis;axon guidance;biological regulation;cell activation;cell migration;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;chemotaxis;defense response;developmental process;enzyme linked receptor protein signaling pathway;immune response;immune system process;innate immune response;intracellular signal transduction;lamellipodium assembly;locomotion;nerve growth factor receptor signaling pathway;platelet activation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of kinase activity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transferase activity;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;signal transduction;small GTPase mediated signal transduction;taxis;transmembrane receptor protein tyrosine kinase signaling pathway binding;cation binding;enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;ion binding;lipid binding;metal ion binding;nucleoside-triphosphatase regulator activity;phospholipid binding;Ras guanyl-nucleotide exchange factor activity;Rho guanyl-nucleotide exchange factor activity;small GTPase regulator activity cell part;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane B cell receptor signaling pathway;Chemokine signaling pathway;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Leukocyte transendothelial migration;Natural killer cell mediated cytotoxicity;Regulation of actin cytoskeleton;T cell receptor signaling pathway 3.00E-43 3 7 7 11.3

O75436;F5H4L7;G3V1N8;O75436-2 Vacuolar protein sorting-associated protein 26A VPS26A >sp|O75436|VP26A_HUMAN Vacuolar protein sorting-associated protein 26A OS=Homo sapiens GN=VPS26A PE=1 SV=2;>tr|F5H4L7|F5H4L7_HUMAN Vacuolar protein sorting-associated protein 26A OS=Homo sapiens GN=VPS26A PE=2 SV=1;>tr|G3V1N8|G3V1N8_HUMAN Vacuolar protein 0.20 -0.02 -0.15 -0.28 -0.26 0.25 0.26 0.16 0.429047777 -0.16634362 "cellular process;endosome transport;establishment of localization;establishment of localization in cell;intracellular transport;retrograde transport, endosome to Golgi;transport;vacuolar transport;vesicle-mediated transport" protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex;retromer complex;vesicle 3.25E-63 4 7 7 29.4

Q9Y6W5;Q9Y6W5-2;Q86VQ2;Q9UPY6 Wiskott-Aldrich syndrome protein family member 2 WASF2 >sp|Q9Y6W5|WASF2_HUMAN Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 PE=1 SV=3;>sp|Q9Y6W5-2|WASF2_HUMAN Isoform 2 of Wiskott-Aldrich syndrome protein family member 2 OS=Homo sapiens GN=WASF2 0.12 -0.11 0.20 0.01 0.05 0.15 0.31 -0.25 0.033819685 -0.01390401 "actin cytoskeleton organization;actin filament organization;actin filament polymerization;actin filament-based movement;actin filament-based process;actin polymerization or depolymerization;ameboidal cell migration;anatomical structure development;anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;cAMP-mediated signaling;cell development;cell migration;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to stimulus;cyclic-nucleotide-mediated signaling;cytoskeleton organization;defense response;developmental process;glial cell development;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;immune response;immune system process;innate immune response;intracellular signal transduction;lamellipodium assembly;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;oligodendrocyte development;organelle organization;positive regulation of biological process;positive regulation of cellular process;positive regulation of multicellular organismal process;positive regulation of myelination;positive regulation of neurological system process;protein complex assembly;protein complex subunit organization;protein polymerization;Rac protein signal transduction;Ras protein signal transduction;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of homeostatic process;regulation of ion homeostasis;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myelination;regulation of nervous system development;regulation of neurological system process;regulation of signaling;regulation of system process;regulation of transmission of nerve impulse;response to stimulus;response to stress;second-messenger-mediated signaling;signal transduction;small GTPase mediated signal transduction" actin binding;binding;cytoskeletal protein binding;protein binding actin cytoskeleton;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;early endosome;endosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane-bounded organelle;non-membrane-bounded organelle;organelle;ruffle Adherens junction;Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Regulation of actin cytoskeleton;Shigellosis 1.55E-73 4 7 7 18.3

Q9GZS3;H0YN81;H0YMF9;H0YL19;H0YM76;H0YLA1;H3BQA8 WD repeat-containing protein 61 WDR61 >sp|Q9GZS3|WDR61_HUMAN WD repeat-containing protein 61 OS=Homo sapiens GN=WDR61 PE=1 SV=1;>tr|H0YN81|H0YN81_HUMAN WD repeat-containing protein 61 (Fragment) OS=Homo sapiens GN=WDR61 PE=2 SV=1;>tr|H0YMF9|H0YMF9_HUMAN WD repeat-containing protein 61 OS=Homo 0.02 0.09 0.05 -0.04 0.00 -0.19 0.05 -0.05 0.585662247 0.08065441 "biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;histone H3-K4 methylation;histone H3-K4 trimethylation;histone lysine methylation;histone methylation;histone modification;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of myeloid cell differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine methylation;peptidyl-lysine modification;peptidyl-lysine trimethylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of histone H3-K4 methylation;positive regulation of histone methylation;positive regulation of histone modification;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of RNA metabolic process;positive regulation of transcription elongation from RNA polymerase II promoter;positive regulation of transcription elongation, DNA-dependent;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromosome organization;regulation of developmental process;regulation of gene expression;regulation of histone H3-K4 methylation;regulation of histone methylation;regulation of histone modification;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of RNA metabolic process;regulation of transcription elongation from RNA polymerase II promoter;regulation of transcription elongation, DNA-dependent;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;small molecule metabolic process;transcription, DNA-dependent;Wnt receptor signaling pathway" Cdc73/Paf1 complex;cell part;chromatin;chromosomal part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;Ski complex;transcription elongation factor complex;transcriptionally active chromatin RNA degradation 7.25E-105 7 7 7 36.4

Q9H6S0;D6RA70;D6R9T8;D6RF50 Probable ATP-dependent RNA helicase YTHDC2 YTHDC2>sp|Q9H6S0|YTDC2_HUMAN Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2 0.15 0.13 0.19 -0.34 -0.15 -0.41 0.02 -0.23 0.623688511 0.223556206 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" 1.46E-21 4 7 7 6.8

A1A528;O43264;F5H3C1 Centromere/kinetochore protein zw10 homolog ZW10 >tr|A1A528|A1A528_HUMAN Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=2 SV=1;>sp|O43264|ZW10_HUMAN Centromere/kinetochore protein zw10 homolog OS=Homo sapiens GN=ZW10 PE=1 SV=3 0.18 -0.11 0.10 -0.03 0.15 -0.10 -0.09 -0.35 0.450380874 0.132671462 anaphase;biological regulation;cell cycle checkpoint;cell cycle phase;cell cycle process;cell division;cellular component assembly;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cytoskeleton organization;ER to Golgi vesicle-mediated transport;establishment of chromosome localization;establishment of localization;establishment of localization in cell;establishment of mitotic spindle localization;establishment of mitotic spindle orientation;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;establishment of spindle orientation;Golgi vesicle transport;intracellular transport;localization;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;meiosis;metaphase plate congression;microtubule cytoskeleton organization;microtubule-based process;mitosis;mitotic anaphase;mitotic cell cycle checkpoint;mitotic metaphase plate congression;mitotic prometaphase;nuclear division;organelle fission;organelle organization;protein complex assembly;protein complex subunit organization;protein localization;protein localization to chromosome;protein localization to kinetochore;protein localization to organelle;protein transport;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;regulation of exit from mitosis;regulation of mitotic cell cycle;transport;vesicle-mediated transport binding;centromeric DNA binding;DNA binding;nucleic acid binding;sequence-specific DNA binding "cell part;chromosomal part;chromosome, centromeric region;condensed chromosome kinetochore;cytoplasmic part;cytoskeletal part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;kinetochore microtubule;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;protein complex;spindle microtubule;spindle pole" 5.32E-48 3 7 7 13.1

P05091;F8W0A9;P05091-2;F8VP50 "Aldehyde dehydrogenase, mitochondrial" ALDH2 ">sp|P05091|ALDH2_HUMAN Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2;>tr|F8W0A9|F8W0A9_HUMAN Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=2 SV=1;>sp|P05091-2|ALDH2_HUMAN Isoform 2 of Aldehyde dehydrogenase, m" -1.39 -0.41 -1.39 0.62 -0.99 0.86 0.08 0.66 0.526134315 -0.796745449 alcohol catabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular metabolic process;cellular process;ethanol catabolic process;ethanol metabolic process;ethanol oxidation;metabolic process;neurotransmitter biosynthetic process;neurotransmitter metabolic process;oxidation-reduction process;primary alcohol catabolic process;primary alcohol metabolic process;primary metabolic process;regulation of biological quality;regulation of neurotransmitter levels;small molecule catabolic process;small molecule metabolic process;xenobiotic metabolic process "aldehyde dehydrogenase (NAD) activity;aldehyde dehydrogenase [NAD(P)+] activity;catalytic activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Chloroalkane and chloroalkene degradation;Fatty acid metabolism;Glycerolipid metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Limonene and pinene degradation;Lysine degradation;Pentose and glucuronate interconversions;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 1.62E-73 4 8 7 19.9

Q52LW3;F8VWZ8;Q52LW3-2 Rho GTPase-activating protein 29 ARHGAP29 >sp|Q52LW3|RHG29_HUMAN Rho GTPase-activating protein 29 OS=Homo sapiens GN=ARHGAP29 PE=1 SV=2;>tr|F8VWZ8|F8VWZ8_HUMAN Rho GTPase-activating protein 29 OS=Homo sapiens GN=ARHGAP29 PE=2 SV=1;>sp|Q52LW3-2|RHG29_HUMAN Isoform 2 of Rho GTPase-activating protein 0.70 0.30 -0.22 -0.54 0.04 -0.04 0.66 0.67 0.325596302 -0.275035145 biological regulation;cellular process;cellular response to stimulus;intracellular signal transduction;Ras protein signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction binding;cation binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;ion binding;metal ion binding;nucleoside-triphosphatase regulator activity;Ras GTPase activator activity;Rho GTPase activator activity;small GTPase regulator activity cell part;cytoplasmic part;cytosol;intracellular;intracellular part 2.71E-31 3 8 7 7.7

Q9BS26 Endoplasmic reticulum resident protein 44 ERP44 >sp|Q9BS26|ERP44_HUMAN Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 0.12 -0.06 -0.30 0.02 -0.13 -0.10 0.28 -0.20 0.037017901 -0.015640884 biological regulation;cell redox homeostasis;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;glycoprotein metabolic process;homeostatic process;macromolecule metabolic process;metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein "catalytic activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;protein disulfide isomerase activity" cell part;cell surface;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part 1.72E-51 1 8 7 18.5

Q16836;E9PF18;Q16836-3;Q16836-2 "Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial" HADH ">sp|Q16836|HCDH_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3;>tr|E9PF18|E9PF18_HUMAN Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=2 SV=1;>sp|Q16836-3|HCDH_HUMAN Isoform 3 of H" -0.41 -0.38 0.25 0.13 -0.33 -0.80 -0.10 -0.52 0.628658034 0.335356189 carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "3-hydroxyacyl-CoA dehydrogenase activity;binding;catalytic activity;coenzyme binding;cofactor binding;NAD binding;NAD+ binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part "Butanoate metabolism;Caprolactam degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Geraniol degradation;Lysine degradation;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 5.72E-31 4 8 7 32.2

Q13151 Heterogeneous nuclear ribonucleoprotein A0 HNRNPA0 >sp|Q13151|ROA0_HUMAN Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1-0.42 0.70 0.08 0.92 -0.13 0.17 -1.36 0.40 0.455384335 0.547240572 "3'-UTR-mediated mRNA stabilization;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;inflammatory response;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;response to stress;response to wounding;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization" AU-rich element binding;binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex 7.01E-75 1 8 7 31.8

P28482;A8CZ64 Mitogen-activated protein kinase 1MAPK1 >sp|P28482|MK01_HUMAN Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3;>tr|A8CZ64|A8CZ64_HUMAN Extracellular signal-regulated kinase-2 splice variant OS=Homo sapiens GN=MAPK1 PE=2 SV=1 0.06 -0.03 -0.36 0.09 0.04 0.12 0.37 -0.14 0.43667715 -0.157903413 "activation of immune response;activation of innate immune response;activation of MAPK activity;activation of MAPKK activity;activation of protein kinase activity;anatomical structure development;anatomical structure morphogenesis;antigen receptor-mediated signaling

pathway;apoptosis;axon guidance;B cell receptor signaling pathway;biological regulation;biosynthetic process;blood vessel development;caveolin-mediated endocytosis;cell activation;cell communication;cell cycle;cell death;cell
proliferation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization or
biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular
process;cellular protein metabolic process;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular
response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to organic
substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chemotaxis;cytosine metabolic process;death;defense response;developmental process;embryonic organ
development;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epithelial cell proliferation;ERK1 and ERK2 cascade;establishment of localization;establishment
of localization in cell;establishment of protein localization;fibroblast growth factor receptor signaling pathway;heterocycle metabolic process;immune response;immune response-activating cell surface receptor signaling
pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;induction of
apoptosis;induction of programmed cell death;innate immune response;innate immune response-activating signal transduction;insulin receptor signaling pathway;interaction with host;interspecies interaction between
organisms;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling
pathway;labyrinthine layer blood vessel development;lipopolysaccharide-mediated signaling pathway;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;mammary
gland epithelial cell proliferation;MAPK import into nucleus;MAPKKK cascade;membrane invagination;membrane organization;metabolic process;multicellular organismal process;multi-organism process;MyD88-dependent
toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative
regulation of developmental process;nerve growth factor receptor signaling pathway;neurological system process;nitrogen compound metabolic process;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase
metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleocytoplasmic transport;organ development;organ morphogenesis;pattern recognition receptor
signaling pathway;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;placenta
blood vessel development;platelet activation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell
death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component
movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of defense response;positive regulation of gene
expression;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of kinase activity;positive regulation of locomotion;positive
regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular
function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidyl-threonine phosphorylation;positive regulation of
phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of protein kinase activity;positive
regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of
response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of translation;posttranscriptional regulation of
gene expression;primary metabolic process;programmed cell death;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein
transport;pyrimidine base metabolic process;pyrimidine-containing compound metabolic process;Ras protein signal transduction;receptor-mediated endocytosis;regulation of apoptosis;regulation of biological process;regulation
of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular
biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular
metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cytoskeleton organization;regulation of defense response;regulation of
developmental process;regulation of early endosome to late endosome transport;regulation of gene expression;regulation of Golgi inheritance;regulation of immune response;regulation of immune system process;regulation of
innate immune response;regulation of intracellular protein kinase cascade;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule
biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of nitrogen
compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of peptidyl-threonine phosphorylation;regulation of phosphate metabolic
process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic
process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of RNA
metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated
protein kinase signaling cascade;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of transport;regulation of vesicle-mediated transport;reproductive
process;response to biotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to dsRNA;response to endogenous stimulus;response to epidermal growth factor stimulus;response to estrogen
stimulus;response to exogenous dsRNA;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to
lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to peptide hormone stimulus;response to steroid hormone stimulus;response to stimulus;response to stress;response to
toxin;RNA biosynthetic process;RNA metabolic process;sensory perception;sensory perception of pain;signal transduction;signaling;small GTPase mediated signal transduction;small molecule metabolic process;stress-activated
MAPK cascade;stress-activated protein kinase signaling cascade;synaptic transmission;system process;T cell receptor signaling pathway;taxis;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like
receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transcription, DNA-dependent;transmembrane
receptor protein tyrosine kinase signaling pathway;transport;TRIF-dependent toll-like receptor signaling pathway;vesicle-mediated transport;viral reproductive process;virus-host interaction" "adenyl nucleotide
binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;kinase activity;MAP kinase activity;molecular transducer activity;nucleic acid binding;nucleotide binding;phosphotransferase activity,
alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein
activity;receptor signaling protein serine/threonine kinase activity;ribonucleotide binding;RNA polymerase II carboxy-terminal domain kinase activity;signal transducer activity;transferase activity;transferase activity, transferring
phosphorus-containing groups" adherens junction;anchoring junction;axon part;caveola;cell junction;cell part;cell projection;cell projection cytoplasm;cell projection part;cell-substrate adherens junction;cell-substrate
junction;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;dendrite cytoplasm;early endosome;endosome;focal adhesion;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded
organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;membrane part;membrane raft;membrane-bounded organelle;microtubule cytoskeleton;microtubule organizing
center;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;perikaryon;plasma membrane part;pseudopodium;spindle Acute myeloid leukemia;Adherens
junction;Aldosterone-regulated sodium reabsorption;Alzheimer's disease;Axon guidance;B cell receptor signaling pathway;Bladder cancer;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Chronic
myeloid leukemia;Colorectal cancer;Dorso-ventral axis formation;Endometrial cancer;ErbB signaling pathway;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Gap junction;Glioma;GnRH
signaling pathway;Hepatitis C;Insulin signaling pathway;ko05152;Leishmaniasis;Long-term depression;Long-term potentiation;MAPK signaling pathway;MAPK signaling pathway - fly;Melanogenesis;Melanoma;mTOR
signaling pathway;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;NOD-like receptor signaling pathway;Non-small cell lung cancer;Oocyte meiosis;Osteoclast differentiation;Pancreatic cancer;Pathways
in cancer;Prion diseases;Progesterone-mediated oocyte maturation;Prostate cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis;T cell receptor signaling pathway;TGF-beta signaling pathway;Thyroid
cancer;Toll-like receptor signaling pathway;Toxoplasmosis;Type II diabetes mellitus;Vascular smooth muscle contraction;VEGF signaling pathway 1.03E-31 2 8 7 26.4
O75439;G3V0E4;E7ERZ4;F8WAZ6;F8WEA6;F8WBE1 Mitochondrial-processing peptidase subunit beta PMPCB >sp|O75439|MPPB_HUMAN Mitochondrial-processing peptidase subunit beta OS=Homo sapiens
GN=PMPCB PE=1 SV=2;>tr|G3V0E4|G3V0E4_HUMAN Mitochondrial-processing peptidase subunit beta OS=Homo sapiens GN=PMPCB PE=2 SV=1;>tr|E7ERZ4|E7ERZ4_HUMAN Mitochondrial-proces -0.01 0.10
-0.21 -0.02 -0.09 -0.39 -0.25 -0.46 1.080579037 0.266753164 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic
process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular
protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to
mitochondrion;protein transport;proteolysis;transport "binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase
activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed

lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part 9.30E-24 6 8 7 18.4

Q9NPQ8-4;Q9NPQ8;Q9NPQ8-3;Q9NPQ8-2;E9PSI0;H0YEN0;E9PI04;E9PLE5;H0YE35;Q9NVN3-4;Q9NVN3-3;Q9NVN3;Q9NVN3-1;B7WPL0 Synembryn-A RIC8A >sp|Q9NPQ8-4|RIC8A_HUMAN Isoform 4 of Synembryn-A OS=Homo sapiens GN=RIC8A;>sp|Q9NPQ8|RIC8A_HUMAN Synembryn-A OS=Homo sapiens GN=RIC8A PE=1 SV=3;>sp|Q9NPQ8-3|RIC8A_HUMAN Isoform 3 of Synembryn-A OS=Homo sapiens GN=RIC8A;>sp|Q9NPQ8-2|RIC8A_HUMAN Isoform 2 o 0.30 -0.04 -0.12 -0.23 0.18 -0.01 0.50 -0.08 0.408778172 -0.173642522 "ameboidal cell migration;anatomical structure development;associative learning;basement membrane organization;behavior;biological adhesion;biological regulation;cAMP-mediated signaling;cell adhesion;cell migration;cell migration involved in gastrulation;cell motility;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-cell adhesion involved in gastrulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;chordate embryonic development;cognition;cyclic-nucleotide-mediated signaling;developmental process;embryo development;embryo development ending in birth or egg hatching;extracellular matrix organization;extracellular structure organization;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;in utero embryonic development;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;learning;learning or memory;locomotion;multicellular organismal process;negative regulation of adenylate cyclase activity;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of molecular function;neurological system process;regulation of adenylate cyclase activity;regulation of biological process;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of G-protein coupled receptor protein signaling pathway;regulation of lyase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to abiotic stimulus;response to light stimulus;response to radiation;response to stimulus;second-messenger-mediated signaling;signal transduction;system development;system process;vasculature development;visual behavior;visual learning" binding;enzyme regulator activity;G-protein alpha-subunit binding;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity;protein binding cell cortex;cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;plasma membrane 3.35E-60 14 8 7 20

O43815;O43815-2 Striatin STRN >sp|O43815|STRN_HUMAN Striatin OS=Homo sapiens GN=STRN PE=1 SV=4;>sp|O43815-2|STRN_HUMAN Isoform 2 of Striatin OS=Homo sapiens GN=STRN -0.05 0.03 0.08 0.11 0.04 0.39 -0.11 0.20 0.293515571 -0.085466168 anatomical structure development;behavior;biological regulation;cell junction assembly;cell junction organization;cell projection organization;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;dendrite development;developmental process;locomotory behavior;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;neuron projection development;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to stimulus;signal transduction;tight junction assembly;Wnt receptor signaling pathway binding;calmodulin binding;enzyme binding;phosphatase binding;protein binding;protein complex binding;protein phosphatase 2A binding;protein phosphatase binding cell body;cell junction;cell part;cell-cell junction;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;membrane;neuronal cell body;occluding junction;organelle part;postsynaptic density;postsynaptic membrane;synapse part;synaptic membrane;tight junction 4.89E-127 2 8 7 16.9

Q9BYX2-2;Q9BYX2;Q9BYX2-3;Q9BYX2-4;Q9BYX2-6;Q9BYX2-5 TBC1 domain family member 2A TBC1D2 >sp|Q9BYX2-2|TBD2A_HUMAN Isoform 2 of TBC1 domain family member 2A OS=Homo sapiens GN=TBC1D2;>sp|Q9BYX2|TBD2A_HUMAN TBC1 domain family member 2A OS=Homo sapiens GN=TBC1D2 PE=1 SV=3;>sp|Q9BYX2-3|TBD2A_HUMAN Isoform 3 of TBC1 domain family member 2A OS=Homo 0.35 0.15 -0.09 -0.37 -0.74 -0.40 0.36 0.08 0.250163491 0.188695103 binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;lipid binding;nucleoside-triphosphatase regulator activity;phospholipid binding;Rab GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell junction;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;vesicle 1.16E-32 6 8 7 11.5

Q15643;H0YJ97;G3V4R7;F5H520;REV__B4DYV3;REV__Q09328;P55268 Thyroid receptor-interacting protein 11 TRIP11 >sp|Q15643|TRIPB_HUMAN Thyroid receptor-interacting protein 11 OS=Homo sapiens GN=TRIP11 PE=1 SV=3;>tr|H0YJ97|H0YJ97_HUMAN Thyroid receptor-interacting protein 11 (Fragment) OS=Homo sapiens GN=TRIP11 PE=4 SV=1 0.14 -0.08 0.32 -0.23 0.49 -0.36 -0.24 -0.25 0.213555602 0.129062193 "anatomical structure development;astrocyte development;axon extension;axon extension involved in development;axon extension involved in regeneration;axon guidance;biological adhesion;biosynthetic process;cell adhesion;cell development;cell growth;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chemotaxis;developmental cell growth;developmental growth;developmental growth involved in morphogenesis;developmental process;epithelial cell development;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;extracellular matrix organization;extracellular structure organization;glial cell development;glomerular basement membrane development;glomerular epithelial cell development;glomerular visceral epithelial cell development;Golgi vesicle transport;growth;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;metanephric glomerular basement membrane development;metanephric glomerular epithelial cell development;metanephric glomerular visceral epithelial cell development;multicellular organismal process;neurological system process;neuromuscular junction development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein targeting;protein targeting to Golgi;protein transport;response to chemical stimulus;response to external stimulus;response to stimulus;retina development in camera-type eye;retrograde transport, vesicle recycling within Golgi;RNA biosynthetic process;RNA metabolic process;Schwann cell development;sensory perception;sensory perception of light stimulus;sprouting of injured axon;synapse organization;system process;taxis;transcription from RNA polymerase II promoter;transcription, DNA-dependent;transport;vesicle-mediated transport;visual perception" protein binding transcription factor activity;structural molecule activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;cytoplasmic part;cytoskeleton;extracellular matrix part;extracellular region part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;laminin complex;laminin-11 complex;laminin-3 complex;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;protein complex;synapse Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 2.60E-21 7 8 7 5.3

B4DXZ6;P51114;P51114-3;P51114-2;E7EU85;E9PFF5;H7C4S4;C9IZ22;C9JZE0;C9JY20;C9JAJ4 Fragile X mental retardation syndrome-related protein 1 FXR1 >tr|B4DXZ6|B4DXZ6_HUMAN Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=2 SV=1;>sp|P51114|FXR1_HUMAN Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3;>sp|P51114-3|FXR1_HUMAN Isofor 0.04 0.10 0.04 0.19 0.05 -0.20 -0.51 -0.43 1.158257217 0.364940888 anatomical structure development;apoptosis;biological regulation;cell death;cell differentiation;cellular developmental process;cellular process;death;developmental process;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;organ development;posttranscriptional regulation of gene expression;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation binding;G-quadruplex RNA binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;RNA binding cell part;contractile fiber part;costamere;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;polysome;ribonucleoprotein complex 2.24E-65 11 9 7 26.5

O14979-3;O14979-2;O14979 Heterogeneous nuclear ribonucleoprotein D-like HNRPDL >sp|O14979-3|HNRDL_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL;>sp|O14979-2|HNRDL_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL;>sp|O14979|HNRDL_HUMAN Heterogeneo -0.10 0.48 0.26 0.45 0.20 -0.08 -1.03 -0.27 0.828667921 0.569474576 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;transcription, DNA-dependent" binding;DNA binding;double-stranded DNA binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly(G) RNA binding;poly-purine tract binding;RNA binding;single-stranded DNA binding;single-stranded RNA binding;structure-specific DNA bindingcell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex 5.52E-42 3 9 7 37.3

O75351 Vacuolar protein sorting-associated protein 4B VPS4B >sp|O75351|VPS4B_HUMAN Vacuolar protein sorting-associated protein 4B OS=Homo sapiens GN=VPS4B PE=1 SV=2 0.10 0.08 -0.07 -0.02 0.05 0.15 0.47 -0.12 0.357630906 -0.11609335 cation transport;cell cycle;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cholesterol transport;early endosome to late endosome transport;endosome organization;endosome to lysosome transport via multivesicular body sorting pathway;endosome transport;endosome transport via multivesicular body sorting pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular cholesterol transport;intracellular lipid transport;intracellular sterol transport;intracellular transport;ion transport;lipid transport;membrane organization;metal ion transport;monovalent inorganic cation transport;organelle organization;organic substance transport;potassium ion transport;protein transport;response to chemical stimulus;response to lipid;response to organic substance;response to stimulus;sterol transport;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;early endosome;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;late endosome membrane;lysosome;lytic vacuole;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;vacuolar membrane;vacuolar part;vacuole Endocytosis 4.97E-36 1 10 7 26.8

Q9Y5A9;Q9Y5A9-2 YTH domain family protein 2YTHDF2 >sp|Q9Y5A9|YTHD2_HUMAN YTH domain family protein 2 OS=Homo sapiens GN=YTHDF2 PE=1 SV=2;>sp|Q9Y5A9-2|YTHD2_HUMAN Isoform 2 of YTH domain family protein 2 OS=Homo sapiens GN=YTHDF2 0.10 -0.13 -0.06 -0.07 -0.08 -0.33 0.22 -0.39 0.275017712 0.104397028 humoral immune response;immune response;immune system process;response to stimulus 1.87E-67 2 10 7 21.1

P09972;A8MVZ9;J3KSV6;J3QKP5;C9J8F3;K7EKH5;J3QKK1 Fructose-bisphosphate aldolase C;Fructose-bisphosphate aldolase ALDOC >sp|P09972|ALDOC_HUMAN Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2;>tr|A8MVZ9|A8MVZ9_HUMAN Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOC PE=2 SV=1;>tr|J3KSV6|J3KSV6_HUMAN Fructose-bisphosphate aldolase C (Fragment) OS=Homo 0.28 -0.03 0.00 0.08 -0.19 -0.18 0.31 -0.19 0.408211127 0.143723006 "aging;alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;anatomical structure morphogenesis;apoptosis;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell death;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular process;death;developmental process;fructose 1,6-bisphosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;organ morphogenesis;organ regeneration;primary metabolic process;programmed cell death;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein heterotetramerization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;regeneration;response to chemical stimulus;response to endogenous stimulus;response to hypoxia;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to oxygen levels;response to stimulus;response to stress;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process" aldehyde-lyase activity;binding;carbon-carbon lyase activity;catalytic activity;cytoskeletal protein binding;fructose-bisphosphate aldolase activity;lyase activity;protein binding axon;cell part;cell projection;cytoplasmic part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;non-membrane-bounded organelle;organelle Carbon fixation in photosynthetic organisms;Fructose and mannose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway 2.28E-191 7 12 7 40.4

P62820;E7END7;B7Z8M7;P62820-2;P62820-3;E7ETK2 Ras-related protein Rab-1A RAB1A >sp|P62820|RAB1A_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3;>tr|E7END7|E7END7_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=2 SV=1;>tr|B7Z8M7|B7Z8M7_HUMAN Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=2 SV=1 -0.09 0.07 -0.32 0.01 -0.02 0.13 -0.09 0.07 0.440098449 -0.105718254 biological regulation;cell cycle phase;cell cycle process;cellular process;cellular response to stimulus;establishment of localization;establishment of protein localization;intracellular signal transduction;M phase;M phase of mitotic cell cycle;mitotic prophase;prophase;protein transport;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part 2.18E-136 6 14 7 60.5

Q9NVI7-2;Q9NVI7;H0Y2W2;Q9NVI7-3;Q5SV16;Q5T9A4-2;A6NFL3 ATPase family AAA domain-containing protein 3A ATAD3A>sp|Q9NVI7-2|ATD3A_HUMAN Isoform 2 of ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A;>sp|Q9NVI7|ATD3A_HUMAN ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2;>tr|H0Y2W2|H0Y2W2_HUMAN ATPase family A -0.10 0.96 0.00 0.86 0.14 0.65 -1.22 0.21 0.402765201 0.485246099 biological regulation;cell growth;cellular process;growth;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle part 1.03E-130 7 24 7 44.9

Q9NUQ8;Q9NUQ8-2;F8WCU6 ATP-binding cassette sub-family F member 3 ABCF3 >sp|Q9NUQ8|ABCF3_HUMAN ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 PE=1 SV=2;>sp|Q9NUQ8-2|ABCF3_HUMAN Isoform 2 of ATP-binding cassette sub-family F member 3 OS=Homo sapiens GN=ABCF3 0.25 0.07 0.00 -0.07 0.18 0.04 0.57 0.13 0.516925211 -0.166249232 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;defense response to virus;heterocycle catabolic process;heterocycle metabolic process;immune effector process;immune system process;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" 1.14E-34 3 8 8 18.3

Q9H3P7 Golgi resident protein GCP60ACBD3 >sp|Q9H3P7|GCP60_HUMAN Golgi resident protein GCP60 OS=Homo sapiens GN=ACBD3 PE=1 SV=4 0.02 0.18 0.06 0.06 0.32 0.34 -0.25 0.27 0.234085592

-0.089040596 biosynthetic process;establishment of localization;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;steroid biosynthetic process;steroid metabolic process;transport binding;carboxylic acid binding;coenzyme binding;cofactor binding;fatty acid binding;fatty-acyl-CoA binding;lipid binding;monocarboxylic acid binding cell part;cytoplasmic part;Golgi apparatus;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part 2.09E-112 1 8 8 25.8

P30566;E7ERF4;P30566-2 Adenylosuccinate lyase ADSL >sp|P30566|PUR8_HUMAN Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2;>tr|E7ERF4|E7ERF4_HUMAN Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=2 SV=1;>sp|P30566-2|PUR8_HUMAN Isoform 2 of Adenylosuccinate lyase OS=Homo sapiens GN=ADSL 0.19 -0.10 -0.25 -0.09 -0.11 -0.42 0.31 -0.36 0.15839886 0.081440583 aerobic respiration;AMP biosynthetic process;AMP metabolic process;biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular respiration;'de novo' AMP biosynthetic process;'de novo' IMP biosynthetic process;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein tetramerization;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;response to activity;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to hypoxia;response to muscle activity;response to nutrient;response to nutrient levels;response to oxygen levels;response to starvation;response to stimulus;response to stress;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "(S)-2-(5-amino-1-(5-phospho-D-ribosyl)imidazole-4-carboxamido)succinate AMP-lyase (fumarate-forming) activity;amidine-lyase activity;carbon-nitrogen lyase activity;catalytic activity;lyase activity;N6-(1,2-dicarboxyethyl)AMP AMP-lyase (fumarate-forming) activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle "Alanine, aspartate and glutamate metabolism;Purine metabolism" 3.62E-41 3 8 8 20.9

Q8N4X5-2;Q8N4X5;Q8N4X5-4;F5GZE1;F6QUH3;Q8N4X5-3 Actin filament-associated protein 1-like 2 AFAP1L2 >sp|Q8N4X5-2|AF1L2_HUMAN Isoform 2 of Actin filament-associated protein 1-like 2 OS=Homo sapiens GN=AFAP1L2;>sp|Q8N4X5|AF1L2_HUMAN Actin filament-associated protein 1-like 2 OS=Homo sapiens GN=AFAP1L2 PE=1 SV=1;>sp|Q8N4X5-4|AF1L2_HUMAN Isoform 4 of Actin f 0.08 -0.02 -0.21 0.09 -1.69 -0.38 0.14 0.30 0.340417489 0.390345072 "biological regulation;defense response;inflammatory response;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of epidermal growth factor receptor signaling pathway;positive regulation of gene expression;positive regulation of interleukin-8 production;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of epidermal growth factor receptor signaling pathway;regulation of gene expression;regulation of interleukin-6 production;regulation of interleukin-8 production;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;response to stimulus;response to stress;response to wounding" binding;enzyme activator activity;enzyme regulator activity;kinase activator activity;kinase regulator activity;lipid binding;phospholipid binding;protein kinase activator activity;protein kinase regulator activity;protein tyrosine kinase activator activity aggresome;cell part;cytoplasm;inclusion body;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 2.11E-40 6 8 8 16.2

Q86V81;E9PB61 THO complex subunit 4 ALYREF >sp|Q86V81|THOC4_HUMAN THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3;>tr|E9PB61|E9PB61_HUMAN THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=2 SV=1 -0.11 0.85 0.23 0.81 0.00 0.18 -1.47 0.12 0.686410275 0.738318247 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;interaction with host;interspecies interaction between organisms;intracellular transport;intronless viral mRNA export from host nucleus;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;reproductive process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport;viral reproductive process;virus-host interaction"binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;single-stranded DNA binding;structure-specific DNA binding catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex;transcription export complex mRNA surveillance pathway;RNA transport;Spliceosome 3.97E-194 2 8 8 42.8

P54709;C9JA36;B7Z1N7;C9JXZ1;H7C547;F8WBY4;H7C4L9 Sodium/potassium-transporting ATPase subunit beta-3ATP1B3 >sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1;>tr|C9JA36|C9JA36_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 (Fragment) OS=Homo sapiens GN=ATP1B3 PE=2 SV=1;>tr|B7Z1N7|B7Z1N7_HUMA -0.24 -0.11 0.05 0.08 -0.53 -0.27 -0.20 -0.32 1.106273374 0.272161626 biological regulation;blood coagulation;cation transport;cell migration;cell motility;cellular component movement;cellular process;coagulation;establishment of localization;hemostasis;immune system process;ion transport;leukocyte migration;locomotion;metal ion transport;monovalent inorganic cation transport;multicellular organismal process;potassium ion transport;regulation of biological quality;regulation of body fluid levels;sodium ion transport;transport "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;potassium ion transmembrane transporter activity;potassium-transporting ATPase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;pyrophosphatase activity;sodium ion transmembrane transporter activity;sodium:potassium-exchanging ATPase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" caveola;cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;melanosome;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;plasma membrane part;protein complex;sodium:potassium-exchanging ATPase complex;vesicle Aldosterone-regulated sodium reabsorption;Bile secretion;Carbohydrate digestion and absorption;Cardiac muscle contraction;Endocrine and other factor-regulated calcium reabsorption;Gastric acid secretion;Mineral absorption;Pancreatic secretion;Protein digestion and absorption;Proximal tubule bicarbonate reclamation;Salivary secretion 2.93E-46 7 8 8 33.3

P24539;Q5QNZ2 "ATP synthase subunit b, mitochondrial" ATP5F1 ">sp|P24539|AT5F1_HUMAN ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2;>tr|Q5QNZ2|Q5QNZ2_HUMAN ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=2 SV=1" -0.48 0.15 -0.16 0.18 0.23 0.17 -1.25 -0.19 0.176387304 0.179366235 "ATP biosynthetic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;cation transport;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle lumen;organelle part;protein complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex, proton-transporting domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 1.48E-72 2 8 8 28.1

Q9BXK5;Q9BXK5-2;B7Z238;E9PDD6;Q9BXK5-4;F2Z2C3;Q8IZP5 Bcl-2-like protein 13 BCL2L13 >sp|Q9BXK5|B2L13_HUMAN Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=1 SV=1;>sp|Q9BXK5-2|B2L13_HUMAN Isoform 1 of Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13;>tr|B7Z238|B7Z238_HUMAN Bcl-2-like protein 13 OS=Homo sapiens GN=BCL2L13 PE=2 SV=1 -0.47 0.05 0.02 0.24 -0.11 0.42 -0.54 -0.07 0.047693397 0.035169292 biological regulation;induction of apoptosis;induction of programmed cell death;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death apoptotic protease activator activity;caspase activator activity;caspase regulator activity;enzyme activator activity;enzyme regulator activity;peptidase activator activity;peptidase regulator activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle membrane;organelle part 1.30E-45 7 8 8 28.7

Q07021;I3L3Q7;I3L3B0 "Complement component 1 Q subcomponent-binding protein, mitochondrial" C1QBP ">sp|Q07021|C1QBP_HUMAN Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP PE=1 SV=1;>tr|I3L3Q7|I3L3Q7_HUMAN Complement component 1 Q subcomponent-binding protein, mitochondrial (Fragment) OS=Homo sapiens GN=C1QBP" 0.07 0.18 -0.07 0.19 -0.04 -0.10 -0.51 0.21 0.514509359 0.19886211 "activation of immune response;apoptosis;biological regulation;biosynthetic process;blood coagulation, intrinsic pathway;cell death;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;complement activation;complement activation, classical pathway;death;defense response;humoral immune response;immune effector process;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;interaction with host;interspecies interaction between organisms;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;mature ribosome assembly;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of defense response;negative regulation of defense response to virus;negative regulation of gene expression;negative regulation of immune effector process;negative regulation of immune system process;negative regulation of interferon-gamma production;negative regulation of interleukin-12 production;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of multicellular organismal process;negative regulation of multi-organism process;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of RNA splicing;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle assembly;phosphatidylinositol 3-kinase cascade;phosphatidylinositol-mediated signaling;positive regulation of apoptosis;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemotaxis;positive regulation of dendritic cell chemotaxis;positive regulation of immune response;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitochondrial translation;positive regulation of mitochondrion organization;positive regulation of neutrophil chemotaxis;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein activation cascade;protein metabolic process;regulation of acute inflammatory response;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of complement activation;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of dendritic cell chemotaxis;regulation of gene expression;regulation of humoral immune response;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of interferon-gamma production;regulation of interleukin-12 production;regulation of intracellular protein kinase cascade;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitochondrial translation;regulation of mitochondrion organization;regulation of mRNA processing;regulation of multicellular organismal process;regulation of multi-organism process;regulation of neutrophil chemotaxis;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein activation cascade;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein processing;regulation of response to biotic stimulus;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA splicing;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;reproductive process;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;signal transduction;transcription, DNA-dependent;viral reproductive process;virus-host interaction" adrenergic receptor binding;binding;carbohydrate binding;complement binding;complement component C1q binding;glycosaminoglycan binding;G-protein-coupled receptor binding;hyaluronic acid binding;kininogen binding;mRNA binding;nucleic acid binding;opsonin binding;pattern binding;polysaccharide binding;protein binding;protein binding transcription factor activity;receptor binding;RNA binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding;transcription factor binding transcription factor activity cell part;cell surface;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle lumen;organelle part;plasma membrane 1.86E-127 3 8 8 42.9

Q6YP21-3;Q6YP21;Q6YP21-2 Kynurenine--oxoglutarate transaminase 3 CCBL2 >sp|Q6YP21-3|KAT3_HUMAN Isoform 3 of Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens GN=CCBL2;>sp|Q6YP21|KAT3_HUMAN Kynurenine--oxoglutarate transaminase 3 OS=Homo sapiens GN=CCBL2 PE=1 SV=1 0.20 -0.26 0.04 0.01 0.62 0.34 0.35 -0.41 0.386925021 -0.229730618 2-oxoglutarate metabolic process;amine catabolic process;amine metabolic process;aromatic amino acid family catabolic process;aromatic amino acid family metabolic process;aromatic compound catabolic process;biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;dicarboxylic acid metabolic process;heterocycle catabolic process;heterocycle metabolic process;indolalkylamine catabolic process;indolalkylamine metabolic process;indole-containing compound catabolic process;indole-containing compound metabolic process;metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;tryptophan catabolic process;tryptophan metabolic process "binding;carbon-sulfur lyase activity;catalytic activity;cofactor binding;cysteine-S-conjugate beta-lyase activity;kynurenine-glyoxylate transaminase activity;kynurenine-oxoglutarate transaminase activity;lyase activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Selenocompound metabolism;Tryptophan metabolism 8.94E-36 3 8 8 22.9

Q9Y5K6 CD2-associated protein CD2AP >sp|Q9Y5K6|CD2AP_HUMAN CD2-associated protein OS=Homo sapiens GN=CD2AP PE=1 SV=1 -0.07 -0.13 0.10 0.02 -0.48 -0.19 0.10 -0.06 0.427651193 0.138022242 "biological regulation;cell cycle phase;cell cycle process;cell division;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;macromolecular complex assembly;macromolecular complex subunit organization;mitosis;nuclear division;organelle fission;organelle organization;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;substrate-dependent cell migration, cell extension" structural constituent of cytoskeleton;structural molecule activity cell part;cell projection;cytoplasm;cytoskeletal part;filamentous actin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;protein complex;ruffle Bacterial invasion of epithelial cells 1.59E-36 1 8 8 15.3

Q9BUQ8;H0YI52;F8VVA2 Probable ATP-dependent RNA helicase DDX23 DDX23 >sp|Q9BUQ8|DDX23_HUMAN Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3 0.02 0.18 0.44 0.25 0.13 -0.33 -1.14 -0.47 1.040463079 0.676821349 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cis assembly of pre-catalytic spliceosome;macromolecular complex assembly;macromolecular complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA helicase activity;RNA-dependent ATPase activity" catalytic step 2 spliceosome;cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U5 snRNP Spliceosome 5.58E-21 3 8 8 11.1

Q13217 DnaJ homolog subfamily C member 3 DNAJC3 >sp|Q13217|DNJC3_HUMAN DnaJ homolog subfamily C member 3 OS=Homo sapiens GN=DNAJC3 PE=1 SV=1 0.13 0.04 -0.29 -0.24 0.53 0.04 0.24 0.23 1.027716761 -0.34970314 activation of signaling protein activity involved in unfolded protein response;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;defense response;defense response to virus;immune effector process;immune system process;macromolecule metabolic process;metabolic process;multi-organism process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus enzyme inhibitor activity;enzyme regulator activity;kinase inhibitor activity;kinase regulator activity;protein kinase inhibitor activity;protein kinase regulator activity cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum Sec complex;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;protein complex Protein processing in endoplasmic reticulum 4.20E-31 1 8 8 25.4

Q99615-2;Q99615;K7EPP7;K7ESP1;K7EIH8;K7EJE9;K7EK03;K7EJ24;K7EJL5;K7EN19;K7EJV7;K7ER44;K7ELJ8 DnaJ homolog subfamily C member 7 DNAJC7 >sp|Q99615-2|DNJC7_HUMAN Isoform 2 of DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7;>sp|Q99615|DNJC7_HUMAN DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7 PE=1 SV=2;>tr|K7EPP7|K7EPP7_HUMAN DnaJ homolog subfamily C member 7 OS=Homo 0.32 0.05 0.06 -0.05 -0.17 -0.26 0.17 -0.19 0.702344058 0.207527265 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone cofactor-dependent protein refolding;chaperone-mediated protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;protein refolding cell part;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 2.95E-68 13 8 8 20.5

Q02413;B7Z845 Desmoglein-1 DSG1 >sp|Q02413|DSG1_HUMAN Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2 -0.63 0.67 -0.69 0.01 0.39 1.72 0.49 -0.01 0.699679131 -0.804393323 biological adhesion;biological regulation;calcium-dependent cell-cell adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion;maternal process involved in female pregnancy;multicellular organismal process;multicellular organismal reproductive process;posttranscriptional regulation of gene expression;protein stabilization;regulation of biological process;regulation of biological quality;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of protein stability;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to progesterone stimulus;response to steroid hormone stimulus;response to stimulus binding;calcium ion binding;cation binding;ion binding;metal ion binding;toxin binding anchoring junction;apical plasma membrane;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;desmosome;integral to membrane;internal side of plasma membrane;intracellular part;intrinsic to membrane;lateral plasma membrane;membrane part;plasma membrane part Staphylococcus aureus infection 2.17E-27 2 8 8 13

P30084 "Enoyl-CoA hydratase, mitochondrial" ECHS1 ">sp|P30084|ECHM_HUMAN Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4" -0.23 -0.26 0.23 0.11 0.28 0.15 -0.04 -0.16 0.235632948 -0.096706845 carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process carbon-oxygen lyase activity;catalytic activity;enoyl-CoA hydratase activity;hydro-lyase activity;lyase activity cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Aminobenzoate degradation;Benzoate degradation;beta-Alanine metabolism;Butanoate metabolism;Caprolactam degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Lysine degradation;Propanoate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 1.72E-129 1 8 8 33.8

O75821;K7EL20;K7ER90;K7ENA8;K7EP16;K7EL60 Eukaryotic translation initiation factor 3 subunit G EIF3G >sp|O75821|EIF3G_HUMAN Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2;>tr|K7EL20|K7EL20_HUMAN Eukaryotic translation initiation factor 3 subunit G (Fragment) OS=Homo sapiens GN=EIF3G PE=3 SV=1;>tr|K7ER90|K7ER90_HUMA 0.04 0.16 -0.37 0.01 -0.10 -0.43 -0.13 -0.19 0.532017618 0.172362294 cellular process;translational initiation "binding;nucleic acid binding;nucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;protein complex RNA transport 2.85E-55 6 8 8 33.8

Q01780-2;Q01780;B4DKG8;K7EJ37 Exosome component 10 EXOSC10 >sp|Q01780-2|EXOSX_HUMAN Isoform 2 of Exosome component 10 OS=Homo sapiens GN=EXOSC10;>sp|Q01780|EXOSX_HUMAN Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2;>tr|B4DKG8|B4DKG8_HUMAN Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=2 SV=1 0.05 0.27 0.23 0.22 0.20 -0.36 -0.70 -0.36 1.088423844 0.49687829 "biological regulation;catabolic process;cellular catabolic process;cellular localization;cellular macromolecule catabolic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;CUT catabolic process;CUT metabolic process;dosage compensation;dosage compensation, by inactivation of X chromosome;histone mRNA catabolic process;histone mRNA metabolic process;intracellular mRNA localization;localization;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;maturation of 5.8S rRNA;metabolic process;modification-dependent macromolecule catabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA catabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear ncRNA surveillance;nuclear polyadenylation-dependent ncRNA catabolic process;nuclear polyadenylation-dependent rRNA catabolic process;nuclear retention of pre-mRNA at the site of transcription;nuclear retention of unspliced pre-mRNA at the site of transcription;nuclear RNA surveillance;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;polyadenylation-dependent ncRNA catabolic process;polyadenylation-dependent RNA catabolic process;primary metabolic process;regulation of biological process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule metabolic process;regulation of metabolic process;RNA catabolic process;RNA localization;RNA metabolic process;RNA processing;RNA surveillance;rRNA catabolic process;rRNA metabolic process;rRNA processing" "3'-5' exonuclease activity;binding;catalytic activity;exonuclease activity;exoribonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding;nucleotide binding;ribonuclease activity;RNA binding" cell part;chromatin;chromosomal part;cytoplasm;exosome (RNase complex);intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear exosome (RNase complex);nuclear part;nucleolus;organelle;organelle part;protein complex;transcriptionally active chromatin RNA degradation 2.69E-26 4 8 8 12.2

Q86Y56;H0Y650;Q86Y56-2;Q86Y56-3;E9PGY2;H7C3B1 HEAT repeat-containing protein 2 HEATR2 >sp|Q86Y56|HEAT2_HUMAN HEAT repeat-containing protein 2 OS=Homo sapiens GN=HEATR2 PE=1 SV=4;>tr|H0Y650|H0Y650_HUMAN HEAT repeat-containing protein 2 (Fragment) OS=Homo sapiens GN=HEATR2 PE=4 SV=1;>sp|Q86Y56-2|HEAT2_HUMAN Isoform 2 of HEAT repeat-containing 0.18 -0.05 0.08 0.01 -0.52 -0.44 0.01 0.09 0.709863645 0.271556104 cell part;cytoplasm;intracellular part 9.37E-60 6 8 8 15

Q12768;E7EQI7;E5RFU6 WASH complex subunit strumpellin KIAA0196 >sp|Q12768|STRUM_HUMAN WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=1 SV=1;>tr|E7EQI7|E7EQI7_HUMAN WASH complex subunit strumpellin OS=Homo sapiens GN=KIAA0196 PE=2 SV=1 0.04 -0.19 0.20 -0.03 -0.01 0.07 0.28 -0.17 0.113030684 -0.039435015 cell death;cellular process;death;endosome transport;establishment of localization;establishment of localization in cell;intracellular transport;transport;vesicle-mediated transport cell part;cytoplasmic part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;organelle;protein complex;WASH complex 9.98E-24 3 8 8 8.3

Q6P9B6;F5GWS3;H3BM75;H3BUB0;H3BTC5 TLD domain-containing protein KIAA1609 KIAA1609;TLDC1 >sp|Q6P9B6|TLDC1_HUMAN TLD domain-containing protein 1 OS=Homo sapiens GN=TLDC1 PE=1 SV=2;>tr|F5GWS3|F5GWS3_HUMAN Protein TLDC1 OS=Homo sapiens GN=TLDC1 PE=2 SV=1;>tr|H3BM75|H3BM75_HUMAN Protein TLDC1 OS=Homo sapiens GN=TLDC1 PE=2 SV=1;>tr|H3BUB0|H3BUB0_HU 0.08 0.06 -0.18 -0.15 -0.42 0.20 0.23 0.13 0.191375848 -0.085523642 6.91E-52 5 8 8 25

P09382;F8WEI7 Galectin-1 LGALS1 >sp|P09382|LEG1_HUMAN Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 -0.61 -0.48 -0.12 0.26 1.70 0.74 0.15 0.50 1.101857424 -1.008570688 apoptosis;B cell activation;B cell activation involved in immune response;B cell differentiation;biological regulation;carbohydrate homeostasis;cell activation;cell activation involved in immune response;cell death;cell differentiation;cellular chemical homeostasis;cellular developmental process;cellular glucose homeostasis;cellular homeostasis;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to monosaccharide stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;death;developmental process;glucose homeostasis;homeostatic process;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;leukocyte differentiation;lymphocyte activation;lymphocyte activation involved in immune response;lymphocyte costimulation;lymphocyte differentiation;mature B cell differentiation;mature B cell differentiation involved in immune response;multicellular organismal process;multicellular organismal response to stress;muscle cell differentiation;myoblast differentiation;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell projection organization;negative regulation of cell-substrate adhesion;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of neuron projection development;plasma cell differentiation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell-cell adhesion;positive regulation of cellular process;positive regulation of erythrocyte aggregation;positive regulation of homotypic cell-cell adhesion;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of T cell activation;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell activation;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cell-cell adhesion;regulation of cell-substrate adhesion;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of erythrocyte aggregation;regulation of homotypic cell-cell adhesion;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of T cell activation;response to axon injury;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to glucose stimulus;response to hexose stimulus;response to monosaccharide stimulus;response to organic cyclic compound;response to organic substance;response to stimulus;response to stress;response to wounding;T cell costimulation binding;carbohydrate binding;disaccharide binding;galactoside binding;lactose binding;molecular transducer activity;monosaccharide binding;signal transducer activity;sugar binding cell part;cell surface;cytoplasm;extracellular matrix;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;proteinaceous extracellular matrix 3.35E-115 2 8 8 63

Q9HCC0;Q9HCC0-2;D6RD67;D6RDF7;D6R9R1 "Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial" MCCC2 ">sp|Q9HCC0|MCCB_HUMAN Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1;>sp|Q9HCC0-2|MCCB_HUMAN Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2;>tr|D6RD67|D6RD67_HUM" -0.06 -0.09 0.28 0.17 -0.09 0.04 -0.27 -0.33 0.835911971 0.241542385 amine catabolic process;amine metabolic process;branched chain family amino acid catabolic process;branched chain family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme A metabolic process;coenzyme metabolic process;cofactor metabolic process;heterocycle metabolic process;leucine catabolic process;leucine metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine nucleoside metabolic process;purine ribonucleoside metabolic process;purine-containing compound metabolic process;ribonucleoside metabolic process;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;CoA carboxylase activity;ligase activity;ligase activity, forming carbon-carbon bonds;methylcrotonoyl-CoA carboxylase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part "Valine, leucine and isoleucine degradation" 2.30E-78 5 8 8 18.7

P23368;P23368-2 "NAD-dependent malic enzyme, mitochondrial" ME2 ">sp|P23368|MAOM_HUMAN NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1;>sp|P23368-2|MAOM_HUMAN Isoform 2 of NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2" 0.14 -0.11 -0.22 -0.07 -0.01 0.01 0.08 -0.24 0.083297 -0.024804497 carboxylic acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;dicarboxylic acid metabolic process;malate metabolic process;metabolic process;organic acid metabolic process;oxoacid metabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;electron carrier activity;ion binding;malate dehydrogenase (decarboxylating) activity;malate dehydrogenase (oxaloacetate-decarboxylating) activity;malate dehydrogenase activity;malic enzyme activity;metal ion binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Pyruvate metabolism;Two-component system 9.21E-65 2 8 8 26.5

B4DUX5;P50579;F8VQZ7;G3V1U3;G3XA91;F8VRR3;F8VSC4;F8VY03;F8VZX9 Methionine aminopeptidase;Methionine aminopeptidase 2 METAP2 >tr|B4DUX5|B4DUX5_HUMAN Methionine aminopeptidase OS=Homo sapiens GN=METAP2 PE=2 SV=1;>sp|P50579|MAP2_HUMAN Methionine aminopeptidase 2 OS=Homo sapiens GN=METAP2 PE=1 SV=1;>tr|F8VQZ7|F8VQZ7_HUMAN Methionine aminopeptidase OS=Homo sapiens GN=METAP2 PE=2 SV= 0.01 0.07 0.00 0.09 0.11 -0.16 -0.19 -0.68 0.690259797 0.268705913 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;N-terminal protein amino acid modification;peptidyl-amino acid modification;peptidyl-methionine modification;primary metabolic process;protein maturation;protein metabolic process;protein modification process;protein processing;proteolysis "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase

activity;ion binding;metal ion binding;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasm;intracellular part 1.19E-85 9 8
8 27.7
H7BY50;Q5JRA6-2;Q5JRA6;G8JLC6;Q5JRA6-3;Q5JRA6-4 Melanoma inhibitory activity protein 3 MIA3 >tr|H7BY50|H7BY50_HUMAN Melanoma inhibitory activity protein 3 (Fragment) OS=Homo sapiens
GN=MIA3 PE=4 SV=1;>sp|Q5JRA6-2|MIA3_HUMAN Isoform 2 of Melanoma inhibitory activity protein 3 OS=Homo sapiens GN=MIA3;>sp|Q5JRA6|MIA3_HUMAN Melanoma inhibitory activi 0.02 -0.12 0.11 -0.22
0.80 -0.18 -0.03 -0.51 0.084394474 -0.070010289 biological regulation;cellular process;establishment of localization;establishment of localization in cell;establishment of protein
localization;exocytosis;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component
movement;negative regulation of cellular process;negative regulation of locomotion;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular
component movement;positive regulation of cellular process;positive regulation of immune system process;positive regulation of leukocyte migration;positive regulation of locomotion;protein transport;regulation of biological
process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of immune system process;regulation of leukocyte
migration;regulation of localization;regulation of locomotion;response to stimulus;response to stress;response to wounding;secretion;secretion by cell;transport;vesicle-mediated transport;wound healing cell
part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle
membrane;organelle part 1.07E-29 6 8 8 11.8
P25325;J3KPV7;B1AH49 3-mercaptopyruvate sulfurtransferase;Sulfurtransferase MPST >sp|P25325|THTM_HUMAN 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1
SV=3;>tr|J3KPV7|J3KPV7_HUMAN Sulfurtransferase OS=Homo sapiens GN=MPST PE=4 SV=1;>tr|B1AH49|B1AH49_HUMAN 3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE -0.15 -0.12
0.16 0.07 -0.34 -0.07 0.56 0.31 0.228076824 -0.127173863 biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound
catabolic process;cellular nitrogen compound metabolic process;cellular process;cyanate catabolic process;cyanate metabolic process;hydrogen sulfide biosynthetic process;hydrogen sulfide metabolic process;metabolic
process;nitrogen compound metabolic process;organic acid metabolic process;response to chemical stimulus;response to stimulus;response to toxin;small molecule metabolic process;sulfur compound biosynthetic process;sulfur
compound metabolic process "3-mercaptopyruvate sulfurtransferase activity;catalytic activity;sulfurtransferase activity;thiosulfate sulfurtransferase activity;transferase activity;transferase activity, transferring sulfur-containing
groups" cell junction;cell part;cell projection;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded
organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;neuron projection;organelle;organelle inner membrane;organelle membrane;organelle part;synapse Cysteine and
methionine metabolism;Sulfur relay system 1.98E-92 3 8 8 34
Q14CX7;Q14CX7-2;H0YHR9;F8VSB9 "N-alpha-acetyltransferase 25, NatB auxiliary subunit"NAA25 ">sp|Q14CX7|NAA25_HUMAN N-alpha-acetyltransferase 25, NatB auxiliary subunit OS=Homo sapiens
GN=NAA25 PE=1 SV=1;>sp|Q14CX7-2|NAA25_HUMAN Isoform 2 of N-alpha-acetyltransferase 25, NatB auxiliary subunit OS=Homo sapiens GN=NAA25" 0.26 0.01 0.14 -0.06 -0.01 -0.05 0.30 -0.23
0.244173525 0.082655649 cell part;cytoplasm;intracellular part 1.99E-21 4 8 8 13.8
F8VZJ2;H0YHX9;Q13765;Q13765-2;E9PAV3;F8W0W4;F8W1N5;F8VNW4;F8VZ58;Q9BZK3 Nascent polypeptide-associated complex subunit alphaNACA >tr|F8VZJ2|F8VZJ2_HUMAN Nascent polypeptide-associated
complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1;>tr|H0YHX9|H0YHX9_HUMAN Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens GN=NACA PE=2
SV=1;>sp|Q13765|NACA_HUMAN N 0.11 0.05 0.00 -0.07 -0.03 -0.24 0.05 -0.16 0.670350395 0.116765557 "anatomical structure development;anatomical structure morphogenesis;biological
regulation;biosynthetic process;cardiac chamber development;cardiac ventricle development;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic
process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;developmental growth;developmental process;establishment of localization;establishment of protein
localization;growth;heart trabecular morphogenesis;interaction with host;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism
process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of muscle cell apoptosis;negative regulation of
programmed cell death;negative regulation of striated muscle cell apoptosis;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of
biological process;positive regulation of cell proliferation;positive regulation of cell proliferation involved in heart morphogenesis;positive regulation of cellular process;positive regulation of developmental growth;positive
regulation of developmental process;positive regulation of growth;positive regulation of skeletal muscle tissue growth;primary metabolic process;protein metabolic process;protein transport;regeneration;regulation of anatomical
structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cell
proliferation involved in heart morphogenesis;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of growth;regulation of heart morphogenesis;regulation of
multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell apoptosis;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of organ
morphogenesis;regulation of programmed cell death;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of skeletal muscle tissue growth;regulation of striated muscle cell
apoptosis;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;reproductive process;RNA biosynthetic process;RNA metabolic process;skeletal muscle tissue regeneration;tissue
development;tissue regeneration;trabecula morphogenesis;transcription, DNA-dependent;translation;transport;viral reproductive process;virus-host interaction" binding;DNA binding;nucleic acid binding;protein binding;protein
binding transcription factor activity;TBP-class protein binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity cell
part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nascent polypeptide-associated complex;nucleus;organelle;protein
complex 1.43E-193 10 8 8 55.1
Q9BYT8;E9PCB6;H0YAK4;H0YAF7 "Neurolysin, mitochondrial" NLN ">sp|Q9BYT8|NEUL_HUMAN Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1;>tr|E9PCB6|E9PCB6_HUMAN Neurolysin,
mitochondrial OS=Homo sapiens GN=NLN PE=2 SV=1;>tr|H0YAK4|H0YAK4_HUMAN Neurolysin, mitochondrial (Fragment) OS=Homo sapiens GN=NLN PE=2 SV=" 0.00 -0.04 -0.16 -0.14 0.11 -0.17
0.51 0.16 0.707080851 -0.237002889 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "binding;catalytic activity;cation binding;endopeptidase
activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular
membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial intermembrane space;mitochondrial
part;mitochondrion;organelle;organelle envelope lumen;organelle part Renin-angiotensin system 6.86E-38 4 8 8 15.1
B7Z382;P49902;Q5JUV6;Q5JUV4;Q5JUV3;H0YHR8 Cytosolic purine 5-nucleotidase NT5C2 >tr|B7Z382|B7Z382_HUMAN Cytosolic purine 5-nucleotidase OS=Homo sapiens GN=NT5C2 PE=2
SV=1;>sp|P49902|5NTC_HUMAN Cytosolic purine 5-nucleotidase OS=Homo sapiens GN=NT5C2 PE=1 SV=1 0.23 -0.03 0.12 -0.19 0.05 0.13 0.60 -0.10 0.309884161 -0.138925563 catabolic
process;cellular aromatic compound metabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;drug
metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic
process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary
metabolic process;purine base metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;small
molecule metabolic process "5'-nucleotidase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;kinase activity;metal ion binding;nucleobase-containing
compound kinase activity;nucleoside phosphotransferase activity;nucleotidase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity;phosphotransferase activity, alcohol group as acceptor;transferase
activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part Nicotinate and nicotinamide metabolism;Purine metabolism;Pyrimidine metabolism 1.14E-25 6
8 8 19.9
Q96RS6-3;Q96RS6-2;Q96RS6 NudC domain-containing protein 1 NUDCD1 >sp|Q96RS6-3|NUDC1_HUMAN Isoform 3 of NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1;>sp|Q96RS6-
2|NUDC1_HUMAN Isoform 2 of NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1;>sp|Q96RS6|NUDC1_HUMAN NudC domain-containing protein 1 OS=Hom 0.39 0.02 0.00 0.01 0.05 -0.19 0.09
-0.34 0.617406035 0.202150312 cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.22E-46 3
8 8 20.4
Q9H4L5-2;Q9H4L5;Q9H4L5-4;Q9H4L5-3;Q9H4L5-6;Q9H4L5-5;Q9H4L5-8;Q9H4L5-7 Oxysterol-binding protein-related protein 3 OSBPL3 >sp|Q9H4L5-2|OSBL3_HUMAN Isoform 1b of Oxysterol-binding protein-
related protein 3 OS=Homo sapiens GN=OSBPL3;>sp|Q9H4L5|OSBL3_HUMAN Oxysterol-binding protein-related protein 3 OS=Homo sapiens GN=OSBPL3 PE=1 SV=1;>sp|Q9H4L5-4|OSBL3_HUMAN Isoform 1d of
Oxyst -0.05 0.07 0.00 0.13 -0.02 0.02 -0.20 0.32 0.020152661 0.007062841 establishment of localization;lipid transport;organic substance transport;transport binding;cholesterol binding;lipid

binding;phospholipid binding;steroid binding;sterol bindingcell part;cytoplasmic part;cytosol;endoplasmic reticulum part;intracellular organelle part;intracellular part;membrane;nuclear membrane;nuclear part;organelle membrane;organelle part;perinuclear endoplasmic reticulum;plasma membrane 1.54E-36 8 8 8 12.3

Q8IXQ6-3;Q8IXQ6-2;Q8IXQ6;G5E9U8 Poly [ADP-ribose] polymerase 9 PARP9 >sp|Q8IXQ6-3|PARP9_HUMAN Isoform 3 of Poly [ADP-ribose] polymerase 9 OS=Homo sapiens GN=PARP9;>sp|Q8IXQ6-2|PARP9_HUMAN Isoform 2 of Poly [ADP-ribose] polymerase 9 OS=Homo sapiens GN=PARP9;>sp|Q8IXQ6|PARP9_HUMAN Poly [ADP-ribose] polymerase 9 OS=Homo sapien 0.22 0.13 0.00 -0.07 -1.54 -0.84 -0.28 0.12 0.826265573 0.705364102 biological regulation;cell migration;cell motility;cellular component movement;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;double-strand break repair;locomotion;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;response to DNA damage stimulus;response to stimulus;response to stress "catalytic activity;NAD+ ADP-ribosyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.00E-55 4 8 8 16.2

P08559-3;P08559;P08559-2;P08559-4;Q5JPU3;P29803;Q5JPU0;Q5JPT9;Q5JPU1;Q5JPU2 "Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial" PDHA1 ">sp|P08559-3|ODPA_HUMAN Isoform 3 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1;>sp|P08559|ODPA_HUMAN Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapien" -0.34 0.25 0.06 0.35 0.00 0.18 -0.94 0.09 0.326124906 0.246967991 acetyl-CoA biosynthetic process;acetyl-CoA biosynthetic process from pyruvate;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol catabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor catabolic process;cofactor metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of metabolic process;small molecule catabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor;pyruvate dehydrogenase (acetyl-transferring) activity;pyruvate dehydrogenase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part;protein complex;pyruvate dehydrogenase complex "Butanoate metabolism;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Pyruvate metabolism;Valine, leucine and isoleucine biosynthesis" 6.53E-30 10 8 8 23.1

E7EPL4;H3BNZ1;Q6P996;E7EMH5;J3KNK7;H3BND4;Q6P996-2;Q86XE2;Q6P474;H3BPV5;H3BM88 Pyridoxal-dependent decarboxylase domain-containing protein 1 PDXDC1 >tr|E7EPL4|E7EPL4_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=2 SV=1;>tr|H3BNZ1|H3BNZ1_HUMAN Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=2 SV=1;>sp|Q6P996|P 0.12 0.05 -0.01 0.02 0.21 0.47 -0.15 0.16 0.40725598 -0.12910097 carboxylic acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;metabolic process;organic acid metabolic process;oxoacid metabolic process;small molecule metabolic process binding;carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;cofactor binding;lyase activity;pyridoxal phosphate binding;vitamin B6 binding;vitamin binding 2.29E-80 11 8 8 13.7

B5MCF9;O00541-2;O00541;B3KXD6;H7C267;C9JXJ1;Q674R7 Pescadillo homolog PES1 >tr|B5MCF9|B5MCF9_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1;>sp|O00541-2|PESC_HUMAN Isoform 2 of Pescadillo homolog OS=Homo sapiens GN=PES1;>sp|O00541|PESC_HUMAN Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1;>tr|B3KXD6|B3KXD6_HUMAN 0.17 0.53 0.17 0.51 -0.10 -0.12 -0.83 -0.13 1.277572736 0.63958344 "autophagic vacuole assembly;biological regulation;cell cycle phase;cell cycle process;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;localization;macromolecule localization;macromolecule metabolic process;maturation of 5.8S rRNA;maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);maturation of LSU-rRNA;maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;metaphase;mitotic metaphase;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleolus organization;nucleus organization;organelle assembly;organelle organization;primary metabolic process;protein localization;protein localization to organelle;regulation of biological process;regulation of cell cycle;regulation of cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;vacuole organization" "autophagic vacuole membrane;cell part;chromosome;condensed chromosome;cytoplasmic part;cytoplasmic vesicle;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;nuclear part;nucleolar part;nucleolus;nucleoplasm;organelle;organelle membrane;organelle part;PeBoW complex;preribosome;preribosome, large subunit precursor;protein complex;ribonucleoprotein complex;vacuolar membrane;vacuolar part;vesicle" 2.42E-16 7 8 8 13.7

Q96HS1;Q96HS1-2;F5GXG4;Q9UBZ9-2;Q9UBZ9 "Serine/threonine-protein phosphatase PGAM5, mitochondrial" PGAM5 ">sp|Q96HS1|PGAM5_HUMAN Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2;>sp|Q96HS1-2|PGAM5_HUMAN Isoform 2 of Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5" -0.31 0.56 0.24 0.78 -0.34 -0.04 -1.19 -0.03 0.852471062 0.722372605 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA biosynthetic process;DNA metabolic process;DNA repair;DNA replication;error-prone translesion synthesis;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;postreplication repair;primary metabolic process;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;translesion synthesis"binding;catalytic activity;cation binding;damaged DNA binding;deoxycytidyl transferase activity;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;magnesium ion binding;metal ion binding;nucleic acid binding;nucleotidyltransferase activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;nuclear part;nucleoplasm;organelle membrane;organelle outer membrane;organelle part;outer membrane 2.23E-44 5 8 8 29.8

P47712;E7EU42 Cytosolic phospholipase A2;Phospholipase A2;Lysophospholipase PLA2G4A >sp|P47712|PA24A_HUMAN Cytosolic phospholipase A2 OS=Homo sapiens GN=PLA2G4A PE=1 SV=2;>tr|E7EU42|E7EU42_HUMAN Lysophospholipase OS=Homo sapiens GN=PLA2G4A PE=2 SV=1 0.12 0.19 -0.20 -0.16 0.01 0.14 0.47 -0.37 0.137671425 -0.075672995 acid secretion;alcohol metabolic process;amine metabolic process;arachidonic acid metabolic process;arachidonic acid secretion;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;cardiolipin acyl-chain remodeling;cardiolipin metabolic process;catabolic process;cell activation;cellular amine metabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to antibiotic;cellular response to chemical stimulus;cellular response to stimulus;establishment of localization;ethanolamine-containing compound metabolic process;fatty acid biosynthetic process;fatty acid metabolic process;fatty acid transport;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;icosanoid biosynthetic process;icosanoid metabolic process;icosanoid secretion;icosanoid transport;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid transport;long-chain fatty acid transport;metabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic acid transport;organic substance transport;organophosphate metabolic process;oxoacid metabolic process;phosphatidic acid biosynthetic process;phosphatidic acid metabolic process;phosphatidylglycerol metabolic process;phospholipid biosynthetic process;phospholipid catabolic process;phospholipid metabolic process;platelet activating factor biosynthetic process;platelet activating factor metabolic process;platelet activation;primary metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to antibiotic;response to chemical stimulus;response to stimulus;secretion;small molecule biosynthetic process;small molecule metabolic process;transport;unsaturated fatty acid biosynthetic process;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process "binding;calcium ion binding;calcium-dependent phospholipase A2 activity;calcium-dependent phospholipid binding;carboxylic ester hydrolase activity;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lipase activity;lipid binding;lysophospholipase activity;metal ion binding;phospholipase A2 activity;phospholipase activity;phospholipid binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle;organelle inner membrane;organelle membrane;organelle part;vesicle alpha-Linolenic acid metabolism;Arachidonic acid metabolism;Ether lipid metabolism;Fat digestion and absorption;Fc epsilon RI signaling pathway;Glycerophospholipid metabolism;GnRH signaling pathway;Linoleic acid metabolism;Long-term depression;MAPK signaling pathway;Pancreatic secretion;Toxoplasmosis;Vascular smooth muscle contraction;VEGF signaling pathway 8.09E-57 2 8 8 13.8

Q99575;E5RK39 Ribonucleases P/MRP protein subunit POP1 POP1 >sp|Q99575|POP1_HUMAN Ribonucleases P/MRP protein subunit POP1 OS=Homo sapiens GN=POP1 PE=1 SV=2;>tr|E5RK39|E5RK39_HUMAN Pyrin domain-containing protein 1 (Fragment) OS=Homo sapiens GN=POP1 PE=2 SV=1 -0.04 0.43 -0.20 0.25 -0.32 -0.02 -0.98 0.05 0.667062403 0.427613512 catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;ncRNA catabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA catabolic process;RNA metabolic process;RNA processing;tRNA 5'-leader removal;tRNA catabolic process;tRNA metabolic process;tRNA processing "catalytic activity;endonuclease activity;endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;endoribonuclease activity;endoribonuclease activity, producing 5'-phosphomonoesters;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;ribonuclease activity;ribonuclease MRP activity;ribonuclease P activity;tRNA-specific ribonuclease activity" cell part;intracellular organelle part;intracellular part;macromolecular complex;multimeric ribonuclease P complex;nuclear part;nucleolar part;nucleolar ribonuclease P complex;organelle part;ribonuclease MRP complex;ribonuclease P complex;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes;RNA transport 1.67E-27 2 8 8 10.7

Q15435;C9J177;Q15435-2;H7C003;B5MBZ8;Q15435-3;C9JD73;B5MCY6;Q15435-4;C9JRC4;H7C3Q5 Protein phosphatase 1 regulatory subunit 7 PPP1R7 >sp|Q15435|PP1R7_HUMAN Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1;>tr|C9J177|C9J177_HUMAN Protein phosphatase 1 regulatory subunit 7 (Fragment) OS=Homo sapiens GN=PPP1R7 PE=2 SV=1;>sp|Q15435-2|PP1R7_HUMAN Isoform 2 of Pr 0.11 -0.19 0.22 0.03 -0.07 -0.14 0.39 -0.48 0.229849089 0.119641396 enzyme regulator activity;phosphatase regulator activity;protein phosphatase regulator activity;protein phosphatase type 1 regulator activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.96E-72 11 8 8 27.5

Q14738-3;Q14738-2;E9PFR3;Q14738;H0Y8C4;H7C5Q9;H0YJ35;Q96B13;Q13362-2;Q13362-3;Q13362;Q13362-4;H0YJ75;Q13362-5 Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform PPP2R5D >sp|Q14738-3|2A5D_HUMAN Isoform Delta-3 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform OS=Homo sapiens GN=PPP2R5D;>sp|Q14738-2|2A5D_HUMAN Isoform Delta-2 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subun 0.00 -0.06 0.04 -0.27 0.59 0.33 0.42 -0.09 1.022920614 -0.388667809 "activation of immune response;activation of innate immune response;alcohol catabolic process;alcohol metabolic process;anatomical structure development;biological regulation;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;cellular response to stress;defense response;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;innate immune response;innate immune response-activating signal transduction;intracellular protein kinase cascade;intracellular signal transduction;macromolecule catabolic process;macromolecule metabolic process;MAPKKK cascade;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;monosaccharide catabolic process;monosaccharide metabolic process;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;nerve growth factor receptor signaling pathway;nervous system development;oxidation-reduction process;pattern recognition receptor signaling pathway;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cell death;positive regulation of cellular process;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of programmed cell death;positive regulation of response to stimulus;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of programmed cell death;regulation of response to stimulus;regulation of response to stress;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule catabolic process;small molecule metabolic process;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;system development;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;TRIF-dependent toll-like receptor signaling pathway;ubiquitin-dependent protein catabolic process" "catalytic activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on ester bonds;peptidase activity;phosphatase activity;phosphatase regulator activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein serine/threonine phosphatase activity" "cell part;chromosomal part;chromosome, centromeric region;cytoplasmic part;cytosol;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex"Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;Wnt signaling pathway6.40E-38 14 8 8 18.3

Q08209-2;Q08209;Q08209-3;A8W6Z8;E7ETC2;A1A441;E9PPC8;E9PK68;F5H0F8;Q5F2F8;P16298-2;P16298-3;P16298;P16298-4;H0YC26;P48454-2;P48454;P48454-3 Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;Serine/threonine-protein phosphatase PPP3CA >sp|Q08209-2|PP2BA_HUMAN Isoform 2 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens GN=PPP3CA;>sp|Q08209|PP2BA_HUMAN Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Homo sapiens GN=PPP3CA 0.13 -0.12 -0.07 -0.11 -0.26 -0.17 0.52 0.09 0.183955465 -0.091101877 "anatomical structure development;axon extension;behavior;behavioral interaction between organisms;biological regulation;calcineurin-NFAT signaling pathway;calcium ion transport;calcium ion-dependent exocytosis;calcium-mediated signaling;carbohydrate homeostasis;cation transport;cell activation;cell cycle process;cell development;cell differentiation;cell growth;cell proliferation;cellular chemical homeostasis;cellular developmental process;cellular glucose homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to drug;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cognition;dephosphorylation;developmental cell growth;developmental growth;developmental growth involved in morphogenesis;developmental process;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;G1/S transition of mitotic cell cycle;glucose homeostasis;growth;heart development;homeostasis of number of cells;homeostatic process;immune system process;inositol phosphate-mediated signaling;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;ion transport;learning;learning or memory;leukocyte activation;leukocyte differentiation;leukocyte homeostasis;leukocyte proliferation;lymphocyte activation;lymphocyte differentiation;lymphocyte homeostasis;lymphocyte proliferation;macromolecule metabolic process;macromolecule modification;membrane depolarization;memory;metabolic process;metal ion transport;mononuclear cell proliferation;multicellular organismal process;multi-organism process;muscle cell development;muscle fiber development;negative regulation of adaptive immune response;negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;negative regulation of biological process;negative regulation of cell killing;negative regulation of cellular process;negative regulation of hormone secretion;negative regulation of immune effector process;negative regulation of immune response;negative regulation of immune system process;negative regulation of insulin secretion;negative regulation of leukocyte mediated cytotoxicity;negative regulation of leukocyte mediated immunity;negative regulation of lymphocyte mediated immunity;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of T cell mediated cytotoxicity;negative regulation of T cell mediated immunity;negative regulation of transport;neurological system process;nuclear import;nuclear transport;nucleocytoplasmic transport;organ development;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of insulin secretion involved in cellular response to glucose stimulus;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of RNA metabolic process;positive regulation of secretion;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transport;primary metabolic process;protein dephosphorylation;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein phosphorylation;protein targeting;protein transport;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell killing;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of excitatory postsynaptic membrane potential;regulation of gene expression;regulation of homeostatic process;regulation of hormone secretion;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of insulin secretion;regulation of insulin secretion involved in cellular response to glucose stimulus;regulation of leukocyte mediated cytotoxicity;regulation of leukocyte mediated immunity;regulation of localization;regulation of lymphocyte mediated immunity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of multicellular organismal process;regulation of muscle adaptation;regulation of muscle system process;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of postsynaptic membrane potential;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of secretion;regulation of signaling;regulation of skeletal muscle adaptation;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of T cell mediated cytotoxicity;regulation of T cell mediated immunity;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmission of nerve impulse;regulation of transport;response to amine stimulus;response to amphetamine;response to calcium ion;response to carbohydrate stimulus;response to chemical stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to glucose stimulus;response to hexose stimulus;response to inorganic substance;response to metal ion;response to monosaccharide stimulus;response to organic nitrogen;response to organic substance;response to stimulus;response to stress;second-messenger-mediated signaling;secretion;secretion by cell;signal transduction;skeletal muscle fiber development;social behavior;striated muscle cell development;system process;T cell activation;T cell differentiation;T cell homeostasis;T cell proliferation;transition between fast and slow fiber;transport;vesicle-mediated transport" "binding;calcium ion binding;calcium-dependent protein serine/threonine phosphatase activity;calmodulin binding;calmodulin-dependent protein phosphatase activity;catalytic activity;cation binding;drug binding;enzyme binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphatase binding;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein binding;protein phosphatase 2B binding;protein phosphatase binding;protein serine/threonine phosphatase activity" calcineurin complex;cell part;contractile fiber part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;nucleus;organelle;organelle part;plasma membrane;protein complex;protein serine/threonine phosphatase complex;Z disc Alzheimer's disease;Amyotrophic lateral sclerosis (ALS);Apoptosis;Axon guidance;B cell receptor signaling pathway;Calcium signaling pathway;ko05152;Long-term potentiation;MAPK signaling pathway;Natural killer cell mediated cytotoxicity;Oocyte meiosis;Osteoclast differentiation;T cell receptor signaling pathway;VEGF signaling pathway;Wnt signaling pathway 4.46E-36 18 8 8 19.4

O00487;C9JW37 26S proteasome non-ATPase regulatory subunit 14 PSMD14 >sp|O00487|PSDE_HUMAN 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 -0.11 0.01 -0.07 0.01 -0.04 0.06 -0.10 -0.03 0.068726983 -0.008734159 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via homologous recombination;double-strand break repair via nonhomologous end joining;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein deubiquitination;protein K63-linked deubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;recombinational repair;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular catabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of proteolysis;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" "binding;catalytic activity;cation binding;endopeptidase activator activity;endopeptidase regulator activity;enzyme activator activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;metallopeptidase activity;peptidase activator activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;peptidase regulator activity;proteasome binding;protein binding;protein complex binding;thiolester hydrolase activity;ubiquitin thiolesterase activity" "cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;proteasome regulatory particle, lid subcomplex;protein complex" Proteasome 5.26E-70 2 8 8 39.7

Q96EY7;B8ZZQ4;B4DF73;Q96EY7-2;F8WE76 "Pentatricopeptide repeat domain-containing protein 3, mitochondrial" PTCD3 ">sp|Q96EY7|PTCD3_HUMAN Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3" -0.17 0.18 0.18 0.11 -0.22 -0.36 -0.99 -0.33 1.189819385 0.551620651 biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrial translation;mitochondrion organization;organelle organization;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;translation binding;nucleic acid binding;ribonucleoprotein binding;ribosomal small subunit binding;RNA binding;rRNA binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 3.78E-44 5 8 8 13.2

P46778;G3V1B3;M0R181 60S ribosomal protein L21 RPL21 >sp|P46778|RL21_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2;>tr|G3V1B3|G3V1B3_HUMAN 60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=2 SV=1;>tr|M0R181|M0R181_HUMAN 60S ribosomal protein L21 (Fragment) OS=Homo sapiens GN=RPL21 PE -0.05 -0.06 -0.69 -0.11 -1.39 -0.53 -0.22 -0.29 0.508214085 0.378160942 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.14E-34 3 8 8 45.6

P31949 Protein S100-A11 S100A11 >sp|P31949|S10AB_HUMAN Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 0.14 -0.02 -0.83 -0.17 -0.50 0.14 0.67 0.20 0.443854038 -0.346664996 biological regulation;cellular process;cellular response to stimulus;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to stimulus;signal transduction binding;calcium ion binding;calcium-dependent protein binding;cation binding;identical protein binding;ion binding;metal ion binding;protein binding;protein dimerization activity;protein homodimerization activity cell part;cell projection;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;ruffle 7.31E-235 1 8 8 86.7

P82979;F8VZQ9;H0YHG0;Q567R9;F8VS12 SAP domain-containing ribonucleoprotein SARNP;CIP29 >sp|P82979|SARNP_HUMAN SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3;>tr|F8VZQ9|F8VZQ9_HUMAN SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=2 SV=1;>tr|H0YHG0|H0YHG0_HUMAN Uncharacterized protein (Fragment) -0.18 0.61 0.17 0.58 0.06 0.10 -1.19 -0.03 0.662127173 0.563678959 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part 6.33E-74 5 8 8 42.9

Q14108;Q14108-2;D6RDG0 Lysosome membrane protein 2 SCARB2 >sp|Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2;>sp|Q14108-2|SCRB2_HUMAN Isoform 2 of Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 -0.56 -0.43 0.05 0.15 1.04 0.92 -0.33 0.27 0.794075466 -0.672091915 biological adhesion;cell adhesion;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;intracellular protein transport;intracellular transport;lysosomal transport;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;transport;vacuolar transport receptor activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lysosomal lumen;lysosomal membrane;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part;plasma membrane part;vacuolar lumen;vacuolar membrane;vacuolar part;vacuole Lysosome 5.58E-22 3 8 8 15.5

Q12765;Q12765-2;Q12765-3;B8ZZP4;C9J7U9;B4DIV7;C9K052 Secernin-1 SCRN1 >sp|Q12765|SCRN1_HUMAN Secernin-1 OS=Homo sapiens GN=SCRN1 PE=1 SV=2;>sp|Q12765-2|SCRN1_HUMAN Isoform 2 of Secernin-1 OS=Homo sapiens GN=SCRN1;>sp|Q12765-3|SCRN1_HUMAN Isoform 3 of Secernin-1 OS=Homo sapiens GN=SCRN1;>tr|B8ZZP4|B8ZZP4_HUMAN Secernin-1 OS=H 0.26 -0.07 -0.28 0.03 0.17 0.04 0.71 0.20 0.681020479 -0.293774289 cellular process;establishment of localization;establishment of localization in cell;exocytosis;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis;secretion;secretion by cell;transport;vesicle-mediated transport "catalytic activity;dipeptidase activity;exopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasm;intracellular organelle part;intracellular part;membrane;nuclear membrane;nuclear part;organelle membrane;organelle part 5.75E-44 7 8 8 22.5

Q9UGP8;A6PVC9 Translocation protein SEC63 homolog SEC63 >sp|Q9UGP8|SEC63_HUMAN Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2 -0.25 0.11 0.11 0.20 0.42 0.41 -0.32 0.17 0.240419155 -0.125944886 "cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transmembrane transport;intracellular protein transport;intracellular transport;posttranslational protein targeting to membrane, translocation;protein targeting;protein targeting to membrane;protein transmembrane transport;protein transport;transmembrane transport;transport" protein transporter activity;receptor activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle partProtein export;Protein processing in endoplasmic reticulum 8.81E-40 2 8 8 12.9

O43765;K7EMD6 Small glutamine-rich tetratricopeptide repeat-containing protein alpha SGTA >sp|O43765|SGTA_HUMAN Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1;>tr|K7EMD6|K7EMD6_HUMAN Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Fragment) OS=Homo sapiens GN=SGTA 0.19 0.07 -0.40 0.03 -0.33 -0.06 0.23 -0.10 0.083871142 0.041699076 interaction with host;interspecies interaction between organisms;multi-organism process;reproductive process;viral reproductive process;virus-host interaction cell part;cytoplasm;intracellular part 4.52E-50 2 8 8 30.4

Q9Y371;Q9Y371-2;Q9Y371-3 Endophilin-B1 SH3GLB1 >sp|Q9Y371|SHLB1_HUMAN Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1;>sp|Q9Y371-2|SHLB1_HUMAN Isoform 2 of Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 0.19 -0.12 0.06 -0.17 0.05 -0.09 0.29 -0.15 0.086531655 -0.032101009 apoptosis;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cell death;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;death;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organic acid biosynthetic process;organic acid metabolic process;organophosphate metabolic process;oxoacid metabolic process;phosphatidic acid biosynthetic process;phosphatidic acid metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of protein complex assembly;positive regulation of protein oligomerization;primary metabolic process;programmed cell death;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein oligomerization;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein oligomerization;small molecule biosynthetic process;small molecule metabolic process "binding;carboxylic acid binding;catalytic activity;fatty acid binding;lipid binding;lysophosphatidic acid acyltransferase activity;lysophospholipid acyltransferase activity;monocarboxylic acid binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasm;cytoplasmic part;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex Endocytosis 1.52E-33 3 8 8 20.5

Q08AF3;Q08AF3-2;B4E128;P0C7X5 Schlafen family member 5 SLFN5 >sp|Q08AF3|SLFN5_HUMAN Schlafen family member 5 OS=Homo sapiens GN=SLFN5 PE=1 SV=1 0.76 0.51 -0.08 -0.35 -0.42 0.03 0.25 0.22 0.244189476 0.19033728 "biological regulation;biosynthetic process;cell differentiation;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 3.08E-48 4 8 8 10.9

P09661;H0YMA0;H0YLR3;H0YKK0 U2 small nuclear ribonucleoprotein A SNRPA1 >sp|P09661|RU2A_HUMAN U2 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA1 PE=1 SV=2;>tr|H0YMA0|H0YMA0_HUMAN U2 small nuclear ribonucleoprotein A (Fragment) OS=Homo sapiens GN=SNRPA1 PE=2 SV=1;>tr|H0YLR3|H0YLR3_HUMAN U2 small nuclear ribonucleo 0.02 0.44 0.16 0.51 -0.24 -0.31 -1.31 -0.18 1.138362973 0.791463334 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U2 snRNP Spliceosome 2.39E-94 4 8 8 30.2

Q9UNH7;Q9UNH7-2;B4DJS7;H0YJF8;G3V4Z5;G3V5X9;G3V5U2;G3V2U1 Sorting nexin-6 SNX6 ">sp|Q9UNH7|SNX6_HUMAN Sorting nexin-6 OS=Homo sapiens GN=SNX6 PE=1 SV=1;>sp|Q9UNH7-2|SNX6_HUMAN Isoform 2 of Sorting nexin-6 OS=Homo sapiens GN=SNX6;>tr|B4DJS7|B4DJS7_HUMAN Sorting nexin 6, isoform CRA_e OS=Homo sapiens GN=SNX6 PE=2 SV=1" 0.14 0.11 -0.41 -0.15 0.02 -0.09 0.31 0.07 0.41863183 -0.156283685 "biological regulation;cell communication;cellular process;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of epidermal growth factor-activated receptor activity;negative regulation of gene expression;negative regulation of kinase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein kinase activity;negative regulation of protein tyrosine kinase activity;negative regulation of receptor activity;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription, DNA-dependent;negative regulation of transferase activity;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of epidermal growth factor receptor signaling pathway;regulation of epidermal growth factor-activated receptor activity;regulation of gene expression;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein tyrosine kinase activity;regulation of receptor activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;retrograde transport, endosome to Golgi;transport;vesicle-mediated transport" binding;lipid binding;phosphatidylinositol binding;phospholipid binding cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome membrane;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;vesicle membrane 2.63E-77 8 8 8 23.2

Q00796;B7Z3A6;H0YKB3;H0YLA4 Sorbitol dehydrogenase SORD >sp|Q00796|DHSO_HUMAN Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4;>tr|B7Z3A6|B7Z3A6_HUMAN Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=2 SV=1;>tr|H0YKB3|H0YKB3_HUMAN Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=2 SV=1;>tr|H0YLA4|H0YL 0.20 -0.17 0.20 0.12 -0.56 -0.68 0.22 -0.67 0.936370143 0.509300711 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;alditol catabolic process;alditol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell motility;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component movement;cellular metabolic process;cellular process;fructose biosynthetic process;fructose metabolic process;glucose metabolic process;hexitol catabolic process;hexitol metabolic process;hexose biosynthetic process;hexose metabolic process;locomotion;L-xylitol catabolic process;L-xylitol metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;pentitol catabolic process;pentitol metabolic process;polyol catabolic process;polyol metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;sorbitol catabolic process;sorbitol metabolic process;sperm motility "binding;carbohydrate binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;ion binding;L-iditol 2-dehydrogenase activity;metal ion binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transition metal ion binding;zinc ion binding" cell part;cell projection;cilium;cytoplasmic part;extracellular region part;extracellular space;intracellular organelle part;intracellular part;membrane;mitochondrial membrane;mitochondrial part;motile cilium;organelle membrane;organelle part Fructose and mannose metabolism 6.69E-78 4 8 8 26.3

Q13501-2;Q13501;E7EMC7;E9PFW8;C9JRJ8;E3W990 Sequestosome-1 SQSTM1 >sp|Q13501-2|SQSTM_HUMAN Isoform 2 of Sequestosome-1 OS=Homo sapiens GN=SQSTM1;>sp|Q13501|SQSTM_HUMAN Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1;>tr|E7EMC7|E7EMC7_HUMAN Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=2 SV=1;>tr|E9PFW8|E9PFW8_HUMAN Sequ -0.08 0.28 -0.41 0.02 0.01 -0.29 -0.01 -0.08 0.100925297 0.045800188 "autophagy;biological regulation;catabolic process;cell communication;cell differentiation;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;developmental process;endosome transport;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;intracellular signal transduction;intracellular transport;localization;macroautophagy;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nerve growth factor receptor signaling pathway;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein localization;protein metabolic process;protein oligomerization;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to external stimulus;response to extracellular stimulus;response to nutrient levels;response to starvation;response to stimulus;response to stress;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;ubiquitin-dependent protein catabolic process;vesicle-mediated transport" "binding;catalytic activity;cation binding;enzyme binding;ion binding;kinase activity;kinase binding;metal ion binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein domain specific binding;protein kinase activity;protein kinase binding;protein serine/threonine kinase activity;receptor binding;receptor tyrosine kinase binding;SH2 domain binding;small conjugating protein binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;ubiquitin binding;zinc ion binding" autophagic vacuole;cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;endosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;lysosome;lytic vacuole;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;pre-autophagosomal structure;ribonucleoprotein complex;RNA granule;vacuole;vesicle Osteoclast differentiation 2.49E-78 6 8 8 42.1

P52630-4;P52630;G3V268;B4DLC8 Signal transducer and activator of transcription 2 STAT2 >sp|P52630-4|STAT2_HUMAN Isoform 2 of Signal transducer and activator of transcription 2 OS=Homo sapiens GN=STAT2;>sp|P52630|STAT2_HUMAN Signal transducer and activator of transcription 2 OS=Homo sapiens GN=STAT2 PE=1 SV=1;>tr|G3V268|G3V268_HUMAN Signal tr 0.02 -0.01 -0.24 0.01 -0.35 -0.14 0.15 0.26 0.08017803 -0.035083198 "biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;defense response;defense response to virus;immune effector process;immune system process;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of gene expression;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to cytokine stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of type I interferon-mediated signaling pathway;reproductive process;response to biotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to type I interferon;response to virus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription, DNA-dependent;type I interferon-mediated signaling pathway;viral reproductive process;virus-host interaction" binding;calcium ion binding;cation binding;DNA binding;ion binding;metal ion binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity;signal transducer activity cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane Chemokine signaling pathway;Hepatitis C;Jak-STAT signaling pathway;ko05152;Measles;Osteoclast differentiation 1.74E-37 4 8 8 13.5

P42226;P42226-2;P42226-3;G3V2X7;H0YJH6;Q5FBW6;G3V2L2;G3V2M3;G3V3E9;G3V2H4;G3V5I8;G3V568;G3V370;G3V5K5;H0YIY2 Signal transducer and activator of transcription 6 STAT6 >sp|P42226|STAT6_HUMAN Signal transducer and activator of transcription 6 OS=Homo sapiens GN=STAT6 PE=1 SV=1;>sp|P42226-2|STAT6_HUMAN Isoform 2 of Signal transducer and activator of transcription 6 OS=Homo sapiens GN=STAT6;>sp|P42226-3|STAT6_HUMAN Isoform -0.04 -0.12 0.07 -0.01 -0.22 -0.07 0.28 -0.23 0.087586591 0.031963211 "anatomical structure morphogenesis;biological regulation;biosynthetic process;cell fate commitment;cell proliferation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;epithelial cell proliferation;gland morphogenesis;macromolecule biosynthetic process;macromolecule metabolic process;mammary gland epithelial cell proliferation;mammary gland morphogenesis;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of immune response;negative regulation of immune system process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of type 2 immune response;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of B cell activation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell activation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA recombination;positive regulation of gene expression;positive regulation of immune effector process;positive regulation of immune system process;positive regulation of isotype switching;positive regulation of isotype switching to IgE isotypes;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of adaptive immune response;regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains;regulation of B cell activation;regulation of B cell mediated immunity;regulation of biological process;regulation of biosynthetic process;regulation of cell activation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA recombination;regulation of gene expression;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of immunoglobulin mediated immune response;regulation of immunoglobulin production;regulation of isotype switching;regulation of isotype switching to IgE isotypes;regulation of leukocyte activation;regulation of leukocyte mediated immunity;regulation of lymphocyte activation;regulation of lymphocyte mediated immunity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of production of molecular mediator of immune response;regulation of response to stimulus;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of type 2 immune response;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;T cell lineage commitment;T-helper 1 cell lineage commitment;T-helper cell lineage commitment;transcription, DNA-dependent" binding;calcium ion binding;cation binding;core promoter binding;core promoter sequence-specific DNA binding;DNA binding;ion binding;metal ion binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II core promoter sequence-specific DNA binding;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;signal transducer activity;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding cell part;chromatin;chromosomal part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear part;nucleus;organelle;organelle part Jak-STAT signaling pathway;ko05152 3.24E-28 15 8 8 11.8

P46977;E9PNQ1;E9PIJ8;E9PN73;E9PI32 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A STT3A >sp|P46977|STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2;>tr|E9PNQ1|E9PNQ1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=S 0.07 0.00 -0.81 -1.11 0.45 1.22 0.46 0.43 1.284802197 -1.102158395 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;co-translational protein modification;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;oligosaccharyltransferase complex;organelle part;protein complex N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis 4.79E-23 5 8 8 9.8

Q96I99;H0Y852;E9PDQ8;Q96I99-2 "Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial" SUCLG2 ">sp|Q96I99|SUCB2_HUMAN Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2;>tr|H0Y852|H0Y852_HUMAN Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (Fragment) OS=Homo sapiens GN=SUCLG2 PE=4 SV=1;>t" 0.09 -0.24 0.22 0.06 0.07 -0.22 0.06 -0.28 0.384330879 0.125764655 acetyl-CoA catabolic process;acetyl-CoA metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;metabolic process;small molecule metabolic process;succinyl-CoA metabolic process;tricarboxylic acid cycle "acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;CoA-ligase activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ligase activity;ligase activity, forming carbon-sulfur bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;succinate-CoA ligase (GDP-forming) activity;succinate-CoA ligase activity" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part Citrate cycle (TCA cycle);Propanoate metabolism 4.83E-62 4 8 8 19.9

Q01995;H0YCU9;E9PJ32 Transgelin TAGLN >sp|Q01995|TAGL_HUMAN Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4;>tr|H0YCU9|H0YCU9_HUMAN Transgelin (Fragment) OS=Homo sapiens GN=TAGLN PE=4 SV=1;>tr|E9PJ32|E9PJ32_HUMAN Transgelin (Fragment) OS=Homo sapiens GN=TAGLN PE=2 SV=1 -3.09 -2.03 -0.05 0.65 -0.26 -0.41 0.47 0.00 0.507800878 -1.079831185 anatomical structure development;developmental process;muscle organ development;muscle structure development;organ development cell part;cytoplasm;intracellular part 6.67E-82 3 8 8 43.8

P52888;K7EP46;K7EKB6;K7EIK4;K7EMU4;K7EL32;B3KSE2;K7EL02 Thimet oligopeptidase THOP1 >sp|P52888|THOP1_HUMAN Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2;>tr|K7EP46|K7EP46_HUMAN Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=3 SV=1 0.12 0.04 -0.14 0.10 -0.07 -0.18 0.30 -0.20 0.190868158 0.066709805 biological regulation;cellular metabolic process;cellular process;cellular response to stimulus;intracellular protein kinase cascade;intracellular signal transduction;macromolecule metabolic process;metabolic process;peptide metabolic process;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction "binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;peptide binding" cell part;cytoplasm;intracellular part African trypanosomiasis;Renin-angiotensin system 2.05E-63 8 8 8 16.3

Q9NQ88 "Fructose-2,6-bisphosphatase TIGAR" TIGAR ">sp|Q9NQ88|TIGAR_HUMAN Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1" -0.05 -0.12 0.05 0.00 -0.28 0.20 0.56 0.38 0.550698756 -0.241408124 "carbohydrate phosphatase activity;catalytic activity;fructose-2,6-bisphosphate 2-phosphatase activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphoric ester hydrolase activity;sugar-phosphatase activity" cell part;intracellular Fructose and mannose metabolism 1.14E-95 1 8 8 38.5

Q9Y5L0-3;Q9Y5L0;Q9Y5L0-5;Q9Y5L0-1;C9J7E5;E9PFH4 Transportin-3 TNPO3 >sp|Q9Y5L0-3|TNPO3_HUMAN Isoform 3 of Transportin-3 OS=Homo sapiens GN=TNPO3;>sp|Q9Y5L0|TNPO3_HUMAN Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=3;>sp|Q9Y5L0-5|TNPO3_HUMAN Isoform 4 of Transportin-3 OS=Homo sapiens GN=TNPO3;>sp|Q9Y5L0-1|TNPO3_HUMAN Isofo 0.21 -0.06 0.24 -0.07 0.06 -0.11 -0.05 -0.40 0.659736571 0.203043746 establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;nuclear import;nuclear transport;nucleocytoplasmic transport;protein import;protein import into nucleus;protein targeting;protein transport;splicing factor protein import into nucleus;transport receptor activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 7.98E-44 6 8 8 15.1

Q9H0E2;F2Z2Y8;B3KR28;E7EN89;B3KXC6;E9PP67;E9PQ25;E9PNS3 Toll-interacting protein TOLLIP >sp|Q9H0E2|TOLIP_HUMAN Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=1 SV=1;>tr|F2Z2Y8|F2Z2Y8_HUMAN Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=2 SV=1;>tr|B3KR28|B3KR28_HUMAN Toll-interacting protein OS=Homo sapiens GN=TOLLIP PE=2 SV=1;>t -0.19 0.07 -0.03 0.08 -0.03 0.43 0.30 0.24 0.937718013 -0.254404149 biological regulation;cell activation;cell communication;cell-cell signaling;cellular metabolic process;cellular process;cellular response to stimulus;defense response;immune response;immune system process;inflammatory response;innate immune response;intracellular signal transduction;leukocyte activation;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein sumoylation;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein sumoylation;response to stimulus;response to stress;response to wounding;signal transduction;signaling molecular transducer activity;signal transducer activitycell part;cytoplasmic part;cytosol;interleukin-1 receptor complex;interleukin-18 receptor complex;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear body;nuclear part;nucleoplasm part;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex;receptor complex Toll-like receptor signaling pathway 7.28E-48 8 8 8 33.6

Q6ZVM7;Q6ZVM7-2;B7Z2L7;Q6ZVM7-3;Q6ZVM7-4;F5H3S6;B7Z2U2 TOM1-like protein 2 TOM1L2 >sp|Q6ZVM7|TM1L2_HUMAN TOM1-like protein 2 OS=Homo sapiens GN=TOM1L2 PE=1 SV=1;>sp|Q6ZVM7-2|TM1L2_HUMAN Isoform 2 of TOM1-like protein 2 OS=Homo sapiens GN=TOM1L2;>tr|B7Z2L7|B7Z2L7_HUMAN TOM1-like protein 2 OS=Homo sapiens GN=TOM1L2 PE=2 SV=1;>sp|Q6ZVM7-3| 0.21 0.13 0.25 0.01 0.15 0.63 0.22 -0.19 0.10713739 -0.053266533 establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;transport cell part;intracellular 3.40E-37 7 8 8 26

Q12888;F8VY86;Q12888-2;A6NNK5;C9JXV0;H7C3N7;M0R142;H7BZY0 Tumor suppressor p53-binding protein 1 TP53BP1 >sp|Q12888|TP53B_HUMAN Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=1 SV=2;>tr|F8VY86|F8VY86_HUMAN Tumor suppressor p53-binding protein 1 OS=Homo sapiens GN=TP53BP1 PE=2 SV=1;>sp|Q12888-2|TP53B_HUMAN Isoform 2 of Tumor suppressor p5 -0.19 1.10 -0.19 0.88 -0.09 -0.18 -0.85 0.07 0.706775135 0.661491198 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via homologous recombination;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;recombinational repair;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress" binding;damaged DNA binding;DNA binding;histone binding;methylated histone residue binding;nucleic acid binding;protein binding;protein binding transcription factor activity;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;sequence-specific DNA binding;telomeric DNA binding;transcription cofactor activity;transcription factor binding transcription factor activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;replication fork 8.15E-31 8 8 8 7.1

Q15642-2;Q15642;Q15642-4;Q15642-3;M0R0F9;Q15642-5;M0R2H7 Cdc42-interacting protein 4 TRIP10 >sp|Q15642-2|CIP4_HUMAN Isoform 2 of Cdc42-interacting protein 4 OS=Homo sapiens GN=TRIP10;>sp|Q15642|CIP4_HUMAN Cdc42-interacting protein 4 OS=Homo sapiens GN=TRIP10 PE=1 SV=3;>sp|Q15642-4|CIP4_HUMAN Isoform 4 of Cdc42-interacting protein 4 OS=Homo sapien 0.30 0.19 0.34 -0.02 0.04 0.08 0.00 -0.07 0.940654213 0.191012469 actin cytoskeleton organization;actin filament-based process;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular response to stimulus;cytoskeleton organization;endocytosis;establishment of localization;intracellular signal transduction;membrane invagination;membrane organization;organelle organization;regulation of biological process;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport;vesicle-mediated transport binding;lipid binding cell cortex;cell part;cell projection;cytoplasmic part;cytoskeleton;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;phagocytic cup;plasma membrane part;vacuole Insulin signaling pathway 5.22E-33 7 8 8 25.1

Q9UBT2;K7EPL2;B3KWB9;K7ES38;K7ESK7 SUMO-activating enzyme subunit 2 UBA2 >sp|Q9UBT2|SAE2_HUMAN SUMO-activating enzyme subunit 2 OS=Homo sapiens GN=UBA2 PE=1 SV=2;>tr|K7EPL2|K7EPL2_HUMAN SUMO-activating enzyme subunit 2 (Fragment) OS=Homo sapiens GN=UBA2 PE=4 SV=1;>tr|B3KWB9|B3KWB9_HUMAN SUMO-activating enzyme subunit 2 OS=Homo 0.23 0.02 0.07 0.09 0.20 -0.28 -0.23 -0.22 0.826284234 0.233987594 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein sumoylation adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;ion binding;ligase activity;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small protein activating enzyme activity;SUMO activating enzyme activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Ubiquitin mediated proteolysis 2.86E-35 5 8 8 15.3

P61081;M0QX69;M0QYI6 NEDD8-conjugating enzyme Ubc12 UBE2M >sp|P61081|UBC12_HUMAN NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1 0.29 -0.03 -0.81 -0.06 0.09 -0.25 0.25 -0.23 0.157960067 -0.1138908 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of neuron apoptosis;positive regulation of programmed cell death;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein neddylation;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of neuron apoptosis;regulation of programmed cell death "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;NEDD8 ligase activity;nucleotide binding;protein-glutamic acid ligase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;ribosomal S6-glutamic acid ligase activity;small conjugating protein ligase activity;ubiquitin-protein ligase activity" Ubiquitin mediated proteolysis 2.10E-32 3 8 8 43.2

Q9C0C9;K7ES11;H0YB81;K7EQ12 Ubiquitin-conjugating enzyme E2 O UBE2O >sp|Q9C0C9|UBE2O_HUMAN Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3;>tr|K7ES11|K7ES11_HUMAN Ubiquitin-conjugating enzyme E2 O (Fragment) OS=Homo sapiens GN=UBE2O PE=4 SV=1 0.16 -0.16 0.01 -0.37 0.16 -0.06 0.26 0.04 0.605352709 -0.191397985 "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small conjugating protein ligase activity;ubiquitin-protein ligase activity" Ubiquitin mediated proteolysis 2.95E-25 4 8 8 8.9

O95155-2;O95155;O95155-3;K7EP75;B1AQ61 Ubiquitin conjugation factor E4 B UBE4B >sp|O95155-2|UBE4B_HUMAN Isoform 2 of Ubiquitin conjugation factor E4 B OS=Homo sapiens GN=UBE4B;>sp|O95155|UBE4B_HUMAN Ubiquitin conjugation factor E4 B OS=Homo sapiens GN=UBE4B PE=1 SV=1;>sp|O95155-3|UBE4B_HUMAN Isoform 3 of Ubiquitin conjugation factor 0.14 -0.11 -0.35 -0.09 -0.11 0.22 0.53 0.15 0.765654697 -0.295869306 anatomical structure morphogenesis;apoptosis;cardiac muscle tissue morphogenesis;catabolic process;cell death;cell projection organization;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;developmental process;heart trabecular morphogenesis;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;muscle tissue morphogenesis;neuron projection development;primary metabolic process;programmed cell death;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;response to abiotic stimulus;response to endoplasmic reticulum stress;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;tissue morphogenesis;trabecula morphogenesis;ubiquitin-dependent protein catabolic process;ventricular cardiac muscle tissue morphogenesis;ventricular trabecular myocardium morphogenesis "acid-amino acid ligase activity;binding;catalytic activity;enzyme binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;protein binding;small conjugating protein ligase activity;ubiquitin-protein ligase activity;ubiquitin-ubiquitin ligase activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;ubiquitin ligase complex Protein processing in endoplasmic reticulum;Ubiquitin mediated proteolysis 5.33E-29 5 8 8 10

Q96TA2-3;Q96TA2-2;Q96TA2;R4GNA5;Q5T8D1;Q5T8D2 ATP-dependent zinc metalloprotease YME1L1 YME1L1 >sp|Q96TA2-3|YMEL1_HUMAN Isoform 3 of ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1;>sp|Q96TA2-2|YMEL1_HUMAN Isoform 2 of ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1;>sp|Q96TA2|YMEL1_HUMAN ATP-dependent zinc me -0.59 0.41 0.27 0.75 -0.34 -0.25 -1.74 -0.62 0.908652127 0.945869848 cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;macromolecule metabolic process;metabolic process;misfolded or incompletely synthesized protein catabolic process;mitochondrion organization;organelle organization;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 1.06E-152 6 8 8 15.2

Q96KR1;H0Y8W1 Zinc finger RNA-binding protein ZFR >sp|Q96KR1|ZFR_HUMAN Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 -0.20 0.71 0.10 0.66 0.36 0.35 -0.93 0.15 0.356814216 0.337186953 developmental process;multicellular organismal development;multicellular organismal processbinding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;RNA binding;transition metal ion binding;zinc ion binding cell part;chromosome;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 1.43E-71 2 8 8 13.5

Q96N67-4;Q96N67-3;Q96N67-5;Q96N67-2;Q96N67-6;Q96N67;Q96NI0;H0Y7L2;A2A369;Q8NF50-4;Q8NF50-3;Q8NF50-2;Q8NF50 Dedicator of cytokinesis protein 7 DOCK7 >sp|Q96N67-4|DOCK7_HUMAN Isoform 4 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7;>sp|Q96N67-3|DOCK7_HUMAN Isoform 3 of Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7;>sp|Q96N67-5|DOCK7_HUMAN Isoform 5 of Dedicator of cytokines 0.39 0.17 0.30 0.13 0.34 -0.09 -0.02 -0.12 0.78847367 0.223489929 activation of Rac GTPase activity;activation of Ras GTPase activity;activation of Rho GTPase activity;anatomical structure morphogenesis;axonogenesis;biological regulation;blood coagulation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;coagulation;cytoskeleton organization;developmental process;establishment of cell polarity;establishment of neuroblast polarity;establishment or maintenance of cell polarity;establishment or maintenance of neuroblast polarity;hemostasis;intracellular signal transduction;microtubule cytoskeleton organization;microtubule-based process;multicellular organismal process;neuron projection morphogenesis;organelle organization;pigmentation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of peptidyl-serine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of Rac GTPase activity;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of peptidyl-serine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Rho GTPase activity;response to stimulus;signal transduction;small GTPase mediated signal transduction binding;enzyme binding;enzyme regulator activity;GTPase binding;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity;protein binding;Rac GTPase binding;Ras GTPase binding;Rho GTPase binding;small GTPase binding axon;basal part of cell;cell part;cell projection;cell projection part;cytoplasmic part;cytosol;growth cone;intracellular part;neuron projection;site of polarized growth 2.51E-26 13 9 8 5.5

Q92538 Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 GBF1 >sp|Q92538|GBF1_HUMAN Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2 -0.01 -0.03 -0.05 -0.05 0.34 0.13 0.45 -0.17 0.67880522 -0.219589864 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;Golgi transport vesicle coating;Golgi vesicle transport;intracellular transport;organelle organization;post-Golgi vesicle-mediated transport;regulation of ARF protein signal transduction;regulation of biological process;regulation of cellular process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" ARF guanyl-nucleotide exchange factor activity;enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity;small GTPase regulator activity cell part;cis-Golgi network;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;Golgi stack;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;peroxisome;trans-Golgi network 1.07E-31 1 9 8 5.8

O75146;H0YH66 Huntingtin-interacting protein 1-related protein HIP1R >sp|O75146|HIP1R_HUMAN Huntingtin-interacting protein 1-related protein OS=Homo sapiens GN=HIP1R PE=1 SV=2 0.16 0.19 -0.04 -0.15 -0.11 0.09 0.17 0.18 0.145887123 -0.042689301 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;membrane invagination;membrane organization;receptor-mediated endocytosis;transport;vesicle-mediated transport actin binding;binding;cytoskeletal protein binding;lipid binding;phosphatidylinositol binding;phospholipid binding;protein binding cell part;clathrin coated vesicle membrane;clathrin-coated vesicle;coated pit;coated vesicle;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;vesicle;vesicle membrane 9.72E-42 2 9 8 12.3

P31942-2;P31942;P31942-3;B4DHY1;P31942-4;P31942-6;P31942-5 Heterogeneous nuclear ribonucleoprotein H3 HNRNPH3 >sp|P31942-2|HNRH3_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3;>sp|P31942|HNRH3_HUMAN Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2;>sp|P31942-3|HNRH3_HUMAN Isoform 3 of Heterog -0.05 0.99 0.16 0.94 0.23 0.38 -1.19 0.24 0.544345178 0.59047109 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex 5.95E-134 7 9 8 37.5

P49257 Protein ERGIC-53 LMAN1 >sp|P49257|LMAN1_HUMAN Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2 -0.14 0.15 -0.18 -0.14 0.78 0.27 -0.39 0.10 0.428637968 -0.26403752 biological regulation;blood coagulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;coagulation;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi organization;Golgi vesicle transport;hemostasis;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of organelle organization;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular process;regulation of organelle organization;transport;vesicle-mediated transport binding;carbohydrate binding;cation binding;ion binding;mannose binding;metal ion binding;monosaccharide binding;protein binding;sugar binding;unfolded protein binding cell part;coated vesicle membrane;contractile fiber part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;ER to Golgi transport vesicle membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;sarcomere;transport vesicle membrane;vesicle membrane Protein processing in endoplasmic reticulum 1.58E-39 1 9 8 19.8

P32119;A6NIW5;P32119-2 Peroxiredoxin-2 PRDX2 ">sp|P32119|PRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5;>tr|A6NIW5|A6NIW5_HUMAN Peroxiredoxin 2, isoform CRA_a OS=Homo sapiens GN=PRDX2 PE=2 SV=2" -0.06 -0.18 0.04 -0.05 0.01 0.11 0.49 0.17 0.962279412 -0.255761851 biological regulation;catabolic process;cellular catabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to oxygen radical;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;cellular response to superoxide;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;reactive oxygen species metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of neuron apoptosis;regulation of programmed cell death;removal of superoxide radicals;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to oxygen radical;response to reactive oxygen species;response to stimulus;response to stress;response to superoxide;superoxide metabolic process "antioxidant activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;peroxiredoxin activity;thioredoxin peroxidase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part 6.80E-81 3 9 8 41.4

Q5QPL9;Q9UKM9-2;Q9UKM9;Q5QPM1;Q5QPM0;Q5QPM2;E5RIX9 RNA-binding protein Raly RALY >tr|Q5QPL9|Q5QPL9_HUMAN RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1;>sp|Q9UKM9-2|RALY_HUMAN Isoform 1 of RNA-binding protein Raly OS=Homo sapiens GN=RALY;>sp|Q9UKM9|RALY_HUMAN RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 -0.23 1.12 0.11 1.09 0.00 0.62 -1.32 0.83 0.33077908 0.492885687 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;ribonucleoprotein complex;spliceosomal complex 1.96E-46 7 9 8 42.2

J3QQT2;J3KRX5;P18621;P18621-3;J3QS96;J3KRB3;J3QLC8;P18621-2;J3KSJ0 60S ribosomal protein L17 RPL17 >tr|J3QQT2|J3QQT2_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1;>tr|J3KRX5|J3KRX5_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1;>sp|P18621|RL17_HUMAN 60S ribosomal protein L17 OS=Homo sapiens -0.44 -0.01 0.02 0.05 -0.22 -0.52 -0.43 -0.48 1.019639533 0.316427517 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytosolic large ribosomal subunit;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;organelle part;ribonucleoprotein complex Ribosome 1.27E-78 9 9 8 48

P30740;B4DNT0 Leukocyte elastase inhibitor SERPINB1 >sp|P30740|ILEU_HUMAN Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1;>tr|B4DNT0|B4DNT0_HUMAN Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=2 SV=1 0.31 -0.02 0.43 -0.12 -0.16 0.34 0.34 0.21 0.053856127 -0.028036952 biological regulation;regulation of biological process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasm;extracellular region part;extracellular space;intracellular part Amoebiasis 1.33E-43 2 9 8 30.1

Q9Y277;Q9Y277-2;F5H740;E5RFP6;E5RJN6;E5RHZ6;E5RHE1;E5RK27;E5RFL1 Voltage-dependent anion-selective channel protein 3 VDAC3 >sp|Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1;>sp|Q9Y277-2|VDAC3_HUMAN Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3;>tr|F5H740|F5H740_HUMAN Voltage -0.28 0.94 -0.32 0.98 0.36 1.08 -1.26 0.64 0.066675221 0.122448705 adenine transport;cellular process;establishment of localization;nitrogen compound transport;nucleobase transport;nucleobase-containing compound transport;purine base transport;purine-containing compound transmembrane transport;transmembrane transport;transport anion channel activity;anion transmembrane transporter activity;binding;channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;nucleotide binding;passive transmembrane transporter activity;porin activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated ion channel activity;wide pore channel activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;pore complex;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease 3.09E-44 9 9 8 32.9

P31689;B7Z5C0;P31689-2;Q9H672-2;Q9H672 DnaJ homolog subfamily A member 1 DNAJA1 >sp|P31689|DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2;>tr|B7Z5C0|B7Z5C0_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=2 SV=1;>sp|P31689-2|DNJA1_HUMAN Isoform 2 of DnaJ homolog subfamily A member 0.28 0.12 -0.15 -0.07 -0.18 -0.49 0.40 -0.13 0.273737307 0.14673245 androgen receptor signaling pathway;biological regulation;cell motility;cellular component movement;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;gamete generation;intracellular receptor mediated signaling pathway;intracellular signal transduction;locomotion;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;primary metabolic process;protein folding;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;regulation of biological process;regulation of cellular process;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to heat;response to organic substance;response to stimulus;response to stress;response to temperature stimulus;response to topologically incorrect protein;response to unfolded protein;signal transduction;sperm motility;spermatogenesis;steroid hormone receptor signaling pathway adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cation binding;ion binding;lipoprotein particle receptor binding;low-density lipoprotein particle receptor binding;metal ion binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding cell part;membrane Protein processing in endoplasmic reticulum 1.14E-60 5 10 8 30.5

Q86TI2;Q86TI2-4;Q86TI2-2;M0R2A8;M0R3C4;M0R2G6;M0R0I1;M0QXG6 Dipeptidyl peptidase 9 DPP9 >sp|Q86TI2|DPP9_HUMAN Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9 PE=1 SV=3;>sp|Q86TI2-4|DPP9_HUMAN Isoform 3 of Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9;>sp|Q86TI2-2|DPP9_HUMAN Isoform 2 of Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9;>tr|M0R2A 0.36 -0.15 -0.02 -0.39 0.25 0.12 0.67 0.14 0.742134265 -0.348788633 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "aminopeptidase activity;catalytic activity;exopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type peptidase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane 1.18E-40 8 10 8 15.9

H0Y507;Q5TCZ1-3;Q5TCZ1;Q5TCZ1-2;F5GZ35;B7Z9C6;F8WCK5 SH3 and PX domain-containing protein 2A SH3PXD2A >tr|H0Y507|H0Y507_HUMAN SH3 and PX domain-containing protein 2A (Fragment) OS=Homo sapiens GN=SH3PXD2A PE=4 SV=1;>sp|Q5TCZ1-3|SPD2A_HUMAN Isoform 3 of SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A;>sp|Q5TCZ1|SPD2A_HUMAN SH3 and PX dom 0.29 0.05 -0.05 -0.19 0.17 0.35 0.28 -0.04 0.528477964 -0.166274291 cell communication;cellular metabolic process;cellular process;metabolic process;reactive oxygen species metabolic process;superoxide metabolic process binding;lipid binding;phosphatidylinositol binding;phospholipid binding cell junction;cell part;cell projection;cytoplasm;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;podosome;protein complex 1.52E-40 7 10 8 13.6

Q6IBS0;D6RG15;H0Y858 Twinfilin-2 TWF2 >sp|Q6IBS0|TWF2_HUMAN Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=1 SV=2;>tr|D6RG15|D6RG15_HUMAN Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=2 SV=1 -0.07 -0.19 0.01 0.11 0.05 0.02 0.34 -0.03 0.531487502 -0.134074703 actin filament capping;activation of immune response;activation of innate immune response;barbed-end actin filament capping;biological regulation;cell communication;cell projection organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to growth factor stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to organic substance;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;defense response;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;maintenance of location;maintenance of protein location;MyD88-dependent toll-like receptor signaling pathway;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;pattern recognition receptor signaling pathway;positive regulation of axon extension;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of defense response;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of immune response;positive regulation of immune system process;positive regulation of inflammatory response;positive regulation of innate immune response;positive regulation of lamellipodium assembly;positive regulation of neurogenesis;positive regulation of neuron projection development;positive regulation of response to external stimulus;positive regulation of response to stimulus;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell projection size;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular localization;regulation of cellular process;regulation of cytokine production;regulation of cytokine secretion;regulation of cytoskeleton organization;regulation of defense response;regulation of developmental growth;regulation of developmental process;regulation of establishment of protein localization;regulation of extent of cell growth;regulation of growth;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of innate immune response;regulation of lamellipodium assembly;regulation of localization;regulation of microvillus length;regulation of microvillus organization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein localization;regulation of protein polymerization;regulation of protein secretion;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of transport;response to biotic stimulus;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to growth factor stimulus;response to molecule of bacterial origin;response to nutrient;response to nutrient levels;response to organic substance;response to retinoic acid;response to stimulus;response to stress;response to vitamin;response to vitamin A;sequestering of actin monomers;signal transduction;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway "actin binding;actin monomer binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cytoskeletal protein binding;lipid binding;molecular transducer activity;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;ribonucleotide binding;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity" cell part;cell projection;cell projection part;contractile fiber;cytoplasmic part;cytoskeleton;filopodium;growth cone;integral to membrane;intracellular;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;lamellipodium;membrane part;microvillus;myofibril;non-membrane-bounded organelle;organelle;organelle part;perinuclear region of cytoplasm;site of polarized growth;stereocilium 1.88E-74 3 10 8 43

Q9UBF2;F6X838;H7C1T7 Coatomer subunit gamma-2 COPG2 >sp|Q9UBF2|COPG2_HUMAN Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1 -0.24 -0.05 0.13 0.26 -0.25 0.00 0.10 -0.26 0.355369481 0.126068435 "cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle-mediated transport" structural molecule activity cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;protein complex;vesicle coat 3.92E-62 3 11 8 15

G5E9S8;Q07866-8;G3V2E7;Q07866-2;Q07866-3;Q07866;F8W6L3;Q07866-7;G3V3H3;Q07866-5;Q07866-10;Q07866-6;G3V5R9;Q07866-4;Q07866-9;E7EVH7;H0YJU9;H0YJL0;H0YJT3;H0YG16;G3V2P7;H0YGB8 Kinesin light chain 1 KLC1 >tr|G5E9S8|G5E9S8_HUMAN Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=2 SV=1;>sp|Q07866-8|KLC1_HUMAN Isoform S of Kinesin light chain 1 OS=Homo sapiens GN=KLC1;>tr|G3V2E7|G3V2E7_HUMAN Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=2 SV=1;>sp|Q07866-2| 0.03 0.16 0.00 0.00 0.41 0.45 0.21 0.06 1.020058471 -0.233528579 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;blood coagulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;coagulation;hemostasis;immune system process;interaction with host;interspecies interaction between organisms;macromolecular complex disassembly;macromolecular complex subunit organization;microtubule-based movement;microtubule-based process;multicellular organismal process;multi-organism process;regulation of biological quality;regulation of body fluid levels;reproductive process;ribonucleoprotein complex disassembly;ribonucleoprotein complex subunit organization;stress granule disassembly;viral reproductive process;virus-host interaction "catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;pyrophosphatase activity" cell part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;kinesin complex;macromolecular complex;microtubule;microtubule associated complex;organelle part;protein complex 2.84E-49 22 12 8 26

P20020-6;P20020-3;P20020-4;P20020;P20020-5;P20020-2;E7ERY9;H0Y7S3;Q01814-6;Q01814-8;Q01814-5;Q01814;H0YHH6;F8W1V5 Plasma membrane calcium-transporting ATPase 1 ATP2B1 >sp|P20020-6|AT2B1_HUMAN Isoform K of Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1;>sp|P20020-3|AT2B1_HUMAN Isoform B of Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1;>sp|P20020-4|AT2B1_HUMAN Isoform C o 0.27 -0.06 -0.22 -0.19 1.29 0.91 0.50 -0.05 0.979219748 -0.711040487 amine metabolic process;anatomical structure development;auditory receptor cell stereocilium organization;behavior;biological regulation;biomineral tissue development;blood coagulation;body fluid secretion;calcium ion homeostasis;cation homeostasis;cell differentiation;cell differentiation in hindbrain;cell projection organization;cellular amine metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine metabolic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;central nervous system neuron differentiation;cerebellar granule cell differentiation;cerebellar Purkinje cell differentiation;cGMP metabolic process;chemical homeostasis;coagulation;cochlea development;cyclic nucleotide metabolic process;cytosolic calcium ion homeostasis;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection of mechanical stimulus involved in sensory perception;detection of mechanical stimulus involved in sensory perception of sound;detection of stimulus;detection of stimulus involved in sensory perception;developmental process;divalent inorganic cation homeostasis;establishment of localization;hemostasis;heterocycle metabolic process;homeostatic process;indolalkylamine metabolic process;indole-containing compound metabolic process;inner ear receptor stereocilium organization;ion homeostasis;lactation;locomotion;locomotory behavior;metabolic process;metal ion homeostasis;multicellular organismal process;multicellular organismal reproductive process;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organelle organization;otolith mineralization;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of ion transport;positive regulation of transport;primary metabolic process;purine nucleotide metabolic process;purine-containing compound metabolic process;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of calcium ion transport;regulation of cell communication;regulation of cell size;regulation of cellular component size;regulation of cellular process;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of multicellular organismal process;regulation of neurological system process;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;reproductive process;response to abiotic stimulus;response to external stimulus;response to mechanical stimulus;response to stimulus;secretion;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;serotonin metabolic process;small molecule metabolic process;synapse organization;system process;tissue development;transport "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;calcium ion binding;calcium ion transmembrane transporter activity;calcium-dependent ATPase activity;calcium-transporting ATPase activity;calmodulin binding;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;divalent inorganic cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;metal ion transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;PDZ domain binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;protein domain specific binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" apical plasma membrane;cell body;cell part;cell projection;cilium;cytoplasm;cytoplasmic part;endoplasmic reticulum;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;neuronal cell body;organelle;plasma membrane;plasma membrane part Calcium signaling pathway;Pancreatic secretion;Salivary secretion 2.20E-152 14 17 8 19.6

O00154-4;O00154-6;O00154-7;O00154;O00154-2;O00154-3;O00154-5;B4DUX0;K7EKP8;F5GWE2 Cytosolic acyl coenzyme A thioester hydrolase ACOT7 >sp|O00154-4|BACH_HUMAN Isoform 4 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7;>sp|O00154-6|BACH_HUMAN Isoform 6 of Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7;>sp|O00154-7|BACH_HUMAN

Isoform 7 of Cyt 0.56 0.24 -0.44 -0.83 0.26 0.13 0.41 0.11 0.441594445 -0.347428624 carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid catabolic process;fatty acid metabolic process;lipid catabolic process;lipid metabolic process;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "acyl-CoA thioesterase activity;binding;carboxylesterase activity;carboxylic acid binding;carboxylic ester hydrolase activity;catalytic activity;CoA hydrolase activity;coenzyme binding;cofactor binding;fatty acid binding;fatty-acyl-CoA binding;hydrolase activity;hydrolase activity, acting on ester bonds;lipid binding;monocarboxylic acid binding;palmitoyl-CoA hydrolase activity;thiolester hydrolase activity" cell body;cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;neuron projection;organelle Biosynthesis of unsaturated fatty acids 1.07E-46 10 9 9 34.3

Q9Y4W6;K7EP56;B7Z651;E9PHW9;Q01484-5;Q01484-2;I6L894;Q01484 AFG3-like protein 2 AFG3L2 >sp|Q9Y4W6|AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 -0.39 -0.03 0.04 0.44 -0.04 0.11 -0.92 -0.45 0.500278843 0.341639854 anatomical structure development;anatomical structure morphogenesis;atrial septum development;axon ensheathment;axon guidance;axonogenesis;biological regulation;calcium ion homeostasis;calcium ion transport;calcium-mediated signaling;cardiac muscle contraction;cardiac septum development;catabolic process;cation homeostasis;cation transport;cell death;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to stimulus;chemical homeostasis;chemotaxis;cristae formation;death;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;ensheathment of neurons;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in membrane;establishment of protein localization in plasma membrane;homeostatic process;inner mitochondrial membrane organization;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;ion transport;localization;locomotion;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;membrane fusion;membrane organization;metabolic process;metal ion homeostasis;metal ion transport;mitochondrial fusion;mitochondrial membrane organization;mitochondrial protein processing;mitochondrion organization;multicellular organismal process;muscle contraction;muscle system process;myelination;nerve development;neuromuscular junction development;neuron projection morphogenesis;organelle fusion;organelle organization;plasma membrane organization;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of gene expression;positive regulation of ion transport;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of potassium ion transport;positive regulation of transport;posttranscriptional regulation of gene expression;primary metabolic process;protein catabolic process;protein localization;protein localization at cell surface;protein localization in endoplasmic reticulum;protein localization in membrane;protein localization in plasma membrane;protein localization to organelle;protein maturation;protein metabolic process;protein processing;protein stabilization;protein targeting;protein targeting to plasma membrane;protein transport;proteolysis;reflex;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cellular localization;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of heart contraction;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transport;regulation of localization;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of membrane repolarization;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of potassium ion transport;regulation of protein stability;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of striated muscle contraction;regulation of system process;regulation of transport;regulation of ventricular cardiomyocyte membrane repolarization;response to chemical stimulus;response to external stimulus;response to stimulus;righting reflex;sarcoplasmic reticulum calcium ion transport;second-messenger-mediated signaling;signal transduction;striated muscle contraction;synapse organization;system process;taxis;transport;T-tubule organization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase binding;binding;binding, bridging;catalytic activity;cation binding;channel regulator activity;endopeptidase activity;enzyme binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;ion channel binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;potassium channel regulator activity;protein binding;protein binding, bridging;purine nucleotide binding;purine nucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transition metal ion binding;unfolded protein binding;zinc ion binding" apical plasma membrane;basolateral plasma membrane;cell junction;cell part;cell-cell contact zone;cell-cell junction;contractile fiber part;costamere;cytoplasmic part;cytoskeleton;cytosol;integral to membrane;integral to plasma membrane;intercalated disc;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;M band;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;non-membrane-bounded organelle;organelle;organelle inner membrane;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;postsynaptic membrane;synapse part;synaptic membrane;T-tubule;Z disc 8.93E-25 8 9 9 11.9

P53367;P53367-2;B4DS69 Arfaptin-1 ARFIP1 >sp|P53367|ARFP1_HUMAN Arfaptin-1 OS=Homo sapiens GN=ARFIP1 PE=1 SV=2;>sp|P53367-2|ARFP1_HUMAN Isoform A of Arfaptin-1 OS=Homo sapiens GN=ARFIP1 -0.02 0.03 0.15 -0.12 0.12 -0.17 0.13 -0.06 0.023701938 0.00658457 biological regulation;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of localization;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of secretion;regulation of transport;transport cell part;cytoplasmic part;cytosol;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part 2.09E-42 3 9 9 32.4

P36543;P36543-3;P36543-2;C9J8H1;Q96A05 V-type proton ATPase subunit E 1 ATP6V1E1 >sp|P36543|VATE1_HUMAN V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1;>sp|P36543-3|VATE1_HUMAN Isoform 3 of V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1;>sp|P36543-2|VATE1_HUMAN Isoform 2 of V-type proton ATPase subu -0.22 0.56 -1.59 0.87 -1.25 0.56 -0.30 0.64 0.004920049 -0.010778453 "ATP hydrolysis coupled proton transport;biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;organelle organization;phagosome maturation;protein transport;proton transport;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrogen-exporting ATPase activity, phosphorylative mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "acrosomal vesicle;apical plasma membrane;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microvillus;mitochondrion;organelle;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain;stored secretory granule;vesicle" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection 3.56E-44 5 9 9 36.3

B4DUS9;O95861;O95861-2;B4DPS5;A6NF51;F8W1J0;F8VZG4;F8VVW8;F8VRY7 "3(2),5-bisphosphate nucleotidase 1" BPNT1 ">tr|B4DUS9|B4DUS9_HUMAN 3(2),5-bisphosphate nucleotidase 1 OS=Homo sapiens

GN=BPNT1 PE=2 SV=1;>sp|O95861|BPNT1_HUMAN 3(2),5-bisphosphate nucleotidase 1 OS=Homo sapiens GN=BPNT1 PE=1 SV=1;>sp|O95861-2|BPNT1_HUMAN Isoform 2 of 3(2),5-bisphosphate nu" -0.24 -0.03 -1.05 0.05 -0.87 0.20 0.60 0.39 0.391111505 -0.398386154 3'-phosphoadenosine 5'-phosphosulfate metabolic process;anatomical structure development;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;glycerolipid metabolic process;glycerophospholipid metabolic process;heterocycle metabolic process;lipid metabolic process;lipid modification;lipid phosphorylation;metabolic process;nervous system development;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphatidylinositol metabolic process;phosphatidylinositol phosphorylation;phospholipid metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;purine nucleoside bisphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside bisphosphate metabolic process;purine-containing compound metabolic process;ribonucleoside bisphosphate metabolic process;small molecule metabolic process;sulfur compound metabolic process;system development;xenobiotic metabolic process "3'(2'),5'-bisphosphate nucleotidase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;inositol bisphosphate phosphatase activity;inositol or phosphatidylinositol phosphatase activity;inositol phosphate phosphatase activity;inositol-1,4-bisphosphate 1-phosphatase activity;ion binding;magnesium ion binding;metal ion binding;nucleotidase activity;phosphatase activity;phosphoric ester hydrolase activity" cell part;cytoplasmic part;cytosol;intracellular part Sulfur metabolism 2.35E-71 9 9 9 37.5

Q03701;C9J9W7 CCAAT/enhancer-binding protein zeta CEBPZ >sp|Q03701|CEBPZ_HUMAN CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3 -0.18 1.03 0.18 1.17 -0.26 0.48 -1.28 0.48 0.553483302 0.695564408 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 6.01E-67 2 9 9 11.9

O76031;H0YK07;H0YM48 "ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial" CLPX ">sp|O76031|CLPX_HUMAN ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2" -0.26 0.05 0.13 0.17 0.02 -0.24 -0.59 -0.03 0.577396369 0.234860214 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cation binding;enzyme activator activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;peptidase activator activity;peptidase regulator activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endopeptidase Clp complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial endopeptidase Clp complex;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;protein complex Cell cycle - Caulobacter 1.39E-33 3 9 9 18

Q99715-4;D6RGG3;Q99715;Q99715-2;H0Y4P7;H0Y5N9 Collagen alpha-1(XII) chain COL12A1 >sp|Q99715-4|COCA1_HUMAN Isoform 4 of Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1;>tr|D6RGG3|D6RGG3_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=2 SV=1;>sp|Q99715|COCA1_HUMAN Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL10.47 0.29 -1.52 -0.89 -0.05 0.58 0.95 1.20 0.84387682 -1.082141628 anatomical structure development;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen fibril organization;collagen metabolic process;developmental process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;skeletal system development;system development extracellular matrix structural constituent;extracellular matrix structural constituent conferring tensile strength;structural molecule activity anchoring collagen;cell part;collagen;collagen type XII;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;FACIT collagen;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vesicle Protein digestion and absorption 4.45E-38 6 9 9 4.6

P61201;P61201-2;B4DIH5;H0YKU5;H0YM03 COP9 signalosome complex subunit 2 COPS2 >sp|P61201|CSN2_HUMAN COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1;>sp|P61201-2|CSN2_HUMAN Isoform 2 of COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2;>tr|B4DIH5|B4DIH5_HUMAN COP9 signalosome complex subunit 2 OS=Homo 0.23 0.05 0.03 0.02 0.07 -0.15 -0.13 -0.13 0.999754177 0.169712487 "biological regulation;biosynthetic process;cell differentiation;cell proliferation;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cullin deneddylation;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;neuron differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein deneddylation;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" molecular transducer activity;protein binding transcription factor activity;signal transducer activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;protein complex;signalosome 7.39E-39 5 9 9 20.8

Q92905;E5RHF2;E5RHH5 COP9 signalosome complex subunit 5 COPS5 >sp|Q92905|CSN5_HUMAN COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4 -0.04 0.04 0.15 0.05 0.22 -0.13 -0.01 -0.16 0.288020503 0.070288468 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cullin deneddylation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein deneddylation;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of gene expression;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" "binding;catalytic activity;cation binding;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;nucleic acid binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding transcription factor activity;RNA binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;eukaryotic translation initiation factor 3 complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;organelle part;perinuclear region of cytoplasm;protein complex;signalosome 2.14E-81 3 9 9 30.5

Q99829;B0QZ18;F2Z2V0;A6PVH9;E7ENH5;Q5JX58;Q5JX59;Q5JX60;Q5JX44;Q5JX56;H0Y524;Q5JX45;Q5JX55;Q5JX61;Q5JX52;Q5JX54 Copine-1 CPNE1 >sp|Q99829|CPNE1_HUMAN Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1;>tr|B0QZ18|B0QZ18_HUMAN Copine-1 OS=Homo sapiens GN=CPNE1 PE=2 SV=1;>tr|F2Z2V0|F2Z2V0_HUMAN Copine-1 (Fragment) OS=Homo sapiens GN=CPNE1 PE=2 SV=1;>tr|A6PVH9|A6PVH9_HUMAN Copine-1 OS=Homo s 0.13 -0.21 0.19 0.10 0.51 0.24 0.15 -0.42 0.111364758 -0.067782255 cellular process;establishment of localization;lipid metabolic process;metabolic process;primary metabolic process;transport;vesicle-mediated transport binding;calcium-dependent phospholipid binding;lipid binding;phosphatidylserine binding;phospholipid binding;transporter activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.55E-84 16 9 9 19.7

Q8IXB1;Q8IXB1-2;E7EP04;Q3B7W8 DnaJ homolog subfamily C member 10 DNAJC10 >sp|Q8IXB1|DJC10_HUMAN DnaJ homolog subfamily C member 10 OS=Homo sapiens GN=DNAJC10 PE=1 SV=2;>sp|Q8IXB1-2|DJC10_HUMAN Isoform 2 of DnaJ homolog subfamily C member 10 OS=Homo sapiens GN=DNAJC10 -0.08 -0.09 -0.16 -0.05 -0.13 0.13 0.22 0.11 0.941926027 -0.173929701 apoptosis;apoptosis in response to endoplasmic reticulum stress;biological regulation;catabolic process;cell death;cell redox homeostasis;cellular catabolic process;cellular homeostasis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;death;ER-associated protein catabolic process;glycerol ether metabolic process;homeostatic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;organic ether metabolic process;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biological quality;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;small molecule metabolic process;ubiquitin-dependent protein catabolic process "ATPase activator activity;ATPase regulator activity;binding;catalytic activity;chaperone binding;disulfide oxidoreductase activity;electron carrier activity;enzyme activator activity;enzyme regulator activity;misfolded protein binding;nucleoside-triphosphatase regulator activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein binding;protein disulfide oxidoreductase activity" cell part;cytoplasmic part;endoplasmic reticulum chaperone complex;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular region;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-enclosed lumen;organelle lumen;organelle part;protein complex Protein processing in endoplasmic reticulum 1.04E-66 4 9 9 12.9

O75165;H0YA63 DnaJ homolog subfamily C member 13 DNAJC13 >sp|O75165|DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens GN=DNAJC13 PE=1 SV=5 0.14 -0.04 -0.23 -0.03 0.45 0.17 0.27 -0.36 0.368345705 -0.172783962 3.01E-44 2 9 9 5.7

Q9NTX5-3;Q9NTX5-6;Q9NTX5-2;Q9NTX5;H0Y5L2;Q9NTX5-4;H0Y525;H0YCS9;J3KP84;E9PPG7;E9PRU6;F2Z2D6;Q9NTX5-5;E9PJS8;E9PLY6 Ethylmalonyl-CoA decarboxylase ECHDC1 >sp|Q9NTX5-3|ECHD1_HUMAN Isoform 3 of Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1;>sp|Q9NTX5-6|ECHD1_HUMAN Isoform 6 of Ethylmalonyl-CoA decarboxylase OS=Homo sapiens GN=ECHDC1;>sp|Q9NTX5-2|ECHD1_HUMAN Isoform 2 of Ethylmalonyl-CoA decarboxyla 0.05 -0.11 -0.02 -0.05 0.00 -0.09 0.28 0.01 0.390538536 -0.083803795 carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;lyase activity;methylmalonyl-CoA decarboxylase activity cell part;cytoplasmic part;cytosol;intracellular part 6.10E-175 15 9 9 50.9

Q9UI10-3;Q9UI10;Q9UI10-2;E7ERK9;H7C2L8;F8W8L6 Translation initiation factor eIF-2B subunit delta EIF2B4 >sp|Q9UI10-3|EI2BD_HUMAN Isoform 3 of Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4;>sp|Q9UI10|EI2BD_HUMAN Translation initiation factor eIF-2B subunit delta OS=Homo sapiens GN=EIF2B4 PE=1 SV=2;>sp|Q9UI10-2|EI2BD_HUMAN Isofor 0.16 -0.01 0.23 -0.02 -0.06 -0.14 0.00 -0.27 1.047437558 0.211043625 anatomical structure development;axon ensheathment;biological regulation;cell development;cellular developmental process;cellular metabolic process;cellular process;cellular response to stimulus;cellular response to stress;developmental process;ensheathment of neurons;glial cell development;metabolic process;myelination;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;negative regulation of translation in response to stress;negative regulation of translational initiation;negative regulation of translational initiation in response to stress;oligodendrocyte development;ovarian follicle development;ovulation cycle process;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translation in response to stress;regulation of translational initiation;regulation of translational initiation in response to stress;response to abiotic stimulus;response to carbohydrate stimulus;response to chemical stimulus;response to endogenous stimulus;response to glucose stimulus;response to heat;response to hexose stimulus;response to hormone stimulus;response to monosaccharide stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;response to temperature stimulus;rhythmic process;translational initiation "binding;nucleic acid binding;protein binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity;translation initiation factor binding" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 2B complex;intracellular part;macromolecular complex;protein complex RNA transport 6.02E-35 6 9 9 27.6

P55010;H0YLZ1;H0YN40;H0YK29;H0YK11;H0YMJ8;H0YM54 Eukaryotic translation initiation factor 5 EIF5 >sp|P55010|IF5_HUMAN Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2 0.06 -0.08 0.14 -0.09 -0.17 -0.60 0.05 -0.49 0.827684006 0.306412394 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;RNA metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part RNA transport 5.28E-48 7 9 9 22.3

Q9NZ08;Q9NZ08-2;H0Y9X5 Endoplasmic reticulum aminopeptidase 1 ERAP1 >sp|Q9NZ08|ERAP1_HUMAN Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 PE=1 SV=3;>sp|Q9NZ08-2|ERAP1_HUMAN Isoform 2 of Endoplasmic reticulum aminopeptidase 1 OS=Homo sapiens GN=ERAP1 0.17 -0.32 -0.13 -0.34 0.10 -0.17 0.62 0.33 0.789047002 -0.377170088 anatomical structure formation involved in morphogenesis;angiogenesis;antigen processing and presentation;antigen processing and presentation of endogenous antigen;antigen processing and presentation of endogenous peptide antigen;antigen processing and presentation of endogenous peptide antigen via MHC class I;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;cell differentiation;cellular developmental process;cellular process;developmental process;fat cell differentiation;immune system process;macromolecule metabolic process;membrane protein ectodomain proteolysis;membrane protein proteolysis;metabolic process;multi-organism process;positive regulation of angiogenesis;positive regulation of biological process;positive regulation of developmental process;primary metabolic process;protein metabolic process;proteolysis;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of biological quality;regulation of blood pressure;regulation of defense response;regulation of developmental process;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of response to stimulus;regulation of response to stress;response to bacterium;response to biotic stimulus;response to other organism;response to stimulus "aminopeptidase activity;binding;catalytic activity;cation binding;cytokine receptor binding;exopeptidase activity;growth factor receptor binding;hydrolase activity;interleukin-1 receptor binding;interleukin-1, Type II receptor binding;ion binding;metal ion binding;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;receptor binding;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular region;integral to membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle membrane;organelle part 4.62E-42 3 9 9 11.9

P10768;H7BZT7 S-formylglutathione hydrolase ESD >sp|P10768|ESTD_HUMAN S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2;>tr|H7BZT7|H7BZT7_HUMAN S-formylglutathione hydrolase (Fragment) OS=Homo sapiens GN=ESD PE=4 SV=1 -0.21 -0.14 0.02 0.03 0.28 -0.17 0.25 -0.17 0.354279893 -0.122996221 aldehyde catabolic process;catabolic process;cellular aldehyde metabolic process;cellular catabolic process;cellular metabolic process;cellular process;formaldehyde catabolic process;formaldehyde metabolic process;metabolic process;small molecule catabolic process;small molecule metabolic process "carboxylesterase activity;carboxylic ester hydrolase activity;catalytic activity;deacetylase activity;hydrolase activity;hydrolase activity, acting on ester bonds;methylumbelliferyl-acetate deacetylase activity;S-formylglutathione hydrolase activity;thiolester hydrolase activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;vesicle Methane metabolism 7.16E-113 2 9 9 39.7

Q8IY81 pre-rRNA processing protein FTSJ3 FTSJ3 >sp|Q8IY81|SPB1_HUMAN pre-rRNA processing protein FTSJ3 OS=Homo sapiens GN=FTSJ3 PE=1 SV=2 -0.30 0.99 0.18 0.88 -0.21 0.16 -1.11 0.26 0.642783387 0.660243854 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;primary metabolic process;RNA metabolic process;RNA methylation;RNA modification;RNA processing;rRNA metabolic process;rRNA processing;small molecule metabolic process "catalytic activity;methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 8.72E-44 1 9 9 13.7

Q5T3Q7;Q9H583;Q6P664 HEAT repeat-containing protein 1 HEATR1 >tr|Q5T3Q7|Q5T3Q7_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=2 SV=1;>sp|Q9H583|HEAT1_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3 0.08 0.90 -0.02 0.66 -0.24 -0.11 -0.79 0.10 0.971317173 0.666994661 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complexRibosome biogenesis in eukaryotes 4.22E-25 3 9 9 5.3

O14964-2;O14964;I3L1P5;I3L1E3;I3L165 Hepatocyte growth factor-regulated tyrosine kinase substrate HGS >sp|O14964-2|HGS_HUMAN Isoform 2 of Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS;>sp|O14964|HGS_HUMAN Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1;>tr|I3L1P5|I3L1P5_HUM 0.15 -0.08 0.33 -0.30 0.35 0.15 0.32 0.03 0.494768166 -0.186131053 biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;endosome to lysosome transport;endosome transport;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;lysosomal transport;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of intracellular protein kinase cascade;negative regulation of JAK-STAT cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;protein transport;regulation of biological process;regulation of catabolic process;regulation of cell communication;regulation of cell proliferation;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of intracellular protein kinase cascade;regulation of JAK-STAT cascade;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vacuolar transport;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;early endosome;early endosome membrane;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome membrane;membrane;membrane-bounded organelle;membrane-bounded vesicle;multivesicular body membrane;organelle;organelle membrane;organelle part;stored secretory granule;vesicle Endocytosis;Phagosome 8.55E-35 5 9 9 15.8

P61604;B8ZZL8;B8ZZ54 "10 kDa heat shock protein, mitochondrial" HSPE1 ">sp|P61604|CH10_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2;>tr|B8ZZL8|B8ZZL8_HUMAN 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=2 SV=1" 0.07 -0.07 -0.49 -0.17 0.27 0.16 0.04 -0.46 0.335087284 -0.168640813 activation of caspase activity;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;chaperone binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part 1.97E-95 3 9 9 68.6

P17931;G3V3R6 Galectin-3 LGALS3 >sp|P17931|LEG3_HUMAN Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5;>tr|G3V3R6|G3V3R6_HUMAN Galectin-3 OS=Homo sapiens GN=LGALS3 PE=2 SV=1 -0.06 -0.01 0.30 0.14 0.45 0.45 -0.06 -0.01 0.264091265 -0.111205839 anatomical structure development;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;developmental process;extracellular matrix organization;extracellular structure organization;immune response;immune system process;innate immune response;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;response to stimulus;response to stress;RNA metabolic process;RNA processing;RNA splicing;skeletal system development;system development binding;carbohydrate binding cell part;cytoplasmic part;extracellular matrix;extracellular region part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;nuclear part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane;proteinaceous extracellular matrix;ribonucleoprotein complex;spliceosomal complex 1.33E-51 2 9 9 35.2

Q9H9A6 Leucine-rich repeat-containing protein 40 LRRC40 >sp|Q9H9A6|LRC40_HUMAN Leucine-rich repeat-containing protein 40 OS=Homo sapiens GN=LRRC40 PE=1 SV=1 0.11 -0.03 -0.01 0.04 -0.06 -0.27 0.21 -0.50 0.488520547 0.18205961 5.05E-39 1 9 9 21.9

P55196-1;P55196;A8MQ02;J3KN01;P55196-5;P55196-2;P55196-6;Q5TIG5;P55196-3;C9JX92;H0Y8L4;H0Y7R8;H0Y948;F8W9I4;E9PFY5 Afadin MLLT4 >sp|P55196-1|AFAD_HUMAN Isoform 2 of Afadin OS=Homo sapiens GN=MLLT4;>sp|P55196|AFAD_HUMAN Afadin OS=Homo sapiens GN=MLLT4 PE=1 SV=3;>tr|A8MQ02|A8MQ02_HUMAN Afadin OS=Homo sapiens GN=MLLT4 PE=2 SV=1;>tr|J3KN01|J3KN01_HUMAN Afadin OS=Homo sapiens GN=MLLT4 P 0.46 0.15 0.25 -0.05 -0.41 -0.42 0.09 -0.18 1.130902796 0.432354833 adherens junction organization;biological adhesion;biological regulation;cell adhesion;cell communication;cell junction assembly;cell junction organization;cell-cell junction organization;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;signaling binding;protein binding;protein C-terminus binding adherens junction;anchoring junction;apical part of cell;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane Adherens junction;Leukocyte transendothelial migration;Tight junction 6.98E-63 15 9 9 7

P53602;H3BP35;H3BQ47;H3BRZ1;H3BVC4 Diphosphomevalonate decarboxylase MVD >sp|P53602|MVD1_HUMAN Diphosphomevalonate decarboxylase OS=Homo sapiens GN=MVD PE=1

SV=1;>tr|H3BP35|H3BP35_HUMAN Diphosphomevalonate decarboxylase (Fragment) OS=Homo sapiens GN=MVD PE=2 SV=1 0.36 -0.07 0.12 -0.05 -0.46 -0.32 0.49 -0.17 0.352073823 0.205184766 alcohol metabolic process;biological regulation;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;isoprenoid biosynthetic process;isoprenoid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;diphosphomevalonate decarboxylase activity;identical protein binding;kinase activity;lyase activity;nucleotide binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part Terpenoid backbone biosynthesis 1.48E-52 5 9 9 36.2

Q16795;F5H0J3;F5GY40;H3BRM9 "NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial" NDUFA9">sp|Q16795|NDUA9_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=NDUFA9 PE=1 SV=2" -0.35 0.96 -0.82 0.96 -1.04 0.59 -1.55 0.04 0.408168983 0.669815251 "biosynthetic process;cation transport;cellular metabolic process;cellular process;electron transport chain;establishment of localization;generation of precursor metabolites and energy;ion transport;lipid biosynthetic process;lipid metabolic process;metabolic process;metal ion transport;mitochondrial electron transport, NADH to ubiquinone;monovalent inorganic cation transport;oxidation-reduction process;primary metabolic process;respiratory electron transport chain;small molecule metabolic process;sodium ion transport;steroid biosynthetic process;steroid metabolic process;transport" "3-beta-hydroxy-delta5-steroid dehydrogenase activity;binding;catalytic activity;coenzyme binding;cofactor binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;NADH dehydrogenase complex;organelle lumen;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 4.89E-43 4 9 9 31.3

P30419;P30419-2;K7EN82;B7Z8J4;B4DXS1;Q5VUC6;F5H594;O60551;Q5VUC7;K7EN42 Glycylpeptide N-tetradecanoyltransferase 1 NMT1 >sp|P30419|NMT1_HUMAN Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens GN=NMT1 PE=1 SV=2;>sp|P30419-2|NMT1_HUMAN Isoform Short of Glycylpeptide N-tetradecanoyltransferase 1 OS=Homo sapiens GN=NMT10.16 -0.05 -0.14 -0.08 0.06 -0.15 0.26 -0.14 0.112667975 -0.037035943 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;egress of virus within host cell;macromolecule metabolic process;macromolecule modification;metabolic process;N-terminal protein amino acid modification;N-terminal protein lipidation;N-terminal protein myristoylation;primary metabolic process;protein acylation;protein lipidation;protein lipoylation;protein maturation;protein metabolic process;protein modification process;protein myristoylation;protein processing;protein-cofactor linkage;reproductive process;viral protein processing;viral reproductive process;virion assembly "catalytic activity;glycylpeptide N-tetradecanoyltransferase activity;myristoyltransferase activity;N-acyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" actin cytoskeleton;cell junction;cell part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;organelle;plasma membrane 2.10E-85 10 9 9 21.6

Q7Z417;A1L3A6 Nuclear fragile X mental retardation-interacting protein 2 NUFIP2 >sp|Q7Z417|NUFP2_HUMAN Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1 -0.07 0.08 0.01 -0.10 -0.03 -0.30 -0.14 0.04 0.442363487 0.08928354 binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;polysomal ribosome;ribonucleoprotein complex;ribosome 2.07E-35 2 9 9 22.6

P22059;H0YCV6;H7C1R2;H7C368;B4DTR3;Q8NA37;H7C428;F5H2A3;Q6ZN50;B4DKE4;Q0VF99;Q969R2 Oxysterol-binding protein 1 OSBP >sp|P22059|OSBP1_HUMAN Oxysterol-binding protein 1 OS=Homo sapiens GN=OSBP PE=1 SV=1 -0.09 -0.13 -0.03 -0.10 -0.03 0.08 0.32 0.11 1.117159234 -0.203331872 establishment of localization;lipid transport;organic substance transport;transport binding;cholesterol binding;lipid binding;oxysterol binding;phospholipid binding;steroid binding;sterol binding cell part;cytoplasmic part;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part 2.12E-86 12 9 9 17.5

Q96FW1;J3KR44;F5GYN4;F5H6Q1;F5GYJ8;F5H3F0;Q96FW1-2 Ubiquitin thioesterase OTUB1 OTUB1 >sp|Q96FW1|OTUB1_HUMAN Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=2;>tr|J3KR44|J3KR44_HUMAN Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=4 SV=1;>tr|F5GYN4|F5GYN4_HUMAN Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE= 0.11 -0.07 0.06 0.00 -0.02 0.01 0.32 -0.10 0.097585388 -0.028012973 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA repair;negative regulation of double-strand break repair;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein deubiquitination;protein K48-linked deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of double-strand break repair;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;response to DNA damage stimulus;response to stimulus;response to stress"binding;catalytic activity;cysteine-type peptidase activity;exopeptidase activity;hydrolase activity;NEDD8-specific protease activity;omega peptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;small conjugating protein binding;small conjugating protein-specific protease activity;ubiquitin binding;ubiquitin-specific protease activity" cell part;cytoplasm;intracellular part 1.03E-164 7 9 9 47.6

P13674-3;P13674-2;P13674 Prolyl 4-hydroxylase subunit alpha-1 P4HA1 >sp|P13674-3|P4HA1_HUMAN Isoform 3 of Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1;>sp|P13674-2|P4HA1_HUMAN Isoform 2 of Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1;>sp|P13674|P4HA1_HUMAN Prolyl 4-hydroxylase subunit alph -0.19 -0.14 -0.30 -0.06 0.91 0.42 -0.24 0.09 0.790666072 -0.463167304 4-hydroxyproline metabolic process;amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;collagen fibril organization;extracellular matrix organization;extracellular structure organization;heterocycle metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-proline hydroxylation;peptidyl-proline hydroxylation to 4-hydroxy-L-proline;peptidyl-proline modification;primary metabolic process;protein metabolic process;protein modification process;small molecule metabolic process"binding;carboxylic acid binding;catalytic activity;cation binding;dioxygenase activity;ion binding;iron ion binding;L-ascorbic acid binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptidyl-proline 4-dioxygenase activity;peptidyl-proline dioxygenase activity;procollagen-proline 4-dioxygenase activity;procollagen-proline dioxygenase activity;transition metal ion binding;vitamin binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrion;organelle;organelle lumen;organelle part Arginine and proline metabolism 5.29E-54 3 9 9 22.9

Q13442;F8WBW6 28 kDa heat- and acid-stable phosphoprotein PDAP1 >sp|Q13442|HAP28_HUMAN 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1 -0.25 0.03 -0.21 -0.10 0.24 -0.18 -0.04 -0.09 0.430329471 -0.115515412 biological regulation;cell proliferation;cellular process;cellular response to stimulus;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction 8.68E-81 2 9 9 45.3

F8WDZ1;Q8IZL8;C9JFV4;Q8IZL8-2;I3L3A8;I3L4M7;I3L445;E7EV54;I3L1P4;I3L4P1 "Proline-, glutamic acid- and leucine-rich protein 1" PELP1 ">tr|F8WDZ1|F8WDZ1_HUMAN Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens GN=PELP1 PE=2 SV=1;>sp|Q8IZL8|PELP1_HUMAN Proline-, glutamic acid- and leucine-rich protein 1 OS=Homo sapiens GN=PELP1 PE=1 SV=2;>tr|C9JFV4|C9JFV4_HUMAN Proline-, g" -0.14 0.68 0.39 0.69 -0.30 -0.11 -1.26 -0.22 1.120751244 0.875136854 "biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" cell part;cytoplasm;histone methyltransferase complex;intracellular organelle part;intracellular part;macromolecular complex;methyltransferase complex;MLL1 complex;nuclear part;nucleoplasm part;organelle part;protein complex 7.09E-34 10 9 9 14.6

O95336;M0R261;M0R1L2;M0R0U3 6-phosphogluconolactonase PGLS >sp|O95336|6PGL_HUMAN 6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2;>tr|M0R261|M0R261_HUMAN 6-phosphogluconolactonase (Fragment) OS=Homo sapiens GN=PGLS PE=4 SV=1 0.06 -0.02 -0.15 -0.01 -0.06 0.15 0.48 0.19 0.782450796 -0.221925988 "alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;glucose catabolic process;glucose metabolic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;NADP metabolic process;NADPH regeneration;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;pentose metabolic process;pentose-phosphate shunt;pentose-phosphate shunt, oxidative branch;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule catabolic process;small molecule metabolic process" "6-phosphogluconolactonase activity;binding;carbohydrate binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;monosaccharide binding;sugar binding" cell part;cytoplasmic part;cytosol;intracellular part Pentose phosphate pathway 3.92E-87 4 9 9 58.9

Q6NYC8;Q6NYC8-2 Phostensin PPP1R18 >sp|Q6NYC8|PPR18_HUMAN Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1;>sp|Q6NYC8-2|PPR18_HUMAN Isoform 2 of Phostensin OS=Homo sapiens GN=PPP1R18 -0.20 0.61 0.08 0.48 0.25 0.75 -0.38 0.74 0.102882223 -0.09544467 cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 3.56E-56 2 9 9 25.3

P48634-2;P48634-3;P48634;P48634-4 Protein PRRC2A PRRC2A >sp|P48634-2|PRC2A_HUMAN Isoform 2 of Protein PRRC2A OS=Homo sapiens GN=PRRC2A;>sp|P48634-3|PRC2A_HUMAN Isoform 3 of Protein PRRC2A OS=Homo sapiens GN=PRRC2A;>sp|P48634|PRC2A_HUMAN Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3;>sp|P48634-4|PRC2A_HUMAN 0.19 0.11 0.14 -0.06 0.02 -0.41 -0.07 0.07 0.680480429 0.194671214 cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 5.25E-23 4 9 9 8.7

G3V295;P60900;G3V5Z7;G3V3I1;B4DXJ9;G3V3U4;B4DQR4;G3V4S5;G3V2S7 Proteasome subunit alpha type;Proteasome subunit alpha type-6 PSMA6 >tr|G3V295|G3V295_HUMAN Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1;>sp|P60900|PSA6_HUMAN Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1;>tr|G3V5Z7|G3V5Z7_HUMAN Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 0.06 -0.02 -0.42 -0.04 -0.23 -0.11 -0.14 -0.10 0.121131874 0.037735014 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of gene expression;regulation of inflammatory response;regulation of ligase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" "binding;catalytic activity;endopeptidase activity;hydrolase activity;nucleic acid binding;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;contractile fiber part;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear matrix;nuclear part;nucleoplasm;nucleus;organelle;organelle part;polysome;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex;ribonucleoprotein complex;RNA granule;sarcomere" Proteasome 1.66E-83 9 9 9 49.8

P51665;B4DXI8;H3BNT7;H3BTM8 26S proteasome non-ATPase regulatory subunit 7 PSMD7 >sp|P51665|PSMD7_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2;>tr|B4DXI8|B4DXI8_HUMAN 26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=2 SV=1;>tr|H3BNT7|H3BNT7_HUMAN 26S proteasome non-AT 0.18 0.16 -0.07 -0.01 -0.04 -0.14 -0.03 -0.25 0.941931889 0.178089944 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction"	cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome complex;proteasome regulatory particle;protein complex	Proteasome	1.25E-67 4	9	9	35.8

Q13308-4;Q13308;Q13308-6;Q13308-3;Q13308-2;Q13308-5;Q86X91;F8WDG7;C9JQR6;C9J9E8;H0Y8F1 Inactive tyrosine-protein kinase 7	PTK7	>sp|Q13308-4|PTK7_HUMAN Isoform 4 of Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7;>sp|Q13308|PTK7_HUMAN Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2;>sp|Q13308-6|PTK7_HUMAN Isoform 6 of Inactive tyrosine-protein kinase	-0.56	-0.24	-0.22	0.07 0.49 0.21 0.26 0.00	1.211291546	-0.474964639	"actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;axis elongation;biological adhesion;biological regulation;canonical Wnt receptor signaling pathway;cell adhesion;cell communication;cell differentiation;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to nutrient;cellular response to nutrient levels;cellular response to retinoic acid;cellular response to stimulus;cellular response to vitamin;cellular response to vitamin A;cochlea morphogenesis;convergent extension;cytoskeleton organization;developmental growth;developmental growth involved in morphogenesis;developmental process;embryonic morphogenesis;epithelial cell differentiation;establishment of apical/basal cell polarity;establishment of cell polarity;establishment of epithelial cell apical/basal polarity;establishment of epithelial cell polarity;establishment of monopolar cell polarity;establishment of planar polarity;establishment of tissue polarity;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;establishment or maintenance of epithelial cell apical/basal polarity;establishment or maintenance of monopolar cell polarity;growth;locomotion;lung-associated mesenchyme development;mesenchyme development;morphogenesis of an epithelium;neural tube closure;non-canonical Wnt receptor signaling pathway;organelle organization;planar cell polarity pathway involved in neural tube closure;polarized epithelial cell differentiation;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of neuron projection development;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of embryonic development;regulation of establishment of planar polarity;regulation of establishment of planar polarity involved in neural tube closure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organ morphogenesis;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to retinoic acid;response to stimulus;response to stress;response to vitamin;response to vitamin A;response to wounding;signal transduction;tissue development;tissue morphogenesis;tube closure;tube formation;Wnt receptor signaling pathway;Wnt receptor signaling pathway, planar cell polarity pathway;wound healing" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;ribonucleotide binding;signal transducer activity;signaling receptor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity"	cell junction;cell part;cell-cell junction;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;plasma membrane part	2.17E-35 11	9	9	11.6

P18031;B4DSN5	Tyrosine-protein phosphatase non-receptor type 1;Tyrosine-protein phosphatase non-receptor type	PTPN1	>sp|P18031|PTN1_HUMAN Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1;>tr|B4DSN5|B4DSN5_HUMAN Tyrosine-protein phosphatase non-receptor type OS=Homo sapiens GN=PTPN1 PE=2 SV=1	0.12 -0.04	-0.01	0.11 0.00 -0.20	-0.52	-0.15	0.964750501	0.261004744	actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based process;biological regulation;cell activation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;cellular response to topologically incorrect protein;cellular response to type I interferon;cellular response to unfolded protein;cytokine-mediated signaling pathway;cytoskeleton organization;dephosphorylation;endoplasmic reticulum unfolded protein response;enzyme linked receptor protein signaling pathway;ER-nucleus signaling pathway;insulin receptor signaling pathway;interferon-gamma-mediated signaling pathway;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of insulin receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle organization;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;platelet activation;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of cell communication;regulation of cellular component organization;regulation of cellular process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of endocytosis;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of insulin receptor signaling pathway;regulation of interferon-gamma-mediated signaling pathway;regulation of localization;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of type I interferon-mediated signaling pathway;regulation of vesicle-mediated transport;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to endoplasmic reticulum stress;response to hormone stimulus;response to insulin stimulus;response to interferon-gamma;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;response to topologically incorrect protein;response to type I interferon;response to unfolded protein;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;type I interferon-mediated signaling pathway	"binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein tyrosine phosphatase activity;transition metal ion binding;zinc ion binding"	cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;early endosome;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;vesicle	Adherens junction;Insulin signaling pathway1.98E-112	2	9	9	27.4

Q9BWH6;H3BRE8;Q9BWH6-2;Q9BWH6-3;H3BPM3 RNA polymerase II-associated protein 1 RPAP1 >sp|Q9BWH6|RPAP1_HUMAN RNA polymerase II-associated protein 1 OS=Homo sapiens GN=RPAP1 PE=1 SV=3;>tr|H3BRE8|H3BRE8_HUMAN RNA polymerase II-associated protein 1 OS=Homo sapiens GN=RPAP1 PE=2 SV=1;>sp|Q9BWH6-2|RPAP1_HUMAN Isoform 2 of RNA polymerase II-assoc 0.32 -0.04 0.31 -0.13 -0.01 -0.39 0.21 -0.49 0.599547172 0.286359348 biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process "binding;catalytic activity;DNA binding;DNA-directed RNA polymerase activity;nucleic acid binding;nucleotidyltransferase activity;RNA polymerase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.93E-54 5 9 9 8.8

M0R210;P62249;M0R3H0;Q6IPX4;M0R1M5;M0QX76 40S ribosomal protein S16 RPS16 >tr|M0R210|M0R210_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=3 SV=1;>sp|P62249|RS16_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2;>tr|M0R3H0|M0R3H0_HUMAN 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=3 SV=1;>tr 0.03 -0.04 -0.06 0.20 -0.84 -0.95 -0.08 -0.40 1.19658894 0.602555016 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal small subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 2.47E-27 6 9 9 58.1

P62979;J3QS39;J3QTR3;F5H6Q2;P62987;F5GYU3;F5H2Z3;F5H265;F5H7Y5;B4DV12;F5H388;F5H747;F5GXK7;J3QKN0;P0CG47;Q96C32;F5H7K6;F5H041;P0CG48;M0R1V7;F5H4D8;M0R1M6;M0R2S1;F5GZ39;J3QLP7;J3QRK5;J3QSA3;K7EMA8;J3KSM4 Ubiquitin-40S ribosomal protein S27a;Ubiquitin;40S ribosomal protein S27a;Ubiquitin-60S ribosomal protein L40;Ubiquitin;60S ribosomal protein L40;Polyubiquitin-B;Ubiquitin;Polyubiquitin-C;Ubiquitin RPS27A;UBB;UBC;UBA52;UBBP4 >sp|P62979|RS27A_HUMAN Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2;>tr|J3QS39|J3QS39_HUMAN Ubiquitin (Fragment) OS=Homo sapiens GN=UBB PE=4 SV=1;>tr|J3QTR3|J3QTR3_HUMAN Ubiquitin (Fragment) OS=Homo sapiens GN=RPS27A PE=1 SV=1;> 0.17 0.32 -0.43 -0.01 0.34 0.22 -0.06 0.02 0.247364689 -0.11924073 "activation of immune response;activation of innate immune response;activation of MAPK activity;adipose tissue development;anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen receptor-mediated signaling pathway;biological regulation;biosynthetic process;catabolic process;cell cycle phase;cell cycle process;cell development;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;central nervous system neuron development;cotranslational protein targeting to membrane;cytokine-mediated signaling pathway;cytoplasmic pattern recognition receptor signaling pathway;defense response;developmental process;developmental process involved in reproduction;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;DNA metabolic process;DNA repair;egress of virus within host cell;endosome transport;energy homeostasis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;fat pad development;female gonad development;female meiosis I;fibroblast growth factor receptor signaling pathway;forebrain neuron development;G1 phase;G1 phase of mitotic cell cycle;G1/S transition of mitotic cell cycle;gonad development;homeostatic process;hypothalamus gonadotrophin-releasing hormone neuron development;I-kappaB kinase/NF-kappaB cascade;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;intracellular protein kinase cascade;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;ion transmembrane transport;ion transport;JNK cascade;M phase;M phase of mitotic cell cycle;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;male meiosis I;MAPKKK cascade;meiosis I;membrane organization;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA catabolic process;mRNA metabolic process;multicellular organismal homeostasis;multicellular organismal process;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of cytokine production;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of gene expression;negative regulation of ligase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of type I interferon production;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nerve growth factor receptor signaling pathway;neuron development;nitrogen compound metabolic process;Notch receptor processing;Notch signaling pathway;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;nucleotide-binding oligomerization domain containing signaling pathway;organ development;pattern recognition receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of gene expression;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of intracellular protein kinase cascade;positive regulation of kinase activity;positive regulation of ligase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of NF-kappaB transcription factor activity;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein serine/threonine kinase activity;positive regulation of protein ubiquitination;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of type I interferon production;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex disassembly;protein complex subunit organization;protein maturation;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein phosphorylation;protein polyubiquitination;protein processing;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of defense response;regulation of epidermal growth factor receptor signaling pathway;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of kinase activity;regulation of ligase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein ubiquitination;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of type I interferon production;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;reproductive structure development;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;response to stress;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;S phase;S phase of mitotic cell cycle;seminiferous tubule development;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;SRP-dependent cotranslational protein targeting to membrane;stress-activated protein kinase signaling cascade;T cell receptor signaling pathway;tissue development;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transforming growth factor beta receptor signaling pathway;translation;translational elongation;translational initiation;translational termination;transmembrane receptor protein serine/threonine kinase signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport;TRIF-dependent toll-like receptor signaling pathway;ubiquitin homeostasis;ubiquitin-dependent protein catabolic process;vesicle-mediated transport;viral protein processing;viral reproductive process;viral transcription;virion assembly" binding;cation binding;ion binding;metal ion binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;cytosolic large ribosomal subunit;cytosolic small ribosomal subunit;endocytic vesicle membrane;endosomal part;endosome membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle membrane;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit;vesicle membrane Parkinson's disease;Ribosome 4.41E-145 29 9 9 43.6

Q9BST9;Q9BST9-3;Q9BST9-2;Q8IZC4-3;Q8IZC4-2;Q8IZC4 Rhotekin RTKN >sp|Q9BST9|RTKN_HUMAN Rhotekin OS=Homo sapiens GN=RTKN PE=1 SV=2;>sp|Q9BST9-3|RTKN_HUMAN Isoform 3 of Rhotekin OS=Homo sapiens GN=RTKN;>sp|Q9BST9-2|RTKN_HUMAN Isoform 2 of Rhotekin OS=Homo sapiens GN=RTKN0.33 0.10 -0.24 -0.11 -1.18 0.00 0.36 0.52 0.078139639 0.091734538 anatomical structure development;apoptosis;biological regulation;cell death;cellular process;cellular response to stimulus;death;developmental process;hemopoiesis;hemopoietic or lymphoid organ development;intracellular signal transduction;organ development;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;programmed cell death;Ras protein signal transduction;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;GTP binding;GTPase binding;GTPase inhibitor activity;GTPase regulator activity;GTP-Rho binding;guanyl nucleotide binding;guanyl ribonucleotide binding;lipid binding;nucleoside-triphosphatase regulator activity;nucleotide binding;phospholipid binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;Ras GTPase binding;Rho GTPase binding;ribonucleotide binding;small GTPase binding cell part;membrane;plasma membrane 4.38E-83 6 9 9 25.6

O76054;O76054-5;B3KRD8;O76054-4;H7C417;C9JZI9;C9IYR5;H7C4C6;F8WEE7;C9JYY7;C9JTM4;H7C1K3;Q9UDX4 SEC14-like protein 2 SEC14L2">sp|O76054|S14L2_HUMAN SEC14-like protein 2 OS=Homo sapiens GN=SEC14L2 PE=1 SV=1;>sp|O76054-5|S14L2_HUMAN Isoform 3 of SEC14-like protein 2 OS=Homo sapiens GN=SEC14L2;>tr|B3KRD8|B3KRD8_HUMAN SEC14-like 2 (S. cerevisiae), isoform CRA_c OS=Homo sapiens GN=SE" 0.10 -1.05 0.37 -0.07 0.35 0.77 0.75 -0.36 0.561114448 -0.542304721 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cholesterol biosynthetic process;regulation of cholesterol metabolic process;regulation of gene expression;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent;transport" binding;lipid binding;phospholipid binding;transporter activity;vitamin binding;vitamin E binding cell part;cytoplasm;integral to membrane;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;nucleus;organelle 1.10E-29 13 9 9 33.3

Q9Y3L3;Q9Y3L3-2;F5GZA8;Q6ZT62 SH3 domain-binding protein 1 SH3BP1 >sp|Q9Y3L3|3BP1_HUMAN SH3 domain-binding protein 1 OS=Homo sapiens GN=SH3BP1 PE=1 SV=3;>sp|Q9Y3L3-2|3BP1_HUMAN Isoform 2 of SH3 domain-binding protein 1 OS=Homo sapiens GN=SH3BP1;>tr|F5GZA8|F5GZA8_HUMAN SH3 domain-binding protein 1 OS=Homo sapiens GN=SH3BP0.06 -0.24 0.44 0.11 -0.95 -0.71 -0.02 -0.01 0.797351056 0.514610953 biological regulation;cellular process;cellular response to stimulus;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;response to stimulus;signal transduction enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity cell part;cytoplasm;intracellular part 3.36E-81 4 9 9 16

Q99961;M0QYE0;M0R0I3;Q99961-3;Q99961-2;F5H5J3;Q99962;M0R2K6 Endophilin-A2SH3GL1 >sp|Q99961|SH3G1_HUMAN Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1;>tr|M0QYE0|M0QYE0_HUMAN Endophilin-A2 (Fragment) OS=Homo sapiens GN=SH3GL1 PE=4 SV=1;>tr|M0R0I3|M0R0I3_HUMAN Endophilin-A2 (Fragment) OS=Homo sapiens GN=SH3GL1 PE=4 SV=1;>sp|Q99961-3| -0.12 -0.18 0.00 -0.17 0.64 0.18 0.43 -0.17 0.928502591 -0.388565327 anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;central nervous system development;chemotaxis;developmental process;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;Golgi vesicle transport;immune system process;intracellular transport;locomotion;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;post-Golgi vesicle-mediated transport;regulation of biological process;regulation of cell communication;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of endocytosis;regulation of epidermal growth factor receptor signaling pathway;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of receptor internalization;regulation of receptor-mediated endocytosis;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;synaptic vesicle endocytosis;synaptic vesicle transport;system development;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport binding;lipid binding cell junction;cell part;cell projection;clathrin coated vesicle membrane;clathrin-coated endocytic vesicle membrane;coated vesicle membrane;cytoplasm;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;early endosome membrane;endocytic vesicle membrane;endosomal part;endosome membrane;Golgi apparatus part;Golgi membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;podosome;protein complex;vesicle membrane Endocytosis 3.85E-63 8 9 9 22.8

I3L1P8;Q02978;Q02978-2 Mitochondrial 2-oxoglutarate/malate carrier protein SLC25A11 >tr|I3L1P8|I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens GN=SLC25A11 PE=2 SV=1;>sp|Q02978|M2OM_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3;>sp|Q02978-2|M2OM_H -0.41 0.44 -0.25 0.59 0.92 0.87 -1.33 0.09 0.026453522 -0.046758441 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;establishment of localization;gluconeogenesis;glucose metabolic process;hexose biosynthetic process;hexose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule metabolic process;transport active transmembrane transporter activity;anion transmembrane transporter activity;anion:anion antiporter activity;antiporter activity;C4-dicarboxylate transmembrane transporter activity;carboxylic acid transmembrane transporter activity;dicarboxylic acid transmembrane transporter activity;ion transmembrane transporter activity;malate transmembrane transporter activity;organic acid transmembrane transporter activity;oxoglutarate:malate antiporter activity;secondary active transmembrane transporter activity;solute:solute antiporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;plasma membrane part 1.60E-80 3 9 9 35.1

J3KP15;Q01130;J3QL05;B4DN89;Q9BRL6-2;Q9BRL6 Serine/arginine-rich splicing factor 2 SRSF2;SFRS2>tr|J3KP15|J3KP15_HUMAN Serine/arginine-rich-splicing factor 2 (Fragment) OS=Homo sapiens GN=SRSF2 PE=4 SV=1;>sp|Q01130|SRSF2_HUMAN Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4;>tr|J3QL05|J3QL05_HUMAN Serine/arginine-rich-splic 0.01 0.09 0.16 0.11 -0.01 -0.48 -0.91 -0.54 1.260797904 0.57664622 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;protein binding transcription factor activity;RNA binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 8.63E-120 6 9 9 61.2

E7END2;P28290-2;E9PHV5;P28290;E7EUL7;P28290-3;H7BZ26 Sperm-specific antigen 2SSFA2 >tr|E7END2|E7END2_HUMAN Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2 PE=2 SV=1;>sp|P28290-2|SSFA2_HUMAN Isoform 2 of Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2;>tr|E9PHV5|E9PHV5_HUMAN Sperm-specific antigen 2 OS=Homo sapiens GN=SSFA2 PE=2 SV=1; -0.09 0.66 0.30 0.60 -0.45 0.62 -0.41 0.65 0.295831026 0.264987633 cell part;cytoplasm;intracellular part;membrane;plasma membrane 3.26E-30 7 9 9 11.4

P50502;Q8NFI4;H7C3I1;F6VDH7;Q8IZP2;F8WAQ7 Hsc70-interacting protein;Putative protein FAM10A5;Putative protein FAM10A4 ST13;ST13P5;ST13P4 >sp|P50502|F10A1_HUMAN Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2;>sp|Q8NFI4|F10A5_HUMAN Putative protein FAM10A5 OS=Homo sapiens GN=ST13P5 PE=5 SV=1;>tr|H7C3I1|H7C3I1_HUMAN Hsc70-interacting protein (Fragment) OS=Homo sapiens GN=ST13 PE=4 0.00 0.01 -0.09 -0.08 -0.03 -0.26 0.27 -0.16 0.016481085 0.006022323 biological regulation;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone cofactor-dependent protein refolding;chaperone-mediated protein folding;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of protein refolding;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein homooligomerization;protein metabolic process;protein oligomerization;protein refolding;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein refolding "adenyl deoxyribonucleotide binding;adenyl nucleotide binding;binding;binding, bridging;dATP binding;deoxyribonucleotide binding;nucleotide binding;protein binding;protein binding, bridging;purine deoxyribonucleotide binding;purine nucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;macromolecular complex;protein complex 1.20E-149 6 9 9 26.8

F5GXC8;Q9P2R7-2;Q9P2R7;F5H5G8;Q5T9Q5;Q5T9Q8;B4E0J1 "Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial" SUCLA2 ">tr|F5GXC8|F5GXC8_HUMAN Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=2 SV=1;>sp|Q9P2R7-2|SUCB1_HUMAN Isoform 2 of Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2;>sp|Q9P2" 0.19 0.06 0.02 -0.18 0.15 -0.12 0.12 -0.39 0.213416602 0.083740111 acetyl-CoA catabolic process;acetyl-CoA metabolic process;biosynthetic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;porphyrin-containing compound biosynthetic process;porphyrin-containing compound metabolic process;small molecule metabolic process;succinate metabolic process;succinyl-CoA metabolic process;succinyl-CoA pathway;tetrapyrrole biosynthetic process;tetrapyrrole metabolic process;tricarboxylic acid cycle "acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;CoA-ligase activity;ion binding;ligase activity;ligase activity, forming carbon-sulfur bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;succinate-CoA ligase (ADP-forming) activity;succinate-CoA ligase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Citrate cycle (TCA cycle);Propanoate metabolism 7.55E-31 7 9 9 22.7

Q3ZCQ8;Q3ZCQ8-2;M0R0C3;M0R2F8;Q330K1;M0R047;M0R003;M0QXC3;M0R2Z3;M0R303;M0R2D2;M0R1Y4 Mitochondrial import inner membrane translocase subunit TIM50 TIMM50 >sp|Q3ZCQ8|TIM50_HUMAN Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2;>sp|Q3ZCQ8-2|TIM50_HUMAN Isoform 2 of Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50;>tr|M0R0C -0.18 0.13 0.03 0.15 -0.23 -0.26 -1.03 -0.29 0.987857831 0.482370236 apoptotic mitochondrial changes;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;membrane organization;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;organelle organization;protein import;protein targeting;protein targeting to mitochondrion;protein transport;release of cytochrome c from mitochondria;transport "binding;catalytic activity;cytokine receptor binding;growth factor receptor binding;hydrolase activity;hydrolase activity, acting on ester bonds;interleukin-2 receptor binding;nucleic acid binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein binding;protein serine/threonine phosphatase activity;protein tyrosine phosphatase activity;receptor binding;ribonucleoprotein binding;RNA binding" cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;mitochondrial inner membrane presequence translocase complex;mitochondrial membrane part;mitochondrial part;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex 3.82E-84 12 9 9 27.8

P10155-3;Q5LJA0;P10155-4;P10155;P10155-2;D6RDN1;D6RE09;H0Y9N5 60 kDa SS-A/Ro ribonucleoprotein TROVE2 >sp|P10155-3|RO60_HUMAN Isoform 3 of 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2;>tr|Q5LJA0|Q5LJA0_HUMAN 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens GN=TROVE2 PE=2 SV=1;>sp|P10155-4|RO60_HUMAN Isoform 4 of 60 kDa SS-A/Ro ribonucleoprote 0.09 -0.10 0.25 0.07 0.23 -0.26 -0.10 -0.47 0.579858175 0.224628026 "anatomical structure morphogenesis;biosynthetic process;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular biosynthetic process;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cilium morphogenesis;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase III promoter;transcription, DNA-dependent" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex Systemic lupus erythematosus 1.84E-55 8 9 9 23

P40222 Alpha-taxilin TXLNA >sp|P40222|TXLNA_HUMAN Alpha-taxilin OS=Homo sapiens GN=TXLNA PE=1 SV=3 0.02 0.13 -0.23 0.08 -0.15 -0.13 0.05 -0.37 0.545473341 0.152249804 cell proliferation;cellular process;establishment of localization;establishment of localization in cell;exocytosis;secretion;secretion by cell;transport;vesicle-mediated transport binding;cytokine activity;growth factor receptor binding;high molecular weight B cell growth factor receptor binding;protein binding;receptor binding cell part;cytoplasm;extracellular region;intracellular part 3.55E-42 1 9 9 28.6

B4DIZ2;P61086;D6RDM7;P61086-3;P61086-2;D6RFX1;A6NF31;O75665 Ubiquitin-conjugating enzyme E2 K UBE2K >tr|B4DIZ2|B4DIZ2_HUMAN Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=2 SV=1;>sp|P61086|UBE2K_HUMAN Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3;>tr|D6RDM7|D6RDM7_HUMAN Ubiquitin-conjugating enzyme E2 K (Fragment) OS 0.04 -0.14 -0.21 -0.04 0.09 -0.12 0.40 -0.10 0.485333762 -0.155155479 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;axoneme assembly;catabolic process;cell cycle process;cell part morphogenesis;cell projection assembly;cell projection morphogenesis;cell projection organization;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cilium axoneme assembly;cilium morphogenesis;cilium movement;cytoskeleton organization;developmental process;epithelial cilium movement;epithelial cilium movement involved in determination of left/right asymmetry;G2/M transition of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;organelle organization;primary metabolic process;protein K48-linked ubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;alpha-tubulin binding;ATP binding;binding;catalytic activity;cytoskeletal protein binding;gamma-tubulin binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small conjugating protein ligase activity;tubulin binding;ubiquitin-protein ligase activity;ubiquitin-ubiquitin ligase activity" cell part;cell projection;cell projection part;centriole;cilium;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule basal body;microtubule cytoskeleton;microtubule organizing center;microtubule organizing center part;non-membrane-bounded organelle;nucleus;organelle;organelle part Ubiquitin mediated proteolysis 6.05E-64 8 9 9 64

O95833;Q5SQ17;Q96NY7-2;Q96NY7 Chloride intracellular channel protein 3 CLIC3 >sp|O95833|CLIC3_HUMAN Chloride intracellular channel protein 3 OS=Homo sapiens GN=CLIC3 PE=1 SV=2;>tr|Q5SQ17|Q5SQ17_HUMAN Chloride intracellular channel protein 3 (Fragment) OS=Homo sapiens GN=CLIC3 PE=2 SV=1 0.02 0.19 0.34 0.05 0.94 1.62 0.82 -0.23 0.69561361 -0.636942585 biological regulation;cellular process;cellular response to stimulus;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction anion channel activity;anion transmembrane transporter activity;channel activity;chloride channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;passive transmembrane transporter activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated chloride channel activity;voltage-gated ion channel activity cell part;chloride channel complex;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane;protein complex 5.51E-69 4 10 9 46.6

Q9Y6G9;E9PHI6;C9JGM7;C9JLW1 Cytoplasmic dynein 1 light intermediate chain 1 DYNC1LI1 >sp|Q9Y6G9|DC1L1_HUMAN Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=1 SV=3;>tr|E9PHI6|E9PHI6_HUMAN Cytoplasmic dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DYNC1LI1 PE=2 SV=1 -0.06 0.05 -0.14 0.01 0.33 0.16 -0.02 0.02 0.749034839 -0.1571001 biological regulation;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;establishment of localization;interaction with host;interspecies interaction between organisms;mitosis;multi-organism process;nuclear division;organelle fission;organelle organization;positive regulation of biological process;positive regulation of mitotic cell cycle spindle assembly checkpoint;positive regulation of spindle checkpoint;regulation of biological process;regulation of cell cycle;regulation of cellular process;regulation of mitotic cell cycle;regulation of mitotic cell cycle spindle assembly checkpoint;regulation of spindle checkpoint;reproductive process;transport;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;centrosome;chromosomal part;condensed chromosome kinetochore;cytoplasm;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;dynein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;spindle pole Phagosome;Vasopressin-regulated water reabsorption 1.15E-90 4 10 9 26.2

Q96C19;H0Y4Y4;Q9BUP0-2;Q9BUP0;C9JTV4;Q8WYH2 EF-hand domain-containing protein D2 EFHD2 >sp|Q96C19|EFHD2_HUMAN EF-hand domain-containing protein D2 OS=Homo sapiens GN=EFHD2 PE=1 SV=1 -0.12 0.53 0.14 0.72 -0.28 0.07 -0.61 0.23 0.744795521 0.462664463 cell projection organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;neuron projection development binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 7.90E-56 6 10 9 32.5

P14324-2;P14324;REV__H0YCZ3;REV__Q5VSG8-3;REV__Q5VSG8 Farnesyl pyrophosphate synthase FDPS >sp|P14324-2|FPPS_HUMAN Isoform 2 of Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS;>sp|P14324|FPPS_HUMAN Farnesyl pyrophosphate synthase OS=Homo sapiens GN=FDPS PE=1 SV=4 0.14 0.15 -0.12 -0.14 -0.38 -0.17 0.32 -0.06 0.176469442 0.079453113 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;farnesyl diphosphate biosynthetic process;farnesyl diphosphate metabolic process;geranyl diphosphate biosynthetic process;geranyl diphosphate metabolic process;interaction with host;interspecies interaction between organisms;isoprenoid biosynthetic process;isoprenoid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;multi-organism process;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;prenol biosynthetic process;prenol metabolic process;primary metabolic process;reproductive process;small molecule biosynthetic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;terpenoid biosynthetic process;terpenoid metabolic process;viral reproductive process;virus-host interaction "binding;catalytic activity;cation binding;dimethylallyltranstransferase activity;geranyltranstransferase activity;ion binding;metal ion binding;prenyltransferase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle Terpenoid backbone biosynthesis 7.12E-111 5 10 9 25.8

Q99729-3;D6R9P3;D6RD18;D6RBZ0;Q99729-2;Q99729-4;Q99729 Heterogeneous nuclear ribonucleoprotein A/B HNRNPAB >sp|Q99729-3|ROAA_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB;>tr|D6R9P3|D6R9P3_HUMAN Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1;>tr|D6RD18|D6RD18_HUMAN Heterogeneous nucle -0.19 0.29 -0.02 0.43 0.26 -0.07 -1.14 -0.45 0.608875524 0.477693216 "anatomical structure morphogenesis;biological regulation;cell morphogenesis;cell morphogenesis involved in differentiation;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;developmental process;epithelial to mesenchymal transition;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent" binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex 1.65E-98 7 10 9 33

Q9UIQ6-3;Q9UIQ6-2;Q9UIQ6;Q8NFU1;REV__Q8N612-3;REV__E9PJK5;REV__Q8N612;REV__Q8N612-2;Q96T58 "Leucyl-cystinyl aminopeptidase;Leucyl-cystinyl aminopeptidase, pregnancy serum form" LNPEP >sp|Q9UIQ6-3|LCAP_HUMAN Isoform 3 of Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP;>sp|Q9UIQ6-2|LCAP_HUMAN Isoform 2 of Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP;>sp|Q9UIQ6|LCAP_HUMAN Leucyl-cystinyl aminopeptidase OS=Homo sapiens G 0.00 0.02 -0.01 -0.13 -0.16 0.04 0.13 0.19 0.394244109 -0.082302806 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;catabolic process;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular chemical homeostasis;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chemical homeostasis;female pregnancy;homeostatic process;immune system process;interaction with host;interspecies interaction between organisms;ion homeostasis;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane depolarization;membrane organization;metabolic process;multicellular organismal process;multi-organism process;neurological system process;Notch signaling pathway;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to stimulus;sensory perception;sensory perception of chemical stimulus;sensory perception of smell;signal transduction;signaling;system process;viral reproductive process;virus-host interaction" "aminopeptidase activity;anion channel activity;anion transmembrane transporter activity;binding;catalytic activity;cation binding;channel activity;chloride channel activity;DNA binding;exopeptidase activity;hydrolase activity;ion binding;ion channel activity;ion transmembrane transporter activity;metal ion binding;metallopeptidase activity;nucleic acid binding;nucleic acid binding transcription factor activity;nucleotide binding;passive transmembrane transporter activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding transcription factor activity;RNA binding;RNA polymerase II transcription factor binding transcription factor activity;RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transition metal ion binding;transmembrane transporter activity;transporter activity;zinc ion binding" cell part;cell projection;chloride channel complex;cilium;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;early endosome lumen;endosomal part;endosome lumen;extracellular region;integral to membrane;integral to plasma membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;ion channel complex;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;nuclear part;nucleoplasm part;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;transcriptional repressor complex;vesicle membrane Renin-angiotensin system;Salivary secretion 1.15E-52 9 10 9 11.7

P61106 Ras-related protein Rab-14 RAB14 >sp|P61106|RAB14_HUMAN Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 -0.09 0.14 -0.43 0.04 0.09 0.02 -0.27 -0.02 0.096954658 -0.040876482 biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;developmental process;embryo development;endocytic recycling;endosome transport;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;fibroblast growth factor receptor signaling pathway;Golgi to endosome transport;Golgi vesicle transport;intracellular signal transduction;intracellular transport;membrane organization;neurotransmitter secretion;neurotransmitter transport;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of localization;regulation of neurotransmitter levels;regulation of protein localization;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;secretion;secretion by cell;signal release;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;early endosome;early endosome membrane;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum;endosomal part;endosome;endosome membrane;Golgi apparatus part;Golgi membrane;Golgi stack;Golgi-associated vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nuclear outer membrane-endoplasmic reticulum membrane network;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;recycling endosome;rough endoplasmic reticulum;trans-Golgi network transport vesicle;transport vesicle;vacuole;vesicle;vesicle membrane 5.26E-74 1 10 9 54.9

Q14160;Q14160-3;Q14160-2;H0YCG0;Q96A19 Protein scribble homolog SCRIB >sp|Q14160|SCRIB_HUMAN Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=4;>sp|Q14160-3|SCRIB_HUMAN Isoform 3 of Protein scribble homolog OS=Homo sapiens GN=SCRIB;>sp|Q14160-2|SCRIB_HUMAN Isoform 2 of Protein scribble homolog OS=Homo sapiens GN=SCR -0.05 -0.12 0.11 0.04 -0.02 -0.34 -0.16 -0.47 0.936456436 0.243058793 activation of Rac GTPase activity;activation of Ras GTPase activity;activation of Rho GTPase activity;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptosis;apoptosis involved in morphogenesis;asymmetric protein localization;biological adhesion;biological regulation;cell adhesion;cell death;cell migration;cell motility;cell proliferation;cell-cell adhesion;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular membrane organization;cellular process;chemotaxis;death;developmental process;developmental programmed cell death;endocytosis;epithelial tube morphogenesis;establishment of apical/basal cell polarity;establishment of cell polarity;establishment of localization;establishment of monopolar cell polarity;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;establishment or maintenance of monopolar cell polarity;interaction with host;interspecies interaction between organisms;localization;locomotion;macromolecule localization;mammary gland duct morphogenesis;membrane invagination;membrane organization;morphogenesis of an epithelium;multi-organism process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;negative regulation of mitotic cell cycle;neural tube closure;positive chemotaxis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of programmed cell death;positive regulation of Rac GTPase activity;positive regulation of Ras GTPase activity;positive regulation of receptor recycling;positive regulation of Rho GTPase activity;positive regulation of signaling;programmed cell death;protein localization;protein localization to adherens junction;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of receptor recycling;regulation of Rho GTPase activity;regulation of signaling;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;response to wounding;synaptic vesicle endocytosis;synaptic vesicle targeting;synaptic vesicle transport;taxis;tissue morphogenesis;transport;tube closure;tube formation;tube morphogenesis;vesicle targeting;vesicle-mediated transport;viral reproductive process;virus-host interaction;wound healing adherens junction;anchoring junction;basolateral plasma membrane;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cytoplasmic part;intracellular part;macromolecular complex;membrane;membrane part;myelin sheath abaxonal region;plasma membrane;plasma membrane part;protein complex;Scrib-APC-beta-catenin complex 8.80E-62 5 10 9 9.1

Q9BWM7 Sideroflexin-3 SFXN3 >sp|Q9BWM7|SFXN3_HUMAN Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=2 -0.70 0.16 -0.50 0.34 0.73 2.01 -0.82 1.44 0.653484678 -1.016028482 biological regulation;cation homeostasis;chemical homeostasis;homeostatic process;ion homeostasis;iron ion homeostasis;regulation of biological quality cation transmembrane transporter activity;ion transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle part 1.79E-65 1 10 9 41.5

P30837;O94788-2 "Aldehyde dehydrogenase X, mitochondrial" ALDH1B1 ">sp|P30837|AL1B1_HUMAN Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3" -0.38 -0.28 -0.10 -0.04 0.30 -0.10 0.15 0.03 1.060023207 -0.295187584 alcohol catabolic process;alcohol metabolic process;carbohydrate metabolic process;catabolic process;ethanol catabolic process;ethanol metabolic process;metabolic process;primary alcohol catabolic process;primary alcohol metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "aldehyde dehydrogenase (NAD) activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Chloroalkane and chloroalkene degradation;Fatty acid metabolism;Glycerolipid metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Limonene and pinene degradation;Lysine degradation;Pentose and glucuronate interconversions;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 4.41E-75 2 11 9 28.2

P60981;F6RFD5;P60981-2 Destrin DSTN >sp|P60981|DEST_HUMAN Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3;>tr|F6RFD5|F6RFD5_HUMAN Destrin OS=Homo sapiens GN=DSTN PE=2 SV=1;>sp|P60981-2|DEST_HUMAN Isoform 2 of Destrin OS=Homo sapiens GN=DSTN 0.05 -0.12 -0.35 0.06 -0.12 0.00 0.69 0.33 0.652284762 -0.316630761 actin cytoskeleton organization;actin filament depolymerization;actin filament organization;actin filament severing;actin filament-based process;actin polymerization or depolymerization;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex disassembly;cytokinesis;cytoskeleton organization;macromolecular complex disassembly;macromolecular complex subunit organization;organelle organization;positive regulation of actin filament depolymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex disassembly;protein complex disassembly;protein complex subunit organization;protein depolymerization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex disassembly actin cytoskeleton;cell cortex part;cell part;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part 1.79E-60 3 11 9 51.5

O75367-2;O75367-3;O75367;D6RCF2;B4DJC3 Core histone macro-H2A.1 H2AFY >sp|O75367-2|H2AY_HUMAN Isoform 1 of Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY;>sp|O75367-3|H2AY_HUMAN Isoform 3 of Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY;>sp|O75367|H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4 -0.23 1.27 0.09 1.31 -0.86 0.00 -1.35 0.50 0.773651502 1.040292952 "biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin modification;chromatin organization;chromosome organization;dosage compensation;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule metabolic process;regulation of metabolic process" binding;chromatin binding;DNA binding;nucleic acid binding Barr body;cell part;chromosomal part;chromosome;condensed chromosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleosome;nucleus;organelle;organelle part;protein-DNA complex;sex chromosome;X chromosome Systemic lupus erythematosus 1.14E-158 5 11 9 37.7

P16401 Histone H1.5 HIST1H1B >sp|P16401|H15_HUMAN Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 -0.79 1.33 0.14 0.71 0.52 0.06 -2.10 -0.94 0.550882536 0.96366779 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organizationbinding;DNA binding;nucleic acid binding cell part;chromatin;chromosomal part;intracellular organelle part;intracellular part;macromolecular complex;nuclear chromatin;nuclear chromosome part;nuclear part;nucleosome;organelle part;protein-DNA complex 5.08E-91 1 11 9 31.9

Q14573 "Inositol 1,4,5-trisphosphate receptor type 3" ITPR3 ">sp|Q14573|ITPR3_HUMAN Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens GN=ITPR3 PE=1 SV=2" -0.38 0.67 -0.31 0.23 -0.24 0.48 -0.62 0.49 0.019099531 0.021697573 activation of phospholipase C activity;biological regulation;calcium ion homeostasis;calcium ion transport;calcium ion transport into cytosol;cation homeostasis;cation transport;cell activation;cell surface receptor linked signaling pathway;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cytosolic calcium ion homeostasis;cytosolic calcium ion transport;defense response;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of cytosolic calcium ion concentration;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;fibroblast growth factor receptor signaling pathway;generation of precursor metabolites and energy;G-protein coupled receptor protein signaling pathway;homeostatic process;immune response;immune system process;innate immune response;ion homeostasis;ion transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;metal ion homeostasis;metal ion transport;multicellular organismal process;nerve growth factor receptor signaling pathway;neurological system process;oxidation-reduction process;platelet activation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of lipase activity;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein homooligomerization;protein oligomerization;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of lipase activity;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phospholipase activity;regulation of secretion;regulation of signaling;regulation of transport;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to stimulus;response to stress;sensory perception;sensory perception of bitter taste;sensory perception of chemical stimulus;sensory perception of sweet taste;sensory perception of taste;sensory perception of umami taste;signal transduction;small molecule metabolic process;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transport "alcohol binding;binding;calcium channel activity;calcium-release channel activity;cation channel activity;cation transmembrane transporter activity;channel activity;gated channel activity;inositol 1,3,4,5 tetrakisphosphate binding;inositol 1,4,5 trisphosphate binding;inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity;inositol hexakisphosphate binding;intracellular ligand-gated calcium channel activity;intracellular ligand-gated ion channel activity;ion channel activity;ion transmembrane transporter activity;ligand-gated channel activity;ligand-gated ion channel activity;lipid binding;molecular transducer activity;passive transmembrane transporter activity;phosphatidylinositol binding;phospholipid binding;receptor activity;signal transducer activity;signaling receptor activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" apical part of cell;brush border;cell body;cell part;cell projection;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;integral to plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;myelin sheath;neuronal cell body;non-membrane-bounded organelle;nuclear membrane;nuclear outer membrane;nuclear part;nucleolus;nucleoplasm;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;plasma membrane part;platelet dense tubular network membrane Alzheimer's disease;Calcium signaling pathway;Gap junction;Gastric acid secretion;GnRH signaling pathway;Long-term depression;Long-term potentiation;Oocyte meiosis;Pancreatic secretion;Phosphatidylinositol signaling system;Salivary secretion;Taste transduction;Vascular smooth muscle contraction 5.96E-48 1 11 9 6

Q99733;F5HFY4;C9JZI7;E9PNW0;E9PJJ2;E9PS34;E9PNJ7;C9J6D1;A8MXH2;E9PKT8;E9PKI2;E9PP22;C9J1B1;H0YCI4 Nucleosome assembly protein 1-like 4 NAP1L4;NAP1L4b >sp|Q99733|NP1L4_HUMAN Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1;>tr|F5HFY4|F5HFY4_HUMAN Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4b PE=2 SV=1;>tr|C9JZI7|C9JZI7_HUMAN Nucleosome assembly protein 1-like 4 (0.15 0.01 -0.04 0.02 0.10 0.00 0.27 -0.09 0.144780509 -0.034413146 cellular component assembly;cellular component assembly at cellular level;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;protein binding;unfolded protein binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.53E-193 14 11 9 30.4

O43290 U4/U6.U5 tri-snRNP-associated protein 1 SART1 >sp|O43290|SNUT1_HUMAN U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1 -0.31 0.21 0.34 0.27 0.11 -0.35 -1.25 -0.67 0.888581934 0.666858129 biological regulation;cell cycle arrest;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of cytotoxic T cell differentiation;positive regulation of developmental process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of T cell activation;positive regulation of T cell differentiation;regulation of biological process;regulation of cell activation;regulation of cell cycle;regulation of cell differentiation;regulation of cellular process;regulation of cytotoxic T cell differentiation;regulation of developmental process;regulation of immune system process;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of T cell activation;regulation of T cell differentiation;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;spliceosomal snRNP assembly Cajal body;catalytic step 2 spliceosome;cell part;cytoplasmic part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 1.60E-83 1 11 9 20.1

Q13492-3;Q13492-2;Q13492-5;Q13492;Q13492-4;E9PKP6;E9PI56;E9PLJ8;H0YCY1;E9PK13;E9PJT1;E5RFU0;E5RHK9;E5RFC6;E5RK51;E5RIJ5;E5RGY9;O60641-3;O60641-4;E9PDG8;O60641;F5GWN7 Phosphatidylinositol-binding clathrin assembly proteinPICALM >sp|Q13492-3|PICAL_HUMAN Isoform 3 of Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM;>sp|Q13492-2|PICAL_HUMAN Isoform 2 of Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM;>sp|Q13492-5|PICAL -0.08 -0.01 -0.21 0.04 0.23 0.18 -0.24 0.25 0.5588484 -0.17237967 "anatomical structure development;anatomical structure morphogenesis;axonogenesis;biological regulation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein complex assembly;clathrin coat assembly;dendrite morphogenesis;developmental process;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;hemopoiesis;hemopoietic or lymphoid organ development;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of endocytosis;negative regulation of receptor-mediated endocytosis;negative regulation of transport;neuron projection morphogenesis;organ development;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;protein complex assembly;protein complex subunit organization;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of endocytosis;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of receptor-mediated endocytosis;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of transport;regulation of vesicle-mediated transport;transport;vesicle coating;vesicle organization;vesicle-mediated transport" 1-phosphatidylinositol binding;binding;clathrin binding;clathrin heavy chain binding;lipid binding;phosphatidylinositol binding;phospholipid binding;protein binding cell part;clathrin coat;clathrin-coated vesicle;coated pit;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane;postsynaptic membrane;presynaptic membrane;protein complex;synapse part;synaptic membrane;vesicle 9.89E-139 22 12 9 32.8

Q8WZ42-5;Q8WZ42-11;Q8WZ42-4;Q8WZ42-7;Q8WZ42-2;Q8WZ42;Q8WZ42-8;Q8WZ42-13;Q8WZ42-12;Q8WZ42-3;Q8WZ42-10;Q8WZ42-9 TitinTTN>sp|Q8WZ42-5|TITIN_HUMAN Isoform 5 of Titin OS=Homo sapiens GN=TTN;>sp|Q8WZ42-11|TITIN_HUMAN Isoform 11 of Titin OS=Homo sapiens GN=TTN;>sp|Q8WZ42-4|TITIN_HUMAN Isoform 4 of Titin OS=Homo sapiens GN=TTN;>sp|Q8WZ42-7|TITIN_HUMAN Isoform 7 of Titin OS=Homo s -0.35 0.65 0.34 1.20 0.02 0.48 -0.29 1.23 0.075909076 0.101911239 actin cytoskeleton organization;actin filament organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;actomyosin structure organization;adult heart development;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;cardiac muscle contraction;cardiac muscle fiber development;cardiac muscle hypertrophy;cardiac muscle tissue morphogenesis;cardiac myofibril assembly;cell activation;cell cycle process;cell development;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;chordate embryonic development;chromosome condensation;chromosome organization;cytoskeleton organization;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection of muscle stretch;detection of stimulus;developmental process;directional locomotion;DNA conformation change;DNA metabolic process;DNA packaging;embryo development;embryo development ending in birth or egg hatching;establishment of localization;establishment of localization in cell;exocytosis;forward locomotion;heart development;in utero embryonic development;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mitotic chromosome condensation;multicellular organismal process;muscle cell development;muscle contraction;muscle fiber development;muscle filament sliding;muscle hypertrophy;muscle system process;muscle tissue morphogenesis;myofibril assembly;myosin filament assembly;myosin filament organization;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle organization;platelet activation;platelet degranulation;primary metabolic process;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to abiotic stimulus;response to calcium ion;response to chemical stimulus;response to external stimulus;response to inorganic substance;response to mechanical stimulus;response to metal ion;response to muscle stretch;response to stimulus;sarcomere organization;sarcomerogenesis;secretion;secretion by cell;skeletal muscle myosin thick filament assembly;skeletal muscle thin filament assembly;striated muscle cell development;striated muscle contraction;striated muscle hypertrophy;striated muscle myosin thick filament assembly;system process;tissue morphogenesis;transport;vesicle-mediated transport "actin binding;actin filament binding;actinin binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;calmodulin binding;catalytic activity;cation binding;cytoskeletal protein binding;ion binding;kinase activity;metal ion binding;nucleic acid binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein self-association;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural constituent of muscle;structural molecule activity;telethonin binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;chromosome;condensed chromosome;condensed nuclear chromosome;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;M band;membrane-bounded organelle;non-membrane-bounded organelle;nuclear chromosome;nuclear part;organelle;organelle part;striated muscle thin filament;Z disc Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM) 8.24E-21 12 12 9 0.4

P47755;C9JUG7;B4DG50;F8W9N7;F8WED3 F-actin-capping protein subunit alpha-2 CAPZA2 >sp|P47755|CAZA2_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3;>tr|C9JUG7|C9JUG7_HUMAN F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=2 SV=1;>tr|B4DG50|B4DG50_HUMAN F-actin-capping protein subunit a -0.17 0.07 -0.16 0.29 0.30 0.56 0.16 0.27 0.970911373 -0.314595047 actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;defense response;hemostasis;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;protein complex assembly;protein complex subunit organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to stimulus;response to stress cell cortex part;cell part;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular region;F-actin capping protein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;protein complex 2.07E-102 5 13 9 57.3

Q9UKV3-5;E7EQT4;Q9UKV3;G3V3B0;Q9UKV3-3;Q9UKV3-2;G3V3T3 Apoptotic chromatin condensation inducer in the nucleus ACIN1 >sp|Q9UKV3-5|ACINU_HUMAN Isoform 4 of Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1;>tr|E7EQT4|E7EQT4_HUMAN Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=2 SV=2;>sp|Q9UKV3|ACINU_HUMAN -0.11 0.59 0.26 0.65 0.02 -0.11 -1.27 -0.06 0.85372027 0.70437116 apoptotic chromosome condensation;biological regulation;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome condensation;chromosome organization;developmental process;DNA conformation change;DNA metabolic process;DNA packaging;erythrocyte differentiation;macromolecule metabolic process;metabolic process;myeloid cell differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of monocyte differentiation;positive regulation of myeloid cell differentiation;positive regulation of myeloid leukocyte differentiation;primary metabolic process;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of monocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation "ATPase activity;binding;catalytic activity;enzyme binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;pyrophosphatase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part mRNA surveillance pathway;RNA transport;Spliceosome 4.23E-90 7 10 10 11.3

P54819-5;P54819-2;F8W1A4;P54819;F8VZG5;P54819-6;P54819-3;G3V213;F8VY04;P54819-4;F8VPP1 "Adenylate kinase 2, mitochondrial" AK2">sp|P54819-5|KAD2_HUMAN Isoform 5 of Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2;>sp|P54819-2|KAD2_HUMAN Isoform 2 of Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2;>tr|F8W1A4|F8W1A4_HUMAN Adenylate kinase 2, mitochondrial OS=Homo sa" -0.13 -0.04 -0.03 0.03 -0.11 -0.34 0.05 -0.33 0.573993922 0.136251021 2'-deoxyribonucleotide metabolic process;ADP biosynthetic process;ADP metabolic process;AMP metabolic process;anatomical structure development;ATP metabolic process;biosynthetic process;brain development;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;dATP metabolic process;deoxyribonucleoside triphosphate metabolic process;deoxyribonucleotide metabolic process;developmental process;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;liver development;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside diphosphate biosynthetic process;nucleoside diphosphate metabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organ development;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;purine deoxyribonucleoside triphosphate metabolic process;purine deoxyribonucleotide metabolic process;purine nucleoside diphosphate biosynthetic process;purine nucleoside diphosphate metabolic process;purine nucleoside monophosphate metabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside diphosphate biosynthetic process;purine ribonucleoside diphosphate metabolic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;response to thyroid hormone stimulus;ribonucleoside diphosphate biosynthetic process;ribonucleoside diphosphate metabolic process;ribonucleoside monophosphate metabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;adenylate kinase activity;ATP binding;binding;catalytic activity;kinase activity;nucleobase-containing compound kinase activity;nucleotide binding;nucleotide kinase activity;phosphotransferase activity, phosphate group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial part;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part Purine metabolism 5.57E-65 11 10 10 53.1

P53004;C9J1E1 Biliverdin reductase A BLVRA >sp|P53004|BIEA_HUMAN Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2 -0.07 -0.19 0.09 -0.02 -0.05 -0.04 0.56 0.12 0.526931642 -0.193535951 catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cofactor catabolic process;cofactor metabolic process;heme catabolic process;heme metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;oxidation-reduction process;pigment catabolic process;pigment metabolic process;porphyrin-containing compound catabolic process;porphyrin-containing compound metabolic process;small molecule metabolic process;tetrapyrrole catabolic process;tetrapyrrole metabolic process "biliverdin reductase activity;binding;catalytic activity;cation binding;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;transition metal ion binding;zinc ion binding"cell part;cytoplasmic part;cytosol;intracellular part Porphyrin and chlorophyll metabolism 2.85E-65 2 10 10 34.5

Q8IVT2 Uncharacterized protein C19orf21 C19orf21 >sp|Q8IVT2|MISP_HUMAN Mitotic interactor and substrate of PLK1 OS=Homo sapiens GN=MISP PE=1 SV=1 0.07 0.10 0.37 0.52 -1.16 0.20 -0.18 0.83 0.313655222 0.341773791 6.70E-33 1 10 10 23.9

P00918;E5RID5;E5RK37 Carbonic anhydrase 2 CA2 >sp|P00918|CAH2_HUMAN Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 -0.30 -0.35 0.11 -0.25 -0.42 0.15 1.20 0.48 0.660106008 -0.547492258 anatomical structure development;anatomical structure morphogenesis;anion transport;bicarbonate transport;biological regulation;carbon dioxide transport;cellular metabolic process;cellular process;developmental process;establishment of localization;gas transport;inorganic anion transport;ion transport;kidney development;metabolic process;morphogenesis of an epithelium;odontogenesis;odontogenesis of dentine-containing tooth;one-carbon metabolic process;organ development;organ morphogenesis;organic anion transport;positive regulation of biological process;positive regulation of bone remodeling;positive regulation of bone resorption;positive regulation of cell differentiation;positive regulation of cellular pH reduction;positive regulation of cellular process;positive regulation of developmental process;positive regulation of homeostatic process;positive regulation of multicellular organismal process;positive regulation of myeloid cell differentiation;positive regulation of myeloid leukocyte differentiation;positive regulation of osteoclast differentiation;positive regulation of tissue remodeling;regulation of biological process;regulation of bone remodeling;regulation of bone resorption;regulation of cell differentiation;regulation of cellular pH reduction;regulation of cellular process;regulation of developmental process;regulation of homeostatic process;regulation of immune system process;regulation of ion homeostasis;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of osteoclast differentiation;regulation of tissue remodeling;response to abiotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to pH;response to steroid hormone stimulus;response to stimulus;response to stress;response to zinc ion;secretion;small molecule metabolic process;tissue morphogenesis;transport binding;carbonate dehydratase activity;carbon-oxygen lyase activity;catalytic activity;cation binding;hydro-lyase activity;ion binding;lyase activity;metal ion binding;transition metal ion binding;zinc ion binding apical part of cell;axon;basolateral plasma membrane;cell part;cell projection;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular part;membrane part;microvillus;neuron projection;plasma membrane part Nitrogen metabolism 3.99E-58 3 10 10 45.8

Q6P1N0;Q6P1N0-2;K7EJY5;K7EMP1 Coiled-coil and C2 domain-containing protein 1ACC2D1A >sp|Q6P1N0|C2D1A_HUMAN Coiled-coil and C2 domain-containing protein 1A OS=Homo sapiens GN=CC2D1A PE=1 SV=1;>sp|Q6P1N0-2|C2D1A_HUMAN Isoform 2 of Coiled-coil and C2 domain-containing protein 1A OS=Homo sapiens GN=CC2D1A -0.03 0.12 0.27 0.06 -0.20 0.16 -0.12 0.16 0.379704949 0.106008808 biological regulation;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signalingbinding;core promoter proximal region DNA binding;core promoter proximal region sequence-specific DNA binding;DNA binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity;RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;signal transducer activity;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding cell part;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;nucleus;organelle;organelle part 2.37E-37 4 10 10 14.2

Q96A33;Q96A33-2;J3QR89 Coiled-coil domain-containing protein 47 CCDC47 >sp|Q96A33|CCD47_HUMAN Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1;>sp|Q96A33-2|CCD47_HUMAN Isoform 2 of Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47-0.08 0.09 0.10 0.18 0.16 0.02 -0.59 -0.14 0.502946969 0.208402698 biological regulation;calcium ion homeostasis;cation homeostasis;cellular process;cellular response to biotic stimulus;cellular response to stimulus;cellular response to stress;chemical homeostasis;developmental process;divalent inorganic cation homeostasis;embryo development;ER overload response;ER-nucleus signaling pathway;homeostatic process;ion homeostasis;metal ion homeostasis;post-embryonic development;regulation of biological process;regulation of biological quality;regulation of cellular process;response to biotic stimulus;response to endoplasmic reticulum stress;response to stimulus;response to stress;signal transduction binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;organelle 1.18E-70 3 10 10 25.3

P46108;P46108-2;I3L297 Adapter molecule crk CRK >sp|P46108|CRK_HUMAN Adapter molecule crk OS=Homo sapiens GN=CRK PE=1 SV=2;>sp|P46108-2|CRK_HUMAN Isoform Crk-I of Adapter molecule crk OS=Homo sapiens GN=CRK;>tr|I3L297|I3L297_HUMAN Adapter molecule crk OS=Homo sapiens GN=CRK PE=2 SV=1 -0.03 -0.17 0.23 -0.03 -0.03 0.22 0.55 0.22 0.713321647 -0.241924 "activation of MAPKK activity;activation of protein kinase activity;biological regulation;cell activation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;defense response;enzyme linked receptor protein signaling pathway;ephrin receptor signaling pathway;immune response;immune system process;innate immune response;insulin receptor signaling pathway;macromolecule metabolic process;macromolecule modification;metabolic process;nerve growth factor receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of gene expression;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of purine nucleotide catabolic process;regulation of Rac protein signal transduction;regulation of Ras GTPase activity;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane Bacterial invasion of epithelial cells;Chemokine signaling pathway;Chronic myeloid leukemia;ErbB signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Insulin signaling pathway;MAPK signaling pathway;Neurotrophin signaling pathway;Pathways in cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis 1.35E-73 3 10 10 44.1

P46109 Crk-like protein CRKL >sp|P46109|CRKL_HUMAN Crk-like protein OS=Homo sapiens GN=CRKL PE=1 SV=1 0.02 -0.05 0.14 -0.04 -0.24 -0.30 0.40 -0.10 0.167906604 0.075684268 activation of MAPKK activity;activation of protein kinase activity;anatomical structure development;anatomical structure morphogenesis;anterior/posterior pattern specification;biological regulation;blood vessel development;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;developmental process;enzyme linked receptor protein signaling pathway;gland development;heart development;hemopoietic or lymphoid organ development;intracellular protein kinase cascade;intracellular signal transduction;JNK cascade;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;nerve growth factor receptor signaling pathway;organ development;organ morphogenesis;parathyroid gland development;pattern specification process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;Ras protein signal transduction;regionalization;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;response to stress;signal transduction;small GTPase mediated signal transduction;stress-activated protein kinase signaling cascade;thymus development;transmembrane receptor protein tyrosine kinase signaling pathway "binding;binding, bridging;molecular transducer activity;protein binding;protein binding, bridging;SH3/SH2 adaptor activity;signal transducer activity;signaling adaptor activity" cell part;cytoplasmic part;cytosol;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle Bacterial invasion of epithelial cells;Chemokine signaling pathway;Chronic myeloid leukemia;ErbB signaling pathway;Fc gamma R-mediated phagocytosis;Focal adhesion;Insulin signaling pathway;MAPK signaling pathway;Neurotrophin signaling pathway;Pathways in cancer;Regulation of actin cytoskeleton;Renal cell carcinoma;Shigellosis 2.41E-85 1 10 10 44.9

P00387-2;P00387;P00387-3;B1AHF3 NADH-cytochrome b5 reductase 3;NADH-cytochrome b5 reductase 3 membrane-bound form;NADH-cytochrome b5 reductase 3 soluble form CYB5R3 >sp|P00387-2|NB5R3_HUMAN Isoform 2 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3;>sp|P00387|NB5R3_HUMAN NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3;>sp|P00387-3|NB5R3_HUMAN Isoform 3 of NADH-cytochrome b5 reductase 3 OS -0.23 0.11 0.02 0.12 0.61 0.70 -0.52 0.32 0.380421679 -0.273243509 alcohol metabolic process;biosynthetic process;blood circulation;carboxylic acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;cholesterol biosynthetic process;cholesterol metabolic process;circulatory system process;L-ascorbic acid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;multicellular organismal process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;system process;vitamin metabolic process;water-soluble vitamin metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;AMP binding;binding;catalytic activity;coenzyme binding;cofactor binding;cytochrome-b5 reductase activity;FAD binding;flavin adenine dinucleotide binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosolic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;hemoglobin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex Amino sugar and nucleotide sugar metabolism 1.01E-133 4 10 10 46

Q9NVP1;H7C452 ATP-dependent RNA helicase DDX18 DDX18 >sp|Q9NVP1|DDX18_HUMAN ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 -0.33 1.08 0.06 0.96 -0.56 -0.11 -1.31 0.13 0.827136031 0.905431633 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 4.15E-36 2 10 10 19.1

B7Z6B8;Q16698;E5RJG7;E5RFV2;E5RJD2;E5RID6;H0YAW3 "2,4-dienoyl-CoA reductase, mitochondrial" DECR1 ">tr|B7Z6B8|B7Z6B8_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=2 SV=1;>sp|Q16698|DECR_HUMAN 2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1;>tr|E5RJG7|E5RJG7_HUMAN 2,4-dienoyl-CoA reductase, mitocho" -0.27 -0.08 -0.08 0.07 0.16 0.36 0.05 0.10 1.125568136 -0.259626246 carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;small molecule catabolic process;small molecule metabolic process "2,4-dienoyl-CoA reductase (NADPH) activity;binding;catalytic activity;coenzyme binding;cofactor binding;NADP binding;NADPH binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part 1.01E-91 7 10 10 38.3

Q92620;B4DVG8;H3BQT9;H3BV01;J3KTG2;J3KRT1 Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 DHX38 >sp|Q92620|PRP16_HUMAN Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16 OS=Homo sapiens GN=DHX38 PE=1 SV=2 0.22 0.22 0.10 -0.06 0.32 -0.11 -0.29 0.08 0.317854752 0.117808083 "biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 1.58E-72 6 10 10 11.1

P36957;B7Z5W8;Q86SW4;H0YJF9;G3V5M3;G3V3F0 "Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial" DLST ">sp|P36957|ODO2_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLST PE=1 SV=4;>tr|B7Z5W8|B7Z5W8_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-" -0.44 0.10 0.10 0.26 0.13 0.02 -1.10 -0.24 0.382566879 0.301303225 acetyl-CoA catabolic process;acetyl-CoA metabolic process;amine catabolic process;amine metabolic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;L-lysine catabolic process;L-lysine catabolic process to acetyl-CoA;L-lysine catabolic process to acetyl-CoA via saccharopine;L-lysine metabolic process;lysine catabolic process;lysine metabolic process;metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;dihydrolipoyllysine-residue succinyltransferase activity;S-acyltransferase activity;S-succinyltransferase activity;succinyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part;oxoglutarate dehydrogenase complex;protein complex Citrate cycle (TCA cycle);Lysine degradation 2.81E-158 6 10 10 23.4

P25685;B4DX52;M0R080;M0QYT3;M0QXK0;M0R128;M0R1D6;M0QZD0 DnaJ homolog subfamily B member 1 DNAJB1 >sp|P25685|DNJB1_HUMAN DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4;>tr|B4DX52|B4DX52_HUMAN DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=2 SV=1 0.05 0.25 -0.09 -0.07 -0.40 -0.19 0.17 -0.05 0.437632271 0.152121578 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone cofactor-dependent protein refolding;chaperone mediated protein folding requiring cofactor;chaperone-mediated protein folding;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;protein refolding;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Protein processing in endoplasmic reticulum 6.26E-61 8 10 10 31.2

Q8TDB6;Q8TDB6-2 E3 ubiquitin-protein ligase DTX3L DTX3L >sp|Q8TDB6|DTX3L_HUMAN E3 ubiquitin-protein ligase DTX3L OS=Homo sapiens GN=DTX3L PE=1 SV=1 0.26 0.16 -0.02 -0.16 -1.77 -0.86 -0.23 0.38 0.617037513 0.681886643 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;DNA metabolic process;DNA repair;double-strand break repair;histone modification;histone monoubiquitination;histone ubiquitination;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein ubiquitination;response to DNA damage stimulus;response to stimulus;response to stress "acid-amino acid ligase activity;binding;catalytic activity;cation binding;histone binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;protein binding;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Notch signaling pathway1.28E-59 2 10 10 17.2

O00303;B3KSH1;B4DEW9;H0YDT6;E9PQV8 Eukaryotic translation initiation factor 3 subunit F EIF3F >sp|O00303|EIF3F_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1;>tr|B3KSH1|B3KSH1_HUMAN Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1;>tr|B4DEW9|B4DEW9_HUMAN Eukaryoti 0.20 0.05 -0.10 -0.07 -0.25 -0.40 -0.06 -0.36 1.156762509 0.283729909 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "binding;catalytic activity;cysteine-type peptidase activity;hydrolase activity;nucleic acid binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport1.29E-227 5 10 10 34.2

Q8N766-2;Q8N766;Q8N766-4;Q8N766-3;H7C4E3 ER membrane protein complex subunit 1 EMC1 >sp|Q8N766-2|EMC1_HUMAN Isoform 2 of ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1;>sp|Q8N766|EMC1_HUMAN ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1;>sp|Q8N766-4|EMC1_HUMAN Isoform 4 of ER membrane protein comple 0.09 0.23 -0.17 -0.05 0.78 0.59 -0.29 0.18 0.478097396 -0.291558346 ER membrane protein complex;macromolecular complex;protein complex 6.76E-51 5 10 10 15.1

Q8N8S7-2;Q8N8S7 Protein enabled homolog ENAH >sp|Q8N8S7-2|ENAH_HUMAN Isoform 2 of Protein enabled homolog OS=Homo sapiens GN=ENAH;>sp|Q8N8S7|ENAH_HUMAN Protein enabled homolog OS=Homo sapiens GN=ENAH PE=1 SV=2 -0.19 -0.26 -0.12 -0.09 -1.15 -0.56 0.84 0.48 0.049757237 -0.068332138 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin polymerization or depolymerization;activation of immune response;anatomical structure formation involved in morphogenesis;antigen receptor-mediated signaling pathway;axon guidance;biological regulation;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;intracellular transport;locomotion;macromolecular complex subunit organization;neural tube closure;organelle organization;positive regulation of biological process;positive regulation of immune response;positive regulation of immune system process;positive regulation of response to stimulus;regulation of biological process;regulation of cellular process;regulation of immune response;regulation of immune system process;regulation of response to stimulus;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;T cell receptor signaling pathway;taxis;transport;tube closure;tube formation actin filament bundle;actomyosin;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytosol;filopodium;focal adhesion;intracellular organelle part;intracellular part;lamellipodium;membrane;organelle part;plasma membrane;stress fiber;synapse Regulation of actin cytoskeleton 1.49E-53 2 10 10 26

P42566;B1AUU8;H7BYP0;P42566-2;A6NL94 Epidermal growth factor receptor substrate 15 EPS15 >sp|P42566|EPS15_HUMAN Epidermal growth factor receptor substrate 15 OS=Homo sapiens GN=EPS15 PE=1 SV=2;>tr|B1AUU8|B1AUU8_HUMAN Epidermal growth factor receptor substrate 15 OS=Homo sapiens GN=EPS15 PE=2 SV=1;>tr|H7BYP0|H7BYP0_HUMAN Epidermal growth factor 0.20 0.24 0.37 0.04 -0.17 -0.04 -0.09 0.53 0.364849575 0.157341294 biological regulation;cell proliferation;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;cellular protein complex assembly;cellular response to stimulus;clathrin coat assembly;endocytic recycling;endocytosis;endosome transport;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle organization;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle coating;vesicle organization;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding AP-2 adaptor complex;AP-type membrane coat adaptor complex;cell part;cell projection membrane;cell projection part;cilium membrane;cilium part;clathrin adaptor complex;coated pit;cytoplasm;cytoplasmic part;cytoplasmic vesicle part;cytosol;early endosome membrane;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex Endocytosis 2.05E-44 5 10 10 17.4

Q9NUQ9;Q9NW21;E5RJE1;E5RIR8;E5RJL8;E5RI16;E5RGI7;Q9H0Q0;E5RK61;E5RFS4;E5RHU5 Protein FAM49B FAM49B >sp|Q9NUQ9|FA49B_HUMAN Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1;>tr|Q9NW21|Q9NW21_HUMAN Protein FAM49B OS=Homo sapiens GN=FAM49B PE=2 SV=1 0.12 -0.03 0.12 -0.05 -0.98 -0.35 0.38 0.08 0.339187337 0.253873715 cell part;cell projection;cilium;intracellular 3.33E-147 11 10 10 37

P02792 Ferritin light chain FTL >sp|P02792|FRIL_HUMAN Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2-0.91 0.53 0.18 0.96 -0.04 0.41 -0.29 -0.43 0.240221552 0.276705952 biological regulation;cation homeostasis;cation transport;cell death;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular membrane organization;cellular metal ion homeostasis;cellular process;chemical homeostasis;death;establishment of localization;establishment of localization in cell;Golgi vesicle transport;homeostatic process;intracellular transport;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;membrane organization;metal ion homeostasis;metal ion transport;post-Golgi vesicle-mediated transport;regulation of biological quality;transition metal ion transport;transmembrane transport;transport;vesicle-mediated transport binding;catalytic activity;cation binding;ferric iron binding;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;transition metal ion binding cell part;cytoplasmic part;cytosol;ferritin complex;intracellular ferritin complex;intracellular part;macromolecular complex;protein complex Mineral absorption;Porphyrin and chlorophyll metabolism 3.61E-58 1 10 10 48

Q96RP9;C9IZ01;Q96RP9-2;F8WAU4 "Elongation factor G, mitochondrial" GFM1 ">sp|Q96RP9|EFGM_HUMAN Elongation factor G, mitochondrial OS=Homo sapiens GN=GFM1 PE=1 SV=2;>tr|C9IZ01|C9IZ01_HUMAN Elongation factor G, mitochondrial OS=Homo sapiens GN=GFM1 PE=2 SV=1;>sp|Q96RP9-2|EFGM_HUMAN Isoform 2 of Elongation factor G, mitochondrial" 0.20 -0.10 0.05 -0.06 -0.60 -0.24 -0.04 -0.50 1.070366686 0.367823062 biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrial translational elongation;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;translational elongation"binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding"	cell part;cytoplasmic part;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle		2.34E-34	4	10	10	20.4

Q9BVP2-2;Q9BVP2;C9JYH9;C9JZT7;B4DMU5	Guanine nucleotide-binding protein-like 3	GNL3	>sp|Q9BVP2-2|GNL3_HUMAN Isoform 2 of Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3;>sp|Q9BVP2|GNL3_HUMAN Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2-0.07	0.48	0.09	0.56	-0.24	-0.27	-1.23	-0.06		0.998055267	0.714568245	biological regulation;cell proliferation;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;ribonucleoprotein complex biogenesis;ribosome biogenesis	"binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding"	cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part	Ribosome biogenesis in eukaryotes	8.98E-45	5	10	10	26.3

Q9UBQ7;Q5T946;Q9H636;Q6IQ16	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR	>sp|Q9UBQ7|GRHPR_HUMAN Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1;>tr|Q5T946|Q5T946_HUMAN Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=2 SV=1	0.12	0.05	0.08	0.07	0.15	0.16	0.16	0.08		1.03422016	-0.056293017	biological regulation;carboxylic acid metabolic process;catabolic process;cellular aldehyde metabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;establishment of localization;excretion;glyoxylate metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;monocarboxylic acid metabolic process;multicellular organismal process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein oligomerization;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;secretion;small molecule metabolic process;system process;transport;ubiquitin-dependent protein catabolic process	"binding;catalytic activity;coenzyme binding;cofactor binding;glycerate dehydrogenase activity;glyoxylate reductase (NADP) activity;hydroxypyruvate reductase activity;identical protein binding;NAD binding;NADP binding;NADPH binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;protein binding;protein dimerization activity;protein homodimerization activity"	cell part;Cul3-RING ubiquitin ligase complex;cullin-RING ubiquitin ligase complex;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-enclosed lumen;microbody lumen;microbody part;nucleus;organelle;organelle lumen;organelle part;peroxisomal matrix;peroxisomal part;protein complex;ubiquitin ligase complex	Glyoxylate and dicarboxylate metabolism;Pyruvate metabolism	2.81E-169	4	10	10	40.5

P51610-2;P51610;P51610-4;A6NEM2;P51610-3;H7C1C4	Host cell factor 1;HCF N-terminal chain 1;HCF N-terminal chain 2;HCF N-terminal chain 3;HCF N-terminal chain 4;HCF N-terminal chain 5;HCF N-terminal chain 6;HCF C-terminal chain 1;HCF C-terminal chain 2;HCF C-terminal chain 3;HCF C-terminal chain 4;HCF C-terminal chain 5;HCF C-terminal chain 6	HCFC1	>sp|P51610-2|HCFC1_HUMAN Isoform 2 of Host cell factor 1 OS=Homo sapiens GN=HCFC1;>sp|P51610|HCFC1_HUMAN Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2;>sp|P51610-4|HCFC1_HUMAN Isoform 4 of Host cell factor 1 OS=Homo sapiens GN=HCFC1;>tr|A6NEM2|A6NE	0.04	0.08	-0.07	-0.01	0.26	0.00	-0.79	-0.38		0.42499125	0.239113716	"biological regulation;biosynthetic process;cell cycle;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;histone acetylation;histone H4 acetylation;histone H4-K16 acetylation;histone H4-K5 acetylation;histone H4-K8 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;positive regulation of biological process;positive regulation of cell cycle;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein stabilization;reactivation of latent virus;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein stability;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent;viral reproductive process"	binding;chromatin binding;nucleic acid binding transcription factor activity;protein binding transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity	cell body;cell part;chromatin remodeling complex;cytoplasmic part;histone acetyltransferase complex;histone methyltransferase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;methyltransferase complex;mitochondrion;MLL1 complex;MLL5-L complex;neuronal cell body;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex;Set1C/COMPASS complex		3.66E-31	6	10	10	7.7

Q32P28;Q32P28-3;H7C0D1;H7C2W6;E2QRI1;Q32P28-2	Prolyl 3-hydroxylase 1	LEPRE1	>sp|Q32P28|P3H1_HUMAN Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1 PE=1 SV=2;>sp|Q32P28-3|P3H1_HUMAN Isoform 3 of Prolyl 3-hydroxylase 1 OS=Homo sapiens GN=LEPRE1	-0.31	-0.07	-0.31	0.01	1.32	0.95	-0.07	-0.03		0.842769115	-0.708856133	biological regulation;cell growth;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen fibril organization;extracellular matrix organization;extracellular structure organization;growth;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of multicellular organismal process;regulation of ossification	"binding;carboxylic acid binding;catalytic activity;cation binding;dioxygenase activity;ion binding;iron ion binding;L-ascorbic acid binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptidyl-proline 3-dioxygenase activity;peptidyl-proline dioxygenase activity;procollagen-proline 3-dioxygenase activity;procollagen-proline dioxygenase activity;transition metal ion binding;vitamin binding"	cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix;extracellular region part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;nucleus;organelle;organelle lumen;organelle part;proteinaceous extracellular matrix		1.99E-39	6	10	10	14.5

Q12907;D6RBV2;D6RIU4;D6RDX1;D6RBH1	Vesicular integral-membrane protein VIP36	LMAN2	>sp|Q12907|LMAN2_HUMAN Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1

SV=1;>tr|D6RBV2|D6RBV2_HUMAN Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=2 SV=1;>tr|D6RIU4|D6RIU4_HUMAN Vesicular integral-membrane pro -0.25 -0.14 -0.30 0.08 0.69 0.35 -0.15 0.02 0.810167176 -0.384614778 establishment of localization;establishment of protein localization;protein transport;transport binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle partProtein processing in endoplasmic reticulum 1.57E-57 5 10 10 29.8

P46013-2;P46013 Antigen KI-67 MKI67 >sp|P46013-2|KI67_HUMAN Isoform Short of Antigen KI-67 OS=Homo sapiens GN=MKI67;>sp|P46013|KI67_HUMAN Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 0.15 1.19 -0.27 1.12 -0.42 0.14 -1.32 -0.14 0.877936506 0.985399399 anatomical structure morphogenesis;cell cycle phase;cell cycle process;cell proliferation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;macromolecule metabolic process;meiosis;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ morphogenesis;organ regeneration;primary metabolic process;regeneration;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding "cell part;chromosomal part;chromosome;chromosome, centromeric region;condensed chromosome;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part" 3.47E-28 2 10 10 6.6

Q96T76;Q96T76-8;Q96T76-9;Q96T76-5;H0Y746;Q5T454;Q96T76-7;H0Y7V3;H7C1W5;B0QZ77;H7C0A9;F8WCH8 MMS19 nucleotide excision repair protein homolog MMS19 >sp|Q96T76|MMS19_HUMAN MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2;>sp|Q96T76-8|MMS19_HUMAN Isoform 5 of MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19;>sp|Q96T76-9|MMS19_HUMAN Isoform 6 of 0.15 0.04 -0.24 -0.02 -0.10 -0.20 0.17 -0.22 0.222454101 0.070910611 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome segregation;cofactor biosynthetic process;cofactor metabolic process;DNA metabolic process;DNA repair;iron-sulfur cluster assembly;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;metallo-sulfur cluster assembly;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to chemical stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;small molecule metabolic process;transcription, DNA-dependent;two-component signal transduction system (phosphorelay)" "binding;binding, bridging;protein binding;protein binding transcription factor activity;protein binding, bridging;protein complex scaffold;receptor signaling complex scaffold activity;structural molecule activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cytoskeletal part;holo TFIIH complex;intracellular organelle part;intracellular part;macromolecular complex;MMXD complex;nuclear part;nucleoplasm part;organelle part;protein complex;transcription factor complex 9.46E-61 12 10 10 14.9

P43246-2;P43246;E9PHA6;C9J809 DNA mismatch repair protein Msh2 MSH2 >sp|P43246-2|MSH2_HUMAN Isoform 2 of DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2;>sp|P43246|MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1;>tr|E9PHA6|E9PHA6_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens 0.12 -0.12 -0.04 0.05 0.07 -0.61 -0.53 -0.59 1.040096697 0.420496637 "anatomical structure development;apoptosis;ATP catabolic process;ATP metabolic process;B cell activation;B cell activation involved in immune response;B cell differentiation;biological regulation;catabolic process;cell activation;cell activation involved in immune response;cell cycle arrest;cell cycle checkpoint;cell cycle process;cell death;cell development;cell differentiation;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular response to stimulus;cellular response to stress;chordate embryonic development;chromosome organization;death;determination of adult lifespan;developmental process;developmental process involved in reproduction;DNA damage checkpoint;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;DNA integrity checkpoint;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;embryo development;embryo development ending in birth or egg hatching;gene conversion;generation of precursor metabolites and energy;germ cell development;gonad development;heterocycle catabolic process;heterocycle metabolic process;immune effector process;immune system process;in utero embryonic development;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;intra-S DNA damage checkpoint;isotype switching;leukocyte activation;leukocyte activation involved in immune response;leukocyte differentiation;lymphocyte activation;lymphocyte activation involved in immune response;lymphocyte differentiation;macromolecule metabolic process;maintenance of DNA repeat elements;male gonad development;meiotic gene conversion;meiotic mismatch repair;metabolic process;mismatch repair;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell death;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA recombination;negative regulation of macromolecule metabolic process;negative regulation of meiosis;negative regulation of metabolic process;negative regulation of neuron apoptosis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of reciprocal meiotic recombination;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organ development;organelle organization;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of helicase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of programmed cell death;postreplication repair;primary metabolic process;programmed cell death;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA recombination;regulation of helicase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of meiosis;regulation of meiosis I;regulation of meiotic cell cycle;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of reciprocal meiotic recombination;reproductive process;reproductive structure development;response to abiotic stimulus;response to DNA damage stimulus;response to ionizing radiation;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;response to UV-B;response to X-ray;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;small molecule metabolic process;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immune receptors via somatic mutation;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic hypermutation of immunoglobulin genes;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;centromeric DNA binding;damaged DNA binding;DNA binding;DNA insertion or deletion binding;DNA secondary structure binding;DNA-dependent ATPase activity;double-strand/single-strand DNA junction binding;double-stranded DNA binding;guanine/thymine mispair binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;loop DNA binding;mismatched DNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;sequence-specific DNA binding;structure-specific DNA binding;Y-form DNA binding" cell part;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mismatch repair complex;MutSalpha complex;MutSbeta complex;non-membrane-bounded organelle;nuclear chromosome;nuclear part;organelle;organelle part;protein complex Colorectal cancer;Mismatch repair;Pathways in cancer 1.70E-31 4 10 10 13.2

O94832;K7EIG7;J3QRN6;J3KRL0 Unconventional myosin-Id MYO1D >sp|O94832|MYO1D_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2;>tr|K7EIG7|K7EIG7_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=4 SV=1;>tr|J3QRN6|J3QRN6_HUMAN Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=4 SV=1 0.10 0.28 0.15 0.29 0.44 0.56 0.07 0.37 0.567628655 -0.154869469 biological regulation;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process "actin-dependent ATPase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" axolemma;axon part;cell part;cell projection membrane;cell projection part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;myosin complex;neuron projection membrane;organelle;organelle part;plasma membrane part;protein complex;smooth endoplasmic reticulum 2.35E-29 4 10 10 14.3

P57740;B4DZ67;Q6PJE1;H0YG15;G3V1T4 Nuclear pore complex protein Nup107 NUP107 >sp|P57740|NU107_HUMAN Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1;>tr|B4DZ67|B4DZ67_HUMAN Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=2 SV=1;>tr|Q6PJE1|Q6PJE1_HUMAN NUP107 protein OS=Homo sapiens GN=NUP107 0.06 0.57 0.26 0.53 -0.15 0.08 -0.74 0.03 1.036744564 0.548612506 anaphase;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular transport;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear export;nuclear pore complex assembly;nuclear pore organization;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process channel activity;nucleocytoplasmic transporter activity;passive transmembrane transporter activity;porin activity;structural constituent of nuclear pore;structural molecule activity;transmembrane transporter activity;transporter activity;wide pore channel activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;Nup107-160 complex;organelle;organelle membrane;organelle part;pore complex;protein complex RNA transport 2.56E-64 5 10 10 13.1

Q12769;G3V198;E9PR16;Q12769-3;E9PQY5;Q12769-2;E9PSI3 Nuclear pore complex protein Nup160 NUP160 >sp|Q12769|NU160_HUMAN Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=1 SV=3;>tr|G3V198|G3V198_HUMAN Nuclear pore complex protein Nup160 OS=Homo sapiens GN=NUP160 PE=2 SV=1;>tr|E9PR16|E9PR16_HUMAN Nuclear pore complex protein Nup160 OS=Ho0.17 0.50 -0.12 0.24 0.03 0.23 -0.37 0.19 0.383248266 0.177017511 anaphase;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular transport;M phase;M phase of mitotic cell cycle;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear export;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;organic substance transport;primary metabolic process;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process nucleocytoplasmic transporter activity;transporter activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;Nup107-160 complex;organelle part;protein complex RNA transport 5.64E-49 7 10 10 10

P52948-6;P52948-2;P52948-5;P52948;J3KP29;H7C3P6;P52948-4;P52948-3;H0YCT1;H0YEN4 Nuclear pore complex protein Nup98-Nup96;Nuclear pore complex protein Nup98;Nuclear pore complex protein Nup96 NUP98 >sp|P52948-6|NUP98_HUMAN Isoform 6 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98;>sp|P52948-2|NUP98_HUMAN Isoform 2 of Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens GN=NUP98;>sp|P52948-5|NUP98_HUMAN Isoform 5 of Nuclear po -0.11 0.76 0.20 0.59 0.04 0.32 -0.85 0.06 0.617316156 0.467635486 "anaphase;biological regulation;biosynthetic process;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;DNA metabolic process;DNA replication;establishment of localization;establishment of RNA localization;glucose transport;hexose transport;interaction with host;interspecies interaction between organisms;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA transport;multi-organism process;nitrogen compound metabolic process;nuclear pore complex assembly;nuclear pore organization;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein import into nucleus, docking;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process;virus-host interaction" binding;peptide binding;structural constituent of nuclear pore;structural molecule activity;transporter activity cell part;cytoplasmic part;cytosol;inclusion body;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear inclusion body;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;nucleoplasm;Nup107-160 complex;organelle membrane;organelle part;pore complex;protein complex RNA transport 1.12E-33 10 10 10 7.2

Q16513-3;Q16513-2;Q16513;Q16513-4;Q16513-5;B1AL79 Serine/threonine-protein kinase N2 PKN2 >sp|Q16513-3|PKN2_HUMAN Isoform 3 of Serine/threonine-protein kinase N2 OS=Homo sapiens GN=PKN2;>sp|Q16513-2|PKN2_HUMAN Isoform 2 of Serine/threonine-protein kinase N2 OS=Homo sapiens GN=PKN2;>sp|Q16513|PKN2_HUMAN Serine/threonine-protein kinase N2 OS=Homo 0.24 0.01 -0.08 -0.03 0.08 -0.03 0.29 -0.15 0.029085237 -0.010345012 "ameboidal cell migration;apical junction assembly;apoptosis;biological adhesion;biological regulation;biosynthetic process;cell adhesion;cell cycle;cell death;cell division;cell junction assembly;cell junction organization;cell migration;cell motility;cell-cell junction assembly;cell-cell junction organization;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;death;epithelial cell migration;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell cycle;positive regulation of cell cycle cytokinesis;positive regulation of cell cycle process;positive regulation of cell division;positive regulation of cellular process;positive regulation of cytokinesis;positive regulation of mitotic cell cycle;primary metabolic process;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle cytokinesis;regulation of cell cycle process;regulation of cell division;regulation of cell motility;regulation of cellular biosynthetic

process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokinesis;regulation of gene expression;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme binding;histone deacetylase binding;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein kinase C activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" apical junction complex;cell division site part;cell junction;cell part;cell projection;cell-cell junction;cleavage furrow;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane;membrane-bounded organelle;midbody;non-membrane-bounded organelle;nucleus;organelle
1.25E-26 6 10 10 16.9

P19174-2;P19174 "1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1" PLCG1 ">sp|P19174-2|PLCG1_HUMAN Isoform 2 of 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Homo sapiens GN=PLCG1;>sp|P19174|PLCG1_HUMAN 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Homo sapiens GN=PLCG1 PE=1 SV=1" 0.20 -0.16 0.22 -0.24 0.75 0.44 0.67 0.23 1.275022031 -0.521235455 activation of immune response;activation of MAPKK activity;activation of phospholipase C activity;activation of protein kinase activity;antigen receptor-mediated signaling pathway;axon guidance;biological regulation;blood coagulation;catabolic process;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component movement;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to epidermal growth factor stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;chemotaxis;chordate embryonic development;coagulation;cytokine-mediated signaling pathway;defense response;developmental process;embryo development;embryo development ending in birth or egg hatching;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway;hemostasis;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;in utero embryonic development;innate immune response;inositol phosphate metabolic process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;leukocyte migration;lipid catabolic process;lipid metabolic process;locomotion;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;multi-organism process;nerve growth factor receptor signaling pathway;organophosphate metabolic process;phosphate-containing compound metabolic process;phospholipid catabolic process;phospholipid metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of angiogenesis;positive regulation of biological process;positive regulation of blood vessel endothelial cell migration;positive regulation of catalytic activity;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of developmental process;positive regulation of endothelial cell migration;positive regulation of epithelial cell migration;positive regulation of hydrolase activity;positive regulation of immune response;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of lipase activity;positive regulation of locomotion;positive regulation of molecular function;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of protein kinase activity;positive regulation of response to stimulus;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of biological quality;regulation of blood vessel endothelial cell migration;regulation of body fluid levels;regulation of catalytic activity;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of endothelial cell migration;regulation of epithelial cell migration;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of kinase activity;regulation of lipase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of phosphate metabolic process;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of transferase activity;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to epidermal growth factor stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;response to stress;signal transduction;T cell receptor signaling pathway;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproductive process;virus-host interaction "binding;calcium ion binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lipase activity;lipid binding;metal ion binding;molecular transducer activity;phosphatidylinositol phospholipase C activity;phospholipase activity;phospholipase C activity;phospholipid binding;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;receptor signaling protein activity;signal transducer activity" cell part;cell projection;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane;nuclear part;organelle part;plasma membrane;protein complex;ruffle;signalosome Calcium signaling pathway;Epithelial cell signaling in Helicobacter pylori infection;ErbB signaling pathway;Fc epsilon RI signaling pathway;Fc gamma R-mediated phagocytosis;Glioma;Inositol phosphate metabolism;Leukocyte transendothelial migration;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Non-small cell lung cancer;Pathways in cancer;Phosphatidylinositol signaling system;VEGF signaling pathway;Vibrio cholerae infection
6.19E-57 2 10 10 9.5

Q99873-4;E9PKG1;Q99873-3;Q99873-2;Q99873;H7C2I1;E9PQ98;E9PIX6;E9PNR9;H0YDE4;Q9NR22-2;Q9NR22;E9PMZ2;E9PMW9;E9PI83 Protein arginine N-methyltransferase 1 PRMT1 >sp|Q99873-4|ANM1_HUMAN Isoform 4 of Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1;>tr|E9PKG1|E9PKG1_HUMAN Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=2 SV=1;>sp|Q99873-3|ANM1_HUMAN Isoform 3 of Protein arginine N-m 0.04 0.09 -0.41 0.07 -0.16 -0.31 -0.19 -0.06 0.395081968 0.126385584 biological regulation;cell projection organization;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chordate embryonic development;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;developmental process;embryo development;embryo development ending in birth or egg hatching;histone arginine methylation;histone methylation;histone modification;in utero embryonic development;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of megakaryocyte differentiation;negative regulation of myeloid cell differentiation;neuron projection development;one-carbon metabolic process;organelle organization;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;regulation of binding;regulation of biological process;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of megakaryocyte differentiation;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of protein binding;response to stimulus;signal transduction;small molecule metabolic process "[cytochrome c]-arginine N-methyltransferase activity;arginine N-methyltransferase activity;binding;catalytic activity;histone methyltransferase activity;histone methyltransferase activity (H4-R3 specific);histone-arginine N-methyltransferase activity;identical protein binding;methyltransferase activity;N-methyltransferase activity;protein binding;protein dimerization activity;protein heterodimerization activity;protein homodimerization activity;protein methyltransferase activity;protein-arginine N-methyltransferase activity;protein-arginine omega-N asymmetric methyltransferase activity;protein-arginine omega-N monomethyltransferase activity;ribonucleoprotein binding;S-adenosylmethionine-dependent methyltransferase activity;snoRNP binding;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane;protein complex 4.07E-62 15 10 10 39.9

Q13523;F5H2U2;H0YDJ3 Serine/threonine-protein kinase PRP4 homolog PRPF4B >sp|Q13523|PRP4B_HUMAN Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens GN=PRPF4B PE=1 SV=3;>tr|F5H2U2|F5H2U2_HUMAN Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens GN=PRPF4B PE=2 SV=1;>tr|H0YDJ3|H0YDJ3_HUMAN Serine/threonine-protei -0.04 0.18 0.26 0.25 0.23 -0.21 -1.06 -0.34 0.791043271 0.508598281 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" catalytic step 2 spliceosome;cell part;chromosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex 1.08E-87 3 10 10 10.8

O94906;O94906-2 Pre-mRNA-processing factor 6 PRPF6 >sp|O94906|PRP6_HUMAN Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1;>sp|O94906-2|PRP6_HUMAN Isoform 2 of Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 0.01 0.19 0.35 0.17 -0.05 -0.61 -1.02 -0.17 1.15511422 0.643579326 "assembly of spliceosomal tri-snRNP;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA localization;spliceosome assembly" binding;nucleic acid binding;protein binding transcription factor activity;ribonucleoprotein binding;RNA binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U4/U6 snRNP;U4/U6 x U5 tri-snRNP complex;U5 snRNP Spliceosome 3.85E-34 2 10 10 11.9

P25788-2;P25788;G3V4X5;G3V3W4;G3V5N4;H0YJ03 Proteasome subunit alpha type-3 PSMA3 >sp|P25788-2|PSA3_HUMAN Isoform 2 of Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3;>sp|P25788|PSA3_HUMAN Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 0.06 0.02 -0.01 -0.02 0.04 -0.03 -0.12 -0.09 0.591048029 0.055615258 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex" Proteasome 3.46E-59 6 10 10 40.7

P25789;H0YN18;H0YMZ1;H0YL69;P25789-2;H0YMA1;H0YKT8;H0YMI6;H0YKS0;H0YLS6;H0YLC2 Proteasome subunit alpha type-4;Proteasome subunit alpha type;Proteasome subunit beta type PSMA4 >sp|P25789|PSA4_HUMAN Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1;>tr|H0YN18|H0YN18_HUMAN Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=2 SV=1;>tr|H0YMZ1|H0YMZ1_HUMAN Proteasome subunit alpha type (Fragment) OS=Homo sap 0.08 0.06 -0.31 0.02 -0.02 -0.10 -0.11 -0.11 0.198615126 0.050087267 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex;ribonucleoprotein complex;RNA granule" Proteasome 3.50E-174 11 10 10 38.3

P28074;P28074-3;P28074-2;H0YJM8;G8JLC2;G3V3K3 Proteasome subunit beta type-5 PSMB5 >sp|P28074|PSB5_HUMAN Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3;>sp|P28074-3|PSB5_HUMAN Isoform 3 of Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5;>sp|P28074-2|PSB5_HUMAN Isoform 2 of Proteasome subunit beta type-5 OS=Homo 0.02 0.04 -0.16 -0.06 0.08 0.14 0.01 -0.09 0.47323029 -0.075812515 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to chemical stimulus;response to DNA damage stimulus;response to oxidative stress;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome core complex;protein complex Proteasome 9.02E-77 6 10 10 36.9

P55036;Q5VWC4;A6PVX3;P55036-2;H0Y3Y9;A2A3N6;H0Y561 26S proteasome non-ATPase regulatory subunit 4PSMD4 >sp|P55036|PSMD4_HUMAN 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1;>tr|Q5VWC4|Q5VWC4_HUMAN 26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=2 SV=1;>tr|A6PVX3|A6PVX3_HUMAN 26S proteasome non-AT 0.10 0.05 -0.06 0.05 0.06 -0.12 -0.19 -0.05 0.750511162 0.11040529 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;glycerolipid metabolic process;glycerophospholipid metabolic process;immune system process;intracellular signal transduction;lipid metabolic process;lipid modification;lipid phosphorylation;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphatidylinositol metabolic process;phosphatidylinositol phosphorylation;phospholipid metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" "catalytic activity;inositol or phosphatidylinositol kinase activity;kinase activity;lipid kinase activity;phosphatidylinositol phosphate kinase activity;phosphotransferase activity, alcohol group as acceptor;transferase activity;transferase activity, transferring phosphorus-containing groups" "cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;proteasome regulatory particle, base subcomplex;protein complex" Proteasome 9.83E-188 7 10 10 34.5

R4GMR5;P48556;K7EJR3;K7EJC1;K7ERW6;K7ENY6 26S proteasome non-ATPase regulatory subunit 8PSMD8 >tr|R4GMR5|R4GMR5_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=4 SV=1;>sp|P48556|PSMD8_HUMAN 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2;>tr|K7EJR3|K7EJR3_HUMAN 26S proteasome non-AT 0.08 0.07 -0.14 0.03 -0.16 0.09 -0.09 -0.18 0.483400264 0.093637016 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome regulatory particle;protein complex Proteasome 1.00E-48 6 10 10 40.1

B4DST5;Q9H3S7 Tyrosine-protein phosphatase non-receptor type 23 PTPN23 >tr|B4DST5|B4DST5_HUMAN Tyrosine-protein phosphatase non-receptor type 23 OS=Homo sapiens GN=PTPN23 PE=2 SV=1;>sp|Q9H3S7|PTN23_HUMAN Tyrosine-protein phosphatase non-receptor type 23 OS=Homo sapiens GN=PTPN23 PE=1 SV=1 0.11 -0.03 -0.03 -0.19 0.30 -0.39 0.35 -0.21 0.078967028 -0.044268263 anatomical structure morphogenesis;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cilium morphogenesis;dephosphorylation;developmental process;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process "catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein tyrosine phosphatase activity" cell part;cell projection;cell projection part;cilium;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;microtubule basal body;microtubule organizing center;nucleus;organelle;organelle part;vesicle 2.88E-62 2 10 10 10.7

P61224-3;P61224;P61224-2;P61224-4;P62834;A6NIZ1;B7ZB78;F5GX62;E7ESV4;F5H7Y6;F5H823;F5GZG1;F5H6R7;F5H004;F5GYB5;F5H4H0;F5GYH7;F5H077;F5GWU8;F5H491;F5H0B7;F5H500;F8WBC0 Ras-related protein Rap-1b;Ras-related protein Rap-1A;Ras-related protein Rap-1b-like protein RAP1B;RAP1A >sp|P61224-3|RAP1B_HUMAN Isoform 3 of Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B;>sp|P61224|RAP1B_HUMAN Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1;>sp|P61224-2|RAP1B_HUMAN Isoform 2 of Ras-related protein Rap-1b OS=Homo sapiens -0.13 0.07 -0.18 0.14 0.28 0.12 -0.37 -0.02 0.05732676 -0.026932932 activation of MAPKK activity;activation of protein kinase activity;biological regulation;cell activation;cell proliferation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;energy derivation by oxidation of organic compounds;energy reserve metabolic process;enzyme linked receptor protein signaling pathway;generation of precursor metabolites and energy;intracellular signal transduction;macromolecule metabolic process;macromolecule modification;metabolic process;nerve growth factor receptor signaling pathway;oxidation-reduction process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;platelet activation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of catalytic activity;regulation of cell communication;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of establishment of cell polarity;regulation of establishment or maintenance of cell polarity;regulation of hormone secretion;regulation of insulin secretion;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of secretion;regulation of signaling;regulation of transferase activity;regulation of transport;response to stimulus;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;guanyl-nucleotide exchange factor complex;intracellular part;lipid particle;macromolecular complex;membrane;plasma membrane;protein complex Chemokine signaling pathway;Focal adhesion;Leukocyte transendothelial migration;Long-term potentiation;MAPK signaling pathway;Neurotrophin signaling pathway;Pancreatic secretion;Renal cell carcinoma 5.73E-46 23 10 10 46.7

P49756;P49756-2;P49756-3;H0YE46;E9PQU5 RNA-binding protein 25 RBM25 >sp|P49756|RBM25_HUMAN RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3;>sp|P49756-2|RBM25_HUMAN Isoform 2 of RNA-binding protein 25 OS=Homo sapiens GN=RBM25;>sp|P49756-3|RBM25_HUMAN Isoform 3 of RNA-binding protein 25 OS=Homo sapiens GN=RBM25 -0.12 0.07 0.11 0.07 -0.07 -0.41

-1.04 -0.52 1.094109503 0.538428072 "apoptosis;biological regulation;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing" binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part Spliceosome 1.26E-40 5 10 10 13.6

P46063;F5H2L2;F8WA66;F8WD97;F5H4P4;F5H3W0 ATP-dependent DNA helicase Q1 RECQL >sp|P46063|RECQ1_HUMAN ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3 0.20 -0.25 -0.05 -0.11 0.80 0.32 -0.12 -0.22 0.39850112 -0.244698698 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA recombination;DNA repair;DNA replication;DNA strand renaturation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;response to DNA damage stimulus;response to stimulus;response to stress "3'-5' DNA helicase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent 3'-5' DNA helicase activity;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-bounded organelle;nucleus;organelle 1.38E-50 6 10 10 19.4

P27694;I3L4R8;I3L524;I3L2M5 Replication protein A 70 kDa DNA-binding subunit RPA1 >sp|P27694|RFA1_HUMAN Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens GN=RPA1 PE=1 SV=2 0.07 -0.01 -0.02 -0.02 0.26 -0.37 -0.15 -0.69 0.506268049 0.243577979 "anatomical structure development;anatomical structure homeostasis;biological regulation;biosynthetic process;catabolic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chordate embryonic development;chromosome organization;developmental process;DNA catabolic process;DNA excision;DNA metabolic process;DNA recombinase assembly;DNA recombination;DNA repair;DNA replication;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA-dependent DNA replication;double-strand break repair;double-strand break repair via homologous recombination;embryo development;embryo development ending in birth or egg hatching;G1/S transition of mitotic cell cycle;hemopoiesis;hemopoietic or lymphoid organ development;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;in utero embryonic development;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;meiosis;metabolic process;mitotic recombination;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;nucleotide-excision repair, DNA damage removal;nucleotide-excision repair, DNA gap filling;organ development;organelle organization;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;recombinational repair;regulation of biological process;regulation of biological quality;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell proliferation;regulation of cellular process;response to DNA damage stimulus;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle;telomere maintenance;telomere maintenance via recombination;telomere maintenance via semi-conservative replication;telomere maintenance via telomere lengthening;telomere organization;tissue homeostasis;transcription-coupled nucleotide-excision repair" binding;cation binding;chromatin binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;single-stranded DNA binding;structure-specific DNA binding actin cytoskeleton;cell part;chromosomal part;cytoplasm;cytoskeleton;DNA replication factor A complex;germ cell nucleus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral element;macromolecular complex;male germ cell nucleus;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear chromosome part;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;PML body;protein complex DNA replication;Homologous recombination;Mismatch repair;Nucleotide excision repair 1.08E-31 4 10 10 25.5

P27635;F8W7C6;Q96L21;H7C123;H7C2C5;A6QRI9;B8A6G2 60S ribosomal protein L10;60S ribosomal protein L10-like RPL10;RPL10L >sp|P27635|RL10_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4;>tr|F8W7C6|F8W7C6_HUMAN 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=2 SV=1;>sp|Q96L21|RL10L_HUMAN 60S ribosomal protein L10-like OS=Homo sapiens GN=RPL10L PE=1 SV= -0.16 -0.06 -0.19 0.02 -0.70 -1.02 -0.20 -0.47 1.159142265 0.499757041 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;gamete generation;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;male gamete generation;metabolic process;mRNA catabolic process;mRNA metabolic process;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;spermatogenesis;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 3.10E-44 7 10 10 36.9

P62750;H7BY10;K7ERT8;A8MUS3;K7EMA7;K7EJV9 60S ribosomal protein L23a RPL23A >sp|P62750|RL23A_HUMAN 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1;>tr|H7BY10|H7BY10_HUMAN 60S ribosomal protein L23a (Fragment) OS=Homo sapiens GN=RPL23A PE=3 SV=1;>tr|K7ERT8|K7ERT8_HUMAN 60S ribosomal protein L23a (Fragment) OS=Homo sa -0.25 0.04 0.16 0.10 -0.13 -0.38 -0.45 -0.35 1.242741447 0.342801237 "biosynthetic process;catabolic process;cell proliferation;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;nucleotide binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 5.43E-54 6 10 10 38.5

P46783;F6U211;Q9NQ39 40S ribosomal protein S10 RPS10 >sp|P46783|RS10_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1;>tr|F6U211|F6U211_HUMAN 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=2 SV=1 -0.02 0.08 -0.10 0.04 0.09 -0.46 -0.12 -0.27 0.669418211 0.191321948 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 4.01E-51 3 10 10 49.7

P06703;R4GN98 Protein S100-A6 S100A6 >sp|P06703|S10A6_HUMAN Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1;>tr|R4GN98|R4GN98_HUMAN Protein S100-A6 (Fragment) OS=Homo sapiens GN=S100A6 PE=4 SV=1 0.20 -0.14 0.12 0.01 0.13 0.62 0.71 0.33 1.101407795 -0.399210937 anatomical structure morphogenesis;axonogenesis;biological regulation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;developmental process;neuron projection morphogenesis;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of fibroblast proliferation;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of fibroblast proliferation;response to stimulus;signal transduction binding;calcium ion binding;calcium-dependent protein binding;cation binding;cytoskeletal protein binding;identical protein binding;ion binding;ion transmembrane transporter activity;metal ion binding;protein binding;protein dimerization activity;protein homodimerization activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transition metal ion binding;transmembrane transporter activity;transporter activity;tropomyosin binding;zinc ion binding cell part;cell projection;cytoplasmic part;cytosol;envelope;extrinsic to internal side of plasma membrane;extrinsic to membrane;extrinsic to plasma membrane;intracellular organelle part;intracellular part;membrane part;nuclear envelope;nuclear part;organelle envelope;organelle part;perinuclear region of cytoplasm;plasma membrane part;ruffle 3.33E-45 2 10 10 97.8

Q9Y3Z3-4;Q9Y3Z3-2;Q9Y3Z3;Q9Y3Z3-3;A6NDZ3 SAM domain and HD domain-containing protein 1 SAMHD1 >sp|Q9Y3Z3-4|SAMH1_HUMAN Isoform 4 of Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1;>sp|Q9Y3Z3-2|SAMH1_HUMAN Isoform 2 of Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1;>sp|Q9Y3Z3|SAMH1 0.23 0.06 0.12 0.03 -1.59 -1.19 -0.81 -0.06 1.27005058 1.019064104 biological regulation;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;metabolic process;multi-organism process;regulation of biological process;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of response to stimulus;regulation of response to stress;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nucleic acid binding;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;RNA binding" cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.03E-87 5 10 10 22.2

Q6NUK1-2;Q6NUK1 Calcium-binding mitochondrial carrier protein SCaMC-1 SLC25A24 >sp|Q6NUK1-2|SCMC1_HUMAN Isoform 2 of Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24;>sp|Q6NUK1|SCMC1_HUMAN Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2 -0.60 0.29 -0.16 0.12 0.77 0.75 -0.98 0.50 0.297079978 -0.349680511 cellular process;establishment of localization;transmembrane transport;transport binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 4.99E-61 2 10 10 27.1

P19623;K7EL89;K7EQ47;K7EKM4;K7ESL0 Spermidine synthase SRM >sp|P19623|SPEE_HUMAN Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1 0.14 0.00 -0.07 -0.11 0.21 0.12 0.57 0.04 0.809488079 -0.243934484 amine biosynthetic process;amine metabolic process;biosynthetic process;cellular amine metabolic process;cellular biogenic amine biosynthetic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;polyamine biosynthetic process;polyamine metabolic process;small molecule metabolic process;spermidine biosynthetic process;spermidine metabolic process "binding;catalytic activity;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity;spermidine synthase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;cytosol;intracellular part Arginine and proline metabolism;beta-Alanine metabolism;Cysteine and methionine metabolism;Glutathione metabolism 7.09E-61 5 10 10 38.1

P23193;P23193-2;E5RJ93;E5RIS7;B7Z4S1;E5RK46;E5RFI1;Q5JRI7;Q15560-2;Q15560 Transcription elongation factor A protein 1 TCEA1 >sp|P23193|TCEA1_HUMAN Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2;>sp|P23193-2|TCEA1_HUMAN Isoform 2 of Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1;>tr|E5RJ93|E5RJ93_HUMAN Transcription elongatio 0.26 0.06 0.08 -0.01 0.02 -0.67 -0.25 -0.85 1.092615671 0.534110811 "biological regulation;biosynthetic process;cell differentiation;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;DNA repair;erythrocyte differentiation;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;myeloid cell differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription elongation, DNA-dependent;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;transcription, DNA-dependent;transcription-coupled nucleotide-excision repair;viral reproductive process" "binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;RNA binding;transition metal ion binding;translation elongation factor activity;translation factor activity, nucleic acid binding;zinc ion binding" cell part;centrosome;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex;transcription elongation factor complex 4.68E-36 10 10 10 29.9

P11172;P11172-2;P11172-3;E9PFD2;P11172-4;F2Z3P2;F2Z303;F8WDG4 Uridine 5-monophosphate synthase;Orotate phosphoribosyltransferase;Orotidine 5-phosphate decarboxylase UMPS >sp|P11172|UMPS_HUMAN Uridine 5-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1;>sp|P11172-2|UMPS_HUMAN Isoform 2 of Uridine 5-monophosphate synthase OS=Homo sapiens GN=UMPS;>sp|P11172-3|UMPS_HUMAN Isoform 3 of Uridine 5-monophosphate synthase -0.04 -0.01 0.07 -0.13 -0.32 -0.61 -0.14 -0.29 1.215920207 0.313806288 biological regulation;biosynthetic process;body fluid secretion;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to drug;cellular response to stimulus;'de novo' pyrimidine base biosynthetic process;'de novo' UMP biosynthetic process;establishment of localization;female pregnancy;heterocycle biosynthetic process;heterocycle metabolic process;lactation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;pyrimidine base biosynthetic process;pyrimidine base metabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside monophosphate biosynthetic process;pyrimidine nucleoside monophosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside monophosphate biosynthetic process;pyrimidine ribonucleoside monophosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;regulation of biological quality;regulation of body fluid levels;reproductive process;response to chemical stimulus;response to drug;response to stimulus;ribonucleoside metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;small molecule metabolic process;transport;UMP biosynthetic process;UMP metabolic process "carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;lyase activity;orotate phosphoribosyltransferase activity;orotidine-5'-phosphate decarboxylase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Drug metabolism - other enzymes;Pyrimidine metabolism 4.12E-61 8 10 10 27.3

Q9BRP8;Q9BRP8-2 Partner of Y14 and mago WIBG >sp|Q9BRP8|WIBG_HUMAN Partner of Y14 and mago OS=Homo sapiens GN=WIBG PE=1 SV=1;>sp|Q9BRP8-2|WIBG_HUMAN Isoform 2 of Partner of Y14 and mago OS=Homo sapiens GN=WIBG -0.24 0.09 0.08 0.19 -0.25 0.01 -0.10 0.00 0.419289045 0.114500395 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;RNA catabolic process;RNA metabolic process" binding;nucleic acid binding;ribonucleoprotein binding;ribosome binding;RNA binding cell part;cytoplasm;exon-exon junction complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;protein complex mRNA surveillance pathway;RNA transport 9.39E-120 2 10 10 70.1

F5GWT4;Q9H4A3-2;Q9H4A3;Q9H4A3-5;Q9H4A3-6;F5H2M7;Q9H4A3-4;F6UYG0;H0YH68;K7ENT7;Q96J92-2;Q9Y3S1-3;C9JGD6;A6PVV2;Q96J92-3;Q96J92;F8W9F9;H0Y7T5;Q9Y3S1-2;Q9Y3S1-4;Q9Y3S1 Serine/threonine-protein kinase WNK1 WNK1 >tr|F5GWT4|F5GWT4_HUMAN Serine/threonine-protein kinase WNK1 OS=Homo sapiens GN=WNK1 PE=2 SV=1;>sp|Q9H4A3-2|WNK1_HUMAN Isoform 2 of Serine/threonine-protein kinase WNK1 OS=Homo sapiens GN=WNK1;>sp|Q9H4A3|WNK1_HUMAN Serine/threonine-protein kinase WNK1 OS=H -0.03 -0.15 0.40 -0.02 0.27 -0.03 0.19 -0.37 0.059709529 0.032991733 anatomical structure development;anion transport;biological regulation;cell development;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chloride transport;developmental process;establishment of localization;inorganic anion transport;intracellular protein kinase cascade;intracellular signal transduction;ion transport;localization;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of digestive system process;negative regulation of ERK1 and ERK2 cascade;negative regulation of hydrolase activity;negative regulation of intracellular protein kinase cascade;negative regulation of kinase activity;negative regulation of MAPKKK cascade;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of pancreatic juice secretion;negative regulation of phosphatase activity;negative regulation of protein kinase activity;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transferase activity;negative regulation of transport;neuron development;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of blood pressure;positive regulation of ion transmembrane transporter activity;positive regulation of molecular function;positive regulation of sodium ion transmembrane transporter activity;positive regulation of systemic arterial blood pressure;positive regulation of transport;positive regulation of transporter activity;primary metabolic process;protein autophosphorylation;protein localization;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biological quality;regulation of blood pressure;regulation of catalytic activity;regulation of cell communication;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of digestive system process;regulation of ERK1 and ERK2 cascade;regulation of homeostatic process;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of pancreatic juice secretion;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of system process;regulation of transferase activity;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to stimulus;signal transduction;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;kinase activity;kinase inhibitor activity;kinase regulator activity;nucleotide binding;phosphatase binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell junction;cell part;cell-cell junction;cytoplasm;intracellular part;membrane;occluding junction;plasma membrane;tight junction 6.58E-61 21 10 10 6.9

Q9BR76;F5H390;E7EW44;F5H0D2 Coronin-1B CORO1B >sp|Q9BR76|COR1B_HUMAN Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1 0.15 0.08 -0.08 0.10 0.34 0.13 0.05 0.01 0.291178634 -0.06642241 actin cytoskeleton organization;actin filament-based process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization actin binding;actin filament binding;binding;cytoskeletal protein binding;protein binding actin cytoskeleton;cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 1.56E-43 4 11 10 33.1

P07942;G3XAI2;E7EPA6 Laminin subunit beta-1 LAMB1 >sp|P07942|LAMB1_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2;>tr|G3XAI2|G3XAI2_HUMAN Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=2 SV=1 0.05 0.34 -0.39 -0.32 0.56 0.16 -0.20 0.36 0.534163446 -0.299401057 anatomical structure morphogenesis;axon guidance;biological adhesion;biological regulation;cell adhesion;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell-substrate adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;chemotaxis;developmental process;embryo implantation;locomotion;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;odontogenesis;organ morphogenesis;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of epithelial cell proliferation;positive regulation of locomotion;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of epithelial cell proliferation;regulation of localization;regulation of locomotion;reproductive process;response to chemical stimulus;response to external stimulus;response to stimulus;substrate adhesion-dependent cell spreading;taxis binding;extracellular matrix structural constituent;glycolipid binding;glycosphingolipid binding;lipid binding;sphingolipid binding;structural molecule activity cell part;cytoplasmic part;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular part;laminin complex;laminin-1 complex;laminin-10 complex;laminin-2 complex;laminin-8 complex;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;perinuclear region of cytoplasm;plasma membrane part;protein complex;vesicle Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 3.75E-100 3 11 10 8.5

Q96PK6;Q96PK6-2 RNA-binding protein 14 RBM14 >sp|Q96PK6|RBM14_HUMAN RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2 0.04 0.98 0.16 1.02 0.15 0.51 -1.25 0.28 0.554928928

0.626425958 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromosome organization;corticosteroid receptor signaling pathway;covalent chromatin modification;DNA metabolic process;DNA recombination;DNA repair;DNA replication;estrogen receptor signaling pathway;glucocorticoid receptor signaling pathway;histone deacetylation;histone modification;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein deacetylation;protein deacylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;response to stress;signal transduction;steroid hormone receptor signaling pathway" "binding;binding, bridging;ligand-dependent nuclear receptor transcription coactivator activity;nucleic acid binding;nucleotide binding;protein binding;protein binding transcription factor activity;protein binding, bridging;RNA binding;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;intracellular organelle part;intracellular part;macromolecular complex;mediator complex;nuclear part;nucleoplasm part;organelle part;protein complex;ribonucleoprotein complex;transcription factor complex 3.39E-79 2 11 10 20.8

Q9H9B4;D6RFI0;D6RDG7;D6RAE9 Sideroflexin-1 SFXN1 >sp|Q9H9B4|SFXN1_HUMAN Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4;>tr|D6RFI0|D6RFI0_HUMAN Sideroflexin-1 (Fragment) OS=Homo sapiens GN=SFXN1 PE=2 SV=1;>tr|D6RDG7|D6RDG7_HUMAN Sideroflexin-1 (Fragment) OS=Homo sapiens GN=SFXN1 PE=2 SV=1 -0.16 0.33 0.13 0.28 0.44 0.21 -1.29 -0.11 0.332472015 0.333584046 biological regulation;cation homeostasis;cation transport;cell differentiation;cellular developmental process;cellular process;chemical homeostasis;developmental process;erythrocyte differentiation;establishment of localization;homeostatic process;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;metal ion transport;myeloid cell differentiation;regulation of biological quality;transition metal ion transport;transport cation transmembrane transporter activity;ion transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part 8.75E-116 4 11 10 45.7

Q9P0L0;Q9P0L0-2;J3QKM9 Vesicle-associated membrane protein-associated protein A VAPA >sp|Q9P0L0|VAPA_HUMAN Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3;>sp|Q9P0L0-2|VAPA_HUMAN Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA -0.34 0.17 -0.02 0.25 0.17 0.29 -0.75 -0.11 0.153117971 0.112506319 biological regulation;biosynthetic process;cell death;cell projection organization;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;death;lipid biosynthetic process;lipid metabolic process;localization;macromolecule localization;membrane fusion;membrane lipid biosynthetic process;membrane lipid metabolic process;membrane organization;metabolic process;neuron projection development;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;protein localization;protein localization in endoplasmic reticulum;protein localization to organelle;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;small molecule metabolic process;sphingolipid biosynthetic process;sphingolipid metabolic process molecular transducer activity;signal transducer activity;structural molecule activity cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;microtubule;organelle;organelle membrane;organelle part;plasma membrane;protein complex;vesicle Tight junction 2.84E-46 3 11 10 49

Q9Y376 Calcium-binding protein 39 CAB39 >sp|Q9Y376|CAB39_HUMAN Calcium-binding protein 39 OS=Homo sapiens GN=CAB39 PE=1 SV=1 0.20 -0.01 0.06 -0.17 -0.21 -0.09 0.22 -0.31 0.344817492 0.119119621 biological regulation;cell cycle arrest;cell cycle process;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;enzyme linked receptor protein signaling pathway;insulin receptor signaling pathway;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;regulation of biological process;regulation of cell cycle;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway enzyme activator activity;enzyme regulator activity;kinase activator activity;kinase regulator activity;protein kinase activator activity;protein kinase regulator activity cell part;cytoplasmic part;cytosol;intracellular part mTOR signaling pathway 8.28E-42 1 12 10 30.5

Q13011;M0R248;M0QZW4 "Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial" ECH1 ">sp|Q13011|ECH1_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2;>tr|M0R248|M0R248_HUMAN Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial (Fragment) OS=Homo sapiens GN=ECH1 PE=3 SV=1" -0.50 -0.23 0.12 0.22 0.88 0.57 0.02 0.17 0.852526999 -0.507346283 carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process catalytic activity;isomerase activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microbody;mitochondrion;organelle;peroxisome Peroxisome 1.98E-119 3 12 10 45.7

P35637-2;P35637;H3BPE7 RNA-binding protein FUS FUS >sp|P35637-2|FUS_HUMAN Isoform Short of RNA-binding protein FUS OS=Homo sapiens GN=FUS;>sp|P35637|FUS_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1;>tr|H3BPE7|H3BPE7_HUMAN RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=2 SV=1 -0.09 0.12 0.05 0.15 0.39 -0.12 -0.65 -0.35 0.437489441 0.240453275 "cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part 1.83E-108 3 12 10 23.8

Q12792;Q12792-3;Q12792-4;F8VS81;F8VRG3;F8W645;F8W1Q9 Twinfilin-1 TWF1 >sp|Q12792|TWF1_HUMAN Twinfilin-1 OS=Homo sapiens GN=TWF1 PE=1 SV=3;>sp|Q12792-3|TWF1_HUMAN Isoform 3 of Twinfilin-1 OS=Homo sapiens GN=TWF1;>sp|Q12792-4|TWF1_HUMAN Isoform 4 of Twinfilin-1 OS=Homo sapiens GN=TWF1;>tr|F8VS81|F8VS81_HUMAN Twinfilin-1 (Fragm0.19 -0.05 0.02 0.01 0.11 0.28 0.32 0.10 0.895135024 -0.158584182 actin filament capping;barbed-end actin filament capping;biological regulation;cellular component organization;cellular component organization or biogenesis;maintenance of location;maintenance of protein location;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin phosphorylation;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytoskeleton organization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of organelle organization;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;sequestering of actin monomers "actin binding;actin monomer binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;cytoskeletal protein binding;lipid binding;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" actin cytoskeleton;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;contractile fiber;cytoplasm;cytoplasmic part;cytoskeleton;filopodium;intracellular;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;leading edge membrane;membrane part;myofibril;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;plasma membrane part;ruffle membrane 5.52E-203 7 12 10 38.6

D6RGI3;Q9NVA2;D6RER5;Q9NVA2-2;D6RDU5;H0Y961;D6RDP1;D6R9Y6;Q14141-2;Q14141-4;B1AMS2;Q14141;F5H1J5;B4E049;H0Y9G8;Q14141-3 Septin-11 11-Sep ">tr|D6RGI3|D6RGI3_HUMAN Septin 11, isoform CRA_b OS=Homo sapiens GN=SEPT11 PE=2 SV=1;>sp|Q9NVA2|SEP11_HUMAN Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3;>tr|D6RER5|D6RER5_HUMAN Septin-11 OS=Homo sapiens GN=SEPT11 PE=2 SV=1;>sp|Q9NVA2-2|SEP11_HUMAN Isoform" -0.12 -0.04 -0.16 0.05 0.76 0.48 0.03 0.09 0.975611272 -0.409161048 cell cycle;cell division;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular process;cytokinesis;interaction with host;interspecies interaction between organisms;macromolecular complex assembly;macromolecular complex subunit organization;multi-organism process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;reproductive process;viral reproductive process;virus-host interaction binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding actin filament bundle;actomyosin;axon;axon part;axon terminus;cell cortex part;cell division site part;cell junction;cell part;cell projection;cell projection part;chromosomal part;clathrin-coated vesicle;cleavage furrow;coated vesicle;condensed chromosome kinetochore;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;dendritic spine;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;midbody;neuron projection;neuron projection terminus;neuron spine;non-membrane-bounded organelle;organelle;organelle part;protein complex;septin complex;spindle;stress fiber;synapse;synapse part;synaptic vesicle;vesicle 5.85E-173 16 13 10 30.8

O60488-2;O60488;D6RF95;D6RFW9;D6RDA8;D6RD96;H0Y9A0 Long-chain-fatty-acid--CoA ligase 4 ACSL4 >sp|O60488-2|ACSL4_HUMAN Isoform Short of Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4;>sp|O60488|ACSL4_HUMAN Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2 0.02 0.00 -0.36 0.00 0.05 -0.23 0.07 -0.25 0.009098133 0.00355113 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;anatomical structure development;biological regulation;biosynthetic process;carboxylic acid transport;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;dendritic spine development;developmental process;embryonic process involved in female pregnancy;establishment of localization;fatty acid transport;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;lipid transport;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid transport;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of fatty acid transport;negative regulation of icosanoid secretion;negative regulation of lipid transport;negative regulation of organic acid transport;negative regulation of prostaglandin secretion;negative regulation of secretion;negative regulation of transport;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid transport;organic ether metabolic process;organic substance transport;positive regulation of biological process;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;primary metabolic process;regulation of biological process;regulation of cell growth;regulation of cellular component organization;regulation of cellular process;regulation of fatty acid transport;regulation of growth;regulation of icosanoid secretion;regulation of lipid transport;regulation of localization;regulation of organic acid transport;regulation of prostaglandin secretion;regulation of secretion;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to extracellular stimulus;response to interleukin-15;response to nutrient;response to nutrient levels;response to organic substance;response to stimulus;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;transport;triglyceride biosynthetic process;triglyceride metabolic process "acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;arachidonate-CoA ligase activity;ATP binding;binding;catalytic activity;fatty acid ligase activity;ligase activity;ligase activity, forming carbon-sulfur bonds;long-chain fatty acid-CoA ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;very long-chain fatty acid-CoA ligase activity" cell body;cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lipid particle;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;neuronal cell body;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;peroxisomal membrane;peroxisomal part;peroxisome Adipocytokine signaling pathway;Fatty acid metabolism;Peroxisome;PPAR signaling pathway 3.54E-88 7 13 10 24.3

Q15365 Poly(rC)-binding protein 1 PCBP1 >sp|Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 0.21 0.04 -0.08 -0.03 -0.20 -0.31 0.12 -0.38 0.756710623 0.225572305 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;DNA binding;nucleic acid binding;RNA binding;single-stranded DNA binding;structure-specific DNA binding cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex Spliceosome 1.48E-244 1 14 10 62.4

P23634-7;P23634-6;P23634-8;P23634;P23634-5;P23634-4;P23634-3;P23634-2;Q01814-4;Q01814-7;Q01814-3;Q01814-2;H0YDG5;H7BZS8;H7BY13 Plasma membrane calcium-transporting ATPase 4 ATP2B4 >sp|P23634-7|AT2B4_HUMAN Isoform ZB of Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4;>sp|P23634-6|AT2B4_HUMAN Isoform XB of Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4;>sp|P23634-8|AT2B4_HUMAN Isoform Z 0.40 0.13 -0.08 -0.38 0.71 0.67 0.52 0.11 0.960210123 -0.483280746 biological regulation;blood coagulation;coagulation;hemostasis;multicellular organismal process;regulation of biological quality;regulation of body fluid levels "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;calcium ion transmembrane transporter activity;calcium-transporting ATPase activity;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;divalent inorganic cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;metal ion transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Calcium signaling pathway;Pancreatic secretion;Salivary secretion 3.27E-134 15 19 10 24.1

G3V4W0;B4DY08;P07910-2;G3V4C1;P07910;P07910-4;G3V2Q1;G3V576;P07910-3;G3V2D6;G3V5V7;G3V555;G3V575;G3V5X6;G3V3K6;G3V251;B4DSU6;G3V4M8;G3V2H6 Heterogeneous nuclear ribonucleoproteins C1/C2 HNRNPC >tr|G3V4W0|G3V4W0_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 (Fragment) OS=Homo sapiens GN=HNRNPC PE=2 SV=1;>tr|B4DY08|B4DY08_HUMAN Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=2 SV=1;>sp|P07910-2|HNRPC_HUMAN Isofor -0.20 1.20 0.04 1.27 -0.34 0.27 -1.58 0.19 0.698574827 0.940558865 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 2.74E-164 19 21 10 63.4

P54652 Heat shock-related 70 kDa protein 2 HSPA2 >sp|P54652|HSP72_HUMAN Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1 0.01 0.32 -0.32 -0.05 -0.63 0.13 0.89 1.02 0.362573206 -0.362792664 anatomical structure development;biological regulation;cell cycle phase;cell cycle process;cell development;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular process involved in reproduction;chromosome organization;developmental process;developmental process involved in reproduction;germ cell development;male meiosis;male meiosis I;meiosis;meiosis I;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle;positive regulation of cellular process;positive regulation of cyclin-dependent protein kinase activity;positive regulation of cyclin-dependent protein kinase activity involved in G2/M;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of cyclin-dependent protein kinase activity involved in G2/M;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of transferase activity;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;spermatid development;synaptonemal complex disassembly;synaptonemal complex organization adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;glycolipid binding;lipid binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;cell surface;chromosomal part;cytoplasmic part;germ cell nucleus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;male germ cell nucleus;membrane-bounded organelle;mitochondrion;nuclear chromosome part;nuclear part;nucleus;organelle;organelle part;synaptonemal complex Antigen processing and presentation;Endocytosis;MAPK signaling pathway;Measles;Protein processing in endoplasmic reticulum;Spliceosome;Toxoplasmosis 0 1 27 10 40.4

Q12904;Q12904-2;D6R937 Aminoacyl tRNA synthase complex-interacting multifunctional protein 1;Endothelial monocyte-activating polypeptide 2 AIMP1 >sp|Q12904|AIMP1_HUMAN Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2;>sp|Q12904-2|AIMP1_HUMAN Isoform 2 of Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=A 0.02 0.04 -0.06 0.07 -0.19 -0.30 -0.04 -0.04 1.00247123 0.164042681 alcohol metabolic process;amine metabolic process;amino acid activation;anatomical structure formation involved in morphogenesis;angiogenesis;apoptosis;biological adhesion;biological regulation;carbohydrate metabolic process;carboxylic acid metabolic process;cell adhesion;cell communication;cell death;cell migration;cell motility;cell-cell signaling;cellular amine metabolic process;cellular amino acid metabolic process;cellular carbohydrate metabolic process;cellular component movement;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chemotaxis;death;defense response;developmental process;glucose metabolic process;hexose metabolic process;immune system process;inflammatory response;leukocyte migration;locomotion;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;response to wounding;RNA metabolic process;signal transduction;signaling;small molecule metabolic process;taxis;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process binding;cell surface binding;cytokine activity;identical protein binding;nucleic acid binding;protein binding;protein dimerization activity;protein homodimerization activity;receptor binding;RNA binding;tRNA binding aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;extracellular region part;extracellular space;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;protein complex;transport vesicle;vesicle 1.36E-90 3 11 11 60.9

D2D4A3;P30038;P30038-2;Q5TF55 "Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial" ALDH4A1 ">tr|D2D4A3|D2D4A3_HUMAN Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=2 SV=1;>sp|P30038|AL4A1_HUMAN Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3;>sp|P30038-2|" -0.50 -0.49 0.29 0.18 -0.85 -0.54 0.20 -0.22 0.27836432 0.220683243 4-hydroxyproline catabolic process;4-hydroxyproline metabolic process;amine biosynthetic process;amine catabolic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid catabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutamate metabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;proline biosynthetic process;proline catabolic process;proline catabolic process to glutamate;proline metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "1-pyrroline-5-carboxylate dehydrogenase activity;aldehyde dehydrogenase (NAD) activity;catalytic activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-NH group of donors;oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism" 4.92E-131 4 11 11 23.4

I3L1D5;O15296;O15296-3;O15296-4;O15296-2 Arachidonate 15-lipoxygenase B ALOX15B >tr|I3L1D5|I3L1D5_HUMAN Arachidonate 15-lipoxygenase B OS=Homo sapiens GN=ALOX15B PE=2 SV=1;>sp|O15296|LX15B_HUMAN Arachidonate 15-lipoxygenase B OS=Homo sapiens GN=ALOX15B PE=2 SV=3;>sp|O15296-3|LX15B_HUMAN Isoform C of Arachidonate 15-lipoxygenase B OS=H -0.18 0.23 0.66 0.39 -0.62 -0.15 -0.12 -0.31 1.156464058 0.57904591 alkene biosynthetic process;anatomical structure development;arachidonic acid metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular alkene metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;developmental process;developmental process involved in reproduction;fatty acid biosynthetic process;fatty acid metabolic process;gland development;icosanoid biosynthetic process;icosanoid metabolic process;induction of apoptosis;induction of programmed cell death;leukotriene biosynthetic process;leukotriene metabolic process;lipid biosynthetic process;lipid metabolic process;lipoxygenase pathway;metabolic process;monocarboxylic acid metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of growth;negative regulation of locomotion;organ development;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;prostate gland development;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular process;regulation of developmental process;regulation of epithelial cell differentiation;regulation of growth;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of programmed cell death;reproductive process;reproductive structure development;small molecule biosynthetic process;small molecule metabolic process;unsaturated fatty acid biosynthetic process;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process "arachidonate 15-lipoxygenase activity;binding;catalytic activity;cation binding;dioxygenase activity;ion binding;iron ion binding;lipoxygenase activity;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;transition metal ion binding" cell part;cytoplasmic part;cytosol;intracellular part Arachidonic acid metabolism 1.50E-36 5 11 11 22.9

P27695;G3V3M6;G3V5Q1;G3V3C7;G3V5D9;G3V5M0;G3V359;H7C4A8;G3V3Y6 "DNA-(apurinic or apyrimidinic site) lyase;DNA-(apurinic or apyrimidinic site) lyase, mitochondrial" APEX1 >sp|P27695|APEX1_HUMAN DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2;>tr|G3V3M6|G3V3M6_HUMAN DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens GN=APEX1 PE=2 SV=1;>tr|G3V5Q1|G3V5Q1_HUMAN DNA-(apurinic or apy -0.09 -0.10 -0.14 -0.04 0.10 -0.47 0.05 -0.48 0.255443749 0.106218064 "aging;base-excision repair;biological regulation;biosynthetic process;cell redox homeostasis;cellular biosynthetic process;cellular homeostasis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to cAMP;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to hydrogen peroxide;cellular response to organic substance;cellular response to oxidative stress;cellular response to peptide hormone stimulus;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;demethylation;developmental process;DNA dealkylation;DNA demethylation;DNA metabolic process;DNA modification;DNA recombination;DNA repair;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of locomotion;negative regulation of smooth muscle cell migration;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;one-carbon metabolic process;positive regulation of biological process;positive regulation of cell cycle;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA repair;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitotic cell cycle;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of S phase of mitotic cell cycle;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of gene expression;regulation of gene expression, epigenetic;regulation of interphase of mitotic cell cycle;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA stability;regulation of S phase;regulation of S phase of mitotic cell cycle;regulation of smooth muscle cell migration;regulation of transcription, DNA-dependent;response to cAMP;response to chemical stimulus;response to DNA damage stimulus;response to drug;response to endogenous stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to reactive oxygen species;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;transcription, DNA-dependent" "3'-5' exonuclease activity;binding;carbon-oxygen lyase activity;catalytic activity;cation binding;chromatin binding;chromatin DNA binding;damaged DNA binding;deoxyribonuclease activity;DNA binding;DNA N-glycosylase activity;DNA-(apurinic or apyrimidinic site) lyase activity;endodeoxyribonuclease activity;endonuclease activity;endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;endoribonuclease activity;endoribonuclease activity, producing 5'-phosphomonoesters;exonuclease activity;hydrolase activity;hydrolase activity, acting on ester bonds;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing N-glycosyl compounds;ion binding;lyase activity;metal ion binding;nuclease activity;nucleic acid binding;oxidoreductase activity;phosphodiesterase I activity;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;protein binding transcription factor activity;ribonuclease activity;ribonuclease H activity;RNA binding;site-specific endodeoxyribonuclease activity, specific for altered base;structure-specific DNA binding;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;uracil DNA N-glycosylase activity" cell part;centrosome;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule organizing center;mitochondrion;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;nucleus;organelle;organelle part;perinuclear region of cytoplasm;protein complex;ribonucleoprotein complex;ribosome;transcription factor complex Base excision repair 2.30E-71 9 11 11 43.4

J3KTF8;P52565;J3QQX2;P52565-2;J3KRY1;J3KRE2;J3KS60 Rho GDP-dissociation inhibitor 1 ARHGDIA >tr|J3KTF8|J3KTF8_HUMAN Rho GDP-dissociation inhibitor 1 (Fragment) OS=Homo sapiens GN=ARHGDIA PE=4 SV=1;>sp|P52565|GDIR1_HUMAN Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA PE=1 SV=3;>tr|J3QQX2|J3QQX2_HUMAN Rho GDP-dissociation inhibitor 1 O 0.24 0.00 -0.04 -0.01 -0.18 0.07 0.25 0.02 0.020803746 0.007006907 biological regulation;cell surface receptor linked signaling pathway;cellular component movement;cellular process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;intracellular signal transduction;negative regulation of apoptosis;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neurogenesis;negative regulation of programmed cell death;nerve growth factor receptor signaling pathway;positive regulation of axonogenesis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of developmental process;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of neurogenesis;Ras protein signal transduction;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of axonogenesis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein localization;regulation of purine nucleotide catabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway enzyme activator activity;enzyme regulator activity;GDP-dissociation inhibitor activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Rho GDP-dissociation inhibitor activity;small GTPase regulator activity cell part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;immunological synapse;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane part;non-membrane-bounded organelle;organelle;plasma membrane part Neurotrophin signaling pathway;Vasopressin-regulated water reabsorption 6.44E-108 7 11 11 55.2

Q92974-3;Q92974-2;Q92974;Q5VY93 Rho guanine nucleotide exchange factor 2 ARHGEF2 >sp|Q92974-3|ARHG2_HUMAN Isoform 3 of Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2;>sp|Q92974-2|ARHG2_HUMAN Isoform 2 of Rho guanine nucleotide exchange factor 2 OS=Homo sapiens GN=ARHGEF2;>sp|Q92974|ARHG2_HUMAN Rho guanine nucleotid 0.13 -0.02 0.08 -0.12 0.92 0.48 0.15 -0.03 0.716772249 -0.36246726 "actin cytoskeleton organization;actin filament organization;actin filament-based process;anatomical structure morphogenesis;biological regulation;cell cycle phase;cell cycle process;cell division;cell morphogenesis;cell surface receptor linked signaling pathway;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular hyperosmotic response;cellular process;cellular response to abiotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to osmotic stress;cellular response to stimulus;cellular response to stress;cellular response to tumor necrosis factor;cytoskeleton organization;developmental process;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of mitotic spindle localization;establishment of mitotic spindle orientation;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;establishment of spindle orientation;hyperosmotic response;intracellular protein transport;intracellular signal transduction;intracellular transport;microtubule cytoskeleton organization;microtubule-based process;mitosis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of developmental process;negative regulation of microtubule depolymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of necrotic cell death;negative regulation of neurogenesis;negative regulation of organelle organization;negative regulation of programmed cell death;negative regulation of protein complex disassembly;nerve growth factor receptor signaling pathway;nuclear division;organelle fission;organelle organization;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;protein transport;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule depolymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of necrotic cell death;regulation of nervous system development;regulation of neurogenesis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex disassembly;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to osmotic stress;response to stimulus;response to stress;response to tumor necrosis factor;signal transduction;small GTPase mediated signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport" binding;cation binding;cytoskeletal protein binding;enzyme binding;enzyme regulator activity;GTPase binding;GTPase regulator activity;guanyl-nucleotide exchange factor activity;ion binding;lipid binding;metal ion binding;microtubule binding;nucleoside-triphosphatase regulator activity;phospholipid binding;protein binding;Rac GTPase binding;Rac guanyl-nucleotide exchange factor activity;Ras GTPase binding;Ras guanyl-nucleotide exchange factor activity;Rho GTPase binding;Rho guanyl-nucleotide exchange factor activity;small GTPase binding;small GTPase regulator activity;transcription factor binding;transition metal ion binding;tubulin binding;zinc ion binding cell body;cell junction;cell part;cell projection membrane;cell projection part;cell-cell junction;cytoplasmic part;cytoskeletal part;cytosol;dendritic shaft;Golgi apparatus;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;microtubule;neuronal cell body;non-membrane-bounded organelle;occluding junction;organelle;organelle part;plasma membrane part;protein complex;ruffle membrane;spindle;tight junction Pathogenic Escherichia coli infection 5.97E-34 4 11 11 14.8

P48047;H7C0C1;H7C086;H7C068 "ATP synthase subunit O, mitochondrial" ATP5O ">sp|P48047|ATPO_HUMAN ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1" -0.52 0.14 0.09 0.28 0.23 0.21 -1.25 -0.25 0.257540116 0.259317303 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "binding;cation transmembrane transporter activity;drug binding;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;lipid binding;monovalent inorganic cation transmembrane transporter activity;steroid binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;mitochondrial proton-transporting ATP synthase complex, coupling factor F(o);organelle part;plasma membrane;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, coupling factor F(o);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, proton-transporting domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 4.21E-114 4 11 11 61

P21281;H0YC04;C9JL73;P15313;E5RGH6;C9J5E3;C9JNS9;H0YAT8 "V-type proton ATPase subunit B, brain isoform" ATP6V1B2 ">sp|P21281|VATB2_HUMAN V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3" -0.17 0.42 -0.27 0.42 0.06 0.68 -0.04 0.19 0.187135273 -0.123236251 "anatomical structure morphogenesis;ATP hydrolysis coupled proton transport;ATP metabolic process;biological regulation;calcium ion homeostasis;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;developmental process;divalent inorganic cation homeostasis;embryonic morphogenesis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;excretion;ferric iron transport;heterocycle metabolic process;homeostatic process;hydrogen transport;inner ear morphogenesis;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;multicellular organismal process;multi-organism process;neurological system process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;organelle organization;ossification;pH reduction;phagosome maturation;primary metabolic process;protein transport;proton transport;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of pH;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;secretion;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal transduction;small molecule metabolic process;system process;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "apical plasma membrane;basolateral plasma membrane;cell part;cell projection;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endomembrane system;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lateral plasma membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microvillus;organelle;organelle part;pigment granule;plasma membrane;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain;proton-transporting V-type ATPase complex;proton-transporting V-type ATPase, V1 domain;vacuolar part;vacuolar proton-transporting V-type ATPase complex;vesicle" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection 2.34E-112 8 11 11 33.9

P16070-18;P16070-12;P16070-14;P16070-13;P16070-11;P16070-10;P16070-16;P16070-8;P16070-17;P16070-6;P16070-4;P16070-3;P16070-7;E7EPC6;P16070-5;P16070;H0YD13;H0Y2P0;H0YE40;H0YDW7;H0YCV9;P16070-15;H0Y5E4;P16070-9;H0YDX6;H0YD17;J3KN83;E9PKC6;Q86UZ1;P16070-19;H0YD90;H0YEV3;H0YEU1 CD44 antigen CD44 >sp|P16070-18|CD44_HUMAN Isoform 18 of CD44 antigen OS=Homo sapiens GN=CD44;>sp|P16070-12|CD44_HUMAN Isoform 12 of CD44 antigen OS=Homo sapiens GN=CD44;>sp|P16070-14|CD44_HUMAN Isoform 14 of CD44 antigen OS=Homo sapiens GN=CD44;>sp|P16070-13|CD44_HUMAN Iso 0.23 0.01 -0.36 -0.18 0.31 0.09 -0.03 0.08 0.538122837 -0.185943477 "amine metabolic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;anatomical structure morphogenesis;biological adhesion;biological regulation;branching involved in prostate gland morphogenesis;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;carbohydrate catabolic process;carbohydrate metabolic process;cartilage development;catabolic process;cell adhesion;cell surface receptor linked signaling pathway;cell-cell adhesion;cell-matrix adhesion;cell-substrate adhesion;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;developmental process involved in reproduction;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;homotypic cell-cell adhesion;hyaluronan catabolic process;hyaluronan metabolic process;interferon-gamma-mediated signaling pathway;leukocyte aggregation;leukocyte cell-cell adhesion;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monocyte aggregation;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular process;negative regulation of DNA damage response, signal transduction by p53 class mediator;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of response to DNA damage stimulus;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nitrogen compound metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell-cell adhesion;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ERK1 and ERK2 cascade;positive regulation of gene expression;positive regulation of heterotypic cell-cell adhesion;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of peptidyl-serine phosphorylation;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;primary metabolic process;prostate gland epithelium morphogenesis;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell-cell adhesion;regulation of cell-cell adhesion involved in gastrulation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of DNA damage response, signal transduction by p53 class mediator;regulation of embryonic development;regulation of endopeptidase activity;regulation of ERK1 and ERK2 cascade;regulation of gastrulation;regulation of gene expression;regulation of heterotypic cell-cell adhesion;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of peptidase activity;regulation of peptidyl-serine phosphorylation;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to interferon-gamma;response to organic substance;response to stimulus;response to stress;response to wounding;signal transduction;small molecule metabolic process;tissue development;tissue morphogenesis;tube morphogenesis;Wnt receptor signaling pathway;wound healing;wound healing involved in inflammatory response" "binding;carbohydrate binding;catalytic activity;collagen binding;glycosaminoglycan binding;hexosaminidase activity;hyaluronic acid binding;hyalurononglucosaminidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;pattern binding;polysaccharide binding;protein binding" basolateral plasma membrane;cell part;cell surface;cytoplasmic part;external side of plasma membrane;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;organelle;plasma membrane;plasma membrane part ECM-receptor interaction;Hematopoietic cell lineage;Shigellosis5.67E-141 33 11 11 28.8

O00748;O00748-2;J3QSC0;Q5XG92-4;Q5XG92-6;Q5XG92-2;F5H5S4;P22303-3;Q5XG92;P22303-4;P22303;P22303-2 Cocaine esterase CES2 >sp|O00748|EST2_HUMAN Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1;>sp|O00748-2|EST2_HUMAN Isoform 2 of Cocaine esterase OS=Homo sapiens GN=CES2 0.52 0.62 -0.35 -0.34 0.93 1.10 0.79 -0.07 0.656666852 -0.574553315 "acetylcholine catabolic process;acetylcholine catabolic process in synaptic cleft;acetylcholine metabolic process;alcohol metabolic process;amine catabolic process;amine metabolic process;amyloid precursor protein metabolic process;anatomical structure development;biological adhesion;biological regulation;biosynthetic process;catabolic process;cell adhesion;cell development;cell proliferation;cellular amine metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;choline metabolic process;developmental process;DNA metabolic process;DNA replication;endocytosis;establishment of localization;ethanolamine-containing compound metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;glycoprotein metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;membrane invagination;membrane organization;metabolic process;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of multicellular organismal process;negative regulation of neurological system process;negative regulation of signaling;negative regulation of synaptic transmission;negative regulation of synaptic transmission, cholinergic;negative regulation of transmission of nerve impulse;neurotransmitter biosynthetic process;neurotransmitter catabolic process;neurotransmitter metabolic process;neurotransmitter receptor biosynthetic process;neurotransmitter receptor metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organophosphate metabolic process;osteoblast development;phosphatidylcholine biosynthetic process;phosphatidylcholine metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;positive regulation of biological process;positive regulation of cellular process;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of secretion;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein tetramerization;receptor biosynthetic process;receptor internalization;receptor metabolic process;receptor-mediated endocytosis;regulation of anatomical structure morphogenesis;regulation of axonogenesis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of establishment of protein localization;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of neurotransmitter levels;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of receptor recycling;regulation of secretion;regulation of signaling;regulation of synaptic transmission;regulation of synaptic transmission, cholinergic;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;response to stimulus;response to stress;response to wounding;retina development in camera-type eye;small molecule metabolic process;synapse assembly;synapse organization;transport;vesicle-mediated transport" "acetylcholine binding;acetylcholinesterase activity;amine binding;beta-amyloid binding;binding;carboxylesterase activity;carboxylic ester hydrolase activity;catalytic activity;cholinesterase activity;collagen binding;deacetylase activity;extracellular matrix binding;hydrolase activity;hydrolase activity, acting on ester bonds;identical protein binding;laminin binding;methyl indole-3-acetate esterase activity;methyl jasmonate esterase activity;methyl salicylate esterase activity;methylumbelliferyl-acetate deacetylase activity;neurotransmitter binding;protein binding;protein dimerization activity;protein homodimerization activity;retinyl-palmitate esterase activity;serine hydrolase activity" anchored to membrane;axon;basal lamina;cell junction;cell part;cell projection;cell surface;cytoplasmic part;dendrite;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region;extracellular region part;extracellular space;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;neuromuscular junction;neuron projection;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane;postsynaptic membrane;presynaptic membrane;synapse;synapse part;synaptic membrane Drug metabolism - other enzymes;Glycerophospholipid metabolism 6.21E-69 12 11 11 28.6

Q9UHQ9;H7C0R7 NADH-cytochrome b5 reductase 1CYB5R1 >sp|Q9UHQ9|NB5R1_HUMAN NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1;>tr|H7C0R7|H7C0R7_HUMAN NADH-cytochrome b5 reductase 1 (Fragment) OS=Homo sapiens GN=CYB5R1 PE=4 SV=1 -0.59 0.12 0.13 0.33 0.08 0.73 -0.75 0.22 0.07023824 -0.075172286 alcohol metabolic process;biosynthetic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "catalytic activity;cytochrome-b5 reductase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor" cell part;cytoplasmic part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle

Amino sugar and nucleotide sugar metabolism 8.54E-47 2 11 11 35.1

P39656;E7EWT1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit DDOST >sp|P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4;>tr|E7EWT1|E7EWT1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN -0.17 -0.01 -0.12 -0.01 0.70 0.27 -0.54 -0.09 0.226535831 -0.159195047 biosynthetic process;carbohydrate metabolic process;cell activation;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glycosylation;immune response;immune system process;innate immune response;intracellular protein transport;intracellular transport;leukocyte activation;lymphocyte activation;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;response to stress;SRP-dependent cotranslational protein targeting to membrane;T cell activation;translation;transport "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;oligosaccharyltransferase complex;organelle membrane;organelle part;protein complex N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis 3.46E-60 2 11 11 36.2

O60443;O60443-3;H7C3W1;H7C147;H7BZJ0;O60443-2 Non-syndromic hearing impairment protein 5 DFNA5 >sp|O60443|DFNA5_HUMAN Non-syndromic hearing impairment protein 5 OS=Homo sapiens GN=DFNA5 PE=1 SV=2;>sp|O60443-3|DFNA5_HUMAN Isoform 3 of Non-syndromic hearing impairment protein 5 OS=Homo sapiens GN=DFNA5 0.50 -0.01 0.07 -0.14 -0.97 -0.31 0.29 -0.21 0.582549043 0.405817921 apoptosis;biological regulation;cell death;cell differentiation;cellular developmental process;cellular process;death;developmental process;induction of apoptosis;induction of programmed cell death;inner ear receptor cell differentiation;mechanoreceptor differentiation;multicellular organismal process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;neurological system process;neuron differentiation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of programmed cell death;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;system process cell part;cytoplasm;intracellular part 2.70E-91 6 11 11 31.7

Q9Y2L1;G3V1J5;Q9Y2L1-2;F2Z2C0 Exosome complex exonuclease RRP44 DIS3 >sp|Q9Y2L1|RRP44_HUMAN Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2;>tr|G3V1J5|G3V1J5_HUMAN Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=2 SV=1;>sp|Q9Y2L1-2|RRP44_HUMAN Isoform 2 of Exosome complex exonuclease RRP44 O 0.45 0.02 0.06 -0.03 0.22 -0.05 -0.16 -0.53 0.564023003 0.255580901 "catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;CUT catabolic process;CUT metabolic process;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA catabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA catabolic process;rRNA metabolic process;rRNA processing" "3'-5' exonuclease activity;3'-5'-exoribonuclease activity;binding;catalytic activity;endonuclease activity;enzyme regulator activity;exonuclease activity;exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;exoribonuclease activity;exoribonuclease activity, producing 5'-phosphomonoesters;GTPase regulator activity;guanyl-nucleotide exchange factor activity;hydrolase activity;hydrolase activity, acting on ester bonds;nuclease activity;nucleic acid binding;nucleoside-triphosphatase regulator activity;ribonuclease activity;RNA binding" cell part;cytoplasmic part;cytosol;exosome (RNase complex);intracellular organelle part;intracellular part;macromolecular complex;nuclear exosome (RNase complex);nuclear part;nucleoplasm;organelle part;protein complex RNA degradation 7.11E-52 4 11 11 17

E9PEX6;P09622;B4DHG0;B4DT69;F8WDM5;F2Z2E3 "Dihydrolipoyl dehydrogenase, mitochondrial;Dihydrolipoyl dehydrogenase" DLD ">tr|E9PEX6|E9PEX6_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=2 SV=1;>sp|P09622|DLDH_HUMAN Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2;>tr|B4DHG0|B4DHG0_HUMAN Dihydrolipoyl dehydrogenase, mitoc" -0.37 0.13 -0.11 0.20 0.36 0.33 -0.63 -0.09 0.041245232 -0.032745907 "acetyl-CoA catabolic process;acetyl-CoA metabolic process;amine catabolic process;amine metabolic process;anatomical structure morphogenesis;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;biological regulation;branched chain family amino acid catabolic process;branched chain family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell maturation;cell redox homeostasis;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular chemical homeostasis;cellular developmental process;cellular homeostasis;cellular ion homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;chemical homeostasis;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental maturation;developmental process;developmental process involved in reproduction;electron transport chain;embryonic morphogenesis;gastrulation;generation of precursor metabolites and energy;homeostatic process;ion homeostasis;lysine catabolic process;lysine metabolic process;macromolecule metabolic process;metabolic process;mitochondrial electron transport, NADH to ubiquinone;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;protein metabolic process;proteolysis;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of membrane potential;regulation of metabolic process;reproductive process;respiratory electron transport chain;small molecule catabolic process;small molecule metabolic process;sperm capacitation;tricarboxylic acid cycle" "binding;catalytic activity;coenzyme binding;cofactor binding;dihydrolipoyl dehydrogenase activity;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on NADH or NADPH" acrosomal matrix;cell part;cytoplasmic part;cytoplasmic vesicle part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part;vacuolar part "Citrate cycle (TCA cycle);Glycine, serine and threonine metabolism;Glycolysis / Gluconeogenesis;Pyruvate metabolism;Valine, leucine and isoleucine degradation" 1.72E-97 6 11 11 26.5

Q6P2E9;Q6P2E9-2;I3L2F4 Enhancer of mRNA-decapping protein 4 EDC4 >sp|Q6P2E9|EDC4_HUMAN Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1;>sp|Q6P2E9-2|EDC4_HUMAN Isoform 2 of Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 0.04 -0.03 0.20 0.00 0.23 -0.08 -0.08 -0.17 0.297876742 0.076465704 "catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay;gene expression;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, exonucleolytic;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA catabolic process;RNA metabolic process" cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex;RNA granule RNA degradation 4.93E-110 3 11 11 11.3

I3L397;P63241;I3L504;P63241-2;Q6IS14;F8WCJ1;C9J7B5;C9J4W5;Q9GZV4 Eukaryotic translation initiation factor 5A-1;Eukaryotic translation initiation factor 5A-1-like EIF5A;EIF5AL1 >tr|I3L397|I3L397_HUMAN Eukaryotic translation initiation factor 5A-1 (Fragment) OS=Homo sapiens GN=EIF5A PE=2 SV=1;>sp|P63241|IF5A1_HUMAN Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2;>tr|I3L504|I3L504_HUMAN Eukaryotic t 0.00 -0.06 -0.25 -0.15 0.04 -0.36 0.35 -0.23 0.136761679 -0.063147001 amine biosynthetic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chemical homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;gamete generation;homeostatic process;hypusine metabolic process;induction of apoptosis;induction of programmed cell death;intracellular protein transport;intracellular transport;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;mRNA export from nucleus;mRNA transport;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-lysine modification;peptidyl-lysine modification to hypusine;polyamine homeostasis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of programmed cell death;positive regulation of protein complex disassembly;positive regulation of protein metabolic process;positive regulation of translation;positive regulation of translational elongation;positive regulation of translational termination;posttranscriptional regulation of gene expression;post-translational protein modification;primary metabolic process;protein export from nucleus;protein metabolic process;protein modification process;protein targeting;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex disassembly;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational termination;reproductive process;RNA export from nucleus;RNA transport;small molecule biosynthetic process;small molecule metabolic process;spermatogenesis;translational frameshifting;transport "binding;nucleic acid binding;ribonucleoprotein binding;ribosome binding;RNA binding;snRNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding;U6 snRNA binding" annulate lamellae;cell part;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear part;nuclear pore;organelle membrane;organelle part;pore complex;protein complex 1.43E-114 9 11 11 76.2

P30040;F8VY02;F8W1G0;P30040-2 Endoplasmic reticulum resident protein 29 ERP29 >sp|P30040|ERP29_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4;>tr|F8VY02|F8VY02_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=2 SV=1 -0.14 -0.11 -0.06 -0.07 0.12 -0.16 0.14 -0.13 0.451005108 -0.088431463 cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein secretion;protein transport;secretion;secretion by cell;transport "catalytic activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;protein disulfide isomerase activity" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;vesicle Protein processing in endoplasmic reticulum 8.65E-167 4 11 11 51.3

H7BXI1;A0FGR8-2;A0FGR8;A0FGR8-6;A0FGR8-4;F2Z3K9;A0FGR8-5 Extended synaptotagmin-2 ESYT2 >tr|H7BXI1|H7BXI1_HUMAN Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=2 SV=1;>sp|A0FGR8-2|ESYT2_HUMAN Isoform 2 of Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2;>sp|A0FGR8|ESYT2_HUMAN Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 0.00 -0.21 0.08 0.15 0.54 0.54 -0.28 -0.03 0.344495769 -0.189517777 cell part;integral to membrane;intrinsic to membrane;membrane;membrane part;plasma membrane 5.84E-48 7 11 11 18

P62495;Q96CG1;B7Z7P8;D6RCB3;I3L492;D6RJE8 Eukaryotic peptide chain release factor subunit 1 ETF1 >sp|P62495|ERF1_HUMAN Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3;>tr|Q96CG1|Q96CG1_HUMAN ETF1 protein OS=Homo sapiens GN=ETF1 PE=2 SV=1;>tr|B7Z7P8|B7Z7P8_HUMAN Eukaryotic peptide chain release factor subunit 1 OS=Ho 0.09 -0.05 0.01 -0.04 -0.07 -0.30 0.21 -0.26 0.357023516 0.107828834 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein complex disassembly;regulation of protein metabolic process;regulation of translation;regulation of translational termination;RNA catabolic process;RNA metabolic process;small molecule metabolic process" "binding;nucleic acid binding;ribonucleoprotein binding;ribosome binding;RNA binding;translation factor activity, nucleic acid binding;translation release factor activity;translation release factor activity, codon specific;translation termination factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part mRNA surveillance pathway 5.87E-119 6 11 11 36.4

Q9Y613;B4DVN5;J3KTH7 FH1/FH2 domain-containing protein 1 FHOD1 >sp|Q9Y613|FHOD1_HUMAN FH1/FH2 domain-containing protein 1 OS=Homo sapiens GN=FHOD1 PE=1 SV=3;>tr|B4DVN5|B4DVN5_HUMAN FH1/FH2 domain-containing protein 1 OS=Homo sapiens GN=FHOD1 PE=2 SV=1 0.12 -0.17 0.01 -0.21 0.57 0.08 0.34 -0.07 0.763419028 -0.288442061 "actin cytoskeleton organization;actin filament-based process;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization;positive regulation of actin filament bundle assembly;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of RNA metabolic process;positive regulation of stress fiber assembly;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of stress fiber assembly;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent" bleb;cell part;cell projection;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 3.71E-77 3 11 11 12.5

Q00688;G3V5F2 Peptidyl-prolyl cis-trans isomerase FKBP3 FKBP3 >sp|Q00688|FKBP3_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1 -0.13 0.03 -0.09 0.01 0.19 0.02 0.31 0.07 1.050287226 -0.188858646 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process binding;catalytic activity;cis-trans isomerase activity;drug binding;FK506 binding;isomerase activity;macrolide binding;peptidyl-prolyl cis-trans isomerase activity;receptor activity cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle 2.39E-76 2 11 11 42

O94915;F5GX82;H0Y9X0;F2Z2S2;D6RJI4;O94915-2 Protein furry homolog-like FRYL >sp|O94915|FRYL_HUMAN Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=1 SV=2;>tr|F5GX82|F5GX82_HUMAN Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=2 SV=1;>tr|H0Y9X0|H0Y9X0_HUMAN Protein furry homolog-like (Fragment) OS=Homo sapiens GN=FRYL PE 0.14 0.02 -0.12 -0.11 -0.34 -0.43 0.12 -0.19 0.60589467 0.192177081 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" 2.26E-43 6 11 11 4.7

P02794;G3V192;G3V1D1;E9PRK8;E9PKY7;E9PQR3;E9PPQ4;E9PKM5;E9PK45 Ferritin heavy chain;Ferritin FTH1 >sp|P02794|FRIH_HUMAN Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2;>tr|G3V192|G3V192_HUMAN Ferritin OS=Homo sapiens GN=FTH1 PE=2 SV=1;>tr|G3V1D1|G3V1D1_HUMAN Ferritin OS=Homo sapiens GN=FTH1 PE=2 SV=1 -0.97 0.56 -0.39 0.84 0.31 0.96 0.70 -0.36 0.303234718 -0.391380563 biological regulation;cation homeostasis;cation transport;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular membrane organization;cellular metal ion homeostasis;cellular process;chemical homeostasis;establishment of localization;establishment of localization in cell;Golgi vesicle transport;homeostatic process;immune response;immune system process;intracellular sequestering of iron ion;intracellular transport;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;maintenance of location;maintenance of location in cell;membrane organization;metal ion homeostasis;metal ion transport;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of fibroblast proliferation;post-Golgi vesicle-mediated transport;regulation of biological process;regulation of biological quality;regulation of cell proliferation;regulation of cellular process;regulation of fibroblast proliferation;response to stimulus;sequestering of metal ion;transition metal ion transport;transmembrane transport;transport;vesicle-mediated transport "binding;catalytic activity;cation binding;ferric iron binding;ferroxidase activity;ion binding;iron ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, oxidizing metal ions;oxidoreductase activity, oxidizing metal ions, oxygen as acceptor;transition metal ion binding" cell part;cytoplasmic part;cytosol;ferritin complex;intracellular ferritin complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;organelle;protein complex Mineral absorption;Porphyrin and chlorophyll metabolism 4.59E-78 9 11 11 51.4

Q92896;Q92896-3;Q92896-2;H3BM42;H3BQT1;H3BRD8;H3BQU9 Golgi apparatus protein 1 GLG1 >sp|Q92896|GSLG1_HUMAN Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2;>sp|Q92896-3|GSLG1_HUMAN Isoform 3 of Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1;>sp|Q92896-2|GSLG1_HUMAN Isoform 2 of Golgi apparatus protein 1 OS=Homo sapiens GN=GL -0.08 0.20 -0.49 0.04 0.20 0.37 -0.40 -0.29 0.07436601 -0.051454488 anatomical structure morphogenesis;biological regulation;bone morphogenesis;developmental process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of protein processing;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of biological process;regulation of cartilage development;regulation of cell communication;regulation of cell differentiation;regulation of cellular process;regulation of chondrocyte differentiation;regulation of developmental process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein processing;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway binding;protein binding;receptor binding cell part;cytoplasmic part;extracellular matrix;extracellular region part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Cell adhesion molecules (CAMs) 2.77E-47 7 11 11 10.9

Q9HC38-2;B7Z403;Q9HC38;I3L3Q4;Q9HC38-3;I3L1I0;I3L1F4 Glyoxalase domain-containing protein 4 GLOD4 >sp|Q9HC38-2|GLOD4_HUMAN Isoform 2 of Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4;>tr|B7Z403|B7Z403_HUMAN Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=2 SV=1;>sp|Q9HC38|GLOD4_HUMAN Glyoxalase domain-containing prot -0.03 -0.11 0.06 0.03 -0.13 -0.13 0.29 -0.32 0.167430803 0.060802035 cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 5.23E-52 7 11 11 45.6

Q9ULT8;H0YJP0;H0YJD4;G3V4V5 E3 ubiquitin-protein ligase HECTD1 HECTD1 >sp|Q9ULT8|HECD1_HUMAN E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3;>tr|H0YJP0|H0YJP0_HUMAN E3 ubiquitin-protein ligase HECTD1 (Fragment) OS=Homo sapiens GN=HECTD1 PE=2 SV=1 0.31 0.04 -0.31 -0.37 0.70 0.15 0.54 -0.16 0.661575526 -0.390417552 anatomical structure formation involved in morphogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;macromolecule metabolic process;macromolecule modification;metabolic process;neural tube closure;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;tube closure;tube formation "acid-amino acid ligase activity;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;small conjugating protein ligase activity;ubiquitin-protein ligase activity" cell part;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.13E-94 4 11 11 7.1

P62805 Histone H4 HIST1H4A >sp|P62805|H4_HUMAN Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 -0.24 1.37 -0.19 1.39 -0.78 -0.01 -1.58 0.07 0.828077054 1.160875283 anatomical structure homeostasis;ATP-dependent chromatin remodeling;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;CenH3-containing nucleosome assembly at centromere;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;DNA metabolic process;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;histone exchange;homeostatic process;inositol lipid-mediated signaling;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of megakaryocyte differentiation;negative regulation of myeloid cell differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;phosphatidylinositol-mediated signaling;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biological quality;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of megakaryocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;response to stimulus;signal transduction;telomere maintenance;telomere organization binding;DNA binding;nucleic acid binding actin cytoskeleton;cell part;chromosomal part;cytoskeleton;extracellular region;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleosome;organelle;organelle part;protein-DNA complex Systemic lupus erythematosus 1.57E-95 1 11 11 60.2

Q53GQ0;E9PI21;Q96EA9 Estradiol 17-beta-dehydrogenase 12 HSD17B12 >sp|Q53GQ0|DHB12_HUMAN Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2 -0.38 -0.03 -0.06 -0.04 0.41 0.33 0.03 0.07 1.109430171 -0.336602735 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;estrogen biosynthetic process;estrogen metabolic process;extracellular matrix organization;extracellular structure organization;fatty acid biosynthetic process;fatty acid metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;hormone biosynthetic process;hormone metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell-substrate adhesion;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular process;regulation of hormone levels;small molecule biosynthetic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;thioester biosynthetic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process "binding;carbohydrate binding;catalytic activity;estradiol 17-beta-dehydrogenase activity;glycosaminoglycan binding;heparin binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;pattern binding;polysaccharide binding;steroid dehydrogenase activity;steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular matrix;extracellular region part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part Biosynthesis of unsaturated fatty acids;Steroid hormone biosynthesis 8.44E-63 3 11 11 31.7

Q12905 Interleukin enhancer-binding factor 2 ILF2 >sp|Q12905|ILF2_HUMAN Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 -0.10 0.53 -0.14 0.56 -0.23 -0.16 -1.16 -0.23 0.920733923 0.658776015 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;immune response;immune system process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;double-stranded RNA binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;transferase activitycell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex 1.27E-147 1 11 11 43.8

P47929 Galectin-7 LGALS7 >sp|P47929|LEG7_HUMAN Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2 -0.66 0.73 0.07 0.70 0.20 1.60 0.11 1.06 0.44935928 -0.527052673 apoptosis;biological adhesion;cell adhesion;cell death;cell-cell adhesion;cellular process;death;heterophilic cell-cell adhesion;programmed cell death binding;carbohydrate binding cell part;cytoplasm;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.21E-127 1 11 11 89.7

P31153;B4DN45;Q00266 S-adenosylmethionine synthase isoform type-2;S-adenosylmethionine synthase MAT2A >sp|P31153|METK2_HUMAN S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1;>tr|B4DN45|B4DN45_HUMAN S-adenosylmethionine synthase OS=Homo sapiens GN=MAT2A PE=2 SV=1 0.37 0.07 -0.17 -0.07 0.04 -0.52 0.18 -0.31 0.422872563 0.205177603 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;methylation;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;one-carbon metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside biosynthetic process;ribonucleoside metabolic process;S-adenosylmethionine biosynthetic process;S-adenosylmethionine metabolic process;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;xenobiotic metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;metal ion binding;methionine adenosyltransferase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;cytosol;intracellular part Cysteine and methionine metabolism 6.08E-79 3 11 11 28.6

B1AHB1;P33992;B1AHB2;B1AHA9 DNA replication licensing factor MCM5 MCM5 >tr|B1AHB1|B1AHB1_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=2 SV=1;>sp|P33992|MCM5_HUMAN DNA replication licensing factor MCM5 OS=Homo sapiens GN=MCM5 PE=1 SV=5 0.42 -0.09 -0.07 -0.01 0.51 -0.40 -0.51 -1.05 0.510744472 0.422776206 biological regulation;biosynthetic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell division;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA replication;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA-dependent DNA replication initiation;G1/S transition of mitotic cell cycle;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;S phase;S phase of mitotic cell cycle "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;DNA helicase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;MCM complex;membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex Cell cycle;Cell cycle - yeast;DNA replication;Meiosis - yeast 1.33E-38 4 11 11 21.1

E9PGF9;O60502;O60502-2;O60502-3;H7C3X0;B4DYV7 Bifunctional protein NCOAT;Protein O-GlcNAcase;Histone acetyltransferase MGEA5 >tr|E9PGF9|E9PGF9_HUMAN Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=2 SV=1;>sp|O60502|NCOAT_HUMAN Bifunctional protein NCOAT OS=Homo sapiens GN=MGEA5 PE=1 SV=2;>sp|O60502-2|NCOAT_HUMAN Isoform 2 of Bifunctional protein NCOAT OS=Homo sapiens GN=M 0.09 0.03 -0.16 -0.08 -0.21 -0.07 0.30 -0.19 0.029192109 0.011573615 2'-deoxyribonucleotide metabolic process;aging;alcohol metabolic process;amino sugar metabolic process;biological regulation;carbohydrate metabolic process;catabolic process;cell death;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;dATP metabolic process;death;deoxyribonucleoside triphosphate metabolic process;deoxyribonucleotide metabolic process;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;glucosamine metabolic process;glycoprotein catabolic process;glycoprotein metabolic process;heterocycle metabolic process;intracellular protein transport;intracellular transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;N-acetylglucosamine metabolic process;necrotic cell death;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of carbohydrate metabolic process;negative regulation of cardiac muscle adaptation;negative regulation of cellular biosynthetic process;negative regulation of cellular carbohydrate metabolic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of glycoprotein biosynthetic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of multicellular organismal process;negative regulation of muscle adaptation;negative regulation of protein glycosylation;negative regulation of protein metabolic process;negative regulation of protein modification process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of calcium ion transport into cytosol;positive regulation of cell killing;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of DNA metabolic process;positive regulation of glucose import;positive regulation of glucose transport;positive regulation of growth hormone secretion;positive regulation of homeostatic process;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of ion transport;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mitochondrial depolarization;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of protein complex disassembly;positive regulation of protein metabolic process;positive regulation of proteolysis;positive regulation of secretion;positive regulation of transport;primary metabolic process;protein targeting;protein targeting to membrane;protein transport;purine deoxyribonucleoside triphosphate metabolic process;purine deoxyribonucleotide metabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of carbohydrate metabolic process;regulation of cardiac muscle adaptation;regulation of cell communication;regulation of cell killing;regulation of cellular biosynthetic process;regulation of cellular carbohydrate metabolic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of DNA metabolic process;regulation of glucose import;regulation of glucose transport;regulation of glycoprotein biosynthetic process;regulation of growth hormone secretion;regulation of homeostatic process;regulation of hormone secretion;regulation of insulin secretion;regulation of ion homeostasis;regulation of ion transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane depolarization;regulation of metabolic process;regulation of metal ion transport;regulation of mitochondrial depolarization;regulation of multicellular organismal process;regulation of muscle adaptation;regulation of muscle system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of primary metabolic process;regulation of protein complex disassembly;regulation of protein glycosylation;regulation of protein metabolic process;regulation of protein modification process;regulation of proteolysis;regulation of secretion;regulation of signaling;regulation of system process;regulation of transport;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus;small molecule metabolic process;transport "acetyltransferase activity;catalytic activity;hexosaminidase activity;histone acetyltransferase activity;hyaluronoglucosaminidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;lysine N-acetyltransferase activity;N-acetyltransferase activity;N-acyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.63E-74 6 11 11 17

Q13126;B4DUC8;Q13126-4;Q13126-3;Q13126-2;Q13126-7;J3QSB7;Q13126-6;Q13126-5;F2Z2F3;F8WES2;J3KRN1 S-methyl-5-thioadenosine phosphorylase;Purine nucleoside phosphorylase MTAP >sp|Q13126|MTAP_HUMAN S-methyl-5-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP PE=1 SV=2;>tr|B4DUC8|B4DUC8_HUMAN S-methyl-5-thioadenosine phosphorylase OS=Homo sapiens GN=MTAP PE=2 SV=1;>sp|Q13126-4|MTAP_HUMAN Isoform 4 of S-methyl-5-thioadenosine0.17 -0.04 0.19 -0.11 0.11 0.07 0.52 0.27 0.642987852 -0.192346108 amine biosynthetic process;amine metabolic process;amino acid salvage;aspartate family amino acid biosynthetic process;aspartate family amino acid metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;heterocycle biosynthetic process;heterocycle metabolic process;L-methionine biosynthetic process;L-methionine salvage;L-methionine salvage from methylthioadenosine;metabolic process;methionine biosynthetic process;methionine metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;nucleoside salvage;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;polyamine metabolic process;primary metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine ribonucleoside salvage;purine-containing compound biosynthetic process;purine-containing compound metabolic process;purine-containing compound salvage;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to testosterone stimulus;ribonucleoside biosynthetic process;ribonucleoside metabolic process;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid biosynthetic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process "catalytic activity;phosphorylase activity;purine-nucleoside phosphorylase activity;S-methyl-5-thioadenosine phosphorylase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Cysteine and methionine metabolism 8.93E-154 12 11 11 51.9

P22033 "Methylmalonyl-CoA mutase, mitochondrial" MUT ">sp|P22033|MUTA_HUMAN Methylmalonyl-CoA mutase, mitochondrial OS=Homo sapiens GN=MUT PE=1 SV=4" -0.32 -0.09 0.02 0.24 0.59 0.39 0.02 0.06 0.719011933 -0.300929753 amine metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;homocysteine metabolic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;post-embryonic development;primary metabolic process;short-chain fatty acid catabolic process;short-chain fatty acid metabolic process;small molecule catabolic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound metabolic process amine binding;amino acid binding;binding;carboxylic acid binding;catalytic activity;cation binding;cobalamin binding;intramolecular transferase activity;ion binding;isomerase activity;metal ion binding;methylmalonyl-CoA mutase activity;modified amino acid binding;tetrapyrrole binding;vitamin binding cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Carbon fixation pathways in prokaryotes;Glyoxylate and dicarboxylate metabolism;Propanoate metabolism;Valine, leucine and isoleucine degradation" 6.77E-36 1 11 11 21.7

Q8NEY1-5;Q8NEY1-2;Q8NEY1-3;Q8NEY1;Q8NEY1-7;Q8NEY1-4;H0Y6F6;Q8NEY1-6 Neuron navigator 1 NAV1 >sp|Q8NEY1-5|NAV1_HUMAN Isoform 5 of Neuron navigator 1 OS=Homo sapiens GN=NAV1;>sp|Q8NEY1-2|NAV1_HUMAN Isoform 2 of Neuron navigator 1 OS=Homo sapiens GN=NAV1;>sp|Q8NEY1-3|NAV1_HUMAN Isoform 3 of Neuron navigator 1 OS=Homo sapiens GN=NAV1;>sp|Q8NEY1|NAV1_ -0.07 -0.37 0.11 0.20 -1.54 -0.29 0.37 0.37 0.190608505 0.239091491 cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;locomotion;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based process;neuron migration;organelle organization "binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;pyrophosphatase activity" cell part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;microtubule;organelle part;protein complex 8.71E-35 8 11 11 10.9

P55809;E9PDW2;B7Z528;Q8N5Z0;Q8N5Z0-2;Q9BYC2 "Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial" OXCT1 ">sp|P55809|SCOT1_HUMAN Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1;>tr|E9PDW2|E9PDW2_HUMAN Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=2 SV=1" -0.21 -0.02 -0.15 0.01 0.20 -0.14 -0.09 -0.20 0.125138744 -0.035850695 2-oxoglutarate metabolic process;acetyl-CoA metabolic process;adipose tissue development;amine catabolic process;amine metabolic process;anatomical structure development;aromatic amino acid family catabolic process;aromatic amino acid family metabolic process;aromatic compound catabolic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;biological regulation;biosynthetic process;brain development;carbohydrate homeostasis;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular catabolic process;cellular chemical homeostasis;cellular glucose homeostasis;cellular homeostasis;cellular ketone body metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to acid;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;coenzyme metabolic process;cofactor metabolic process;developmental process;dicarboxylic acid metabolic process;glucose homeostasis;glutamate metabolic process;glutamine family amino acid metabolic process;heart development;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;indolalkylamine catabolic process;indolalkylamine metabolic process;indole-containing compound catabolic process;indole-containing compound metabolic process;ketone body catabolic process;ketone catabolic process;kynurenine metabolic process;lipid metabolic process;L-lysine catabolic process;L-lysine catabolic process to acetyl-CoA;L-lysine catabolic process to acetyl-CoA via saccharopine;L-lysine metabolic process;lysine catabolic process;lysine metabolic process;metabolic process;nitrogen compound metabolic process;organ development;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular process;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of secretion;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;response to acid;response to activity;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to monosaccharide stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to starvation;response to stimulus;response to stress;small molecule catabolic process;small molecule metabolic process;tissue development;tryptophan catabolic process;tryptophan catabolic process to kynurenine;tryptophan metabolic process "2-aminoadipate transaminase activity;3-oxoacid CoA-transferase activity;binding;catalytic activity;CoA-transferase activity;cofactor binding;identical protein binding;kynurenine-oxoglutarate transaminase activity;protein binding;protein dimerization activity;protein homodimerization activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;transferase activity, transferring sulfur-containing groups;vitamin B6 binding;vitamin binding"cell part;cell projection;cilium;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;motile cilium;organelle;organelle lumen;organelle part "Butanoate metabolism;Lysine biosynthesis;Lysine degradation;Synthesis and degradation of ketone bodies;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 1.58E-68 6 11 11 30

O00764;F2Z2Y4;O00764-2;O00764-3;A8MV33 Pyridoxal kinase PDXK >sp|O00764|PDXK_HUMAN Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1;>tr|F2Z2Y4|F2Z2Y4_HUMAN Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=2 SV=1;>sp|O00764-2|PDXK_HUMAN Isoform 2 of Pyridoxal kinase OS=Homo sapiens GN=PDXK;>sp|O00764-3|PDXK_HUMAN Isofor 0.34 0.05 0.16 -0.01 -0.32 -0.38 0.03 -0.25 1.249874226 0.364631442 biosynthetic process;cell proliferation;cellular biosynthetic process;cellular metabolic compound salvage;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;heterocycle metabolic process;metabolic process;pyridoxal 5'-phosphate salvage;pyridoxal phosphate biosynthetic process;pyridoxal phosphate metabolic process;small molecule biosynthetic process;small molecule metabolic process;vitamin B6 biosynthetic process;vitamin B6 metabolic process;vitamin biosynthetic process;vitamin metabolic process;water-soluble vitamin biosynthetic process;water-soluble vitamin metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;alkali metal ion binding;ATP binding;binding;catalytic activity;cation binding;cofactor binding;identical protein binding;ion binding;kinase activity;lithium ion binding;magnesium ion binding;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;potassium ion binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyridoxal kinase activity;pyridoxal phosphate binding;ribonucleotide binding;sodium ion binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;vitamin B6 binding;vitamin binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Vitamin B6 metabolism 1.54E-111 5 11 11 40.4

P07737;K7EJ44;I3L3D5;CON__P02584 Profilin-1 PFN1 ">sp|P07737|PROF1_HUMAN Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2;>tr|K7EJ44|K7EJ44_HUMAN Profilin 1, isoform CRA_b OS=Homo sapiens GN=PFN1 PE=4 SV=1" 0.01 -0.19 -0.22 -0.03 -0.38 -0.21 0.46 -0.04 0.1236955 -0.065513879 "actin cytoskeleton organization;actin filament-based process;anatomical structure formation involved in morphogenesis;biological regulation;cell activation;cell death;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;death;developmental process;establishment of localization;establishment of localization in cell;exocytosis;neural tube closure;organelle organization;platelet activation;platelet degranulation;positive regulation of actin filament bundle assembly;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of DNA metabolic process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of stress fiber assembly;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoskeleton organization;regulation of DNA metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of stress fiber assembly;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;secretion;secretion by cell;transport;tube closure;tube formation;vesicle-mediated transport" "binding;lipid binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding" cell part;cell projection;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nucleus;organelle;synapse Regulation of actin cytoskeleton;Shigellosis 9.49E-198 4 11 11 86.4

Q99959-2;Q99959 Plakophilin-2 PKP2 >sp|Q99959-2|PKP2_HUMAN Isoform 1 of Plakophilin-2 OS=Homo sapiens GN=PKP2;>sp|Q99959|PKP2_HUMAN Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2 0.44 0.48 -0.16 0.21 -2.16 -0.79 -0.94 0.02 1.080319738 1.2104968 adherens junction maintenance;adherens junction organization;anatomical structure morphogenesis;biological adhesion;biological regulation;cardiac muscle tissue morphogenesis;cell adhesion;cell junction assembly;cell junction maintenance;cell junction organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component maintenance;cellular component maintenance at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemical homeostasis;cytoskeleton organization;desmosome assembly;developmental process;gap junction assembly;homeostatic process;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;lipid homeostasis;maintenance of organ identity;muscle tissue morphogenesis;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of developmental process;negative regulation of locomotion;organelle organization;positive regulation of biological process;positive regulation of ion transport;positive regulation of sodium ion transport;positive regulation of transport;regulation of biological process;regulation of biological quality;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of ion transport;regulation of localization;regulation of locomotion;regulation of metal ion transport;regulation of sodium ion transport;regulation of tight junction assembly;regulation of transport;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis binding;channel regulator activity;intermediate filament binding;ion channel binding;protein binding;protein complex binding;protein complex scaffold;sodium channel regulator activity;structural molecule activity adherens junction;anchoring junction;cell junction;cell part;cell-cell contact zone;cell-cell junction;cytoskeletal part;desmosome;integral to membrane;intercalated disc;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC) 3.03E-111 2 11 11 20.9

Q8WVV4;Q8WVV4-1;F2Z2D5;Q8WVV4-3 Protein POF1B POF1B >sp|Q8WVV4|POF1B_HUMAN Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3;>sp|Q8WVV4-1|POF1B_HUMAN Isoform 1 of Protein POF1B OS=Homo sapiens GN=POF1B;>tr|F2Z2D5|F2Z2D5_HUMAN Protein POF1B OS=Homo sapiens GN=POF1B PE=2 SV=1;>sp|Q8WVV4-3|POF1B_HUMAN Isoform 3 0.08 0.60 0.24 0.27 0.16 0.94 0.14 0.54 0.254426774 -0.144297505 2.03E-39 4 11 11 22.2

Q06124-2;Q06124;Q06124-3;H0YF12 Tyrosine-protein phosphatase non-receptor type 11 PTPN11 >sp|Q06124-2|PTN11_HUMAN Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11;>sp|Q06124|PTN11_HUMAN Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens GN=PTPN11 PE=1 SV=2;>sp|Q06124-3|PTN11_HUMAN Isoform0.22 -0.06 0.08 -0.07 -0.09 -0.05 0.49 0.30 0.307900827 -0.121365157 activation of MAPK activity;acylglycerol metabolic process;anatomical structure development;anatomical structure morphogenesis;axon guidance;biological regulation;blood coagulation;brain development;carbohydrate homeostasis;cell cycle checkpoint;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component movement;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;cellular response to type I interferon;chemical homeostasis;chemotaxis;coagulation;cytokine-mediated signaling pathway;developmental process;developmental process involved in reproduction;DNA damage checkpoint;DNA integrity checkpoint;enzyme linked receptor protein signaling pathway;ephrin receptor signaling pathway;epidermal growth factor receptor signaling pathway;face morphogenesis;fibroblast growth factor receptor signaling pathway;genitalia development;glucose homeostasis;glycerol ether metabolic process;glycerolipid metabolic process;growth;hemostasis;homeostatic process;hormone metabolic process;hormone-mediated signaling pathway;immune system process;inner ear development;inositol lipid-mediated signaling;insulin receptor signaling pathway;interferon-gamma-mediated signaling pathway;intracellular signal transduction;leukocyte migration;lipid metabolic process;locomotion;lymphocyte costimulation;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cellular process;negative regulation of corticosteroid hormone secretion;negative regulation of cortisol secretion;negative regulation of glucocorticoid secretion;negative regulation of growth hormone secretion;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of secretion;negative regulation of steroid hormone secretion;negative regulation of transport;nerve growth factor receptor signaling pathway;neutral lipid metabolic process;organ development;organ growth;organic ether metabolic process;phosphate-containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell activation;positive regulation of cellular process;positive regulation of hormone secretion;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of secretion;positive regulation of T cell activation;positive regulation of transferase activity;positive regulation of transport;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of catalytic activity;regulation of cell activation;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation of cell communication;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of corticosteroid hormone secretion;regulation of cortisol secretion;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of endocrine process;regulation of establishment of protein localization;regulation of glucocorticoid secretion;regulation of growth;regulation of growth hormone secretion;regulation of hormone levels;regulation of hormone secretion;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of insulin secretion;regulation of interferon-gamma-mediated signaling pathway;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of leukocyte activation;regulation of localization;regulation of lymphocyte activation;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of nucleocytoplasmic transport;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of steroid hormone secretion;regulation of system process;regulation of T cell activation;regulation of transferase activity;regulation of transport;regulation of type I interferon-mediated signaling pathway;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to insulin stimulus;response to interferon-gamma;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;response to type I interferon;signal transduction;small molecule metabolic process;T cell costimulation;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;triglyceride metabolic process;type I interferon-mediated signaling pathway "binding;binding, bridging;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;non-membrane spanning protein tyrosine phosphatase activity;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein binding;protein binding, bridging;protein tyrosine phosphatase activity;SH3/SH2 adaptor activity;signaling adaptor activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nucleus;organelle;protein complex Adipocytokine signaling pathway;Chronic myeloid leukemia;Epithelial cell signaling in Helicobacter pylori infection;Jak-STAT signaling pathway;Leukocyte transendothelial migration;MAPK signaling pathway - fly;Natural killer cell mediated cytotoxicity;Neurotrophin signaling pathway;Renal cell carcinoma 1.89E-96 4 11 11 25.6

H0YEH2;Q14671-2;Q14671;Q14671-3;Q5T1Z4;Q5T1Z8;E9PR38;E7EWT3;B4DG92;H0YDK8;E9PMX1;Q8TB72-2;B4E2B6;Q8TB72-3;Q8TB72;E9PM68;E9PL65 Pumilio homolog 1 PUM1 >tr|H0YEH2|H0YEH2_HUMAN Pumilio homolog 1 (Fragment) OS=Homo sapiens GN=PUM1 PE=4 SV=1;>sp|Q14671-2|PUM1_HUMAN Isoform 2 of Pumilio homolog 1 OS=Homo sapiens GN=PUM1;>sp|Q14671|PUM1_HUMAN Pumilio homolog 1 OS=Homo sapiens GN=PUM1 PE=1 SV=3;>sp|Q14671-3|PUM 0.22 -0.02 0.29 -0.11 -0.05 -0.35 0.02 -0.18 0.80016044 0.233443397 biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;membrane organization;post-Golgi vesicle-mediated transport;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;stress granule assembly;transport;vesicle-mediated transport binding;nucleic acid binding;RNA binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;perinuclear region of cytoplasm;ribonucleoprotein complex;RNA granule;stress granule 3.83E-63 17 11 11 14

Q9P0K7-4;Q9P0K7-3;E7EMX7;Q9P0K7;Q9P0K7-2;D6RB25;D6RBW6;D6RB27;D6R9G4;D6RBY4;D6REL2;D6R9G6;D6RF74;D6RE17 Ankycorbin RAI14 >sp|Q9P0K7-4|RAI14_HUMAN Isoform 4 of Ankycorbin OS=Homo sapiens GN=RAI14;>sp|Q9P0K7-3|RAI14_HUMAN Isoform 3 of Ankycorbin OS=Homo sapiens GN=RAI14;>tr|E7EMX7|E7EMX7_HUMAN Ankycorbin OS=Homo sapiens GN=RAI14 PE=2 SV=1;>sp|Q9P0K7|RAI14_HUMAN Ankycorbin OS=H -0.53 0.63 -0.20 0.71 0.98 1.16 -0.33 0.87 0.468989043 -0.518624771 cell cortex;cell part;cytoplasmic part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nucleus;organelle 8.46E-36 14 11 11 14.3

Q63HN8;Q63HN8-4;H3BLU6;Q63HN8-6;Q63HN8-5;J3QTP8 E3 ubiquitin-protein ligase RNF213 RNF213 >sp|Q63HN8|RN213_HUMAN E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3;>sp|Q63HN8-4|RN213_HUMAN Isoform 2 of E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213;>tr|H3BLU6|H3BLU6_HUMAN E3 ubiquitin-protein ligase RNF213 OS=H 0.24 -0.05 0.06 -0.14 0.41 -0.13 -0.03 0.02 0.097007728 -0.03954153 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein autoubiquitination;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;cytoplasm;intracellular part 1.86E-28 6 11 11 3

P50914;E7EPB3 60S ribosomal protein L14 RPL14 >sp|P50914|RL14_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4;>tr|E7EPB3|E7EPB3_HUMAN 60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=2 SV=1 -0.25 0.02 0.21 0.08 -0.04 -0.50 -0.61 -0.50 1.116298055 0.425552371 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 7.10E-87 2 11 11 43.3

Q9NQC3-2;Q9NQC3-5;Q9NQC3;F8W914;Q9NQC3-4;F8WAM4;Q9NQC3-3;H7C106;Q9NQC3-6 Reticulon-4 RTN4 >sp|Q9NQC3-2|RTN4_HUMAN Isoform 2 of Reticulon-4 OS=Homo sapiens GN=RTN4;>sp|Q9NQC3-5|RTN4_HUMAN Isoform 5 of Reticulon-4 OS=Homo sapiens GN=RTN4;>sp|Q9NQC3|RTN4_HUMAN Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2;>tr|F8W914|F8W914_HUMAN Reticulon-4 OS=Hom -0.38 0.07 -0.19 -0.06 0.73 0.53 -0.29 0.03 0.66167397 -0.391931665 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;apoptosis;axonal fasciculation;biological regulation;cardiac epithelial to mesenchymal transition;cell death;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell recognition;cell surface receptor linked signaling pathway;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;cerebral cortex cell migration;cerebral cortex radial glia guided migration;cerebral cortex radially oriented cell migration;death;developmental process;endoplasmic reticulum organization;endoplasmic reticulum tubular network organization;enzyme linked receptor protein signaling pathway;epithelial to mesenchymal transition;forebrain cell migration;locomotion;negative regulation of axon extension;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental growth;negative regulation of developmental process;negative regulation of growth;negative regulation of neurogenesis;nerve growth factor receptor signaling pathway;neuron recognition;organelle organization;programmed cell death;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of branching morphogenesis of a nerve;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell motility;regulation of cell projection organization;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of localization;regulation of locomotion;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of programmed cell death;response to stimulus;signal transduction;telencephalon cell migration;transmembrane receptor protein tyrosine kinase signaling pathway cell body;cell part;cell projection;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum part;envelope;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;membrane;membrane part;membrane-bounded organelle;neuronal cell body;nuclear envelope;nuclear part;organelle;organelle envelope;organelle part;plasma membrane 1.16E-118 9 11 11 59.2

P61011;P61011-2;G3V4F7;G3V480;G3V346;G3V3L9 Signal recognition particle 54 kDa protein SRP54 >sp|P61011|SRP54_HUMAN Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1;>sp|P61011-2|SRP54_HUMAN Isoform 2 of Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54;>tr|G3V4F7|G3V4F7_HUMAN Signal recognition partic 0.02 -0.02 0.06 0.04 -0.04 -0.24 0.03 -0.40 0.823307321 0.188787091 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;intracellular protein transmembrane transport;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transmembrane transport;protein transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;response to chemical stimulus;response to drug;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;SRP-dependent cotranslational protein targeting to membrane;SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition;SRP-dependent cotranslational protein targeting to membrane, translocation;translation;transmembrane transport;transport" "7S RNA binding;binding;catalytic activity;drug binding;endoplasmic reticulum signal peptide binding;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;peptide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleoprotein binding;ribonucleotide binding;RNA binding;signal sequence binding" "cell part;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;signal recognition particle;signal recognition particle, endoplasmic reticulum targeting" Bacterial secretion system;Protein export 2.45E-143 6 11 11 29.4

Q9Y5M8;H7C4H2;C9J5Z8 Signal recognition particle receptor subunit beta SRPRB >sp|Q9Y5M8|SRPRB_HUMAN Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3;>tr|H7C4H2|H7C4H2_HUMAN Signal recognition particle receptor subunit beta (Fragment) OS=Homo sapiens GN=SRPRB PE=4 SV=1 -0.02 0.00 0.03 0.07 0.49 -0.07 -0.45 -0.02 0.057506252 0.032904213 activation of signaling protein activity involved in unfolded protein response;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular signal transduction;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;signal transduction;small GTPase mediated signal transduction;SRP-dependent cotranslational protein targeting to membrane;translation;transport binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;microtubule;organelle membrane;organelle part;protein complex Protein export 7.58E-102 3 11 11 36.9

O00267-2;O00267;M0QYL9 Transcription elongation factor SPT5 SUPT5H >sp|O00267-2|SPT5H_HUMAN Isoform 2 of Transcription elongation factor SPT5 OS=Homo sapiens GN=SUPT5H;>sp|O00267|SPT5H_HUMAN Transcription elongation factor SPT5 OS=Homo sapiens GN=SUPT5H PE=1 SV=1 0.13 0.46 0.10 0.29 0.05 0.08 -0.44 -0.06 0.990333696 0.337647136 "biological regulation;biosynthetic process;cell cycle;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;macromolecule metabolic process;metabolic process;mRNA capping;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription elongation, DNA-dependent;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of autophagy;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macroautophagy;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of response to external stimulus;positive regulation of response to extracellular stimulus;positive regulation of response to nutrient levels;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription elongation from RNA polymerase II promoter;positive regulation of transcription elongation, DNA-dependent;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;regulation of autophagy;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of gene expression;regulation of macroautophagy;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription elongation from RNA polymerase II promoter;regulation of transcription elongation, DNA-dependent;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;retroviral genome replication;RNA biosynthetic process;RNA capping;RNA metabolic process;RNA processing;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;viral genome replication;viral reproductive process" cell part;DSIF complex;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm part;organelle part;protein complex;transcription elongation factor complex 2.58E-66 3 11 11 15.4

Q9BTW9;J3KR97;Q9BTW9-4;Q9BTW9-5;I3L439;C9J1U4;I3L0V3;I3L163;I3L120;I3L4D2;I3L3H4;Q9BTW9-3;I3L131;Q9BTW9-2;I3L143;I3L500 Tubulin-specific chaperone D TBCD >sp|Q9BTW9|TBCD_HUMAN Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2;>tr|J3KR97|J3KR97_HUMAN Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=4 SV=1;>sp|Q9BTW9-4|TBCD_HUMAN Isoform 4 of Tubulin-specific chaperone D OS=Homo sapiens GN 0.27 0.06 0.07 -0.21 -0.07 -0.46 0.21 -0.10 0.36305946 0.152124962 adherens junction assembly;adherens junction organization;biological regulation;cell junction assembly;cell junction organization;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell-substrate adhesion;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of microtubule polymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein polymerization;post-chaperonin tubulin folding pathway;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of cell adhesion;regulation of cell-substrate adhesion;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;tight junction assembly beta-tubulin binding;binding;chaperone binding;cytoskeletal protein binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;tubulin binding adherens junction;anchoring junction;cell junction;cell part;cell-cell junction;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;microtubule;occluding junction;organelle part;plasma membrane part;protein complex;tight junction 1.94E-66 16 11 11 13

P26368-2;P26368;K7ENG2 Splicing factor U2AF 65 kDa subunit U2AF2 >sp|P26368-2|U2AF2_HUMAN Isoform 2 of Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2;>sp|P26368|U2AF2_HUMAN Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4;>tr|K7ENG2|K7ENG2_HUMAN Splicing factor U2AF 65 kDa subunit OS= 0.02 0.19 0.02 0.32 -0.02 -0.34 -0.91 -0.27 1.090988415 0.524740497 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of RNA localization;intracellular transport;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA export from nucleus;mRNA metabolic process;mRNA processing;mRNA transport;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear export;nuclear mRNA splicing, via spliceosome;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA 3'-end processing;RNA biosynthetic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;termination of RNA polymerase II transcription;transcription termination, DNA-dependent;transport" binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 1.63E-99 3 11 11 27.8

Q96K76-2;E9PM46;Q96K76;Q96K76-3 Ubiquitin carboxyl-terminal hydrolase;Ubiquitin carboxyl-terminal hydrolase 47 USP47 >sp|Q96K76-2|UBP47_HUMAN Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens GN=USP47;>tr|E9PM46|E9PM46_HUMAN Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP47 PE=2 SV=1;>sp|Q96K76|UBP47_HUMAN Ubiquitin carboxyl-terminal hydr 0.02 -0.01 0.04 -0.06 0.17 0.11 0.43 -0.06 0.705218313 -0.170829067 "base-excision repair;biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to light stimulus;cellular response to radiation;cellular response to stimulus;cellular response to stress;cellular response to UV;DNA metabolic process;DNA repair;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;monoubiquitinated protein deubiquitination;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of G2/M transition of mitotic cell cycle;negative regulation of gene expression;negative regulation of hydrolase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitotic cell cycle;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;primary metabolic process;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of G2/M transition of mitotic cell cycle;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of interphase of mitotic cell cycle;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to drug;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;ubiquitin-dependent protein catabolic process" "catalytic activity;cysteine-type peptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;peptidase activity;peptidase activity, acting on L-amino acid peptides;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" cell part;cullin-RING ubiquitin ligase complex;cytoplasm;intracellular part;macromolecular complex;protein complex;SCF ubiquitin ligase complex;ubiquitin ligase complex 7.81E-47 4 11 11 12.3

Q9BVJ6-3;Q9BVJ6;F8WD00;Q9BVJ6-2;Q5TAP6 U3 small nucleolar RNA-associated protein 14 homolog A UTP14A >sp|Q9BVJ6-3|UT14A_HUMAN Isoform 3 of U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A;>sp|Q9BVJ6|UT14A_HUMAN U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1;>tr|F8WD00|F8WD00_HUMAN -0.31 1.07 0.23 1.09 -0.83 -0.29 -1.18 0.15 0.995877158 1.056014139 cell cycle phase;cell cycle process;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;gamete generation;macromolecule metabolic process;male gamete generation;meiosis;metabolic process;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;reproductive process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;spermatogenesis cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;ribonucleoprotein complex;small-subunit processome Ribosome biogenesis in eukaryotes 3.96E-52 5 11 11 21.6

Q86V21;Q86V21-2;Q86V21-3;F5H790;E7EW25;F5GYN1;F5H8J5;F5H3E3;F5GYW2;F5GWW7;F5H6X9;F5H4V2;F8W8B5;Q8N108-19;Q8N108-16;Q8N108-14;Q8N108-18;Q8N108-17;Q8N108-15;REV__Q96RS6-3;Q8N108;Q8N108-13;REV__Q96RS6-2;Q8N108-12;REV__Q96RS6 Acetoacetyl-CoA synthetase AACS >sp|Q86V21|AACS_HUMAN Acetoacetyl-CoA synthetase OS=Homo sapiens GN=AACS PE=1 SV=1;>sp|Q86V21-2|AACS_HUMAN Isoform 2 of Acetoacetyl-CoA synthetase OS=Homo sapiens GN=AACS;>sp|Q86V21-3|AACS_HUMAN Isoform 3 of Acetoacetyl-CoA synthetase OS=Homo sapiens GN=AA -0.05

-0.19 0.09 -0.03 -0.53 -0.36 0.57 -0.01 0.05374548 0.039714751 "adipose tissue development;anatomical structure development;biological regulation;biosynthetic process;carbohydrate homeostasis;carboxylic acid metabolic process;cell differentiation;cellular biosynthetic process;cellular chemical homeostasis;cellular developmental process;cellular glucose homeostasis;cellular homeostasis;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to cholesterol;cellular response to endogenous stimulus;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to hormone stimulus;cellular response to lipid;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to testosterone stimulus;chemical homeostasis;developmental process;fat cell differentiation;fatty acid metabolic process;glucose homeostasis;homeostatic process;lipid metabolic process;liver development;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of chromatin silencing;positive regulation of hormone secretion;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of insulin secretion;positive regulation of intracellular protein kinase cascade;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of response to stimulus;positive regulation of secretion;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of chromatin silencing;regulation of gene expression;regulation of gene silencing;regulation of hormone secretion;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of insulin secretion;regulation of intracellular protein kinase cascade;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transport;response to carbohydrate stimulus;response to chemical stimulus;response to cholesterol;response to drug;response to endogenous stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to fatty acid;response to glucose stimulus;response to hexose stimulus;response to hormone stimulus;response to lipid;response to monosaccharide stimulus;response to nutrient;response to nutrient levels;response to oleic acid;response to organic cyclic compound;response to organic substance;response to purine-containing compound;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;tissue development;transcription, DNA-dependent;white fat cell differentiation" "acetoacetate-CoA ligase activity;acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;butyrate-CoA ligase activity;catalytic activity;chromatin binding;DNA binding;ligase activity;ligase activity, forming carbon-sulfur bonds;molecular transducer activity;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;signal transducer activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm part;organelle part;protein complex;transcriptional repressor complex Butanoate metabolism 8.99E-59 25 12 11 17.7

B4DT77;P20073-2;P20073 Annexin;Annexin A7 ANXA7 >tr|B4DT77|B4DT77_HUMAN Annexin OS=Homo sapiens GN=ANXA7 PE=2 SV=1;>sp|P20073-2|ANXA7_HUMAN Isoform 2 of Annexin A7 OS=Homo sapiens GN=ANXA7;>sp|P20073|ANXA7_HUMAN Annexin A7 OS=Homo sapiens GN=ANXA7 PE=1 SV=3 0.05 -0.04 0.30 -0.45 0.28 0.08 0.33 0.07 0.562701344 -0.225057465 behavior;behavioral interaction between organisms;biological regulation;calcium ion homeostasis;cation homeostasis;cell proliferation;cell volume homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular water homeostasis;chemical homeostasis;divalent inorganic cation homeostasis;hemostasis;homeostatic process;ion homeostasis;metal ion homeostasis;multicellular organismal process;multi-organism process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to abiotic stimulus;response to osmotic stress;response to salt stress;response to stimulus;response to stress;social behavior;water homeostasis binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;ion binding;lipid binding;metal ion binding;phospholipid binding cell part;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;nuclear envelope;nuclear part;nucleus;organelle;organelle envelope;organelle membrane;organelle part;plasma membrane;vesicle 4.50E-84 3 12 11 37.2

B4DJV2;O75390;H0YIC4;F8VPF9;F8VPA1;F8VTT8;F8W1S4;F8W4S1;H0YH82;F8W642;F8VZK9;F8VX07;F8VRP1;F8VX68;F8VWQ5;F8VRI6;F8VR34 "Citrate synthase;Citrate synthase, mitochondrial" CS ">tr|B4DJV2|B4DJV2_HUMAN Citrate synthase OS=Homo sapiens GN=CS PE=2 SV=1;>sp|O75390|CISY_HUMAN Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2" 0.15 -0.08 -0.14 -0.07 0.29 0.04 0.15 -0.13 0.45994996 -0.121740754 acetyl-CoA catabolic process;acetyl-CoA metabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;citrate (Si)-synthase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism 7.83E-59 17 12 11 24.7

O43237;B4DZP4;J3KRI4;J3KRZ2;B4E2E0;H3BUM4;E7EPL8;J3KSD2 Cytoplasmic dynein 1 light intermediate chain 2 DYNC1LI2 >sp|O43237|DC1L2_HUMAN Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=1 SV=1;>tr|B4DZP4|B4DZP4_HUMAN Cytoplasmic dynein 1 light intermediate chain 2 OS=Homo sapiens GN=DYNC1LI2 PE=2 SV=1;>tr|J3KRI4|J3KRI4_HUMAN Cytoplasmic d -0.03 0.06 0.07 0.05 0.08 0.17 0.04 0.05 0.495900539 -0.044995038 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular process;centrosome localization;cytoskeleton organization;establishment of localization;immune system process;localization;microtubule cytoskeleton organization;microtubule-based process;organelle localization;organelle organization;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;centrosome;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex Phagosome;Vasopressin-regulated water reabsorption 8.07E-142 8 12 11 33.1

P48739;B7Z7Q0;P48739-2;B3KYB6;B3KYB7 Phosphatidylinositol transfer protein beta isoform PITPNB >sp|P48739|PIPNB_HUMAN Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=1 SV=2;>tr|B7Z7Q0|B7Z7Q0_HUMAN Phosphatidylinositol transfer protein beta isoform OS=Homo sapiens GN=PITPNB PE=2 SV=1;>sp|P48739-2|PIPNB_HUMAN Isoform 2 0.06 -0.05 -0.30 0.07 -0.21 -0.11 0.27 0.01 0.124493323 -0.046559555 biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;establishment of localization;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;in utero embryonic development;lipid biosynthetic process;lipid metabolic process;lipid transport;metabolic process;organic substance transport;organophosphate metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;phospholipid transport;primary metabolic process;small molecule metabolic process;transport binding;lipid binding cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;intracellular;intracellular organelle part;intracellular part;membrane;membrane part;organelle membrane;organelle part 2.19E-79 5 12 11 48

O15305;H3BV55;H3BRM0;F5H0W0;H3BPH4;B7Z6R0;B7Z419;H3BR08;H3BM92;H3BV34;H3BT06;H3BNY9 Phosphomannomutase 2 PMM2 >sp|O15305|PMM2_HUMAN Phosphomannomutase 2 OS=Homo sapiens GN=PMM2 PE=1 SV=1;>tr|H3BV55|H3BV55_HUMAN Phosphomannomutase 2 OS=Homo sapiens GN=PMM2 PE=2 SV=1;>tr|H3BRM0|H3BRM0_HUMAN Phosphomannomutase 2 OS=Homo sapiens GN=PMM2 PE=2 SV=1;>tr|F5H0W0|F5H0W0_HUM 0.04 -0.08 -0.03 -0.03 0.02 -0.13 0.41 0.03 0.358349004 -0.106121884 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;dolichol-linked oligosaccharide biosynthetic process;GDP-mannose biosynthetic process;GDP-mannose metabolic process;glycosylation;hexose biosynthetic process;hexose metabolic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;mannose biosynthetic process;mannose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar biosynthetic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;small molecule biosynthetic process;small molecule metabolic process "catalytic activity;intramolecular transferase activity;intramolecular transferase activity, phosphotransferases;isomerase activity;phosphomannomutase activity" cell body;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;neuronal cell body Amino sugar and nucleotide sugar metabolism;Fructose and mannose metabolism 2.87E-32 12 12 11 52

B4DMK0;Q15907;P62491-2;J3KQP6;H3BMH2;H3BSC1;P62491;B4DQU5;M0R2D0;M0R377;H3BN38 Ras-related protein Rab-11B;Ras-related protein Rab-11A RAB11B;RAB11A >tr|B4DMK0|B4DMK0_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=2 SV=1;>sp|Q15907|RB11B_HUMAN Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4;>sp|P62491-2|RB11A_HUMAN Isoform 2 of Ras-related protein Rab-11A OS=Homo sapiens -0.15 0.06 -0.49 0.11 -0.16 0.33 -0.01 0.24 0.514909959 -0.21764693 biological regulation;catabolic process;cell cycle;cell projection organization;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular response to stimulus;cytokinesis;establishment of localization;establishment of localization in cell;establishment of melanosome localization;establishment of organelle localization;establishment of pigment granule localization;establishment of protein localization;establishment of vesicle localization;fluid transport;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;intracellular protein transport;intracellular signal transduction;intracellular transport;localization;macromolecule localization;melanosome transport;membrane organization;metabolic process;neuron projection development;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;pigment granule transport;plasma membrane organization;plasma membrane to endosome transport;primary metabolic process;protein localization;protein localization in membrane;protein localization in plasma membrane;protein transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular process;regulation of establishment of protein localization;regulation of localization;regulation of long-term neuronal synaptic plasticity;regulation of multicellular organismal process;regulation of neurological system process;regulation of neuronal synaptic plasticity;regulation of protein localization;regulation of protein transport;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small GTPase mediated signal transduction;small molecule metabolic process;transmembrane transport;transport;water transport "binding;catalytic activity;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;SNARE binding;syntaxin binding" cell division site part;cell part;cleavage furrow;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;organelle membrane;organelle part;phagocytic vesicle;phagocytic vesicle membrane;plasma membrane;protein complex;recycling endosome;recycling endosome membrane;trans-Golgi network;transport vesicle;vesicle;vesicle membrane Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Pancreatic secretion;Vasopressin-regulated water reabsorption 1.76E-92 11 12 11 65.9

P54727;Q5W0S5;P54727-2;Q5W0S4;H0Y579 UV excision repair protein RAD23 homolog B RAD23B >sp|P54727|RD23B_HUMAN UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1;>tr|Q5W0S5|Q5W0S5_HUMAN UV excision repair protein RAD23 homolog B (Fragment) OS=Homo sapiens GN=RAD23B PE=2 SV=1;>sp|P54727-2|RD23B_HUMAN Isoform 2 of UV 0.15 0.10 -0.09 0.04 0.08 0.07 0.18 -0.18 0.034856231 0.009705811 "biological regulation;catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;DNA catabolic process;DNA excision;DNA metabolic process;gamete generation;macromolecule catabolic process;macromolecule metabolic process;male gamete generation;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair, DNA damage recognition;nucleotide-excision repair, DNA damage removal;organelle organization;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of proteolysis;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;spermatogenesis;ubiquitin-dependent protein catabolic process" binding;damaged DNA binding;DNA binding;nucleic acid binding;polyubiquitin binding;protein binding;single-stranded DNA binding;small conjugating protein binding;structure-specific DNA binding;ubiquitin binding cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;nucleotide-excision repair complex;organelle part;proteasome complex;protein complex;XPC complex Nucleotide excision repair;Protein processing in endoplasmic reticulum 1.21E-99 5 12 11 34.2

F5H0L8;Q9Y6Y8;Q9Y6Y8-2;H7C0V8;REV__Q9NYY3 SEC23-interacting protein SEC23IP >tr|F5H0L8|F5H0L8_HUMAN SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=2 SV=1;>sp|Q9Y6Y8|S23IP_HUMAN SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1;>sp|Q9Y6Y8-2|S23IP_HUMAN Isoform 2 of SEC23-interacting protein OS=Homo sapiens GN= 0.05 -0.08 -0.09 -0.08 0.34 0.18 0.28 -0.07 1.009227306 -0.229692263 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi organization;intracellular protein transport;intracellular transport;organelle organization;protein transport;transport binding;cation binding;ion binding;metal ion binding cell part;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endoplasmic reticulum;endoplasmic reticulum-Golgi intermediate compartment;ER to Golgi transport vesicle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;transport vesicle membrane;vesicle membrane 2.43E-57 5 12 11 21.2

Q92734-2;Q92734;C9JJP5;C9JUE0;C9JTY3;REV__K7EPD6;REV__Q8N4Y2;Q6A163;CON__Q6IFU6;REV__H7C4G9;REV__O15083;REV__G8JLD3;REV__Q8IUD2-3;REV__Q8IUD2;REV__Q6ZRS2-3;REV__Q6ZRS2-2;REV__Q6ZRS2 Protein TFG TFG >sp|Q92734-2|TFG_HUMAN Isoform 2 of Protein TFG OS=Homo sapiens GN=TFG;>sp|Q92734|TFG_HUMAN Protein TFG OS=Homo sapiens GN=TFG PE=1 SV=2;>tr|C9JJP5|C9JJP5_HUMAN Protein TFG (Fragment) OS=Homo sapiens GN=TFG PE=2 SV=1;>tr|C9JUE0|C9JUE0_HUMAN Protein TFG (Fr 0.05 -0.10 0.16 -0.25 0.13 -0.03 0.30 -0.16 0.283317749 -0.097069789 biological regulation;cell death;cellular process;death;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of response to stimulus;regulation of signal transduction;regulation of signaling molecular transducer activity;signal transducer activity;structural molecule activity cell part;cytoplasm;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex Pathways in cancer;Thyroid cancer 1.75E-156 17 12 11 41.9

Q7Z460;Q7Z460-2;B7ZLX3;F5GWS0;Q7Z460-3;F8WA11;F5GWM7;F5H2E2;H0Y5T1;C9J151;C9JP76;H0YHV8 CLIP-associating protein 1 CLASP1 >sp|Q7Z460|CLAP1_HUMAN CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=1;>sp|Q7Z460-2|CLAP1_HUMAN Isoform 2 of CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1;>tr|B7ZLX3|B7ZLX3_HUMAN CLASP1 protein OS=Homo sapiens GN=CLASP1 PE=2 SV=1;>tr| 0.22 -0.06 0.01 -0.28 0.09 -0.01 0.38 -0.12 0.297265247 -0.112590272 anaphase;axon guidance;biological regulation;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of spindle localization;establishment of spindle orientation;exit from mitosis;G2/M transition of mitotic cell cycle;locomotion;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;microtubule anchoring;microtubule bundle formation;microtubule cytoskeleton organization;microtubule nucleation;microtubule organizing center organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of microtubule depolymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of organelle organization;negative regulation of protein complex disassembly;organelle organization;regulation of biological process;regulation of biological quality;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule depolymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of organelle organization;regulation of protein complex disassembly;response to chemical stimulus;response to external stimulus;response to stimulus;taxis binding;cytoskeletal protein binding;kinetochore binding;microtubule binding;microtubule plus-end binding;protein binding;tubulin binding cell cortex part;cell part;centrosomal corona;chromosomal part;condensed chromosome kinetochore;cortical cytoskeleton;cortical microtubule cytoskeleton;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;kinetochore microtubule;macromolecular complex;membrane-bounded organelle;microtubule;microtubule organizing center part;non-membrane-bounded organelle;organelle;organelle part;protein complex;spindle microtubule 9.84E-55 12 13 11 11.7

E3W994;F5H604;E9PBA6;J3KR49;O75122;E7ERI8;E7EW49;F5H3X0;H7C5M8;H7C4X8;O75122-2;B3KR06;E7ENG2;C9J668;H7C4I5;D6RBU8 CLIP-associating protein 2 CLASP2 >tr|E3W994|E3W994_HUMAN CLIP-associating protein 2 OS=Homo sapiens GN=CLASP2 PE=2 SV=2;>tr|F5H604|F5H604_HUMAN CLIP-associating protein 2 OS=Homo sapiens GN=CLASP2 PE=2 SV=1;>tr|E9PBA6|E9PBA6_HUMAN CLIP-associating protein 2 OS=Homo sapiens GN=CLASP2 PE=2 0.20 -0.11 0.30 -0.08 -0.15 -0.17 0.25 -0.28 0.430392745 0.161941562 anaphase;axon guidance;biological regulation;cell cycle phase;cell cycle process;cell division;cell migration;cell motility;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;cytoskeleton organization;establishment or maintenance of cell polarity;locomotion;M phase;M phase of mitotic cell cycle;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;microtubule anchoring;microtubule cytoskeleton organization;microtubule nucleation;microtubule organizing center organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of microtubule depolymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of organelle organization;negative regulation of protein complex disassembly;organelle organization;regulation of biological process;regulation of biological quality;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule depolymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of organelle organization;regulation of protein complex disassembly;response to chemical stimulus;response to external stimulus;response to stimulus;taxis "alpha(1,2)-fucosyltransferase activity;binding;catalytic activity;cytoskeletal protein binding;fucosyltransferase activity;galactoside 2-alpha-L-fucosyltransferase activity;microtubule binding;microtubule plus-end binding;protein binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;tubulin binding" cell cortex;cell part;cell projection membrane;cell projection part;chromosomal part;condensed chromosome kinetochore;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytosol;Golgi apparatus;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;kinetochore microtubule;leading edge membrane;macromolecular complex;membrane part;membrane-bounded organelle;microtubule;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;protein complex;ruffle membrane;spindle microtubule;trans-Golgi network 3.64E-116 16 13 11 13.8

Q15417;F8WA86;B4DFK6;E9PDU6 Calponin-3 CNN3 >sp|Q15417|CNN3_HUMAN Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1;>tr|F8WA86|F8WA86_HUMAN Calponin-3 OS=Homo sapiens GN=CNN3 PE=2 SV=1;>tr|B4DFK6|B4DFK6_HUMAN Calponin-3 OS=Homo sapiens GN=CNN3 PE=2 SV=1;>tr|E9PDU6|E9PDU6_HUMAN Calponin-3 (Fragment) OS=Ho 0.57 -0.02 -0.35 -0.20 0.90 0.58 0.06 0.35 0.751567988 -0.469863947 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;multicellular organismal process;muscle contraction;muscle system process;negative regulation of ATPase activity;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;organelle organization;regulation of ATPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;smooth muscle contraction;system process actin binding;binding;calmodulin binding;cytoskeletal protein binding;protein binding;tropomyosin binding;troponin C binding cell body;cell part;cytoskeletal part;intracellular organelle part;intracellular part;neuronal cell body;organelle part;postsynaptic density;synapse part 6.61E-105 4 13 11 46.2

P24534;C9JZW3;F2Z2G2;F8WF65 Elongation factor 1-beta EEF1B2 >sp|P24534|EF1B_HUMAN Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 -0.06 0.01 -0.01 -0.01 0.20 0.03 -0.16 -0.12 0.01482831 -0.00375506 "binding;nucleic acid binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular part;macromolecular complex;protein complex 3.73E-120 4 13 11 55.6

Q15437;Q5QPE2;Q5QPE1 Protein transport protein Sec23B SEC23B >sp|Q15437|SC23B_HUMAN Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2;>tr|Q5QPE2|Q5QPE2_HUMAN Protein transport protein Sec23B (Fragment) OS=Homo sapiens GN=SEC23B PE=2 SV=1 0.30 0.10 -0.35 -0.14 -0.47 -0.63 0.02 0.01 0.466945258 0.244935004 cellular process;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular protein transport;intracellular transport;protein transport;transport;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;COPII vesicle coat;cytoplasmic part;cytoplasmic vesicle part;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;vesicle coat Protein processing in endoplasmic reticulum 1.23E-112 3 14 11 26.2

Q9BUF5;K7ESM5;K7EL29;K7ES63;K7EN98;K7ESQ3;K7EQT3;K7EJ64;K7ERA8;K7EJZ4;K7EPE5 Tubulin beta-6 chain TUBB6 >sp|Q9BUF5|TBB6_HUMAN Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1;>tr|K7ESM5|K7ESM5_HUMAN Tubulin beta-6 chain (Fragment) OS=Homo sapiens GN=TUBB6 PE=3 SV=1 0.09 -0.10 -0.34 -0.05 -0.08 0.05 0.30 0.24 0.775973086 -0.228785958 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein polymerization "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasm;cytoskeletal part;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;organelle part;plasma membrane;protein complex Gap junction;Pathogenic Escherichia coli infection;Phagosome 0 11 25 11 66.1

P11940;E7EQV3;P11940-2;E7ERJ7;H0YAR2;H0YBN4;E5RGH3;E5RJB9;H0YAP2;E5RH24;H0YB86;H0YAS6;H0YB75;Q4VXU2;Q4VY17;H0YAS7;E5RHG7;H0YAW6;H0YC10;Q96DU9-2;Q96DU9;E5RGC4;E5RFD8 Polyadenylate-binding protein 1 PABPC1 >sp|P11940|PABP1_HUMAN Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2;>tr|E7EQV3|E7EQV3_HUMAN Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=2 SV=1;>sp|P11940-2|PABP1_HUMAN Isoform 2 of Polyadenylate-binding protein 1 OS= 0.20 0.01 0.01 -0.10 0.00 -0.27 -0.14 -0.38 0.936024678 0.226603532 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;gene silencing;gene silencing by RNA;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA polyadenylation;mRNA processing;mRNA stabilization;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA 3'-end processing;positive regulation of mRNA catabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear-transcribed mRNA poly(A) tail shortening;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA 3'-end processing;regulation of mRNA catabolic process;regulation of mRNA processing;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;regulation of nuclear-transcribed mRNA poly(A) tail shortening;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA polyadenylation;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization;translational initiation" "binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;RNA binding;single-stranded RNA binding;translation activator activity;translation regulator activity;translation regulator activity, nucleic acid binding" catalytic step 2 spliceosome;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;organelle;organelle part;ribonucleoprotein complex;RNA granule;spliceosomal complex;stress granule mRNA surveillance pathway;RNA degradation;RNA transport 0 23 35 11 56.6

O00571;O00571-2;B4E3C4;B4DLA0;C9J8G5;D6RCM4;Q9NQI0-3;Q9NQI0-2;Q9NQI0-4;Q9NQI0;H0Y960 ATP-dependent RNA helicase DDX3X DDX3X >sp|O00571|DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3;>sp|O00571-2|DDX3X_HUMAN Isoform 2 of ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X 0.10 0.36 -0.05 0.26 0.26 0.45 -0.07 0.31 0.178621591 -0.068422536 "biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell motility;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to abiotic stimulus;cellular response to arsenic-containing substance;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to osmotic stress;cellular response to stimulus;cellular response to stress;chromosome segregation;defense response;developmental process;gamete generation;immune response;immune system process;induction of apoptosis;induction of apoptosis by extracellular signals;induction of apoptosis via death domain receptors;induction of programmed cell death;innate immune response;interaction with host;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;leptotene;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;male gamete generation;male meiosis I;mature ribosome assembly;meiosis I;metabolic process;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of growth;negative regulation of hydrolase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;negative regulation of protein complex assembly;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle assembly;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of chemokine (C-C motif) ligand 5 production;positive regulation of chemokine production;positive regulation of cytokine production;positive regulation of gene expression;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of interferon-beta production;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of protein metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of translation;positive regulation of translational initiation;positive regulation of type I interferon production;posttranscriptional regulation of gene expression;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell death;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemokine (C-C motif) ligand 5 production;regulation of chemokine production;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of cytokine production;regulation of endopeptidase activity;regulation of gene expression;regulation of growth;regulation of hydrolase activity;regulation of interferon-beta production;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein localization;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;regulation of type I interferon production;reproductive process;response to abiotic stimulus;response to arsenic-containing substance;response to biotic stimulus;response to chemical stimulus;response to inorganic substance;response to osmotic stress;response to other organism;response to stimulus;response to stress;response to virus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;RNA biosynthetic process;RNA metabolic process;RNA secondary structure unwinding;signal transduction;sperm motility;spermatogenesis;stress granule assembly;transcription, DNA-dependent;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;eukaryotic initiation factor 4E binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mRNA 5'-UTR binding;mRNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;protein binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleoprotein binding;ribonucleotide binding;ribosomal small subunit binding;RNA binding;RNA helicase activity;RNA stem-loop binding;RNA-dependent ATPase activity;single-stranded RNA binding;transcription factor binding;translation initiation factor binding" cell part;chromatoid body;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;P granule;perinuclear region of cytoplasm;pi-body;piP-body;ribonucleoprotein complex;RNA granule;stress granule RIG-I-like receptor signaling pathway 0 11 40 11 65.6

O95433;B4DUR9;G3V438;H0YJG7;H0YJ63;H0YJU2;G3V3W9;H0YJG6 Activator of 90 kDa heat shock protein ATPase homolog 1 AHSA1 >sp|O95433|AHSA1_HUMAN Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=1 SV=1;>tr|B4DUR9|B4DUR9_HUMAN Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHSA1 PE=2 SV=1;>tr|G3V438|G3V438_HUMAN Act 0.37 0.07 0.03 -0.07 -0.12 -0.28 0.36 -0.42 0.455554905 0.214512714 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;positive regulation of ATPase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;primary metabolic process;protein folding;protein metabolic process;regulation of ATPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;response to stimulus;response to stress ATPase activator activity;ATPase regulator activity;binding;chaperone binding;enzyme activator activity;enzyme regulator activity;nucleoside-triphosphatase regulator activity;protein binding cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle 8.05E-51 8 12 12 45.3

Q13740-2;Q13740;F5GXJ9;H7C543;Q6ZS95 CD166 antigen ALCAM >sp|Q13740-2|CD166_HUMAN Isoform 2 of CD166 antigen OS=Homo sapiens GN=ALCAM;>sp|Q13740|CD166_HUMAN CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2;>tr|F5GXJ9|F5GXJ9_HUMAN CD166 antigen OS=Homo sapiens GN=ALCAM PE=2 SV=1 0.06 0.02 -0.26 -0.15 0.64 0.41 -0.10 -0.09 0.637551232 -0.296570172 axon guidance;biological adhesion;biological regulation;cell adhesion;cellular process;cellular response to stimulus;chemotaxis;locomotion;motor axon guidance;regulation of biological process;regulation of cellular process;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;taxis binding;protein binding;receptor binding axon;cell body;cell part;cell projection;external side of plasma membrane;integral to membrane;intrinsic to membrane;membrane;membrane part;neuron projection;neuronal cell body;plasma membrane part Cell adhesion molecules (CAMs) 8.50E-72 5 12 12 24.2

P36542;B4DL14;P36542-2 "ATP synthase subunit gamma, mitochondrial;ATP synthase subunit gamma" ATP5C1 ">sp|P36542|ATPG_HUMAN ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1;>tr|B4DL14|B4DL14_HUMAN ATP synthase subunit gamma OS=Homo sapiens GN=ATP5C1 PE=2 SV=1;>sp|P36542-2|ATPG_HUMAN Isoform Heart of ATP synthase subunit gamma," -0.31 0.16 0.08 0.31 0.26 0.18 -1.16 -0.24 0.340712841 0.300762741 "ATP biosynthetic process;ATP catabolic process;ATP metabolic process;ATP synthesis coupled proton transport;biosynthetic process;catabolic process;cation transport;cellular biosynthetic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;electron transport chain;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport""active transmembrane transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex, catalytic core F(1);organelle inner membrane;organelle lumen;organelle membrane;organelle part;protein complex;proton-transporting ATP synthase complex, catalytic core F(1);proton-transporting two-sector ATPase complex, catalytic domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 7.14E-66 3 12 12 37.6

P80723;P80723-2 Brain acid soluble protein 1 BASP1 >sp|P80723|BASP1_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2;>sp|P80723-2|BASP1_HUMAN Isoform 2 of Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 -0.52 0.49 -0.45 0.19 0.52 0.86 -0.45 0.59 0.496526327 -0.451537214 "anatomical structure development;anatomical structure morphogenesis;anterior/posterior pattern specification;biological regulation;cell differentiation;cell differentiation involved in kidney development;cell morphogenesis;cell morphogenesis involved in differentiation;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;developmental process;developmental process involved in reproduction;diaphragm development;epithelial cell differentiation;epithelial cell differentiation involved in kidney development;epithelial cell morphogenesis;glomerular epithelial cell differentiation;glomerular visceral epithelial cell differentiation;gonad development;kidney mesenchyme development;mesenchymal to epithelial transition;mesenchyme development;metanephric mesenchyme development;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;organ development;pattern specification process;positive regulation of biological process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of growth;positive regulation of heart growth;positive regulation of metanephric ureteric bud development;positive regulation of organ growth;regionalization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of gene expression;regulation of growth;regulation of heart growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metanephric ureteric bud development;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ growth;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;renal filtration cell differentiation;reproductive process;reproductive structure development;skeletal muscle organ development;thorax and anterior abdomen determination;tissue development" binding;DNA binding;nucleic acid binding;protein binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding cell part;cell projection part;cytoplasm;cytoskeleton;growth cone;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part;plasma membrane;site of polarized growth 7.38E-95 2 12 12 84.6

Q9BT78;D6RAX7;D6RFN0;Q9BT78-2;D6RD63 COP9 signalosome complex subunit 4 COPS4 >sp|Q9BT78|CSN4_HUMAN COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1;>tr|D6RAX7|D6RAX7_HUMAN COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=2 SV=1;>tr|D6RFN0|D6RFN0_HUMAN COP9 signalosome complex subunit 4 OS=Homo sap 0.11 0.02 -0.17 0.00 -0.01 -0.13 0.09 -0.34 0.321685661 0.088400665 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cullin deneddylation;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein deneddylation;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleus;organelle;organelle part;protein complex;signalosome 6.96E-74 5 12 12 40.4

Q8IY21;H0Y8Z7;H0Y8H0;Q5H9U9-2;Q5H9U9 Probable ATP-dependent RNA helicase DDX60 DDX60 >sp|Q8IY21|DDX60_HUMAN Probable ATP-dependent RNA helicase DDX60 OS=Homo sapiens GN=DDX60 PE=1 SV=3 0.48 0.22 0.22 1.29 -1.50 2.67 -0.25 -0.40 0.168820515 0.424454041 defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;multi-organism process;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;DNA binding;double-stranded DNA binding;double-stranded RNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;single-stranded RNA binding;structure-specific DNA binding" cell part;cytoplasm;intracellular part 2.38E-43 5 12 12 9.1

P10515;H0YDD4;F5H7M3;E9PEJ4 "Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial" DLAT ">sp|P10515|ODP2_HUMAN Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Homo sapiens GN=DLAT PE=1 SV=3;>tr|H0YDD4|H0YDD4_HUMAN Dihydrolipoyllysine-residue acetyltransferase component of pyruvate deh" -0.35 0.40 0.01 0.36 -0.08 0.09 -1.21 -0.09 0.521280945 0.43206108 acetyl-CoA biosynthetic process;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor catabolic process;cofactor metabolic process;glucose metabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of cofactor metabolic process;regulation of metabolic process;small molecule metabolic process;tricarboxylic acid cycle "acetyltransferase activity;catalytic activity;dihydrolipoamide S-acyltransferase activity;dihydrolipoyllysine-residue acetyltransferase activity;S-acetyltransferase activity;S-acyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial part;mitochondrial pyruvate dehydrogenase complex;organelle part;protein complex;pyruvate dehydrogenase complex Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Pyruvate metabolism 3.39E-94 4 12 12 23.6

P20042 Eukaryotic translation initiation factor 2 subunit 2 EIF2S2 >sp|P20042|IF2B_HUMAN Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2 0.05 -0.05 0.07 -0.09 0.08 -0.12 -0.02 -0.53 0.420511126 0.143549315 "binding;cation binding;ion binding;metal ion binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 2 complex;intracellular part;macromolecular complex;protein complex RNA transport 5.71E-94 1 12 12 36

P41091;Q2VIR3;Q2VIR3-2;F8W810;H7BZU1 Eukaryotic translation initiation factor 2 subunit 3;Putative eukaryotic translation initiation factor 2 subunit 3-like protein EIF2S3;EIF2S3L >sp|P41091|IF2G_HUMAN Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3;>sp|Q2VIR3|IF2GL_HUMAN Putative eukaryotic translation initiation factor 2 subunit 3-like protein OS=Homo sapiens GN=EIF2S3L PE=5 SV=2;>sp|Q2VIR3 0.14 0.03 -0.10 0.00 0.04 -0.10 0.07 -0.22 0.309207131 0.065316035 catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;intracellular part RNA transport 8.29E-119 5 12 12 41.5

Q13347;Q5TFK1 Eukaryotic translation initiation factor 3 subunit I EIF3I >sp|Q13347|EIF3I_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens GN=EIF3I PE=1 SV=1 0.07 0.03 -0.06 -0.02 0.04 -0.25 -0.03 -0.23 0.662583158 0.121291247 cellular process;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport 6.18E-71 2 12 12 39.7

O75822;F5H425;B4DUI3;H0YGJ7;H0YLP3 Eukaryotic translation initiation factor 3 subunit J EIF3J >sp|O75822|EIF3J_HUMAN Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2;>tr|F5H425|F5H425_HUMAN Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=2 SV=1;>tr|B4DUI3|B4DUI3_HUMAN Eukaryoti -0.01 -0.06 0.07 -0.02 -0.09 -0.25 0.10 -0.15 0.498276245 0.094217817 cellular process;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport 9.50E-115 5 12 12 42.2

P50402;Q5HY57;F8WEQ1 Emerin EMD >sp|P50402|EMD_HUMAN Emerin OS=Homo sapiens GN=EMD PE=1 SV=1;>tr|Q5HY57|Q5HY57_HUMAN Emerin OS=Homo sapiens GN=EMD PE=2 SV=1 -0.08 0.12 0.22 0.15 0.60 0.34 -0.59 -0.07 0.039297416 0.031667542 anaphase;anatomical structure development;biological regulation;cell cycle phase;cell cycle process;cell differentiation;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;developmental process;M phase;M phase of mitotic cell cycle;membrane disassembly;membrane organization;mitotic anaphase;mitotic nuclear envelope disassembly;mitotic nuclear envelope reassembly;mitotic prophase;multicellular organismal process;muscle cell differentiation;muscle contraction;muscle organ development;muscle structure development;muscle system process;negative regulation of biological process;negative regulation of catenin import into nucleus;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of fibroblast proliferation;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of nucleocytoplasmic transport;negative regulation of protein import into nucleus;negative regulation of protein transport;negative regulation of transmembrane transport;negative regulation of transport;nuclear envelope disassembly;nuclear envelope organization;nuclear envelope reassembly;organ development;positive regulation of biological process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein export from nucleus;positive regulation of protein transport;positive regulation of transport;prophase;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of catenin import into nucleus;regulation of cell proliferation;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of fibroblast proliferation;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of nucleocytoplasmic transport;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of transmembrane transport;regulation of transport;regulation of Wnt receptor signaling pathway;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;skeletal muscle cell differentiation;striated muscle cell differentiation;system process actin binding;beta-tubulin binding;binding;cytoskeletal protein binding;protein binding;tubulin binding cell part;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;nuclear inner membrane;nuclear membrane;nuclear outer membrane;nuclear part;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;Hypertrophic cardiomyopathy (HCM) 1.27E-121 3 12 12 52.8

Q5T0W9 Protein FAM83B FAM83B >sp|Q5T0W9|FA83B_HUMAN Protein FAM83B OS=Homo sapiens GN=FAM83B PE=1 SV=1 -0.21 1.15 0.29 1.01 -1.28 0.27 -0.83 0.74 0.62519515 0.835705694 2.52E-64 1 12 12 15.2

P22087;M0R299;M0QXL5;M0R0P1;M0R2Q4;M0R2U2;M0R1H0;M0R2B0;A6NHQ2;R4GMW7 rRNA 2-O-methyltransferase fibrillarin FBL >sp|P22087|FBRL_HUMAN rRNA 2-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2;>tr|M0R299|M0R299_HUMAN rRNA 2-O-methyltransferase fibrillarin (Fragment) OS=Homo sapiens GN=FBL PE=3 SV=1;>tr|M0QXL5|M0QXL5_HUMAN rRNA 2-O-methyltransferase f -0.35 1.04 -0.01 1.04 -0.34 0.24 -1.38 0.34 0.560192274 0.710091127 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;methylation;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;small molecule metabolic process;snoRNA metabolic process;tRNA metabolic process;tRNA processing "binding;catalytic activity;methyltransferase activity;nucleic acid binding;RNA binding;transferase activity;transferase activity, transferring one-carbon groups" box C/D snoRNP complex;Cajal body;cell part;granular component;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleolar part;nucleolus;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes 1.34E-57 10 12 12 39.3

P48506;D6R959;D6RGF8;H0YAB6;H0Y9I7 Glutamate--cysteine ligase catalytic subunit GCLC >sp|P48506|GSH1_HUMAN Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2 0.01 -0.22 -0.08 -0.16 -0.21 0.23 1.06 0.23 0.704603295 -0.443231756 "amine biosynthetic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cell redox homeostasis;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular homeostasis;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;circulatory system process;cysteine metabolic process;glutamate metabolic process;glutamine family amino acid metabolic process;glutathione biosynthetic process;glutathione metabolic process;homeostatic process;L-ascorbic acid metabolic process;metabolic process;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron apoptosis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptide biosynthetic process;peptide metabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of proteolysis;primary metabolic process;regulation of anatomical structure size;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood vessel size;regulation of catabolic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of homeostatic process;regulation of ion homeostasis;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane depolarization;regulation of metabolic process;regulation of mitochondrial depolarization;regulation of neuron apoptosis;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of proteolysis;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of tube size;response to abiotic stimulus;response to arsenic-containing substance;response to chemical stimulus;response to endogenous stimulus;response to heat;response to hormone stimulus;response to inorganic substance;response to nitrosative stress;response to organic substance;response to oxidative stress;response to stimulus;response to stress;response to temperature stimulus;response to xenobiotic stimulus;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;system process;vascular process in circulatory system;vitamin metabolic process;water-soluble vitamin metabolic process;xenobiotic metabolic process" "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;amine binding;amino acid binding;ATP binding;binding;carboxylic acid binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;glutamate binding;glutamate-cysteine ligase activity;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;magnesium ion binding;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;glutamate-cysteine ligase complex;intracellular part;macromolecular complex;protein complex Glutathione metabolism 1.99E-52 5 12 12 23.1

O76003 Glutaredoxin-3 GLRX3 >sp|O76003|GLRX3_HUMAN Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2 0.16 -0.03 0.04 -0.03 -0.32 -0.41 0.26 -0.19 0.530809664 0.199604745 biological regulation;cell redox homeostasis;cellular homeostasis;cellular process;homeostatic process;negative regulation of biological process;negative regulation of cardiac muscle hypertrophy;negative regulation of multicellular organismal process;negative regulation of muscle hypertrophy;regulation of biological process;regulation of biological quality;regulation of cardiac muscle hypertrophy;regulation of cellular process;regulation of heart contraction;regulation of multicellular organismal process;regulation of muscle adaptation;regulation of muscle hypertrophy;regulation of muscle system process;regulation of system process;regulation of the force of heart contraction "binding;catalytic activity;cation binding;disulfide oxidoreductase activity;electron carrier activity;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide oxidoreductase activity" cell cortex;cell part;contractile fiber part;cytoplasmic part;intracellular part;organelle part;Z disc 2.55E-144 1 12 12 44.8

P48637;P48637-2;B7Z514 Glutathione synthetase GSS >sp|P48637|GSHB_HUMAN Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1;>sp|P48637-2|GSHB_HUMAN Isoform 2 of Glutathione synthetase OS=Homo sapiens GN=GSS;>tr|B7Z514|B7Z514_HUMAN Glutathione synthetase OS=Homo sapiens GN=GSS PE=2 SV=1 0.17 -0.10 0.09 -0.21 0.02 -0.19 0.50 -0.11 0.139123426 -0.068704997 aging;anatomical structure development;cellular metabolic process;cellular process;developmental process;metabolic process;nervous system development;response to acid;response to amine stimulus;response to amino acid stimulus;response to cadmium ion;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to inorganic substance;response to metal ion;response to nutrient levels;response to organic nitrogen;response to organic substance;response to oxidative stress;response to stimulus;response to stress;response to tumor necrosis factor;response to xenobiotic stimulus;system development;xenobiotic metabolic process "acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;ATP binding;binding;carboxylic acid binding;catalytic activity;cation binding;glutathione binding;glutathione synthase activity;glycine binding;identical protein binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;magnesium ion binding;metal ion binding;modified amino acid binding;nucleotide binding;peptide binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part Glutathione metabolism 4.06E-91 3 12 12 25.9

Q5SSJ5;Q5SSJ5-2;B0QZK4;Q5SWC8;Q5SSJ5-3;B0QZK9;B0QZK8;Q5SSJ5-5 Heterochromatin protein 1-binding protein 3 HP1BP3 >sp|Q5SSJ5|HP1B3_HUMAN Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1;>sp|Q5SSJ5-2|HP1B3_HUMAN Isoform 2 of Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3;>tr|B0QZK4|B0QZK4_HUMAN Heterochromatin prote -0.53 0.89 0.42 0.80 0.09 0.33 -1.77 -0.06 0.542466829 0.745474839 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;chromatin organization;chromosome organization;macromolecular complex assembly;macromolecular complex subunit organization;nucleosome assembly;nucleosome organization;organelle organization;protein-DNA complex assembly;protein-DNA complex subunit organization binding;DNA binding;nucleic acid binding cell part;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleosome;nucleus;organelle;organelle part;protein-DNA complex 2.61E-55 8 12 12 20.4

Q96CX2;Q68DU8;Q6ZWB6 BTB/POZ domain-containing protein KCTD12 KCTD12 >sp|Q96CX2|KCD12_HUMAN BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1 0.34 -0.01 -0.05 -0.13 1.10 0.30 -0.01 -0.29 0.287667684 -0.234442258 biological regulation;cellular component assembly;cellular component organization;cellular component organization or biogenesis;macromolecular complex assembly;macromolecular complex subunit organization;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;regulation of biological process;regulation of cellular process;regulation of G-protein coupled receptor protein signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling cell junction;cell part;macromolecular complex;membrane;plasma membrane;postsynaptic membrane;presynaptic membrane;protein complex;receptor complex;synapse part;synaptic membrane 8.84E-109 3 12 12 39.1

Q07666;Q07666-2;Q07666-3;O75525-2;O75525;Q5VWX1;E5RG12;E5RJZ9;H0YAQ1;H0YAQ3;Q9UBC1-2;Q5STV6;Q9UBC1-3;Q9UBC1 "KH domain-containing, RNA-binding, signal transduction-associated protein 1" KHDRBS1 ">sp|Q07666|KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1;>sp|Q07666-2|KHDR1_HUMAN Isoform 2 of KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Hom" -0.38 0.46 0.04 0.49 0.17 -0.03 -1.38 -0.25 0.552109596 0.528452173 "biological regulation;biosynthetic process;cell cycle arrest;cell cycle process;cell proliferation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to biotic stimulus;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to stimulus;cytoplasmic sequestering of protein;cytoplasmic sequestering of transcription factor;G2/M transition of mitotic cell cycle;gamete generation;I-kappaB kinase/NF-kappaB cascade;intracellular protein kinase cascade;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;male gamete generation;metabolic process;mRNA metabolic process;mRNA processing;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of gene expression;negative regulation of immune system process;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of lipopolysaccharide-mediated signaling pathway;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of NF-kappaB transcription factor activity;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleocytoplasmic transport;negative regulation of protein import into nucleus;negative regulation of protein transport;negative regulation of response to biotic stimulus;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of signal transduction;negative regulation of signaling;negative regulation of toll-like receptor signaling pathway;negative regulation of transcription factor import into nucleus;negative regulation of transcription, DNA-dependent;negative regulation of transmembrane transport;negative regulation of transport;negative regulation of tumor necrosis factor production;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nucleobase-containing compound transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein metabolic process;positive regulation of RNA export from nucleus;positive regulation of translation;positive regulation of translational initiation;positive regulation of transport;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine production;regulation of establishment of protein localization;regulation of gene expression;regulation of immune system process;regulation of intracellular protein transport;regulation of intracellular transport;regulation of lipopolysaccharide-mediated signaling pathway;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleobase-containing compound transport;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of RNA export from nucleus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of toll-like receptor signaling pathway;regulation of transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;regulation of transmembrane transport;regulation of transport;regulation of tumor necrosis factor production;reproductive process;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;signal transduction;spermatogenesis;transcription, DNA-dependent" binding;DNA binding;mRNA binding;nucleic acid binding;poly(A) RNA binding;poly(U) RNA binding;poly-purine tract binding;poly-pyrimidine tract binding;RNA binding;single-stranded RNA binding cell part;cytoplasm;cytoplasmic part;cytosol;Grb2-Sos complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;plasma membrane part;protein complex 1.48E-59 14 12 12 30.7

P29966 Myristoylated alanine-rich C-kinase substrate MARCKS >sp|P29966|MARCS_HUMAN Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4 -0.40 0.08 -0.23 0.13 0.88 0.77 -0.24 0.29 0.795616757 -0.530362019 biological regulation;cellular metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;small molecule metabolic process actin binding;actin filament binding;binding;calmodulin binding;cytoskeletal protein binding;protein binding actin cytoskeleton;cell cortex;cell part;centrosome;cytoplasmic part;cytoskeletal part;cytoskeleton;female germ cell nucleus;germ cell nucleus;germinal vesicle;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane Fc gamma R-mediated phagocytosis 3.86E-92 1 12 12 51.8

P52701;F5H2F9;P52701-2;B4DF41;F8WAX8;C9JH55;C9J8Y8;C9J7Y7 DNA mismatch repair protein Msh6 MSH6 >sp|P52701|MSH6_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2;>tr|F5H2F9|F5H2F9_HUMAN DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=2 SV=1;>sp|P52701-2|MSH6_HUMAN Isoform GTBP-alt of DNA mismatch repair protein Msh6 0.21 -0.25 -0.12 0.06 -0.01 -0.77 -0.24 -0.05 0.504325892 0.243498019 "B cell activation;B cell activation involved in immune response;biological regulation;cell activation;cell activation involved in immune response;cell cycle process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;determination of adult lifespan;DNA damage response, signal transduction resulting in induction of apoptosis;DNA metabolic process;DNA recombination;DNA repair;immune effector process;immune system process;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;isotype switching;leukocyte activation;leukocyte activation involved in immune response;lymphocyte activation;lymphocyte activation involved in immune response;macromolecule metabolic process;meiotic mismatch repair;metabolic process;mismatch repair;multicellular organismal process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of DNA metabolic process;negative regulation of DNA recombination;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cellular process;positive regulation of helicase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of programmed cell death;primary metabolic process;reciprocal DNA recombination;reciprocal meiotic recombination;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA recombination;regulation of helicase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;response to abiotic stimulus;response to DNA damage stimulus;response to light stimulus;response to radiation;response to stimulus;response to stress;response to UV;signal transduction;signal transduction in response to DNA damage;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immune receptors via somatic mutation;somatic diversification of immunoglobulins;somatic diversification of immunoglobulins involved in immune response;somatic hypermutation of immunoglobulin genes;somatic recombination of immunoglobulin gene segments;somatic recombination of immunoglobulin genes involved in immune response" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;chromatin binding;damaged DNA binding;DNA binding;DNA-dependent ATPase activity;double-stranded DNA binding;guanine/thymine mispair binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mismatched DNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structure-specific DNA binding" cell part;chromatin;chromosomal part;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mismatch repair complex;MutSalpha complex;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome;nuclear chromosome part;nuclear part;organelle;organelle part;protein complex Colorectal cancer;Mismatch repair;Pathways in cancer 7.92E-49 8 12 12 12

M0R0Y2;P54920;M0R2M1;M0R213;M0R027;M0R058;M0R0I4;M0QZM9;M0QZN5;M0R031;Q4G0M0;B4DK44;Q9H115 Alpha-soluble NSF attachment protein NAPA >tr|M0R0Y2|M0R0Y2_HUMAN Napsin-A OS=Homo sapiens GN=NAPA PE=4 SV=1;>sp|P54920|SNAA_HUMAN Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3;>tr|M0R2M1|M0R2M1_HUMAN Napsin-A (Fragment) OS=Homo sapiens GN=NAPA PE=4 SV=1 0.06 0.08 -0.02 0.01 0.36 0.36 0.36 0.02 1.146194435 -0.242348936 "anatomical structure development;apical protein localization;asymmetric protein localization;biological regulation;brain development;cell communication;cell differentiation;cell-cell signaling;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular membrane fusion;cellular membrane organization;cellular process;cellular protein complex disassembly;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;localization;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule localization;membrane fusion;membrane organization;neuron differentiation;neuron-neuron synaptic transmission;organ development;post-Golgi vesicle-mediated transport;protein complex disassembly;protein complex subunit organization;protein localization;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of exocytosis;regulation of localization;regulation of multicellular organismal process;regulation of neurological system process;regulation of neurotransmitter secretion;regulation of neurotransmitter transport;regulation of protein complex assembly;regulation of secretion;regulation of signaling;regulation of synaptic transmission;regulation of synaptic vesicle exocytosis;regulation of synaptic vesicle priming;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;regulation of vesicle-mediated transport;signaling;SNARE complex disassembly;synaptic transmission;synaptic transmission, glutamatergic;transport;vesicle-mediated transport" cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;membrane part;protein complex;SNARE complex;synaptobrevin 2-SNAP-25-syntaxin-1a complex 2.76E-155 13 12 12 59

Q9NQR4;H7C579;F8WF70 Omega-amidase NIT2 NIT2 >sp|Q9NQR4|NIT2_HUMAN Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1;>tr|H7C579|H7C579_HUMAN Omega-amidase NIT2 (Fragment) OS=Homo sapiens GN=NIT2 PE=4 SV=1 0.15 -0.02 0.21 -0.11 -0.01 -0.13 0.33 -0.02 0.030834473 0.011444138 metabolic process;nitrogen compound metabolic process "catalytic activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;omega-amidase activity" cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;mitochondrion;non-membrane-bounded organelle;organelle;organelle part "Alanine, aspartate and glutamate metabolism" 9.90E-118 3 12 12 53.3

I3L0N3;P46459;B4DFA2;I3L0L3;I3L2G1;K7EQD6 Vesicle-fusing ATPase NSF >tr|I3L0N3|I3L0N3_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1;>sp|P46459|NSF_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3;>tr|B4DFA2|B4DFA2_HUMAN Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=2 SV=1 -0.18 -0.06 -0.04 0.06 0.97 0.84 0.11 0.12 1.029936277 -0.569379098 biological regulation;cation transport;cell communication;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular membrane fusion;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;ion transport;membrane fusion;membrane organization;metal ion transport;monovalent inorganic cation transport;plasma membrane fusion;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of receptor recycling;positive regulation of signaling;potassium ion transport;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of receptor recycling;regulation of signaling;secretion;secretion by cell;signaling;synaptic transmission;transport;vesicle-mediated transport"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein complex binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Vasopressin-regulated water reabsorption 7.76E-72 6 12 12 20.2

Q9Y266 Nuclear migration protein nudC NUDC >sp|Q9Y266|NUDC_HUMAN Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1 0.02 -0.09 -0.04 -0.03 -0.11 -0.62 -0.01 -0.75 0.788400818 0.340488101 anaphase;cell cycle phase;cell cycle process;cell proliferation;cellular process;cytokinesis;developmental process;M phase;M phase of mitotic cell cycle;mitotic anaphase;mitotic prometaphase;multicellular organismal development;multicellular organismal process cell part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;microtubule;nuclear part;nucleoplasm;organelle part;protein complex 1.84E-55 1 12 12 40.8

Q9UKK9;A6NFX8;A6NJU6;A6NHE8;A6NCQ0;C9JYY9;H0YEY4 ADP-sugar pyrophosphatase NUDT5 >sp|Q9UKK9|NUDT5_HUMAN ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1;>tr|A6NFX8|A6NFX8_HUMAN ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=2 SV=1;>tr|A6NJU6|A6NJU6_HUMAN ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=2 SV=2;>t 0.21 0.02 0.16 -0.06 0.02 -0.23 0.22 -0.27 0.471609495 0.147476155 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;D-ribose catabolic process;D-ribose metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule catabolic process;nucleobase-containing small molecule metabolic process;nucleoside diphosphate catabolic process;nucleoside diphosphate metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;pentose catabolic process;pentose metabolic process;primary metabolic process;ribonucleoside diphosphate catabolic process;ribonucleoside diphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule catabolic process;small molecule metabolic process "ADP-ribose diphosphatase activity;ADP-sugar diphosphatase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;magnesium ion binding;metal ion binding;nucleic acid binding;nucleoside-diphosphatase activity;pyrophosphatase activity;RNA binding;snoRNA binding" cell part;cytoplasmic part;cytosol;intracellular part Purine metabolism 1.92E-95 7 12 12 51.1

O95747;C9JIG9;Q9UEW8 Serine/threonine-protein kinase OSR1 OXSR1 >sp|O95747|OXSR1_HUMAN Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=1 SV=1;>tr|C9JIG9|C9JIG9_HUMAN Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OXSR1 PE=2 SV=1 0.29 0.07 0.01 -0.11 0.36 0.21 0.37 -0.08 0.457697996 -0.148775069 biological regulation;cellular process;cellular response to stimulus;intracellular protein kinase cascade;intracellular signal transduction;positive regulation of biological process;positive regulation of ion transport;positive regulation of potassium ion transport;positive regulation of transport;regulation of biological process;regulation of cellular process;regulation of defense response;regulation of inflammatory response;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of potassium ion transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of transport;response to chemical stimulus;response to oxidative stress;response to stimulus;response to stress;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;magnesium ion binding;metal ion binding;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;ribonucleotide binding;signal transducer activity;transferase activity;transferase activity, transferring phosphorus-containing groups" apical plasma membrane;basolateral plasma membrane;cell part;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;plasma membrane part 3.73E-111 3 12 12 25.8

Q9UNF0-2;Q9UNF0;B0QYG7;B0QYG8;H0Y923 Protein kinase C and casein kinase substrate in neurons protein 2PACSIN2 >sp|Q9UNF0-2|PACN2_HUMAN Isoform 2 of Protein kinase C and casein kinase substrate in neurons protein 2 OS=Homo sapiens GN=PACSIN2;>sp|Q9UNF0|PACN2_HUMAN Protein kinase C and casein kinase substrate in neurons protein 2 OS=Homo sapiens GN=PACSIN2 PE=1 SV=2 0.17 -0.19 0.00 -0.14 0.41 0.11 0.27 0.10 1.025949937 -0.263137398 actin cytoskeleton organization;actin filament-based process;anatomical structure morphogenesis;biological regulation;caveola assembly;caveolin-mediated endocytosis;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cytoskeleton organization;developmental process;endocytosis;establishment of localization;membrane invagination;membrane organization;membrane raft assembly;membrane raft organization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of endocytosis;negative regulation of transport;organelle organization;receptor-mediated endocytosis;regulation of biological process;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of transport;regulation of vesicle-mediated transport;transport;vesicle-mediated transport transporter activity caveola;cell part;cytoplasm;cytoplasmic part;cytosol;extrinsic to membrane;intracellular part;membrane part;membrane raft;plasma membrane part 5.12E-42 5 12 12 28.5

Q99497;K7ELW0;K7EN27 Protein DJ-1 PARK7 >sp|Q99497|PARK7_HUMAN Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2;>tr|K7ELW0|K7ELW0_HUMAN Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=4 SV=1;>tr|K7EN27|K7EN27_HUMAN Protein DJ-1 (Fragment) OS=Homo sapiens GN=PARK7 PE=4 SV=1 -0.10 -0.18 -0.24 -0.02 -0.05 -0.12 0.30 -0.14 0.477511221 -0.130436656 adult behavior;adult locomotory behavior;amine transport;autophagy;behavior;biological regulation;catabolic process;catecholamine transport;catecholamine uptake involved in synaptic transmission;cell death;cellular catabolic process;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;chemical homeostasis;death;defense response;dopamine transport;dopamine uptake;establishment of localization;fertilization;homeostatic process;hydrogen peroxide metabolic process;inflammatory response;ion homeostasis;locomotory behavior;macromolecule metabolic process;membrane depolarization;membrane hyperpolarization;metabolic process;mitochondrion organization;monoamine transport;multicellular organismal process;negative regulation of apoptosis;negative regulation of binding;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of molecular function;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of protein binding;neurotransmitter transport;neurotransmitter uptake;nitrogen compound transport;organelle organization;organic alcohol transport;organic substance transport;positive regulation of biological process;positive regulation of molecular function;positive regulation of oxidative phosphorylation uncoupler activity;positive regulation of transport;positive regulation of transporter activity;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;protein stabilization;proteolysis;reactive oxygen species metabolic process;regulation of androgen receptor signaling pathway;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;regulation of defense response;regulation of gene expression;regulation of inflammatory response;regulation of ion

transport;regulation of localization;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of
neurotransmitter levels;regulation of oxidative phosphorylation uncoupler activity;regulation of programmed cell death;regulation of protein binding;regulation of protein stability;regulation of proton transport;regulation of
response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of
transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;reproductive process;response to chemical stimulus;response to hydrogen peroxide;response to
inorganic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;response to wounding;single fertilization;transport"antioxidant activity;binding;catalytic
activity;hydrolase activity;identical protein binding;mRNA binding;nucleic acid binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular
oxygen;oxidoreductase activity, acting on peroxide as acceptor;peptidase activity;peroxidase activity;peroxiredoxin activity;protein binding;protein dimerization activity;protein homodimerization activity;RNA binding" cell
part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle Parkinson's disease 6.79E-113 3 12 12 62.4
Q9UHG3;B7Z3Y2;B7Z9P8;F8W8W4;C9K055;C9JM55;C9JGT6 Prenylcysteine oxidase 1PCYOX1>sp|Q9UHG3|PCYOX_HUMAN Prenylcysteine oxidase 1 OS=Homo sapiens GN=PCYOX1 PE=1
SV=3;>tr|B7Z3Y2|B7Z3Y2_HUMAN Prenylcysteine oxidase 1 OS=Homo sapiens GN=PCYOX1 PE=2 SV=1;>tr|B7Z9P8|B7Z9P8_HUMAN Prenylcysteine oxidase 1 OS=Homo sapiens GN=PCYOX1 PE=2 SV=1;>t -0.25
-0.24 -0.07 -0.06 0.76 0.69 0.22 0.00 1.243092941 -0.572447404 amine catabolic process;amine metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular
amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular macromolecule catabolic process;cellular macromolecule
metabolic process;cellular metabolic process;cellular modified amino acid catabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule
catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nitrogen compound metabolic process;organic
acid catabolic process;organic acid metabolic process;oxoacid metabolic process;prenylated protein catabolic process;prenylcysteine catabolic process;prenylcysteine metabolic process;primary metabolic process;protein
metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;small molecule catabolic process;small molecule metabolic process "active transmembrane transporter activity;anion transmembrane
transporter activity;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane
movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;catalytic activity;chloride transmembrane transporter activity;chloride-transporting ATPase activity;hydrolase
activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing
anhydrides;inorganic anion transmembrane transporter activity;ion transmembrane transporter activity;nucleoside-triphosphatase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of
donors;oxidoreductase activity, acting on a sulfur group of donors, oxygen as acceptor;P-P-bond-hydrolysis-driven transmembrane transporter activity;prenylcysteine oxidase activity;primary active transmembrane transporter
activity;pyrophosphatase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" cell part;cytoplasmic part;extracellular
region part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;macromolecular complex;membrane;membrane-bounded organelle;organelle;plasma lipoprotein
particle;plasma membrane;protein-lipid complex;triglyceride-rich lipoprotein particle;vacuole;very-low-density lipoprotein particle 1.53E-77 7 12 12 29.1
P11177-2;P11177;P11177-3;C9J634;F8WF02 "Pyruvate dehydrogenase E1 component subunit beta, mitochondrial"PDHB ">sp|P11177-2|ODPB_HUMAN Isoform 2 of Pyruvate dehydrogenase E1 component subunit
beta, mitochondrial OS=Homo sapiens GN=PDHB;>sp|P11177|ODPB_HUMAN Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3;>sp|P11177-" -0.48 0.08
0.01 0.39 0.28 0.35 -1.03 0.11 0.071259875 0.077072191 acetyl-CoA biosynthetic process;acetyl-CoA biosynthetic process from pyruvate;acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol
metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular
catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme biosynthetic process;coenzyme catabolic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor
catabolic process;cofactor metabolic process;glucose metabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;organic acid metabolic
process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;regulation of acetyl-CoA biosynthetic process from pyruvate;regulation of biological process;regulation of biosynthetic
process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of coenzyme metabolic process;regulation of
cofactor metabolic process;regulation of metabolic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of
donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor;pyruvate dehydrogenase (acetyl-transferring) activity;pyruvate dehydrogenase activity" cell part;cytoplasmic part;intracellular
organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part;protein complex;pyruvate
dehydrogenase complex "Butanoate metabolism;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Pyruvate metabolism;Valine, leucine and isoleucine biosynthesis" 6.46E-120 5 12 12 41.3
Q8TF05-2;Q8TF05;J3QL26;J3KSB0;J3QLA6;J3QQV0;J3KRU1;J3QRV2;F8WAJ9;J3KSS1 Serine/threonine-protein phosphatase 4 regulatory subunit 1PPP4R1 >sp|Q8TF05-2|PP4R1_HUMAN Isoform 2 of Serine/threonine-protein
phosphatase 4 regulatory subunit 1 OS=Homo sapiens GN=PPP4R1;>sp|Q8TF05|PP4R1_HUMAN Serine/threonine-protein phosphatase 4 regulatory subunit 1 OS=Homo sapiens GN=PPP4R1 PE=1 SV=1;>tr|J3QL26|J3
0.23 -0.01 0.15 -0.02 -0.24 -0.07 0.27 -0.06 0.359763654 0.110519483 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein
metabolic process;cellular response to stimulus;macromolecule metabolic process;macromolecule modification;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic
process;phosphorylation;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of cellular process;response to stimulus;signal
transduction enzyme regulator activity;phosphatase regulator activity;protein phosphatase regulator activity;protein phosphatase type 4 regulator activitycell part;intracellular part;macromolecular complex;protein
complex;protein phosphatase 4 complex;protein serine/threonine phosphatase complex 1.23E-65 10 12 12 15.3
Q9UMS4;F5GY56;H0YGF3;F5H2I0;H0YGZ5 Pre-mRNA-processing factor 19 PRPF19 >sp|Q9UMS4|PRP19_HUMAN Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1 -0.03 0.22
0.09 0.26 -0.06 -0.39 -0.96 0.08 0.840696153 0.46847697 "biological regulation;biosynthetic process;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular
component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex
assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic
process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;inner cell mass cell proliferation;lipid biosynthetic process;lipid metabolic process;macromolecular complex
assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell
differentiation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neuron differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing
compound metabolic process;positive regulation of astrocyte differentiation;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation
of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of glial cell differentiation;positive regulation of gliogenesis;positive regulation of
macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive
regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;primary
metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein
ubiquitination;regulation of astrocyte differentiation;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cellular metabolic process;regulation of cellular
process;regulation of developmental process;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of macromolecule metabolic process;regulation of metabolic process;regulation
of mRNA processing;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron
differentiation;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic
process;regulation of RNA metabolic process;regulation of RNA splicing;response to DNA damage stimulus;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit
organization;spliceosome assembly" "acid-amino acid ligase activity;binding;catalytic activity;DNA binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleic acid binding;small conjugating protein ligase
activity;ubiquitin-protein ligase activity;ubiquitin-ubiquitin ligase activity"catalytic step 2 spliceosome;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded
organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear
part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part;protein complex;Prp19 complex;ribonucleoprotein complex;spindle;spliceosomal complex;ubiquitin ligase complex Spliceosome;Ubiquitin mediated
proteolysis 7.25E-73 5 12 12 31.9
Q9Y617;Q9Y617-2Phosphoserine aminotransferase PSAT1 >sp|Q9Y617|SERC_HUMAN Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2;>sp|Q9Y617-2|SERC_HUMAN Isoform 2 of

Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1-0.67 -0.69 0.15 0.12 -0.26 -0.89 0.54 -0.58 0.019043564 0.022591582 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;heterocycle metabolic process;L-serine biosynthetic process;L-serine metabolic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyridoxine biosynthetic process;pyridoxine metabolic process;serine family amino acid biosynthetic process;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule metabolic process;vitamin B6 biosynthetic process;vitamin B6 metabolic process;vitamin biosynthetic process;vitamin metabolic process;water-soluble vitamin biosynthetic process;water-soluble vitamin metabolic process "binding;catalytic activity;cofactor binding;O-phospho-L-serine:2-oxoglutarate aminotransferase activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;cytosol;intracellular part "Glycine, serine and threonine metabolism;Methane metabolism;Vitamin B6 metabolism" 3.49E-73 2 12 12 32.4

Q15042;A6H8Z3;C9J837 Rab3 GTPase-activating protein catalytic subunit RAB3GAP1 >sp|Q15042|RB3GP_HUMAN Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens GN=RAB3GAP1 PE=1 SV=3;>tr|A6H8Z3|A6H8Z3_HUMAN RAB3GAP1 protein OS=Homo sapiens GN=RAB3GAP1 PE=2 SV=1;>tr|C9J837|C9J837_HUMAN Rab3 GTPase-activating protein catalytic su 0.02 -0.08 -0.01 -0.07 0.08 -0.05 0.44 0.18 0.792641086 -0.19627246 anatomical structure development;anatomical structure morphogenesis;biological regulation;camera-type eye development;developmental process;eye development;face morphogenesis;hypothalamus development;organ development;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Rab GTPase activity;positive regulation of Ras GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Rab GTPase activity;regulation of Ras GTPase activity;sensory organ development enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Rab GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part 7.40E-39 3 12 12 18

Q9P258 Protein RCC2 RCC2 >sp|Q9P258|RCC2_HUMAN Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 0.13 -0.13 -0.07 -0.03 -0.50 -0.94 0.04 -0.50 0.931652793 0.453219987 anaphase;cell cycle phase;cell cycle process;cell division;cellular process;M phase;M phase of mitotic cell cycle;mitotic anaphase;mitotic prometaphase "cell part;chromosomal part;chromosome, centromeric region;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex;spindle" 2.48E-87 1 12 12 29.9

O76021;J3QSV6;I3L3C4;I3L3U9;B4DJ58;I3L234 Ribosomal L1 domain-containing protein 1 RSL1D1 >sp|O76021|RL1D1_HUMAN Ribosomal L1 domain-containing protein 1 OS=Homo sapiens GN=RSL1D1 PE=1 SV=3;>tr|J3QSV6|J3QSV6_HUMAN Ribosomal L1 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=RSL1D1 PE=4 SV=1;>tr|I3L3C4|I3L3C4_HUMAN Ribosomal L1 domain- -0.32 1.35 0.17 1.16 -0.43 0.20 -1.39 0.24 0.725402554 0.933568563 biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;regulation of biological process;regulation of localization;regulation of protein localization;translation binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex 1.08E-40 6 12 12 24.3

Q9Y3A5;F8WE72 Ribosome maturation protein SBDS SBDS >sp|Q9Y3A5|SBDS_HUMAN Ribosome maturation protein SBDS OS=Homo sapiens GN=SBDS PE=1 SV=4 0.02 -0.06 0.01 -0.03 0.00 -0.02 0.42 -0.02 0.406141767 -0.110251608 anatomical structure development;biological regulation;biomineral tissue development;bone marrow development;bone mineralization;cell chemotaxis;cell cycle process;cell migration;cell motility;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemotaxis;developmental process;hemopoietic or lymphoid organ development;immune system process;inner cell mass cell proliferation;leukocyte chemotaxis;leukocyte migration;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;mature ribosome assembly;metabolic process;mitotic spindle stabilization;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of microtubule depolymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of organelle organization;negative regulation of protein complex disassembly;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle assembly;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cell cycle process;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule depolymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of mitotic cell cycle;regulation of mitotic spindle organization;regulation of organelle organization;regulation of protein complex disassembly;regulation of spindle organization;response to chemical stimulus;response to external stimulus;response to stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex biogenesis;ribonucleoprotein complex subunit organization;ribosomal large subunit biogenesis;ribosome assembly;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;spindle stabilization;taxis;tissue development binding;cytoskeletal protein binding;microtubule binding;nucleic acid binding;protein binding;ribonucleoprotein binding;ribosome binding;RNA binding;rRNA binding;tubulin binding cell part;cytoplasm;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;spindle pole Ribosome biogenesis in eukaryotes 1.59E-60 2 12 12 46

P16949;P16949-2;A2A2D0;E5RGX5;Q93045;Q93045-2;B7Z2Z7;Q9H169;G5EA16;Q9H169-2;E5RIR6;E7EVN3 Stathmin STMN1 >sp|P16949|STMN1_HUMAN Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3;>sp|P16949-2|STMN1_HUMAN Isoform 2 of Stathmin OS=Homo sapiens GN=STMN1;>tr|A2A2D0|A2A2D0_HUMAN Stathmin (Fragment) OS=Homo sapiens GN=STMN1 PE=2 SV=1 -0.09 -0.08 -0.28 -0.01 0.62 -0.21 0.00 -0.38 0.207243162 -0.124225164 anatomical structure morphogenesis;axonogenesis;biological regulation;cell cycle process;cell differentiation;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component disassembly;cellular component disassembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex disassembly;cellular response to stimulus;cytoskeleton organization;developmental process;intracellular signal transduction;macromolecular complex disassembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule depolymerization;microtubule polymerization or depolymerization;microtubule-based process;mitotic spindle organization;multi-organism process;negative regulation of biological process;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of microtubule depolymerization;negative regulation of microtubule polymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of neuron projection development;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;neuron differentiation;neuron projection morphogenesis;organelle organization;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of microtubule depolymerization;positive regulation of microtubule polymerization or depolymerization;positive regulation of neuron projection development;positive regulation of organelle organization;positive regulation of protein complex disassembly;protein complex disassembly;protein complex subunit organization;protein depolymerization;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of localization;regulation of microtubule cytoskeleton organization;regulation of microtubule depolymerization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to biotic stimulus;response to other organism;response to stimulus;response to virus;signal transduction;spindle organization binding;cytoskeletal protein binding;molecular transducer activity;protein binding;signal transducer activity;tubulin binding axon;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;endosome;Golgi apparatus;growth cone;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule;neuron projection;organelle;organelle part;perinuclear region of cytoplasm;protein complex;site of polarized growth MAPK signaling pathway 2.12E-103 12 12 12 62.4

B4E1K7;Q9UJZ1;F2Z2I8 "Stomatin-like protein 2, mitochondrial" STOML2 ">tr|B4E1K7|B4E1K7_HUMAN Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=2 SV=1;>sp|Q9UJZ1|STML2_HUMAN Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1" -0.40 0.52 0.14 0.60 -0.01 0.07 -1.36 0.57 0.333560352 0.395412227 "activation of immune response;alpha-beta T cell activation;antigen receptor-mediated signaling pathway;ATP biosynthetic process;ATP metabolic process;ATP synthesis coupled proton transport;biological regulation;biosynthetic process;calcium ion homeostasis;calcium ion transport;cation homeostasis;cation transport;CD4-positive, alpha-beta T cell activation;cell activation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;chemical homeostasis;cytokine production;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;heterocycle biosynthetic process;heterocycle metabolic process;homeostatic process;hydrogen transport;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;interleukin-2 production;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;leukocyte activation;lipid localization;localization;lymphocyte activation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;metabolic process;metal ion homeostasis;metal ion transport;mitochondrial ATP synthesis coupled proton transport;mitochondrial calcium ion transport;mitochondrial protein processing;mitochondrial transport;monovalent inorganic cation transport;multicellular organismal process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of DNA-dependent DNA replication;positive regulation of immune response;positive regulation of immune system process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of membrane potential;positive regulation of metabolic process;positive regulation of mitochondrial DNA replication;positive regulation of mitochondrial membrane potential;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;primary metabolic process;protein complex assembly;protein complex subunit organization;protein maturation;protein metabolic process;protein oligomerization;protein processing;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of immune response;regulation of immune system process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of membrane potential;regulation of metabolic process;regulation of mitochondrial DNA replication;regulation of mitochondrial membrane potential;regulation of mitochondrion organization;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of response to stimulus;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;T cell activation;T cell receptor signaling pathway;transmembrane transport;transport" binding;protein binding;receptor binding cell part;cytoplasmic part;cytoskeleton;extrinsic to membrane;extrinsic to plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;organelle;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part;plasma membrane part 1.49E-175 3 12 12 52.7

P22735;H0YN27;B4DWR7;H0YNM4;H0YLJ6;H0YKI6;H0YMQ8 Protein-glutamine gamma-glutamyltransferase K TGM1 >sp|P22735|TGM1_HUMAN Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4 -0.41 0.67 1.07 0.74 -0.03 -0.49 -0.92 -0.82 1.191944681 1.082867684 anatomical structure morphogenesis;cell differentiation;cell envelope organization;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;external encapsulating structure organization;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;organ morphogenesis;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process "binding;catalytic activity;cation binding;ion binding;metal ion binding;protein-glutamine gamma-glutamyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring amino-acyl groups" adherens junction;anchoring junction;cell junction;cell part;cell-cell adherens junction;cell-cell junction;cornified envelope;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;non-membrane-bounded organelle;organelle 1.41E-94 7 12 12 20.4

Q8IZW8 Tensin-4 TNS4 >sp|Q8IZW8|TENS4_HUMAN Tensin-4 OS=Homo sapiens GN=TNS4 PE=1 SV=3 0.64 0.40 -0.77 -0.04 -1.76 -0.21 0.35 0.43 0.227136721 0.354353286 apoptosis;cell death;cellular process;death;localization;macromolecule localization;programmed cell death;protein localization adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoskeleton;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 3.81E-132 1 12 12 23.6

O43396;K7ER96;K7EML9;G3V1K0;K7EPB7;K7EKG2;K7EME7 Thioredoxin-like protein 1 TXNL1 >sp|O43396|TXNL1_HUMAN Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3;>tr|K7ER96|K7ER96_HUMAN Thioredoxin-like protein 1 (Fragment) OS=Homo sapiens GN=TXNL1 PE=4 SV=1;>tr|K7EML9|K7EML9_HUMAN Thioredoxin-like protein 1 (Fragment) OS=Homo sapi 0.01 0.00 -0.18 0.00 0.17 0.19 0.32 -0.09 0.838762505 -0.189993869 biological regulation;cell redox homeostasis;cellular homeostasis;cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;glycerol ether metabolic process;homeostatic process;metabolic process;organic ether metabolic process;oxidation-reduction process;regulation of biological process;regulation of biological quality;regulation of cellular process;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide oxidoreductase activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;proteasome complex;protein complex 1.47E-116 7 12 12 52.2

O43592;F5GZM3;F8WDU6;F5GYW6 Exportin-T XPOT >sp|O43592|XPOT_HUMAN Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2 0.16 -0.02 0.15 -0.05 0.11 -0.15 0.09 -0.48 0.464860216 0.166749743 establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;intracellular protein transport;intracellular transport;nuclear export;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;protein transport;RNA export from nucleus;RNA transport;transport;tRNA export from nucleus;tRNA transport binding;nucleic acid binding;protein transporter activity;RNA binding;substrate-specific transporter activity;transporter activity;tRNA binding cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;nucleoplasm;organelle part;pore complex;protein complex RNA transport 2.77E-57 4 12 12 15.1

Q7Z2W4;C9J6P4;Q7Z2W4-2;Q7Z2W4-3;Q7Z2W4-4;Q7Z2W4-5;H7C5K1 Zinc finger CCCH-type antiviral protein 1 ZC3HAV1 >sp|Q7Z2W4|ZCCHV_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3;>tr|C9J6P4|C9J6P4_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=2 SV=1;>sp|Q7Z2W4-2|ZCCHV_HUMAN Isoform 2 of Zinc finger C 0.03 0.03 0.15 0.07 0.01 -0.03 -0.15 0.09 0.689204631 0.093049351 biological regulation;cellular process;cellular response to chemical stimulus;cellular response to dsRNA;cellular response to exogenous dsRNA;cellular response to organic substance;cellular response to stimulus;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;multi-organism process;negative regulation of biological process;negative regulation of reproductive process;negative regulation of viral genome replication;negative regulation of viral reproduction;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of interferon-alpha production;positive regulation of interferon-beta production;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA catabolic process;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of type I interferon production;regulation of biological process;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of interferon-alpha production;regulation of interferon-beta production;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA catabolic process;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of type I interferon production;regulation of viral genome replication;regulation of viral reproduction;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus "binding;catalytic activity;cation binding;ion binding;metal ion binding;NAD+ ADP-ribosyltransferase activity;nucleic acid binding;RNA binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 1.76E-107 7 12 12 21.3

Q7L1Q6;Q7L1Q6-4;Q7L1Q6-3;Q7L1Q6-2;C9IZ80;H0Y503;C9JFN4;C9JV57;C9J188;C9JWF5 Basic leucine zipper and W2 domain-containing protein 1 BZW1 >sp|Q7L1Q6|BZW1_HUMAN Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1;>sp|Q7L1Q6-4|BZW1_HUMAN Isoform 4 of Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1;>sp|Q7L1Q6-3|BZW1_HUMAN Iso 0.25 0.03 -0.11 -0.14 0.10 -0.21 0.17 -0.26 0.161226911 0.061313221 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" cell part;cytoplasm;intracellular part 2.62E-40 10 13 12 29.4

P09497-2;P09497;D6RJD1;H0Y9Q6;Q2TAC6-3;Q2TAC6-2;F8VW50;Q2TAC6 Clathrin light chain B CLTB >sp|P09497-2|CLCB_HUMAN Isoform Non-brain of Clathrin light chain B OS=Homo sapiens GN=CLTB;>sp|P09497|CLCB_HUMAN Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1 -0.15 0.02 0.06 0.08 -0.22 0.24 -0.10 0.24 0.117583604 -0.042944701 axonemal microtubule depolymerization;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex disassembly;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;microtubule cytoskeleton organization;microtubule depolymerization;microtubule polymerization or depolymerization;microtubule-based movement;microtubule-based process;organelle organization;plus-end specific microtubule depolymerization;protein complex disassembly;protein complex subunit organization;protein depolymerization;protein transport;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;peptide binding;plus-end-directed microtubule motor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural molecule activity" cell part;cell projection;cell projection membrane;cell projection part;cilium;cilium membrane;cilium part;clathrin coat;clathrin coat of coated pit;clathrin coat of trans-Golgi network vesicle;clathrin vesicle coat;cytoplasm;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;microtubule;microtubule associated complex;organelle part;plasma membrane part;protein complex;trans-Golgi network;vesicle coat Bacterial invasion of epithelial cells;Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease;Lysosome 1.36E-64 8 13 12 37.4

P51178;P51178-2 "1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1" PLCD1 ">sp|P51178|PLCD1_HUMAN 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Homo sapiens GN=PLCD1 PE=1 SV=2;>sp|P51178-2|PLCD1_HUMAN Isoform 2 of 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1 OS=Homo sapiens GN=PLCD1" -0.08 0.12 0.50 0.13 0.22 0.57 0.29 -0.21 0.084141759 -0.049131017 anatomical structure development;anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;blood vessel development;catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to stimulus;developmental process;embryonic organ development;inositol phosphate metabolic process;intracellular signal transduction;labyrinthine layer blood vessel development;lipid catabolic process;lipid metabolic process;metabolic process;organ development;organophosphate metabolic process;phospholipid metabolic process;placenta blood vessel development;primary metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;response to stimulus;signal transduction "binding;calcium ion binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lipase activity;lipid binding;metal ion binding;molecular transducer activity;phosphatidylinositol phospholipase C activity;phospholipase activity;phospholipase C activity;phospholipid binding;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;signal transducer activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Calcium signaling pathway;Inositol phosphate metabolism;Phosphatidylinositol signaling system 1.38E-55 2 13 12 25.7

P51149;C9J592;C9J4V0;C9J8S3;C9IZZ0;C9J7D1;C9J4S4;E9PQX4;Q9HC10-4;Q9HC10-2;Q9HC10-3;Q9HC10-5;Q9HC10 Ras-related protein Rab-7a RAB7A >sp|P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1;>tr|C9J592|C9J592_HUMAN Ras-related protein Rab-7a (Fragment) OS=Homo sapiens GN=RAB7A PE=2 SV=1;>tr|C9J4V0|C9J4V0_HUMAN Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7 -0.10 0.09 -0.23 0.03 0.14 0.23 -0.30 0.04 0.238313875 -0.083908964 anatomical structure homeostasis;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;bone resorption;catabolic process;cation homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular monovalent inorganic cation homeostasis;cellular process;cellular protein catabolic process;cellular protein metabolic process;cellular response to stimulus;chemical homeostasis;early endosome to late endosome transport;endosome to lysosome transport;endosome transport;epidermal growth factor catabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;exocytosis;homeostatic process;immune system process;intracellular pH reduction;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;lysosomal transport;macromolecule catabolic process;macromolecule metabolic process;membrane fusion;membrane organization;metabolic process;monovalent inorganic cation homeostasis;multicellular organismal process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;neurological system process;organelle fusion;organelle organization;pH reduction;phagosome acidification;phagosome-lysosome fusion;primary metabolic process;protein catabolic process;protein metabolic process;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular pH;regulation of cellular process;regulation of epidermal growth factor receptor signaling pathway;regulation of intracellular pH;regulation of pH;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to stimulus;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal transduction;small GTPase mediated signal transduction;synaptic vesicle exocytosis;synaptic vesicle transport;system process;tissue homeostasis;transport;vacuolar transport;vesicle-mediated transport "binding;calcium ion binding;catalytic activity;cation binding;GDP binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" basolateral plasma membrane;cell junction;cell part;clathrin coated vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endocytic vesicle;endocytic vesicle membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endosome;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;late endosome;lysosomal membrane;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-

bounded vesicle;organelle;organelle membrane;organelle part;phagocytic vesicle;phagocytic vesicle membrane;pigment granule;plasma membrane part;synapse part;synaptic vesicle membrane;vacuolar membrane;vacuolar part;vesicle;vesicle membrane	Amoebiasis;Endocytosis;ko05152;Phagosome	9.43E-183	13	13	12	54.6
P53814-5;P53814;P53814-6;P53814-2;C9JGQ0;C9JQZ8;H7BZZ8;C9JP19;H7C372	Smoothelin	SMTN	>sp|P53814-5|SMTN_HUMAN Isoform B2 of Smoothelin OS=Homo sapiens GN=SMTN;>sp|P53814|SMTN_HUMAN Smoothelin OS=Homo sapiens GN=SMTN PE=1 SV=7;>sp|P53814-6|SMTN_HUMAN Isoform B3 of Smoothelin OS=Homo sapiens GN=SMTN	0.59 0.31 -0.11	0.10 -0.21 -0.13	-0.37	0.06	0.932414429	0.383048054	anatomical structure development;developmental process;multicellular organismal process;muscle contraction;muscle organ development;muscle structure development;muscle system process;organ development;smooth muscle contraction;system process	actin binding;binding;cytoskeletal protein binding;protein binding;structural constituent of muscle;structural molecule activity	actin cytoskeleton;cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle	2.20E-160	9	14	12	19.5
O60749;B4DEK4;D6RC15	Sorting nexin-2	SNX2	>sp|O60749|SNX2_HUMAN Sorting nexin-2 OS=Homo sapiens GN=SNX2 PE=1 SV=2;>tr|B4DEK4|B4DEK4_HUMAN Sorting nexin-2 OS=Homo sapiens GN=SNX2 PE=2 SV=1	0.25 0.08 0.02 -0.20	0.28 0.12 0.31 -0.26	0.182769436	-0.078855332	cell communication;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;membrane invagination;membrane organization;protein transport;transport;vesicle-mediated transport	binding;lipid binding;phosphatidylinositol binding;phospholipid binding;protein transporter activity;substrate-specific transporter activity;transporter activity	cell part;cytoplasmic part;early endosome membrane;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part	1.04E-138	3	14	12	32
E9PRI4;E9PGT3;Q15418;Q15418-2;Q15418-3;B7Z3B5;Q15349;Q15349-3;Q15349-2;F2Z2J1;Q5SVM6;E9PMM7;D6R910;Q5TI62;B1AXG1;Q5SVM7;E9PAN7;Q9UK32;B7ZL90	Ribosomal protein S6 kinase;Ribosomal protein S6 kinase alpha-1	RPS6KA1	>tr|E9PRI4|E9PRI4_HUMAN Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=2 SV=1;>tr|E9PGT3|E9PGT3_HUMAN Ribosomal protein S6 kinase OS=Homo sapiens GN=RPS6KA1 PE=2 SV=1;>sp|Q15418|KS6A1_HUMAN Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=	0.01 -0.14	0.16 0.06 -1.80	-1.00	0.34 0.05	0.52549919	0.622902991	"activation of immune response;activation of innate immune response;anatomical structure development;apoptosis;axon guidance;biological regulation;brain renin-angiotensin system;cardiac muscle cell apoptosis;cell communication;cell cycle;cell cycle phase;cell cycle process;cell death;cell maturation;cell surface receptor linked signaling pathway;cell-cell signaling;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;central nervous system development;chemotaxis;circulatory system process;death;defense response;developmental maturation;developmental process;developmental process involved in reproduction;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator;DNA damage response, signal transduction resulting in transcription;endocrine process;enzyme linked receptor protein signaling pathway;heart contraction;heart development;heart process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;intracellular protein kinase cascade;intracellular signal transduction;locomotion;macromolecule metabolic process;macromolecule modification;MAPKKK cascade;metabolic process;metaphase;mitotic metaphase;multicellular organismal process;muscle cell apoptosis;MyD88-dependent toll-like receptor signaling pathway;MyD88-independent toll-like receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of embryonic development;negative regulation of ERK1 and ERK2 cascade;negative regulation of intracellular protein kinase cascade;negative regulation of MAPKKK cascade;negative regulation of mesoderm development;negative regulation of programmed cell death;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;neurological system process;neurological system process involved in regulation of systemic arterial blood pressure;oocyte maturation;organ development;pattern recognition receptor signaling pathway;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell activation;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cell growth;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of defense response;positive regulation of developmental process;positive regulation of gene expression;positive regulation of growth;positive regulation of hepatic stellate cell activation;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein metabolic process;protein modification process;protein phosphorylation;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of blood volume by renin-angiotensin;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of developmental process;regulation of DNA-dependent transcription in response to stress;regulation of embryonic development;regulation of ERK1 and ERK2 cascade;regulation of gene expression;regulation of growth;regulation of hepatic stellate cell activation;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of intracellular protein kinase cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of mesoderm development;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein processing;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of systemic arterial blood pressure;regulation of systemic arterial blood pressure by hormone;regulation of systemic arterial blood pressure by renin-angiotensin;regulation of systemic arterial blood pressure mediated by a chemical signal;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of translation in response to stress;reproductive process;response to carbohydrate stimulus;response to chemical stimulus;response to DNA damage stimulus;response to external stimulus;response to organic substance;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signaling;stress-activated MAPK cascade;stress-activated protein kinase signaling cascade;striated muscle cell apoptosis;synaptic transmission;system development;system process;taxis;toll-like receptor 10 signaling pathway;toll-like receptor 2 signaling pathway;toll-like receptor 3 signaling pathway;toll-like receptor 4 signaling pathway;toll-like receptor 5 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;transmembrane receptor protein tyrosine kinase signaling pathway;TRIF-dependent toll-like receptor signaling pathway"	"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;caspase inhibitor activity;caspase regulator activity;catalytic activity;cation binding;cysteine-type endopeptidase inhibitor activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;ion binding;kinase activity;magnesium ion binding;metal ion binding;nucleotide binding;peptidase inhibitor activity;peptidase regulator activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;ribosomal protein S6 kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups"	cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome;spindle	Long-term potentiation;MAPK signaling pathway;mTOR signaling pathway;Neurotrophin signaling pathway;Oocyte meiosis;Progesterone-mediated oocyte maturation	6.73E-58	19	16	12	28.7
P09429;Q5T7C4;Q5T7C6;Q5T7C0;B2RPK0	High mobility group protein B1	HMGB1	>sp|P09429|HMGB1_HUMAN High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3;>tr|Q5T7C4|Q5T7C4_HUMAN High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=2 SV=1;>tr|Q5T7C6|Q5T7C6_HUMAN High mobility group protein B1 (Fragment) OS=Homo sap	-0.04 0.02 -0.11	0.07 0.22 -0.57	-0.36	-0.98	0.687621959	0.407112972	"anatomical structure development;base-excision repair, DNA ligation;biological regulation;catabolic process;cell activation;cell chemotaxis;cell migration;cell motility;cell projection organization;cellular catabolic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemotaxis;defense response;dendritic cell chemotaxis;developmental process;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA conformation change;DNA fragmentation involved in apoptotic nuclear change;DNA ligation;DNA ligation involved in DNA repair;DNA metabolic process;DNA recombination;DNA topological change;eye development;immune response;immune system process;inflammatory response;inflammatory response to antigenic stimulus;innate immune response;leukocyte activation;leukocyte chemotaxis;leukocyte

migration;locomotion;lung development;macromolecule catabolic process;macromolecule metabolic process;metabolic process;myeloid dendritic cell activation;myeloid leukocyte activation;negative regulation of apoptotic cell clearance;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of endocytosis;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of phagocytosis;negative regulation of RNA metabolic process;negative regulation of RNA polymerase II transcriptional preinitiation complex assembly;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transport;neuron projection development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;organ development;positive regulation of apoptosis;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of carbohydrate metabolic process;positive regulation of caspase activity;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular carbohydrate metabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of DNA binding;positive regulation of gene expression;positive regulation of glucose metabolic process;positive regulation of glycogen catabolic process;positive regulation of glycogen metabolic process;positive regulation of hydrolase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of myeloid cell differentiation;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of peptidase activity;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of apoptosis;regulation of apoptotic cell clearance;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell death;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of DNA binding;regulation of endocytosis;regulation of endopeptidase activity;regulation of gene expression;regulation of generation of precursor metabolites and energy;regulation of glucose metabolic process;regulation of glycogen catabolic process;regulation of glycogen metabolic process;regulation of hydrolase activity;regulation of immune system process;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidase activity;regulation of phagocytosis;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of RNA metabolic process;regulation of RNA polymerase II transcriptional preinitiation complex assembly;regulation of transcription from RNA polymerase II promoter;regulation of transcription initiation from RNA polymerase II promoter;regulation of transcription initiation, DNA-dependent;regulation of transcription, DNA-dependent;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;sensory organ development;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;taxis;V(D)J recombination"	binding;calcium-dependent protein kinase regulator activity;chemoattractant activity;cytokine activity;damaged DNA binding;DNA bending activity;DNA binding;double-stranded DNA binding;enzyme activator activity;enzyme regulator activity;kinase activator activity;kinase regulator activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein kinase activator activity;protein kinase regulator activity;RAGE receptor binding;receptor binding;sequence-specific DNA binding transcription factor activity;single-stranded DNA binding;structure-specific DNA bindingcell part;cell projection;cell surface;chromosome;condensed chromosome;cytoplasm;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part	Base excision repair	2.49E-120	5	17	12	40.9

O00468-6;O00468-3;O00468-7;O00468-2;O00468-5;O00468-4;O00468;H0Y5U1	Agrin;Agrin N-terminal 110 kDa subunit;Agrin C-terminal 110 kDa subunit;Agrin C-terminal 90 kDa fragment;Agrin C-terminal 22 kDa fragment	AGRN	>sp|O00468-6|AGRIN_HUMAN Isoform 6 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-3|AGRIN_HUMAN Isoform 3 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-7|AGRIN_HUMAN Isoform 7 of Agrin OS=Homo sapiens GN=AGRN;>sp|O00468-2|AGRIN_HUMAN Isoform 2 of Agrin OS=Homo	0.18 0.18 -0.16	0.03 -1.09	-0.89	-0.13	0.03	0.862067477	0.579949756	"amine metabolic process;aminoglycan biosynthetic process;aminoglycan catabolic process;aminoglycan metabolic process;axon guidance;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular metabolic process;cellular process;cellular protein localization;cellular response to stimulus;chemotaxis;chondroitin sulfate metabolic process;clustering of voltage-gated sodium channels;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;diterpenoid metabolic process;glycosaminoglycan biosynthetic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;G-protein coupled receptor protein signaling pathway;isoprenoid metabolic process;lipid metabolic process;localization;locomotion;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;muscarinic acetylcholine receptor signaling pathway;neuronal ion channel clustering;nitrogen compound metabolic process;phototransduction;phototransduction, visible light;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell projection organization;positive regulation of cellular biosynthetic process;positive regulation of cellular component biogenesis;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental growth;positive regulation of developmental process;positive regulation of filopodium assembly;positive regulation of gene expression;positive regulation of growth;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nervous system development;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;positive regulation of RNA metabolic process;positive regulation of synapse assembly;positive regulation of synaptic growth at neuromuscular junction;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein localization;protein localization in membrane;receptor clustering;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell development;regulation of cell differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of filopodium assembly;regulation of gene expression;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of nervous system development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;regulation of synapse assembly;regulation of synapse organization;regulation of synaptic growth at neuromuscular junction;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to light stimulus;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;sulfur compound metabolic process;synapse organization;taxis;terpenoid metabolic process"	binding;calcium ion binding;carbohydrate binding;cation binding;chondroitin sulfate binding;dystroglycan binding;extracellular matrix binding;glycoprotein binding;glycosaminoglycan binding;heparan sulfate proteoglycan binding;ion binding;laminin binding;metal ion binding;monosaccharide binding;pattern binding;polysaccharide binding;protein binding;proteoglycan binding;sialic acid binding;structural constituent of cytoskeleton;structural molecule activity;sugar binding	basal lamina;cell junction;cell part;cytoplasmic part;extracellular matrix part;extracellular region part;Golgi apparatus part;Golgi lumen;integral to membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal lumen;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;synapse;vacuolar lumen;vacuolar part	ECM-receptor interaction	1.41E-59	8	13	13	8.5

P49189;B4DXY7 4-trimethylaminobutyraldehyde dehydrogenase ALDH9A1 >sp|P49189|AL9A1_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3;>tr|B4DXY7|B4DXY7_HUMAN 4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=2 SV=1 -0.04 -0.06 -0.68 0.15 -0.27 0.20 0.35 -0.16 0.321003953 -0.1874033 amine biosynthetic process;amine metabolic process;betaine biosynthetic process;betaine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carnitine biosynthetic process;carnitine metabolic process;cellular aldehyde metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;hormone metabolic process;metabolic process;neurotransmitter biosynthetic process;neurotransmitter metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of biological quality;regulation of hormone levels;regulation of neurotransmitter levels;small molecule biosynthetic process;small molecule metabolic process "1-pyrroline dehydrogenase activity;3-chloroallyl aldehyde dehydrogenase activity;4-trimethylammoniobutyraldehyde dehydrogenase activity;aminobutyraldehyde dehydrogenase activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle;plasma membrane "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Fatty acid metabolism;Glycerolipid metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Lysine degradation;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 1.27E-47 2 13 13 26.7

Q14677-3;Q14677;Q14677-2;H0YD52 Clathrin interactor 1 CLINT1 >sp|Q14677-3|EPN4_HUMAN Isoform 3 of Clathrin interactor 1 OS=Homo sapiens GN=CLINT1;>sp|Q14677|EPN4_HUMAN Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 PE=1 SV=1;>sp|Q14677-2|EPN4_HUMAN Isoform 2 of Clathrin interactor 1 OS=Homo sapiens GN=CLINT1 -0.01 -0.05 0.08 0.00 -0.26 -0.08 0.25 -0.02 0.099240692 0.031037648 cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;membrane invagination;membrane organization;post-Golgi vesicle-mediated transport;transport;vesicle-mediated transport binding;lipid binding cell part;clathrin-coated vesicle;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;perinuclear region of cytoplasm;vesicle 9.08E-134 4 13 13 26.7

A5YKK6;A5YKK6-2;A5YKK6-3;B5MDN3;A5YKK6-4;H3BMZ2;H3BR89;H3BMH0;H3BNB1;H3BVC9 CCR4-NOT transcription complex subunit 1 CNOT1 >sp|A5YKK6|CNOT1_HUMAN CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2;>sp|A5YKK6-2|CNOT1_HUMAN Isoform 2 of CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1;>sp|A5YKK6-3|CNOT1_HUMAN Isoform 3 of CCR4-NOT transc 0.19 -0.08 0.06 -0.10 0.16 -0.30 0.15 -0.16 0.162582974 0.058976682 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of estrogen receptor signaling pathway;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of retinoic acid receptor signaling pathway;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytoplasmic mRNA processing body assembly;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA 3'-end processing;positive regulation of mRNA catabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear-transcribed mRNA poly(A) tail shortening;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytoplasmic mRNA processing body assembly;regulation of developmental process;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA 3'-end processing;regulation of mRNA catabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear-transcribed mRNA poly(A) tail shortening;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stem cell differentiation;regulation of stem cell maintenance;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;transcription, DNA-dependent" binding;estrogen receptor binding;hormone receptor binding;nuclear hormone receptor binding;protein binding;receptor binding;retinoic acid receptor binding;steroid hormone receptor binding;transcription factor binding CCR4-NOT complex;cell part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microbody;microbody membrane;microbody part;non-membrane-bounded organelle;nuclear part;nucleoplasm part;organelle;organelle membrane;organelle part;peroxisomal membrane;peroxisomal part;protein complex;ribonucleoprotein complex;RNA granule;transcription factor complex RNA degradation 5.33E-47 10 13 13 6.8

O14579;M0QXB4;O14579-3;O14579-2;M0R061 Coatomer subunit epsilon COPE ">sp|O14579|COPE_HUMAN Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3;>tr|M0QXB4|M0QXB4_HUMAN Coatomer protein complex, subunit epsilon, isoform CRA_g OS=Homo sapiens GN=COPE PE=4 SV=1;>sp|O14579-3|COPE_HUMAN Isoform 3 of Coatomer subunit epsilo" 0.02 0.03 -0.12 -0.05 0.09 0.20 -0.04 0.05 0.732786955 -0.103721765 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular transport;intra-Golgi vesicle-mediated transport;organelle organization;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" structural molecule activity cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;protein complex;vesicle coat 7.96E-72 5 13 13 44.2

Q08257;Q08257-3;A6NP24;C9JH92;Q08257-2 Quinone oxidoreductase CRYZ >sp|Q08257|QOR_HUMAN Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1;>sp|Q08257-3|QOR_HUMAN Isoform 3 of Quinone oxidoreductase OS=Homo sapiens GN=CRYZ;>tr|A6NP24|A6NP24_HUMAN Quinone oxidoreductase (Fragment) OS=Homo sapiens GN=CRYZ PE=2 SV=1;>tr -0.77 -0.52 -0.04 0.38 0.55 0.95 -0.04 -0.01 0.732443877 -0.600113915 catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multicellular organismal process;neurological system process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;sensory perception;sensory perception of light stimulus;system process;visual perception;xenobiotic catabolic process;xenobiotic metabolic process "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;ion binding;metal ion binding;mRNA 3'-UTR binding;mRNA binding;NADP binding;NADPH binding;NADPH:quinone reductase activity;nucleic acid binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;RNA binding;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle 3.15E-59 5 13 13 56.8

O43491-4;E9PHY5;O43491;O43491-3;E9PK52;O43491-2;E9PII3;Q6R5J7;Q6ZSX4;E9PQD2;E9PPC9;E9PQN0;E9PRG1;E9PIG0;E9PN54;E9PJP4;E9PMV8;H0Y5B0 Band 4.1-like protein 2 EPB41L2>sp|O43491-4|E41L2_HUMAN Isoform 4 of Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2;>tr|E9PHY5|E9PHY5_HUMAN Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=2 SV=1;>sp|O43491|E41L2_HUMAN Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV= 0.21 0.01 -0.13 0.04 0.68 0.04 -0.40 -0.71 0.152759113 0.129867616 actin cytoskeleton organization;actin filament-based process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;organelle organization structural molecule activity cell cortex part;cell junction;cell part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;extrinsic to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;spectrin Tight junction 2.84E-69 18 13 13 22.7

O94925-3;O94925;H7BZD1;B8ZZA8;B8ZZC5;O94925-2;C9JIJ6 "Glutaminase kidney isoform, mitochondrial" GLS ">sp|O94925-3|GLSK_HUMAN Isoform 3 of Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS;>sp|O94925|GLSK_HUMAN Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1" -0.21 -0.02 -0.08 0.17 -0.50 0.74 -0.18 1.17 0.344573746 -0.34241323 amine biosynthetic process;amine catabolic process;amine metabolic process;behavior;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell communication;cell-cell signaling;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;glutamate biosynthetic process;glutamate metabolic process;glutamate secretion;glutamine catabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multicellular organismal process;neurological system process;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;regulation of biological process;regulation of biological quality;regulation of multicellular organismal process;regulation of neurotransmitter levels;regulation of respiratory gaseous exchange;regulation of respiratory gaseous exchange by neurological system process;regulation of respiratory system process;regulation of system process;response to stimulus;secretion;secretion by cell;signal release;signaling;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;synaptic transmission;system process;transport "catalytic activity;glutaminase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides" cell part;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;D-Glutamine and D-glutamate metabolism;Nitrogen metabolism;Proximal tubule bicarbonate reclamation" 5.86E-145 7 13 13 32.8

Q13439-3;Q13439-4;Q13439;Q13439-5;H0Y6I0;C9JHJ5;C9J0Y3;Q86W71;E7EVX2 Golgin subfamily A member 4 GOLGA4>sp|Q13439-3|GOGA4_HUMAN Isoform 3 of Golgin subfamily A member 4 OS=Homo sapiens GN=GOLGA4;>sp|Q13439-4|GOGA4_HUMAN Isoform 4 of Golgin subfamily A member 4 OS=Homo sapiens GN=GOLGA4;>sp|Q13439|GOGA4_HUMAN Golgin subfamily A member 4 OS=Homo sapiens GN=GO -0.02 0.06 0.13 -0.10 0.01 -0.23 -0.20 0.40 0.046650287 0.021267639 "cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;post-Golgi vesicle-mediated transport;protein targeting;protein targeting to Golgi;protein transport;retrograde transport, vesicle recycling within Golgi;transport;vesicle-mediated transport" cell part;cytoplasmic part;Golgi apparatus;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;trans-Golgi network 1.25E-51 9 13 13 7.8

P17174;B7Z7E9 "Aspartate aminotransferase, cytoplasmic;Aspartate aminotransferase" GOT1 ">sp|P17174|AATC_HUMAN Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3;>tr|B7Z7E9|B7Z7E9_HUMAN Aspartate aminotransferase OS=Homo sapiens GN=GOT1 PE=2 SV=1" 0.03 -0.12 0.08 0.02 -0.19 -0.25 0.37 -0.37 0.254781635 0.111786126 2-oxoglutarate metabolic process;alcohol biosynthetic process;alcohol metabolic process;alditol biosynthetic process;alditol metabolic process;amine biosynthetic process;amine catabolic process;amine metabolic process;amino acid salvage;aspartate biosynthetic process;aspartate catabolic process;aspartate family amino acid biosynthetic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;aspartate metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;dicarboxylic acid metabolic process;fatty acid homeostasis;fumarate metabolic process;gluconeogenesis;glucose metabolic process;glutamate catabolic process;glutamate catabolic process to 2-oxoglutarate;glutamate catabolic process to aspartate;glutamate metabolic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glycerol biosynthetic process;glycerol metabolic process;hexose biosynthetic process;hexose metabolic process;homeostatic process;lipid homeostasis;L-methionine biosynthetic process;L-methionine salvage;L-methionine salvage from methylthioadenosine;metabolic process;methionine biosynthetic process;methionine metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxaloacetate metabolic process;oxoacid metabolic process;polyamine metabolic process;polyol biosynthetic process;polyol metabolic process;primary metabolic process;regulation of biological quality;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to steroid hormone stimulus;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;sulfur amino acid biosynthetic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process "binding;carbon-carbon lyase activity;carboxylic acid binding;carboxy-lyase activity;catalytic activity;cofactor binding;L-aspartate:2-oxoglutarate aminotransferase activity;L-cysteine:2-oxoglutarate aminotransferase activity;L-phenylalanine aminotransferase activity;L-phenylalanine:2-oxoglutarate aminotransferase activity;lyase activity;phosphatidylserine decarboxylase activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;vitamin B6 binding;vitamin binding" axon part;axon terminus;cell part;cell projection part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane-bounded organelle;neuron projection terminus;organelle;vacuole "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;Cysteine and methionine metabolism;Phenylalanine metabolism;Phenylalanine, tyrosine and tryptophan biosynthesis;Tyrosine metabolism" 1.76E-147 2 13 13 47

P09211;A8MX94 Glutathione S-transferase P GSTP1 >sp|P09211|GSTP1_HUMAN Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2;>tr|A8MX94|A8MX94_HUMAN Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=2 SV=1 0.12 -0.06 -0.34 -0.15 -0.33 -0.10 0.60 0.16 0.34504455 -0.191747986 amine metabolic process;anatomical structure development;biological regulation;carboxylic acid metabolic process;cell proliferation;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to biotic stimulus;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to stimulus;central nervous system development;common myeloid progenitor cell proliferation;developmental process;glutathione metabolic process;localization;metabolic process;negative regulation of acute inflammatory response;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of chemokine production;negative regulation of cytokine production;negative regulation of cytokine-mediated signaling pathway;negative regulation of defense response;negative regulation of ERK1 and ERK2 cascade;negative regulation of fibroblast proliferation;negative regulation of I-kappaB kinase/NF-kappaB cascade;negative regulation of inflammatory response;negative regulation of interleukin-1 beta production;negative regulation of interleukin-1 production;negative regulation of intracellular protein kinase cascade;negative regulation of JUN kinase activity;negative regulation of kinase activity;negative regulation of leukocyte proliferation;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of MAPKKK cascade;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of monocyte chemotactic protein-1 production;negative regulation of multicellular organismal process;negative regulation of necrotic cell death;negative regulation of nitric-oxide synthase biosynthetic process;negative regulation of programmed cell death;negative regulation of protein kinase activity;negative regulation of protein serine/threonine kinase activity;negative regulation of response to cytokine stimulus;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of stress-activated MAPK cascade;negative regulation of stress-activated protein kinase signaling cascade;negative regulation of transferase activity;negative regulation of tumor necrosis factor production;negative regulation of tumor necrosis factor-mediated signaling pathway;nitric oxide storage;nitrogen compound metabolic process;organic acid metabolic process;oxoacid metabolic process;peptide metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;positive regulation of reactive oxygen species metabolic process;positive regulation of superoxide anion generation;primary metabolic process;regulation of acute inflammatory response;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of chemokine production;regulation of cytokine production;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of ERK1 and ERK2 cascade;regulation of fibroblast proliferation;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of inflammatory response;regulation of interleukin-1 beta production;regulation of interleukin-1 production;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of leukocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of monocyte chemotactic protein-1 production;regulation of multicellular organismal process;regulation of necrotic cell death;regulation of nitric-oxide synthase biosynthetic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of reactive oxygen species metabolic process;regulation of response to cytokine stimulus;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated MAPK cascade;regulation of stress-activated protein kinase signaling cascade;regulation of superoxide anion generation;regulation of superoxide metabolic process;regulation of transferase activity;regulation of tumor necrosis factor production;regulation of tumor necrosis factor-mediated signaling pathway;response to biotic stimulus;response to chemical stimulus;response to inorganic substance;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress;small molecule metabolic process;sulfur compound metabolic process;system development;xenobiotic metabolic process "binding;catalytic activity;dinitrosyl-iron complex binding;enzyme binding;enzyme regulator activity;glutathione transferase activity;JUN kinase binding;kinase binding;kinase regulator activity;nitric oxide binding;protein binding;protein kinase binding;S-nitrosoglutathione binding;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups"cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nucleus;organelle;protein complex;TRAF2-GSTP1 complexDrug metabolism - cytochrome P450;Glutathione metabolism;Metabolism of xenobiotics by cytochrome P450 0 2 13 13 70

P51858;A8K8G0;P51858-2;P51858-3 Hepatoma-derived growth factor HDGF >sp|P51858|HDGF_HUMAN Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1;>tr|A8K8G0|A8K8G0_HUMAN Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=2 SV=1;>sp|P51858-2|HDGF_HUMAN Isoform 2 of Hepatoma-derived growth factor OS=Homo sapi -0.18 0.07 0.07 0.15 0.23 -0.17 -0.26 -0.28 0.436201767 0.14882935 activation of signaling protein activity involved in unfolded protein response;biological regulation;cell proliferation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity binding;carbohydrate binding;DNA binding;glycosaminoglycan binding;heparin binding;nucleic acid binding;nucleotide binding;pattern binding;polysaccharide binding;protein binding transcription factor activity;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription corepressor activity;RNA polymerase II transcription factor binding transcription factor activity;RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;cytoplasm;extracellular region part;extracellular space;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm part;organelle part;protein complex;transcriptional repressor complex 2.81E-113 4 13 13 57.5

P07686;Q5URX0;H0YA83;H0Y9B6;D6REQ8;H0Y9M3 Beta-hexosaminidase subunit beta;Beta-hexosaminidase subunit beta chain B;Beta-hexosaminidase subunit beta chain A HEXB >sp|P07686|HEXB_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3;>tr|Q5URX0|Q5URX0_HUMAN Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=2 SV=1;>tr|H0YA83|H0YA83_HUMAN Beta-hexosaminidase subunit beta (Fragment) OS=Homo 0.01 -0.09 0.07 -0.08 0.79 0.44 0.24 -0.11 0.807716358 -0.363359306 "amine metabolic process;aminoglycan catabolic process;aminoglycan metabolic process;anatomical structure development;astrocyte cell migration;axon ensheathment;behavior;biological regulation;biosynthetic process;calcium ion homeostasis;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cation homeostasis;cell death;cell migration;cell motility;cellular biosynthetic process;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein metabolic process;ceramide metabolic process;chemical homeostasis;chondroitin sulfate catabolic process;chondroitin sulfate metabolic process;death;developmental process;divalent inorganic cation homeostasis;ensheathment of neurons;female gamete generation;gamete generation;ganglioside catabolic process;ganglioside metabolic process;glial cell migration;glycolipid catabolic process;glycolipid metabolic process;glycosaminoglycan catabolic process;glycosaminoglycan metabolic process;glycosphingolipid catabolic process;glycosphingolipid metabolic process;homeostatic process;hyaluronan catabolic process;hyaluronan metabolic process;ion homeostasis;keratan sulfate catabolic process;keratan sulfate metabolic process;lipid biosynthetic process;lipid catabolic process;lipid localization;lipid metabolic process;lipid storage;localization;locomotion;locomotory behavior;lysosome organization;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;male courtship behavior;male mating behavior;membrane lipid catabolic process;membrane lipid metabolic process;metabolic process;metal ion homeostasis;multicellular organismal process;multicellular organismal reproductive behavior;multicellular organismal reproductive process;myelination;neurological system process;neuromuscular process;neuromuscular process controlling balance;nitrogen compound metabolic process;oligosaccharide catabolic process;oligosaccharide metabolic process;oogenesis;organelle organization;organophosphate metabolic process;penetration of zona pellucida;phospholipid biosynthetic process;phospholipid metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein metabolic process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive behavior;reproductive process;response to stimulus;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;skeletal system development;sphingoid metabolic process;sphingolipid catabolic process;sphingolipid metabolic process;sulfur compound catabolic process;sulfur compound metabolic process;system development;system process;vacuole organization" "beta-N-acetylhexosaminidase activity;binding;catalytic activity;hexosaminidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;identical protein binding;protein binding;protein dimerization activity;protein heterodimerization activity;protein homodimerization activity" acrosomal vesicle;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;lysosome;lytic vacuole;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;stored secretory granule;vacuolar lumen;vacuolar part;vacuole;vesicle Amino sugar and nucleotide sugar metabolism;Glycosaminoglycan degradation;Glycosphingolipid biosynthesis - ganglio series;Glycosphingolipid biosynthesis - globo series;Lysosome;Other glycan degradation 1.20E-62 6 13 13 21.9

Q9BUJ2-4;B7Z4B8;Q9BUJ2-2;Q9BUJ2;Q9BUJ2-3;M0QYZ0;M0R3F1;M0R203;M0QZV6;M0R0K8;M0QYI8;M0QYM5 Heterogeneous nuclear ribonucleoprotein U-like protein 1 HNRNPUL1 >sp|Q9BUJ2-4|HNRL1_HUMAN Isoform 4 of Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1;>tr|B7Z4B8|B7Z4B8_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=2 SV=1;>sp|Q9BUJ2-2|H -0.33 0.08 0.09 0.19 0.24 -0.12 -0.79 -0.29 0.42135273 0.249386055 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to biotic stimulus;response to other organism;response to stimulus;response to virus;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;nucleic acid binding;RNA binding cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex 9.76E-101 12 13 13 24.5

P42345;B1AKP8 Serine/threonine-protein kinase mTOR MTOR >sp|P42345|MTOR_HUMAN Serine/threonine-protein kinase mTOR OS=Homo sapiens GN=MTOR PE=1 SV=10.05 0.12 -0.12 -0.02 -0.15 -0.29 0.13 0.11 0.19530272 0.059835452 "anatomical structure development;biological regulation;catabolic process;cell communication;cell development;cell growth;cell projection organization;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to hormone stimulus;cellular response to hypoxia;cellular response to insulin stimulus;cellular response to nutrient levels;cellular response to organic substance;cellular response to oxygen levels;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;defense response;developmental process;developmental process involved in reproduction;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;fibroblast growth factor receptor signaling pathway;germ cell development;growth;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;insulin receptor signaling pathway;intracellular signal transduction;lymphocyte costimulation;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of autophagy;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cell communication;negative regulation of cell size;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of macroautophagy;negative regulation of metabolic process;negative regulation of NFAT protein import into nucleus;negative regulation of nucleocytoplasmic transport;negative regulation of protein import into nucleus;negative regulation of protein transport;negative regulation of response to external stimulus;negative regulation of response to extracellular stimulus;negative regulation of response to nutrient levels;negative regulation of response to stimulus;negative regulation of transcription factor import into nucleus;negative regulation of transmembrane transport;negative regulation of transport;nerve growth factor receptor signaling pathway;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;peptidyl-threonine modification;peptidyl-threonine phosphorylation;phosphate-containing compound metabolic process;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;positive regulation of actin filament bundle assembly;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell activation;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of endothelial cell proliferation;positive regulation of epithelial cell proliferation;positive regulation of gene expression;positive regulation of immune system process;positive regulation of intracellular protein kinase cascade;positive regulation of lamellipodium assembly;positive regulation of leukocyte activation;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of muscle cell differentiation;positive regulation of myotube differentiation;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organelle organization;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein complex assembly;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein polymerization;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of skeletal muscle cell differentiation;positive regulation of stress fiber assembly;positive regulation of striated muscle cell differentiation;positive regulation of T cell activation;positive regulation of transcription from RNA polymerase III promoter;positive regulation of transcription, DNA-dependent;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;protein autophosphorylation;protein catabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of autophagy;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of carbohydrate biosynthetic process;regulation of carbohydrate metabolic process;regulation of carbohydrate utilization;regulation of catabolic process;regulation of catalytic activity;regulation of cell activation;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cell proliferation;regulation of cell size;regulation of cellular biosynthetic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cytoskeleton organization;regulation of developmental process;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;regulation of establishment of protein localization;regulation of fatty acid beta-oxidation;regulation of fatty acid metabolic process;regulation of fatty acid oxidation;regulation of gene expression;regulation of generation of precursor metabolites and energy;regulation of glucan biosynthetic process;regulation of glucose metabolic process;regulation of glycogen biosynthetic process;regulation of glycogen metabolic process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of lamellipodium assembly;regulation of leukocyte activation;regulation of lipid biosynthetic process;regulation of lipid catabolic process;regulation of lipid metabolic process;regulation of localization;regulation of lymphocyte activation;regulation of macroautophagy;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of muscle organ development;regulation of myotube differentiation;regulation of NFAT protein import into nucleus;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organelle organization;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of polysaccharide biosynthetic process;regulation of polysaccharide metabolic process;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein polymerization;regulation of protein transport;regulation of purine nucleotide catabolic process;regulation of Rac GTPase activity;regulation of Ras GTPase activity;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to food;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of skeletal muscle fiber development;regulation of skeletal muscle tissue development;regulation of stress fiber assembly;regulation of striated muscle cell differentiation;regulation of striated muscle tissue development;regulation of T cell activation;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase III promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of transmembrane transport;regulation of transport;reproductive process;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to hormone stimulus;response to hypoxia;response to insulin stimulus;response to nutrient;response to nutrient levels;response to organic nitrogen;response to organic substance;response to oxygen levels;response to peptide hormone stimulus;response to stimulus;response to stress;ruffle organization;signal transduction;T cell costimulation;TOR signaling cascade;transmembrane receptor protein tyrosine kinase signaling pathway" "5S rDNA binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;drug binding;kinase activity;nucleic acid binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;rDNA binding;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleoprotein binding;ribonucleotide binding;ribosome binding;RNA polymerase III regulatory region DNA binding;RNA polymerase III transcription factor binding;RNA polymerase III type 1 promoter DNA binding;RNA polymerase III type 2 promoter DNA binding;RNA polymerase III type 3 promoter DNA binding;sequence-specific DNA binding;TFIIIC-class transcription factor binding;transcription factor binding;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;cytosolic part;endomembrane system;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lysosome;lytic vacuole;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mTOR-FKBP12-rapamycin complex;nuclear body;nuclear part;nucleoplasm part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;phosphatidylinositol 3-kinase complex;PML body;protein complex;TORC1 complex;TORC2 complex;vacuole Acute myeloid leukemia;Adipocytokine signaling pathway;ErbB

signaling pathway;Glioma;Insulin signaling pathway;mTOR signaling pathway;Pathways in cancer;Prostate cancer;Type II diabetes mellitus 1.11E-45 2 13 13 7.6
Q99707;B7ZLW7;B1ANE3 Methionine synthase MTR >sp|Q99707|METH_HUMAN Methionine synthase OS=Homo sapiens GN=MTR PE=1 SV=2;>tr|B7ZLW7|B7ZLW7_HUMAN MTR protein OS=Homo sapiens GN=MTR PE=2 SV=1;>tr|B1ANE3|B1ANE3_HUMAN Methionine synthase (Fragment) OS=Homo sapiens GN=MTR PE=2 SV=1 0.09 -0.08 -0.12 -0.09 -0.01 -0.40 0.53 -0.21 0.041758889 -0.025743532 amine metabolic process;anatomical structure development;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;heterocycle metabolic process;metabolic process;methylation;nervous system development;nitrogen compound metabolic process;one-carbon metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pteridine-containing compound metabolic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound metabolic process;system development;xenobiotic metabolic process "5-methyltetrahydrofolate-dependent methyltransferase activity;binding;catalytic activity;cation binding;cobalamin binding;homocysteine S-methyltransferase activity;ion binding;metal ion binding;methionine synthase activity;methyltransferase activity;S-adenosylmethionine-dependent methyltransferase activity;S-methyltransferase activity;tetrapyrrole binding;transferase activity;transferase activity, transferring one-carbon groups;transition metal ion binding;vitamin binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular;intracellular part Cysteine and methionine metabolism;One carbon pool by folate;Selenocompound metabolism 7.47E-88 3 13 13 14.2
Q13564-2;Q13564;A6NCK0;A8MU28;J3KRK3;J3QRA5;H3BMR3;J3QLH4;J3KTE3;H3BQW6 NEDD8-activating enzyme E1 regulatory subunit NAE1 >sp|Q13564-2|ULA1_HUMAN Isoform 2 of NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1;>sp|Q13564|ULA1_HUMAN NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1;>tr|A6NCK0|A6NCK0_HUMAN NEDD8-activating enzyme 0.34 -0.10 0.15 -0.10 0.08 -0.14 0.19 -0.31 0.29451185 0.116884205 apoptosis;biological regulation;biosynthetic process;cell cycle checkpoint;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;death;DNA integrity checkpoint;DNA metabolic process;DNA replication;DNA replication checkpoint;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic cell cycle checkpoint;mitotic cell cycle DNA replication checkpoint;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cellular process;negative regulation of G2/M transition of mitotic cell cycle;negative regulation of mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein neddylation;regulation of apoptosis;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular process;regulation of G2/M transition of mitotic cell cycle;regulation of interphase of mitotic cell cycle;regulation of mitotic cell cycle;regulation of programmed cell death;response to stimulus;signal transduction catalytic activity cell part;cytoplasm;intracellular part;membrane;plasma membrane Alzheimer's disease 3.75E-81 10 13 13 40.9
Q9NTK5;J3KQ32;Q9NTK5-2;Q9NTK5-3;C9JTK6;C9JCJ9 Obg-like ATPase 1 OLA1 >sp|Q9NTK5|OLA1_HUMAN Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2;>tr|J3KQ32|J3KQ32_HUMAN Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=4 SV=1;>sp|Q9NTK5-2|OLA1_HUMAN Isoform 2 of Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 0.05 -0.08 -0.07 -0.04 -0.25 -0.22 0.35 -0.04 0.017351338 0.007547334 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 3.35E-79 6 13 13 32.8
Q9UKK3 Poly [ADP-ribose] polymerase 4 PARP4 >sp|Q9UKK3|PARP4_HUMAN Poly [ADP-ribose] polymerase 4 OS=Homo sapiens GN=PARP4 PE=1 SV=3 0.22 -0.04 -0.13 -0.27 0.69 0.35 0.23 0.25 1.215631806 -0.434004488 cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;defense response;DNA metabolic process;DNA repair;establishment of localization;inflammatory response;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein ADP-ribosylation;protein metabolic process;protein modification process;response to chemical stimulus;response to DNA damage stimulus;response to drug;response to stimulus;response to stress;response to wounding;transport "binding;catalytic activity;DNA binding;enzyme binding;NAD+ ADP-ribosyltransferase activity;nucleic acid binding;protein binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasm;cytoskeletal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spindle microtubule Base excision repair 1.64E-51 1 13 13 9
P12004 Proliferating cell nuclear antigen PCNA >sp|P12004|PCNA_HUMAN Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 0.37 0.12 -0.55 0.06 0.08 -0.57 -0.44 -0.60 0.651368721 0.383227053 "anatomical structure development;anatomical structure homeostasis;base-excision repair;biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;developmental process;DNA biosynthetic process;DNA metabolic process;DNA recombination;DNA repair;DNA replication;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA-dependent DNA replication;heart development;homeostatic process;inositol lipid-mediated signaling;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mismatch repair;mitotic recombination;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;nucleotide-excision repair, DNA gap filling;organ development;organelle organization;phosphatidylinositol-mediated signaling;positive regulation of catalytic activity;positive regulation of deoxyribonuclease activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of nuclease activity;postreplication repair;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of deoxyribonuclease activity;regulation of DNA metabolic process;regulation of DNA replication;regulation of gene expression;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription involved in G1/S phase of mitotic cell cycle;regulation of transcription, DNA-dependent;response to cadmium ion;response to chemical stimulus;response to DNA damage stimulus;response to inorganic substance;response to lipid;response to metal ion;response to organic substance;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle;signal transduction;telomere maintenance;telomere maintenance via recombination;telomere maintenance via semi-conservative replication;telomere maintenance via telomere lengthening;telomere organization;transcription-coupled nucleotide-excision repair;translesion synthesis" "binding;catalytic activity;dinucleotide insertion or deletion binding;DNA binding;DNA insertion or deletion binding;DNA N-glycosylase activity;DNA polymerase processivity factor activity;double-stranded DNA binding;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing N-glycosyl compounds;mismatch base pair DNA N-glycosylase activity;mismatch repair complex binding;mismatched DNA binding;MutLalpha complex binding;nucleic acid binding;protein binding;protein complex binding;purine-specific mismatch base pair DNA N-glycosylase activity;structure-specific DNA binding" cell part;chromosomal part;cytoplasm;cytoskeleton;DNA replication factor C complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule cytoskeleton;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nuclear replication fork;nucleoplasm;organelle;organelle part;PCNA complex;PCNA-p21 complex;protein complex;replication fork Base excision repair;Cell cycle;DNA replication;Mismatch repair;Nucleotide excision repair 2.40E-227 1 13 13 69.3
O14818;O14818-2;H0Y586;O14818-4;Q8TAA3-2;Q8TAA3-5;Q8TAA3;F5GY34 Proteasome subunit alpha type-7 PSMA7 >sp|O14818|PSA7_HUMAN Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1;>sp|O14818-2|PSA7_HUMAN Isoform 2 of Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7;>tr|H0Y586|H0Y586_HUMAN Proteasome subunit alpha type-7 (Fragment) OS=Hom -0.02 0.06 -0.13 0.06 0.07 -0.06 -0.18 -0.12 0.375038668 0.064220985 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen

processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex"Proteasome 0 8 13 13 58.9

P62333;H0YJC0;H0YJS8;H0YJX2;H0YJE9;H0YJT1 26S protease regulatory subunit 10B PSMC6 >sp|P62333|PRS10_HUMAN 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1;>tr|H0YJC0|H0YJC0_HUMAN 26S protease regulatory subunit 10B (Fragment) OS=Homo sapiens GN=PSMC6 PE=4 SV=1;>tr|H0YJS8|H0YJS8_HUMAN 26S protease regulatory subunit 0.07 0.06 0.01 0.04 0.03 -0.19 -0.19 -0.28 1.231044997 0.201839902 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;binding, bridging;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane;proteasome accessory complex;protein complex Proteasome 8.59E-178 6 13 13 44.7

Q15008;C9IZE4;E9PHI9;Q6UV22;C9J7B7;C9J0E9;H7C531 26S proteasome non-ATPase regulatory subunit 6PSMD6 >sp|Q15008|PSMD6_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1;>tr|C9IZE4|C9IZE4_HUMAN 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=2 SV=1;>tr|E9PHI9|E9PHI9_HUMAN 26S proteasome non-AT 0.05 0.04 -0.11 -0.02 -0.02 -0.16 -0.01 -0.40 0.595463409 0.137325994 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction" "ATPase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;pyrophosphatase activity" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;proteasome complex;protein complex Proteasome 4.85E-62 7 13 13 34.4

Q9UL46;H0YM70;H0YKU2;H0YLG1;H0YLD2 Proteasome activator complex subunit 2 PSME2 >sp|Q9UL46|PSME2_HUMAN Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4;>tr|H0YM70|H0YM70_HUMAN Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=2 SV=1 -0.07 -0.12 0.13 0.06 -0.13 -0.36 0.12 -0.15 0.462611191 0.128505367 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome activator complex;proteasome complex;protein complex Antigen processing and presentation;Proteasome 1.37E-152 5 13 13 66.1

Q9Y3P9;Q9Y3P9-2;Q9Y3P9-3;B7Z2B4;C9JGR5;B7ZAP0;Q9Y3P9-4;F5H8L0;Q5R372-7;Q5R372-8;Q5R372-6;Q5R372-5;B5MCD9;E9PS63 Rab GTPase-activating protein 1 RABGAP1 >sp|Q9Y3P9|RBGP1_HUMAN Rab GTPase-activating protein 1 OS=Homo sapiens GN=RABGAP1 PE=1 SV=3;>sp|Q9Y3P9-2|RBGP1_HUMAN Isoform 2 of Rab GTPase-activating protein 1 OS=Homo sapiens GN=RABGAP1 0.15 0.03 0.04 0.06 -0.24 -0.07 0.19 -0.31 0.650265715 0.176741015 biological regulation;cell cycle;cellular process;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Rab GTPase activity;positive regulation of Ras GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Rab GTPase activity;regulation of Ras GTPase activity binding;cytoskeletal protein binding;DNA binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleic acid binding;nucleoside-triphosphatase regulator activity;protein binding;Rab GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity;tubulin binding cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex 1.85E-58 14 13 13 14.2

Q15293;B7Z1M1;E9PP27 Reticulocalbin-1 RCN1 >sp|Q15293|RCN1_HUMAN Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1;>tr|B7Z1M1|B7Z1M1_HUMAN Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=2 SV=1 -0.23 -0.16 -0.29 -0.04 1.45 0.82 0.26 -0.11 0.969388057 -0.785744788 anatomical structure development;camera-type eye development;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;eye development;in utero embryonic development;organ development;sensory organ development binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part 6.88E-90 3 13 13 58.6

Q9BW04;Q9BW04-2 Specifically androgen-regulated gene protein SARG >sp|Q9BW04|SARG_HUMAN Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG PE=1 SV=2;>sp|Q9BW04-

2|SARG_HUMAN Isoform 2 of Specifically androgen-regulated gene protein OS=Homo sapiens GN=SARG 0.13 0.24 0.17 -0.07 -0.48 0.13 0.21 0.27 0.172476136 0.087061564 cell part;cytoplasm;intracellular part;membrane;plasma membrane 8.72E-124 2 13 13 35.3

Q12874;E7EUT8 Splicing factor 3A subunit 3 SF3A3 >sp|Q12874|SF3A3_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1;>tr|E7EUT8|E7EUT8_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=2 SV=1 -0.28 0.42 -0.04 0.45 0.05 -0.23 -1.19 -0.47 0.794635093 0.596587091 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;mRNA splice site selection;nuclear mRNA 3'-splice site recognition;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization binding;cation binding;ion binding;metal ion binding;nucleic acid binding;transition metal ion binding;zinc ion binding catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 3.39E-80 2 13 13 28.1

Q00325-2;Q00325;F8VVM2;F8VZL5;F8VWR4;F8VWQ0 "Phosphate carrier protein, mitochondrial" SLC25A3 ">sp|Q00325-2|MPCP_HUMAN Isoform B of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3;>sp|Q00325|MPCP_HUMAN Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2;>tr|F8VVM2|F8VVM2_HUMAN Phosphate carrier protein," -1.03 -0.18 -0.04 -0.16 -0.74 0.71 -1.19 -0.05 0.024739711 -0.03573884 cellular metabolic process;cellular process;establishment of localization;generation of precursor metabolites and energy;metabolic process;transport active transmembrane transporter activity;anion transmembrane transporter activity;inorganic anion transmembrane transporter activity;ion transmembrane transporter activity;phosphate ion carrier activity;phosphate ion transmembrane transporter activity;secondary active transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;symporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane part 1.23E-51 6 13 13 29.4

Q5T6F2;F5H2U4;A6NCA8;E7EWG4;Q5JV03;A2A305;A2A306;Q5JV08 Ubiquitin-associated protein 2 UBAP2 >sp|Q5T6F2|UBAP2_HUMAN Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBAP2 PE=1 SV=1;>tr|F5H2U4|F5H2U4_HUMAN Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBAP2 PE=2 SV=1;>tr|A6NCA8|A6NCA8_HUMAN Ubiquitin-associated protein 2 OS=Homo sapiens GN=UBA 0.34 0.10 -0.18 -0.10 -0.30 -0.13 0.18 0.09 0.185501317 0.079033718 1.42E-84 8 13 13 22.9

P45880;P45880-2;P45880-1;Q5JSD2;Q5JSD1;B4DKM5;A2A3S1 Voltage-dependent anion-selective channel protein 2 VDAC2 >sp|P45880|VDAC2_HUMAN Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2;>sp|P45880-2|VDAC2_HUMAN Isoform 2 of Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2;>sp|P45880-1|VDAC2_HUMAN Isofor -0.32 0.85 -0.27 0.80 0.08 0.95 -1.19 0.71 0.074006594 0.124504078 biological regulation;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of protein complex assembly;negative regulation of protein polymerization;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of protein complex assembly;regulation of protein polymerization anion channel activity;anion transmembrane transporter activity;binding;channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;nucleotide binding;passive transmembrane transporter activity;porin activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated ion channel activity;wide pore channel activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial outer membrane;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;pore complex;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease 9.73E-123 7 13 13 56.5

Q9NQW7;Q9NQW7-3;Q5T6H7;Q9NQW7-2;G8JLB2;Q5T6H3;Q5T6H2;E9PFW2;O00462 Xaa-Pro aminopeptidase 1 XPNPEP1 >sp|Q9NQW7|XPP1_HUMAN Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=1 SV=3;>sp|Q9NQW7-3|XPP1_HUMAN Isoform 3 of Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1;>tr|Q5T6H7|Q5T6H7_HUMAN Xaa-Pro aminopeptidase 1 OS=Homo sapiens GN=XPNPEP1 PE=2 SV 0.08 0.01 -0.15 -0.14 -0.08 -0.01 0.42 0.01 0.436591124 -0.134983792 bradykinin catabolic process;carbohydrate metabolic process;catabolic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycoprotein catabolic process;glycoprotein metabolic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;peptide catabolic process;peptide metabolic process;primary metabolic process;protein metabolic process;protein modification process;proteolysis "aminopeptidase activity;beta-mannosidase activity;binding;carbohydrate binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;ion binding;manganese ion binding;mannose binding;mannosidase activity;metal ion binding;metalloaminopeptidase activity;metalloexopeptidase activity;metallopeptidase activity;monosaccharide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;sugar binding;transition metal ion binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane-bounded organelle;organelle;vacuole Lysosome;Other glycan degradation 2.72E-90 9 13 13 30.2

P14550;Q5T621;G3V1C1;Q96JD6-4;Q96JD6 Alcohol dehydrogenase [NADP(+)] AKR1A1 >sp|P14550|AK1A1_HUMAN Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3 0.09 0.16 -0.85 -0.43 0.01 0.32 0.76 0.36 0.929714495 -0.61784109 alcohol metabolic process;aldehyde catabolic process;biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular aldehyde metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;D-glucuronate catabolic process;D-glucuronate metabolic process;glucose metabolic process;glucuronate catabolic process;glucuronate metabolic process;hexose metabolic process;L-ascorbic acid biosynthetic process;L-ascorbic acid metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;uronic acid metabolic process;vitamin biosynthetic process;vitamin metabolic process;water-soluble vitamin biosynthetic process;water-soluble vitamin metabolic process "1,5-anhydro-D-fructose reductase activity;alcohol dehydrogenase (NADP+) activity;alditol:NADP+ 1-oxidoreductase activity;aldo-keto reductase (NADP) activity;catalytic activity;electron carrier activity;L-glucuronate reductase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" apical plasma membrane;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane part;plasma membrane part Caprolactam degradation;Glycerolipid metabolism;Glycolysis / Gluconeogenesis 3.47E-107 5 14 13 50.5

O00299;A6PVS0;Q9NZA1-3;O15247;Q9NZA1-2;Q9NZA1 Chloride intracellular channel protein 1 CLIC1 >sp|O00299|CLIC1_HUMAN Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 0.17 -0.08 -0.12 -0.06 0.05 -0.16 0.38 0.18 0.429338129 -0.136725831 anion transport;auditory receptor cell stereocilium organization;biological regulation;calcium-mediated signaling;cell projection organization;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;chloride transport;diet induced thermogenesis;establishment of localization;female pregnancy;homeostatic process;inner ear receptor stereocilium organization;inorganic anion transport;intracellular signal transduction;ion homeostasis;ion transport;localization;macromolecule localization;multicellular organismal process;multi-organism process;negative regulation of biological process;negative regulation of ion transmembrane transporter activity;negative regulation of molecular function;negative regulation of ryanodine-sensitive calcium-release channel activity;negative regulation of transport;negative regulation of transporter activity;neurological system process;neuromuscular process;neuromuscular process controlling balance;positive regulation of binding;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal metabolic process;positive regulation of multicellular organismal process;positive regulation of osteoblast differentiation;protein localization;regulation of binding;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cell differentiation;regulation of cellular localization;regulation of cellular process;regulation of developmental process;regulation of heart contraction;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of membrane potential;regulation of metabolic process;regulation of metal ion transport;regulation of mitochondrial membrane potential;regulation of molecular function;regulation of multicellular organismal metabolic process;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of ossification;regulation of osteoblast differentiation;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;reproductive process;response to stimulus;second-messenger-mediated signaling;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal transduction;system process;transport "anion channel activity;anion transmembrane transporter activity;antioxidant activity;catalytic activity;channel activity;chloride channel activity;gated channel activity;glutathione peroxidase activity;ion channel activity;ion transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on peroxide as acceptor;passive transmembrane transporter activity;peroxidase activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated chloride channel activity;voltage-gated ion channel activity" actin cytoskeleton;brush border;cell cortex;cell part;cell projection;chloride channel complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;envelope;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule organizing center;microvillus;mitochondrion;non-membrane-bounded organelle;nuclear envelope;nuclear membrane;nuclear part;nucleus;organelle;organelle envelope;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;protein complex;stereocilium 0 6 14 13 63.9

Q7Z2Z2-2;Q7Z2Z2Elongation factor Tu GTP-binding domain-containing protein 1 EFTUD1 >sp|Q7Z2Z2-2|ETUD1_HUMAN Isoform 2 of Elongation factor Tu GTP-binding domain-containing protein 1 OS=Homo sapiens GN=EFTUD1;>sp|Q7Z2Z2|ETUD1_HUMAN Elongation factor Tu GTP-binding domain-containing protein 1 OS=Homo sapiens GN=EFTUD1 PE=1 SV=2 0.43 0.01 0.20 -0.15 0.25 0.14 0.56 -0.13 0.169727489 -0.086739531 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;mature ribosome assembly;organelle assembly;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleoprotein binding;ribonucleotide binding;ribosome binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" Ribosome biogenesis in eukaryotes 1.21E-148 2 14 13 19.3

O94776;Q68DB1;F8VSM3;H0Y4T7 Metastasis-associated protein MTA2 MTA2;DKFZp686F2281 >sp|O94776|MTA2_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1;>tr|Q68DB1|Q68DB1_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens GN=DKFZp686F2281 PE=2 SV=1 0.03 0.51 -0.02 0.31 -0.22 -0.29 -1.03 -0.05 1.034634394 0.609882173 "biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin assembly or disassembly;chromatin organization;chromosome organization;DNA alkylation;DNA metabolic process;DNA methylation;DNA modification;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;secretory granule organization;small molecule metabolic process;vesicle organization" "binding;catalytic activity;cation binding;chromatin binding;deacetylase activity;DNA binding;histone deacetylase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding transcription factor activity;protein deacetylase activity;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transition metal ion binding;zinc ion binding" cell part;chromatin remodeling complex;cytoplasm;cytoplasmic part;endoplasmic reticulum;histone deacetylase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;protein complex;transcription factor complex;transcriptional repressor complex 8.68E-84 4 14 13 26.5

P49321;P49321-3;P49321-4;P49321-2;Q5T624;H0YDS9;E9PRH9;H0YF33;E9PPR5;E9PI86;E9PPQ8 Nuclear autoantigenic sperm protein NASP >sp|P49321|NASP_HUMAN Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2;>sp|P49321-3|NASP_HUMAN Isoform 3 of Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP;>sp|P49321-4|NASP_HUMAN Isoform 4 of Nuclear autoantigenic sperm pr 0.03 0.02 0.01 0.02 0.50 -0.53 -0.72 -1.08 0.595528331 0.476686593 anatomical structure development;ATP-dependent chromatin remodeling;biosynthetic process;blastocyst development;cell cycle;cell proliferation;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;developmental process;DNA metabolic process;DNA replication;establishment of localization;establishment of protein localization;histone exchange;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome organization;organelle organization;primary metabolic process;protein transport;transport binding;heat shock protein binding;Hsp90 protein binding;protein binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.51E-104 11 14 13 30.3

P52907 F-actin-capping protein subunit alpha-1 CAPZA1 >sp|P52907|CAZA1_HUMAN F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3 0.03 0.14 0.00 0.30 0.26 0.36 0.06 0.21 0.472174665 -0.104249538 actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cellular component assembly;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;defense response;hemostasis;immune response;immune system process;innate immune response;macromolecular complex assembly;macromolecular complex subunit organization;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;protein complex assembly;protein complex subunit organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to stimulus;response to stress actin binding;binding;cytoskeletal protein binding;protein binding cell part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region;F-actin capping protein complex;intracellular organelle part;intracellular part;macromolecular complex;organelle part;protein complex;WASH complex 4.56E-288 1 17 13 66.4

Q04917;A2IDB2;F8WEB6;A2IDB1 14-3-3 protein eta YWHAH >sp|Q04917|1433F_HUMAN 14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4;>tr|A2IDB2|A2IDB2_HUMAN 14-3-3 protein eta (Fragment) OS=Homo sapiens GN=YWHAH PE=2 SV=1 0.03 -0.01 -0.20 0.03 -0.05 0.05 0.08 0.24 0.629730241 -0.121183183 "biological regulation;C21-steroid hormone catabolic process;C21-steroid hormone metabolic process;catabolic process;cellular component organization;cellular component organization or biogenesis;cellular hormone metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular response to stimulus;corticosteroid receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;glucocorticoid catabolic process;glucocorticoid metabolic process;glucocorticoid receptor signaling pathway;hormone catabolic process;hormone metabolic process;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular transport;lipid catabolic process;lipid metabolic process;membrane organization;metabolic process;negative regulation of biological process;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of dendrite morphogenesis;negative regulation of developmental process;negative regulation of neurogenesis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein transport;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of gene expression;regulation of hormone levels;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of signaling;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transmission of nerve impulse;regulation of transport;regulation of transporter activity;response to stimulus;signal transduction;steroid catabolic process;steroid hormone receptor signaling pathway;steroid metabolic process;transport" binding;channel regulator activity;insulin-like growth factor receptor binding;ion channel binding;protein binding;protein domain specific binding;receptor binding;sodium channel regulator activity cell junction;cell part;cell-cell contact zone;cell-cell junction;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intercalated disc;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis 1.82E-281 4 18 13 57.3

Q15424;Q15424-4;Q15424-3;Q15424-2;F5GZU3;B7Z2F6;K7EII0;K7ES42 Scaffold attachment factor B1 SAFB >sp|Q15424|SAFB1_HUMAN Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4;>sp|Q15424-4|SAFB1_HUMAN Isoform 4 of Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB;>sp|Q15424-3|SAFB1_HUMAN Isoform 3 of Scaffold attachment factor B1 OS=Homo s -0.34 1.00 0.12 1.06 -0.05 0.37 -1.24 -0.01 0.600154538 0.693517115 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chromatin organization;chromosome organization;estrogen receptor signaling pathway;growth;hormone metabolic process;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of hormone levels;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;signal transduction;steroid hormone receptor signaling pathway;transcription, DNA-dependent" binding;chromatin binding;core promoter binding;DNA binding;double-stranded DNA binding;nucleic acid binding;nucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;structure-specific DNA binding;transcription regulatory region DNA binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 8.64E-102 8 23 13 29.6

E7EPM6;P33121-2;P33121;B7Z452;B7Z3Z9;H0Y9U7;D6RER0;H0Y9Z9;D6RG07;B4DX30;Q9ULC5-4;Q9ULC5;Q9ULC5-3 Long-chain-fatty-acid--CoA ligase 1 ACSL1 >tr|E7EPM6|E7EPM6_HUMAN Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=2 SV=1;>sp|P33121-2|ACSL1_HUMAN Isoform 2 of Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1;>sp|P33121|ACSL1_HUMAN Long-chain-fatty-acid--CoA ligase 1 OS= -0.04 0.14 0.11 0.03 0.77 0.70 -0.16 -0.86 0.045714994 -0.053008011 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;adiponectin-mediated signaling pathway;biological regulation;biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;cytokine-mediated signaling pathway;establishment of localization;fatty acid metabolic process;fatty acid transport;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;linoleic acid metabolic process;lipid biosynthetic process;lipid metabolic process;lipid transport;long-chain fatty acid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;neutral lipid biosynthetic process;neutral lipid metabolic process;organic acid metabolic process;organic acid transport;organic ether metabolic process;organic substance transport;oxoacid metabolic process;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of transferase activity;response to chemical stimulus;response to cytokine stimulus;response to drug;response to external stimulus;response to extracellular stimulus;response to fatty acid;response to lipid;response to nutrient;response to nutrient levels;response to oleic acid;response to organic cyclic compound;response to organic substance;response to stimulus;signal transduction;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;transport;triglyceride biosynthetic process;triglyceride metabolic process;unsaturated fatty acid metabolic process;xenobiotic catabolic process;xenobiotic metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;fatty acid ligase activity;ligase activity;ligase activity, forming carbon-sulfur bonds;long-chain fatty acid-CoA ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;peroxisomal membrane;peroxisomal part;plasma membrane Adipocytokine signaling pathway;Fatty acid metabolism;Peroxisome;PPAR signaling pathway1.90E-39 13 14 14 24.5

O00116;B8ZZ81 "Alkyldihydroxyacetonephosphate synthase, peroxisomal" AGPS ">sp|O00116|ADAS_HUMAN Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1;>tr|B8ZZ81|B8ZZ81_HUMAN Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=2 SV=1" 0.07 0.55 0.01 -0.02 -0.18 -0.18 -0.16 0.42 0.36067153 0.180165786 biosynthetic process;cellular biosynthetic process;cellular lipid metabolic process;cellular metabolic process;cellular process;ether lipid biosynthetic process;ether lipid metabolic process;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;organic ether metabolic process;primary metabolic process;small molecule metabolic process "alkylglycerone-phosphate synthase activity;binding;catalytic activity;coenzyme binding;cofactor binding;FAD binding;flavin adenine dinucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups;UDP-N-acetylmuramate dehydrogenase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part Ether lipid metabolism;Peroxisome 1.72E-120 2 14 14 28.7

O95831-3;O95831;O95831-2;E9PMA0;O95831-6;O95831-5;O95831-4 "Apoptosis-inducing factor 1, mitochondrial" AIFM1 ">sp|O95831-3|AIFM1_HUMAN Isoform 3 of Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1;>sp|O95831|AIFM1_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1;>sp|O95831-2|AIFM1_HUMAN Isoform 2 of Apoptosis-i" -0.29 -0.02 -0.04 0.11 0.20 0.17 -0.32 -0.04 0.149850732 -0.060658161 "activation of caspase activity;apoptosis;apoptosis in response to endoplasmic reticulum stress;biological regulation;catabolic process;cell death;cell differentiation;cell redox homeostasis;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular homeostasis;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;death;developmental process;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mitochondrial respiratory chain complex assembly;mitochondrial respiratory chain complex I assembly;mitochondrial respiratory chain complex I biogenesis;NADH dehydrogenase complex assembly;neuron apoptosis;neuron death;neuron differentiation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;primary metabolic process;programmed cell death;protein complex assembly;protein complex biogenesis;protein complex subunit organization;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity" binding;catalytic activity;coenzyme binding;cofactor binding;DNA binding;electron carrier activity;flavin adenine dinucleotide binding;nucleic acid binding;oxidoreductase activity cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle part;perinuclear region of cytoplasm Apoptosis 2.01E-116 7 14 14 29.6

Q9P2R3;Q9P2R3-2;Q9P2R3-4;I3L1Z9;I3L3P8;K7EPT2 Ankyrin repeat and FYVE domain-containing protein 1 ANKFY1>sp|Q9P2R3|ANFY1_HUMAN Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2;>sp|Q9P2R3-2|ANFY1_HUMAN Isoform 2 of Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1;>sp|Q9P2R3-4|ANFY1_HUMAN Isof 0.08 0.04 0.02 -0.03 -0.18 0.05 0.21 0.12 0.102810702 -0.025367197 binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;endosomal part;endosome membrane;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part 1.31E-58 6 14 14 19.1

P51572;P51572-2;C9JSP1;C9JQ75;C9J0M4;C9JMD7 B-cell receptor-associated protein 31 BCAP31 >sp|P51572|BAP31_HUMAN B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3;>sp|P51572-2|BAP31_HUMAN Isoform 2 of B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31;>tr|C9JSP1|C9JSP1_HUMAN B-cell receptor-associated protei -0.41 0.17 -0.27 0.09 0.85 0.86 -0.31 0.41 0.772632904 -0.558236424 antigen processing and presentation;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;calcium ion homeostasis;calcium-mediated signaling;calcium-mediated signaling using intracellular calcium source;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;cytosolic calcium ion homeostasis;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion concentration;elevation of mitochondrial calcium ion concentration;endoplasmic reticulum calcium ion homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;gamete generation;homeostatic process;immune response;immune system process;intracellular protein transport;intracellular signal transduction;intracellular transport;ion homeostasis;male gamete generation;metal ion homeostasis;mitochondrial calcium ion homeostasis;multicellular organismal process;multicellular organismal reproductive process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of peptidase activity;protein transport;reduction of endoplasmic reticulum calcium ion concentration;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;reproductive process;response to stimulus;second-messenger-mediated signaling;signal transduction;spermatogenesis;transport;vesicle-mediated transport binding;protein binding;receptor binding cell part;cytoplasmic part;cytosol;endoplasmic reticulum;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment membrane;Golgi apparatus part;Golgi membrane;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;intrinsic to plasma membrane;lipid particle;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part Protein processing in endoplasmic reticulum 8.85E-51 6 14 14 40.2

O95786-2;O95786;B3KWW1;A2A376;F5H5W6 Probable ATP-dependent RNA helicase DDX58 DDX58 >sp|O95786-2|DDX58_HUMAN Isoform 2 of Probable ATP-dependent RNA helicase DDX58 OS=Homo sapiens GN=DDX58;>sp|O95786|DDX58_HUMAN Probable ATP-dependent RNA helicase DDX58 OS=Homo sapiens GN=DDX58 PE=1 SV=2;>tr|B3KWW1|B3KWW1_HUMAN Probable ATP-dependent RNA 0.13 0.06 0.08 -0.03 -1.29 -0.49 0.19 0.12 0.517043261 0.427622184 "biological regulation;defense response;detection of biotic stimulus;detection of external stimulus;detection of stimulus;detection of symbiont;detection of virus;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of type I interferon production;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cytokine production;positive regulation of defense response to virus by host;positive regulation of gene expression;positive regulation of interferon-alpha production;positive regulation of interferon-beta production;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of RNA metabolic process;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transcription factor import into nucleus;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of type I interferon production;regulation of biological process;regulation of biosynthetic process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine production;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by host;regulation of establishment of protein localization;regulation of gene expression;regulation of immune effector process;regulation of immune system process;regulation of interferon-alpha production;regulation of interferon-beta production;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal process;regulation of multi-organism process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription factor import into nucleus;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of type I interferon production;regulation of type III interferon production;reproductive process;response to biotic stimulus;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to external stimulus;response to organic substance;response to other organism;response to stimulus;response to stress;response to symbiont;response to virus;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;cation binding;DNA binding;double-stranded DNA binding;double-stranded RNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;single-stranded RNA binding;structure-specific DNA binding;transition metal ion binding;zinc ion binding" actin cytoskeleton;cell junction;cell part;cell projection membrane;cell projection part;cell-cell junction;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;leading edge membrane;membrane part;non-membrane-bounded organelle;occluding junction;organelle;plasma membrane part;ruffle membrane;tight junction Cytosolic DNA-sensing pathway;Hepatitis C;Measles;RIG-I-like receptor signaling pathway 5.91E-60 5 14 14 22

P38117;P38117-2;M0QY67 Electron transfer flavoprotein subunit beta ETFB >sp|P38117|ETFB_HUMAN Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3;>sp|P38117-2|ETFB_HUMAN Isoform 2 of Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB;>tr|M0QY67|M0QY67_HUMAN Electron transfer flavoprot -0.30 -0.20 0.02 0.18 0.18 0.23 0.27 -0.03 0.79253847 -0.23489378 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic processelectron carrier activity cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part 3.58E-60 3 14 14 48.6

Q14C86-4;Q14C86-5;Q14C86-2;Q14C86;Q14C86-6;F8W9S7;Q14C86-3;C9IZ08;B4DGD8;H0Y4E7;H0Y7I9;B0QZ65;C9IZX9 GTPase-activating protein and VPS9 domain-containing protein 1 GAPVD1>sp|Q14C86-4|GAPD1_HUMAN Isoform 4 of GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1;>sp|Q14C86-5|GAPD1_HUMAN Isoform 5 of GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1;>s 0.34 0.05 0.18 -0.16 -0.04 -0.13 0.24 -0.24 0.409826444 0.148653111 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;endocytosis;establishment of localization;membrane invagination;membrane organization;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of establishment of protein localization;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of protein transport;regulation of purine nucleotide catabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transport;response to stimulus;signal transduction;transport;vesicle-mediated transport binding;enzyme activator activity;enzyme regulator activity;GTPase activating protein binding;GTPase activator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;nucleoside-triphosphatase regulator activity;protein binding cell part;cytoplasmic part;cytosol;endosome;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle 6.38E-120 13 14 14 16.3

P78417;Q5TA02;P78417-3;P78417-2;Q5TA01 Glutathione S-transferase omega-1GSTO1 >sp|P78417|GSTO1_HUMAN Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2;>tr|Q5TA02|Q5TA02_HUMAN Glutathione S-transferase omega-1 (Fragment) OS=Homo sapiens GN=GSTO1 PE=2 SV=1;>sp|P78417-3|GSTO1_HUMAN Isoform 3 of Glutathione S-transfer 0.02 0.00 -0.31 -0.09 0.79 0.41 0.38 0.05 1.223952482 -0.499408219 biological regulation;calcium-mediated signaling;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;cellular response to arsenic-containing substance;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to stimulus;intracellular signal transduction;L-ascorbic acid metabolic process;metabolic process;negative regulation of biological process;negative regulation of ion transmembrane transporter activity;negative regulation of molecular function;negative regulation of ryanodine-sensitive calcium-release channel activity;negative regulation of transport;negative regulation of transporter activity;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of ion transmembrane transporter activity;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of ryanodine-sensitive calcium-release channel activity;positive regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion;positive regulation of striated muscle contraction;positive regulation of transport;positive regulation of transporter activity;regulation of biological process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cellular localization;regulation of cellular process;regulation of heart contraction;regulation of homeostatic process;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of ryanodine-sensitive calcium-release channel activity;regulation of skeletal muscle contraction;regulation of skeletal muscle contraction by calcium ion signaling;regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion;regulation of striated muscle contraction;regulation of system process;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to arsenic-containing substance;response to chemical stimulus;response to inorganic substance;response to stimulus;second-messenger-mediated signaling;signal transduction;small molecule metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process;xenobiotic catabolic process;xenobiotic metabolic process "antioxidant activity;catalytic activity;disulfide oxidoreductase activity;glutathione dehydrogenase (ascorbate) activity;glutathione disulfide oxidoreductase activity;glutathione transferase activity;methylarsonate reductase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, quinone or similar compound as acceptor;oxidoreductase activity, acting on phosphorus or arsenic in donors;oxidoreductase activity, acting on phosphorus or arsenic in donors, disulfide as acceptor;peptide disulfide oxidoreductase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Drug metabolism - cytochrome P450;Glutathione metabolism;Metabolism of xenobiotics by cytochrome P450 4.12E-42 5 14 14 49

Q96P70 Importin-9 IPO9 >sp|Q96P70|IPO9_HUMAN Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3 0.18 -0.01 0.00 -0.08 0.20 -0.17 0.28 -0.19 0.021539195 -0.008909924 establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;nuclear import;nuclear transport;nucleocytoplasmic transport;protein import;protein import into nucleus;protein targeting;protein transport;transport binding;histone binding;protein binding;protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;organelle part;pore complex;protein complex 3.23E-164 1 14 14 18.4

P52292;J3QLL0;J3KS65;J3QL07;A9QM74 Importin subunit alpha-2KPNA2 >sp|P52292|IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 0.63 0.42 -0.59 -0.09 -0.16 -0.59 -0.25 -0.69 0.727893561 0.515871922 biological regulation;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;DNA metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;G2 phase;G2 phase of mitotic cell cycle;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;M phase specific microtubule process;macromolecule metabolic process;metabolic process;microtubule-based process;multi-organism process;nitrogen compound metabolic process;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA recombination;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;signal transduction;transport;viral reproductive process;virus-host interaction binding;nuclear localization sequence binding;peptide binding;protein transporter activity;signal sequence binding;substrate-specific transporter activity;transporter activity cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part 0 5 14 14 33.6

Q3KQU3-4;Q3KQU3;Q3KQU3-2;Q3KQU3-3;H0YF21;C9JIR3;E9PLH3 MAP7 domain-containing protein 1 MAP7D1>sp|Q3KQU3-4|MA7D1_HUMAN Isoform 4 of MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1;>sp|Q3KQU3|MA7D1_HUMAN MAP7 domain-containing protein 1 OS=Homo sapiens GN=MAP7D1 PE=1 SV=1;>sp|Q3KQU3-2|MA7D1_HUMAN Isoform 2 of MAP7 domain-containing protei 0.04 0.57 -0.24 0.27 -0.36 0.33 -0.66 0.36 0.305706911 0.238633547 cell part;cytoplasm;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;spindle 2.42E-86 7 14 14 23.9

P40925;P40925-3;P40925-2;B9A041;B8ZZ51;C9JF79;C9JRL4;C9JLV6 "Malate dehydrogenase, cytoplasmic;Malate dehydrogenase" MDH1 ">sp|P40925|MDHC_HUMAN Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4;>sp|P40925-3|MDHC_HUMAN Isoform 3 of Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1;>sp|P40925-2|MDHC_HUMAN Isoform 2 of Malate dehydrogenase, cytoplasmic" 0.21 0.00 -0.01 -0.06 -0.12 -0.16 0.16 -0.15 0.445156902 0.104941184 acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;gluconeogenesis;glucose metabolic process;heterocycle metabolic process;hexose biosynthetic process;hexose metabolic process;malate metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;NAD metabolic process;NADH metabolic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxaloacetate metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule biosynthetic process;small molecule metabolic process;tricarboxylic acid cycle "binding;catalytic activity;coenzyme binding;cofactor binding;diiodophenylpyruvate reductase activity;L-malate dehydrogenase activity;malate dehydrogenase activity;malic enzyme activity;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;microtubule organizing center;mitochondrion;non-membrane-bounded organelle;organelle;organelle part Carbon fixation in photosynthetic organisms;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism;Proximal tubule bicarbonate reclamation;Pyruvate metabolism 4.26E-194 8 14 14 48.5

J3KSW8;Q6WCQ1-3;Q6WCQ1;Q6WCQ1-2;H0Y2S9;H0Y7E2;H7C3G6;J3QRL2;K7EL39 Myosin phosphatase Rho-interacting protein MPRIP >tr|J3KSW8|J3KSW8_HUMAN Myosin phosphatase Rho-interacting protein (Fragment) OS=Homo sapiens GN=MPRIP PE=4 SV=1;>sp|Q6WCQ1-3|MPRIP_HUMAN Isoform 3 of Myosin phosphatase Rho-interacting protein OS=Homo sapiens GN=MPRIP;>sp|Q6WCQ1|MPRIP_HUMAN Myosin phospha 0.10 1.09 0.27 1.03 0.12 0.91 -1.18 0.57 0.403070758 0.519564399 binding;lipid binding;phospholipid binding cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 1.11E-119 9 14 14 24.6

Q9Y2X3;H7BZ72;F8WED0 Nucleolar protein 58 NOP58 >sp|Q9Y2X3|NOP58_HUMAN Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 -0.55 1.10 0.13 1.18 -0.40 0.14 -1.47 0.11 0.661953948 0.868605385 cell growth;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;growth;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear import;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;snRNP protein import into nucleus;transport binding;nucleic acid binding;RNA binding;snoRNA binding box C/D snoRNP complex;Cajal body;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nucleolar part;nucleoplasm part;organelle part;pre-snoRNP complex;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes 8.48E-173 3 14 14 35

Q9UNZ2;Q9UNZ2-5;J3QK90;Q9UNZ2-4;Q9UNZ2-6;F2Z2K0;R4GNE6 NSFL1 cofactor p47 NSFL1C >sp|Q9UNZ2|NSF1C_HUMAN NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2;>sp|Q9UNZ2-5|NSF1C_HUMAN Isoform 3 of NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C;>tr|J3QK90|J3QK90_HUMAN NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=4 SV=1;>sp|Q9UNZ2-4|NSF0.24 -0.08 0.11 0.03 -0.35 -0.22 0.29 -0.25 0.546472203 0.208936134 binding;lipid binding cell part;chromosome;cytoplasmic part;Golgi apparatus part;Golgi stack;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part Protein processing in endoplasmic reticulum 4.36E-209 7 14 14 44.3

F5H5C2;Q8WUM0;Q5T8N1;Q5TDI3 Nuclear pore complex protein Nup133 NUP133 >tr|F5H5C2|F5H5C2_HUMAN Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=2 SV=1;>sp|Q8WUM0|NU133_HUMAN Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=1 SV=2;>tr|Q5T8N1|Q5T8N1_HUMAN Nuclear pore complex protein Nup133 OS=Ho 0.02 0.62 0.14 0.49 0.10 0.25 -0.59 0.14 0.612964784 0.342093005 anaphase;anatomical structure development;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular transport;M phase;M phase of mitotic cell cycle;macromolecular complex subunit organization;mesoderm development;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear export;nuclear pore organization;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;nucleus organization;organelle organization;organic substance transport;paraxial mesoderm development;primary metabolic process;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;tissue development;transmembrane transport;transport;viral reproductive process nucleocytoplasmic transporter activity;transporter activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane part;non-membrane-bounded organelle;nuclear part;Nup107-160 complex;organelle;organelle part;protein complex RNA transport 4.36E-96 4 14 14 16.9

O60568;H7C2V1;H7C2S8;H7C0B8;C9JIX5;H7C2A8;C9JU11 "Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3" PLOD3 ">sp|O60568|PLOD3_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1;>tr|H7C2V1|H7C2V1_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 (Fragment) OS=Homo sapiens GN=PLOD3 PE=4 SV=1" -0.34 -0.11 0.04 0.12 0.81 0.37 -0.40 -0.09 0.348984227 -0.24699769 anatomical structure development;anatomical structure morphogenesis;basement membrane assembly;basement membrane organization;biological regulation;cell morphogenesis;cell morphogenesis involved in differentiation;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to stimulus;chordate embryonic development;circulatory system process;collagen fibril organization;developmental process;embryo development;embryo development ending in birth or egg hatching;endothelial cell morphogenesis;epidermis morphogenesis;epithelial cell morphogenesis;extracellular matrix organization;extracellular structure organization;in utero embryonic development;localization;lung morphogenesis;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;neural tube development;organ morphogenesis;primary metabolic process;protein localization;protein metabolic process;protein modification process;regulation of anatomical structure size;regulation of biological quality;regulation of blood vessel size;regulation of tube size;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;system process;tissue morphogenesis;vascular process in circulatory system;vasodilation "binding;carboxylic acid binding;catalytic activity;cation binding;dioxygenase activity;galactosyltransferase activity;glucosyltransferase activity;ion binding;iron ion binding;L-ascorbic acid binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptidyl-lysine 5-dioxygenase activity;procollagen galactosyltransferase activity;procollagen glucosyltransferase activity;procollagen-lysine 5-dioxygenase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;transition metal ion binding;UDP-galactosyltransferase activity;UDP-glycosyltransferase activity;vitamin binding" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;rough endoplasmic reticulum membrane Lysine degradation;Other types of O-glycan biosynthesis 2.64E-71 7 14 14 25.2

P00491;G3V5M2;G3V2H3;G3V393 Purine nucleoside phosphorylase PNP >sp|P00491|PNPH_HUMAN Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2;>tr|G3V5M2|G3V5M2_HUMAN Purine nucleoside phosphorylase (Fragment) OS=Homo sapiens GN=PNP PE=2 SV=1 0.32 0.01 -0.17 -0.12 0.06 0.24 0.43 0.13 0.633423986 -0.204568149 biological regulation;biosynthetic process;catabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;cytokine secretion;establishment of localization;establishment of localization in cell;establishment of protein localization;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;immune response;immune system process;inosine catabolic process;inosine metabolic process;interleukin-2 secretion;metabolic process;NAD biosynthesis via nicotinamide riboside salvage pathway;NAD biosynthetic process;NAD metabolic process;nicotinamide nucleotide biosynthetic process;nicotinamide nucleotide metabolic process;nicotinamide riboside catabolic process;nicotinamide riboside metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside catabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide catabolic process;nucleotide metabolic process;organic acid metabolic process;oxidoreduction coenzyme metabolic process;positive regulation of alpha-beta T cell activation;positive regulation of alpha-beta T cell differentiation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of leukocyte proliferation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of lymphocyte proliferation;positive regulation of mononuclear cell proliferation;positive regulation of T cell activation;positive regulation of T cell differentiation;positive regulation of T cell proliferation;primary metabolic process;protein secretion;protein transport;purine base metabolic process;purine nucleoside catabolic process;purine nucleoside metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside catabolic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;purine-containing compound salvage;pyridine nucleoside catabolic process;pyridine nucleoside metabolic process;pyridine nucleotide biosynthetic process;pyridine nucleotide metabolic process;pyridine-containing compound biosynthetic process;pyridine-containing compound catabolic process;pyridine-containing compound metabolic process;regulation of alpha-beta T cell activation;regulation of alpha-beta T cell differentiation;regulation of biological process;regulation of cell activation;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of lymphocyte proliferation;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of T cell activation;regulation of T cell differentiation;regulation of T cell proliferation;response to chemical stimulus;response to drug;response to stimulus;ribonucleoside catabolic process;ribonucleoside metabolic process;secretion;secretion by cell;small molecule biosynthetic process;small molecule metabolic process;transport;urate biosynthetic process;urate metabolic process "anion binding;binding;catalytic activity;drug binding;ion binding;nucleobase binding;nucleoside binding;phosphate ion binding;purine base binding;purine-nucleoside phosphorylase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle Nicotinate and nicotinamide metabolism;Purine metabolism;Pyrimidine metabolism 2.71E-139 4 14 14 59.9

P23284 Peptidyl-prolyl cis-trans isomerase B PPIB >sp|P23284|PPIB_HUMAN Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 0.05 -0.12 -0.27 -0.19 0.59 0.04 0.50 0.13 1.225131178 -0.447184621 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;extracellular matrix organization;extracellular structure organization;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process binding;catalytic activity;cis-trans isomerase activity;isomerase activity;peptide binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;unfolded protein binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;vesicle 1.88E-141 1 14 14 55.6

O15355 Protein phosphatase 1G PPM1G >sp|O15355|PPM1G_HUMAN Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 0.14 0.08 -0.11 0.01 0.03 -0.36 -0.31 -0.41 1.083686438 0.292205955 biological regulation;cell cycle arrest;cell cycle process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;dephosphorylation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;peptidyl-threonine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of cell cycle;regulation of cellular process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.92E-69 1 14 14 35.9

Q9UNM6;Q9UNM6-2;J3KNQ3;E9PL38;H0YD73;E9PQG3 26S proteasome non-ATPase regulatory subunit 13 PSMD13 >sp|Q9UNM6|PSD13_HUMAN 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2;>sp|Q9UNM6-2|PSD13_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13;>tr|J3KNQ3|J3KNQ3_HUMAN 26S proteasom 0.01 0.07 -0.15 -0.01 -0.04 -0.12 -0.06 -0.24 0.59888334 0.093021578 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;meiosis I;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome regulatory particle;protein complex Proteasome 2.18E-122 6 14 14 43.9

Q16401;Q16401-2;F2Z3J2;Q4VXH0 26S proteasome non-ATPase regulatory subunit 5PSMD5 >sp|Q16401|PSMD5_HUMAN 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3;>sp|Q16401-2|PSMD5_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 0.10 -0.05 -0.09 -0.02 -0.31 -0.48 0.17 -0.41 0.68495491 0.244087465 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;proteasome assembly;proteasome regulatory particle assembly;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;protein complex 4.28E-147 4 14 14 38.1

Q06323;H0YNE3;Q06323-2;H0YKK6;H0YLU2 Proteasome activator complex subunit 1 PSME1 >sp|Q06323|PSME1_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1;>tr|H0YNE3|H0YNE3_HUMAN Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=2 SV=1;>sp|Q06323-2|PSME1_HUMAN Isoform 2 of Proteasome activator co -0.18 -0.12 0.01 0.09 -0.31 -0.31 0.09 -0.21 0.500628614 0.135632597 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome activator complex;proteasome complex;protein complex Antigen processing and presentation;Proteasome 7.37E-148 5 14 14 53

Q92696;H0YLH3;H0YLG7;H0YKZ8;H0YMG5;H0YKP6 Geranylgeranyl transferase type-2 subunit alpha RABGGTA >sp|Q92696|PGTA_HUMAN Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens GN=RABGGTA PE=1 SV=2;>tr|H0YLH3|H0YLH3_HUMAN Geranylgeranyl transferase type-2 subunit alpha OS=Homo sapiens GN=RABGGTA PE=2 SV=1;>tr|H0YLG7|H0YLG7_HUMAN Geranylgeranyl t 0.42 0.21 -0.14 -0.02 -0.27 -0.20 0.19 -0.52 0.694504986 0.316193522 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;neurological system process;primary metabolic process;protein geranylgeranylation;protein metabolic process;protein modification process;protein prenylation;sensory perception;sensory perception of light stimulus;system process;visual perception "binding;catalytic activity;cation binding;ion binding;metal ion binding;prenyltransferase activity;protein geranylgeranyltransferase activity;protein prenyltransferase activity;Rab geranylgeranyltransferase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups;transition metal ion binding;zinc ion binding" 5.08E-88 6 14 14 24

P13489;E9PMJ3;E9PLZ3;E9PIM9;H0YCR7;E9PMN0;E9PIK5;E9PMA9;E9PR82;E9PMI1 Ribonuclease inhibitor RNH1 >sp|P13489|RINI_HUMAN Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2 0.10 -0.10 -0.77 0.04 0.10 0.26 0.60 -0.22 0.597105765 -0.368801178 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;RNA catabolic process;RNA metabolic process enzyme inhibitor activity;enzyme regulator activity;ribonuclease inhibitor activity angiogenin-PRI complex;cell part;cytoplasm;extracellular region part;intracellular part;macromolecular complex;protein complex 1.97E-211 10 14 14 37.7

P62269;J3JS69 40S ribosomal protein S18 RPS18 >sp|P62269|RS18_HUMAN 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 0.13 -0.02 0.03 -0.04 -0.16 -0.60 -0.03 -0.28 0.989125125 0.293670471 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;collagen;cytosolic small ribosomal subunit;extracellular matrix part;extracellular region part;intracellular organelle part;intracellular part;macromolecular complex;organelle part;ribonucleoprotein complex;small ribosomal subunit Ribosome 8.10E-141 2 14 14 57.9

P39019;M0R2L9;M0QXK4;M0QYF7;M0R140 40S ribosomal protein S19 RPS19 >sp|P39019|RS19_HUMAN 40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 0.01 0.00 -0.16 0.09 -0.69 -0.87 -0.12 -0.40 1.210454204 0.505781378 "biological regulation;biosynthetic process;catabolic process;cell chemotaxis;cell differentiation;cell migration;cell motility;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to stimulus;chemotaxis;cotranslational protein targeting to membrane;developmental process;erythrocyte differentiation;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;immune system process;intracellular protein transport;intracellular transport;leukocyte chemotaxis;leukocyte migration;locomotion;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;maturation of SSU-rRNA;maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);metabolic process;monocyte chemotaxis;mRNA catabolic process;mRNA metabolic process;myeloid cell differentiation;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of defense response;negative regulation of immune effector process;negative regulation of immune response;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of innate immune response;negative regulation of metabolic process;negative regulation of multicellular organismal process;negative regulation of respiratory burst;negative regulation of respiratory burst involved in inflammatory response;negative regulation of response to external stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleolus organization;nucleus organization;organelle organization;positive regulation of biological process;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of defense response;positive regulation of immune effector process;positive regulation of immune response;positive regulation of immune system process;positive regulation of inflammatory response;positive regulation of innate immune response;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of respiratory burst;positive regulation of respiratory burst involved in inflammatory response;positive regulation of response to external stimulus;positive regulation of response to stimulus;primary metabolic process;protein complex assembly;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein oligomerization;protein targeting;protein targeting to ER;protein targeting to membrane;protein tetramerization;protein transport;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cellular component movement;regulation of cellular process;regulation of defense response;regulation of developmental process;regulation of immune effector process;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of innate immune response;regulation of localization;regulation of metabolic process;regulation of multicellular organismal process;regulation of respiratory burst;regulation of respiratory burst involved in inflammatory response;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;reproductive process;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;taxis;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;identical protein binding;protein binding;protein dimerization activity;protein homodimerization activity;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Ribosome 1.07E-43 5 14 14 62.8

Q15637-4;Q15637-6;Q15637-3;Q15637-2;Q15637;Q15637-5;Q15637-7;B4DX42;F8WEV5;C9J792;H7C561 Splicing factor 1 SF1 >sp|Q15637-4|SF01_HUMAN Isoform 4 of Splicing factor 1 OS=Homo sapiens GN=SF1;>sp|Q15637-6|SF01_HUMAN Isoform 6 of Splicing factor 1 OS=Homo sapiens GN=SF1;>sp|Q15637-3|SF01_HUMAN Isoform 3 of Splicing factor 1 OS=Homo sapiens GN=SF1;>sp|Q15637-2|SF01_HUMA -0.14 0.18 -0.07 0.21 -0.03 -0.16 -0.69 -0.31 0.883430031 0.342874491 "biological regulation;biosynthetic process;cell cycle process;cell differentiation;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;developmental process;developmental process involved in reproduction;Leydig cell differentiation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;male sex determination;metabolic process;mRNA splice site selection;nitrogen compound metabolic process;nuclear mRNA 3'-splice site recognition;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of steroid biosynthetic process;regulation of steroid metabolic process;regulation of transcription, DNA-dependent;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA biosynthetic process;RNA metabolic process;sex determination;transcription, DNA-dependent" binding;cation binding;ion binding;metal ion binding;nucleic acid binding;protein binding transcription factor activity;RNA binding;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;organelle;organelle part;ribonucleoprotein complex;ribosome;spliceosomal complex 2.98E-81 11 14 14 41.1

B4DIT7;P21980;F5H6P0;P21980-2;A2A299;P21980-3;A2A2A0 Protein-glutamine gamma-glutamyltransferase 2 TGM2 >tr|B4DIT7|B4DIT7_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=2 SV=1;>sp|P21980|TGM2_HUMAN Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2;>tr|F5H6P0|F5H6P0_HUMAN Protein-glutamine gamma-gl 0.84 -0.41 -0.38 -0.26 2.11 2.01 0.06 0.75 0.943641943 -1.284874617 anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;apoptotic cell clearance;biological regulation;blood vessel remodeling;branching involved in salivary gland morphogenesis;calcium ion homeostasis;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein metabolic process;chemical homeostasis;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion concentration;elevation of cytosolic calcium ion concentration involved in G-protein signaling coupled to IP3 second messenger;endocytosis;establishment of localization;homeostatic process;induction of apoptosis;induction of programmed cell death;ion homeostasis;isopeptide cross-linking;isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;metabolic process;metal ion homeostasis;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;peptide cross-linking;peptidyl-amino acid modification;peptidyl-glutamine modification;peptidyl-lysine modification;phagocytosis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of defense response;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of inflammatory response;positive regulation of intracellular protein kinase cascade;positive regulation of programmed cell death;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smooth muscle cell proliferation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein modification process;protein oligomerization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of defense response;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of inflammatory response;regulation of intracellular protein kinase cascade;regulation of programmed cell death;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of smooth muscle cell proliferation;salivary gland cavitation;tissue morphogenesis;tissue remodeling;transport;tube formation;tube lumen cavitation;vesicle-mediated transport "binding;catalytic activity;cation binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ion binding;metal ion binding;nucleotide binding;protein-glutamine gamma-glutamyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle;plasma membrane Huntington's disease 6.23E-97 7 14 14 28.2

P50552;K7EM16;K7ENR7;K7ENL7;K7EQD0;K7EIG8 Vasodilator-stimulated phosphoprotein VASP >sp|P50552|VASP_HUMAN Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3 -0.12 -0.16 0.05 -0.04 0.03 -0.30 0.05 -0.24 0.180118529 0.049611086 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin polymerization or depolymerization;activation of immune response;anatomical structure formation involved in morphogenesis;antigen receptor-mediated signaling pathway;axon guidance;biological regulation;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;neural tube closure;organelle organization;positive regulation of biological process;positive regulation of immune response;positive regulation of immune system process;positive regulation of response to stimulus;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;regulation of biological process;regulation of cellular process;regulation of immune response;regulation of immune system process;regulation of response to stimulus;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;T cell receptor signaling pathway;taxis;tube closure;tube formation actin cytoskeleton;adherens junction;anchoring junction;cell junction;cell part;cell projection membrane;cell projection part;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeleton;cytosol;filopodium membrane;focal adhesion;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium membrane;leading edge membrane;membrane;membrane part;non-membrane-bounded organelle;organelle;plasma membrane;plasma membrane part Fc gamma R-mediated phagocytosis;Focal adhesion;Leukocyte transendothelial migration 9.04E-83 6 14 14 46.3

B4DVE7;P50995;H0Y6E1;Q5T0G9 Annexin;Annexin A11 ANXA11 >tr|B4DVE7|B4DVE7_HUMAN Annexin OS=Homo sapiens GN=ANXA11 PE=2 SV=1;>sp|P50995|ANX11_HUMAN Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 0.34 -0.07 0.03 -0.13 0.37 -0.02 0.20 -0.43 0.022118324 0.013641003 "cell cycle;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cytokinesis, completion of separation;cytokinetic process;endocytosis;establishment of localization;membrane invagination;membrane organization;phagocytosis;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;transport;vesicle-mediated transport" binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;ion binding;lipid binding;metal ion binding;phosphatidylethanolamine binding;phospholipid binding azurophil granule;cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;endocytic vesicle;envelope;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lysosome;lytic vacuole;melanosome;membrane-bounded organelle;membrane-bounded vesicle;midbody;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleoplasm;organelle;organelle envelope;organelle part;phagocytic vesicle;pigment granule;primary lysosome;specific granule;spindle;stored secretory granule;vacuole;vesicle 6.94E-92 4 15 14 35.2

O75131;E5RG68;H0YB26;E5RHZ0;E5RJ85;E5RG97;E5RFT7;Q86VY2;Q7Z6C8;Q96A23;O95741;Q9UBL6-2;Q96A23-2;F5GXN1;Q9UBL6 Copine-3 CPNE3 >sp|O75131|CPNE3_HUMAN Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1;>tr|E5RG68|E5RG68_HUMAN Copine-3 (Fragment) OS=Homo sapiens GN=CPNE3 PE=2 SV=1 0.39 -0.09 -0.07 -0.08 0.36 0.11 0.45 -0.22 0.278349464 -0.135230619 anatomical structure development;cell communication;cell-cell signaling;cellular process;developmental process;establishment of localization;lipid metabolic process;metabolic process;nervous system development;primary metabolic process;signaling;synaptic transmission;system development;transport;vesicle-mediated transport "binding;calcium ion binding;calcium-dependent phospholipid binding;catalytic activity;cation binding;ion binding;kinase activity;lipid binding;metal ion binding;phosphatidylserine binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transporter activity" axon;cell body;cell part;cell projection;cytoplasmic part;cytosol;dendrite;intracellular part;membrane;neuron projection;neuronal cell body 1.86E-113 15 15 14 35

Q15691;Q9UPY8-2;Q15555-4;G5E9I6;Q15555-3;Q15555 Microtubule-associated protein RP/EB family member 1 MAPRE1>sp|Q15691|MARE1_HUMAN Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3 0.12 0.09 -0.24 -0.13 0.19 0.15 0.27 0.09 0.982186209 -0.216101624 anaphase;biological regulation;cell cycle phase;cell cycle process;cell division;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular process;cellular protein localization;cellular response to stimulus;G2/M transition of mitotic cell cycle;localization;M phase;M phase of mitotic cell cycle;macromolecule localization;mitosis;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of microtubule polymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein polymerization;nuclear division;organelle fission;organelle organization;protein localization;protein localization to microtubule;protein localization to organelle;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;signal transduction binding;cytoskeletal protein binding;microtubule binding;microtubule plus-end binding;protein binding;protein C-terminus binding;tubulin binding cell cortex part;cell part;cell projection membrane;cell projection part;centrosome;cortical cytoskeleton;cortical microtubule cytoskeleton;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;microtubule;microtubule cytoskeleton;microtubule organizing center;microtubule plus end;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;protein complex 2.04E-207 6 15 14 64.9

O95487-2;O95487;B7ZKM8 Protein transport protein Sec24B SEC24B >sp|O95487-2|SC24B_HUMAN Isoform 2 of Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B;>sp|O95487|SC24B_HUMAN Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2;>tr|B7ZKM8|B7ZKM8_HUMAN Protein transport protein Sec24B OS=Homo sa 0.22 -0.06 0.18 -0.30 -0.10 -0.04 0.32 -0.18 0.027107253 0.013459633 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;small molecule metabolic process;transport;vesicle coating;vesicle organization;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;transporter activity;zinc ion binding cell part;coated vesicle membrane;COPII vesicle coat;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;ER to Golgi transport vesicle membrane;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;transport vesicle membrane;vesicle coat;vesicle membrane Protein processing in endoplasmic reticulum 5.05E-112 3 15 14 16.4

Q96I24;Q96I24-2;REV__P16234-3 Far upstream element-binding protein 3 FUBP3 >sp|Q96I24|FUBP3_HUMAN Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2;>sp|Q96I24-2|FUBP3_HUMAN Isoform 2 of Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 0.08 0.44 0.07 0.34 0.12 0.35 -0.58 0.51 0.195778157 0.135370439 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;RNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 5.64E-94 3 17 14 40.6

P08237;P08237-3;P08237-2;F8VP00;F8VX13;F8VNX2;F8VZQ1;F8W1J8;F8VSF7;F8VW30;F8VSL1;F8VUB8;F8VTQ3;F8VYK8;F8VZI0;F8VVE3 "6-phosphofructokinase, muscle type" PFKM ">sp|P08237|K6PF_HUMAN 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2;>sp|P08237-3|K6PF_HUMAN Isoform 3 of 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM;>sp|P08237-2|K6PF_HUMAN Isoform 2 of 6-phosphofructokinase, muscle ty" 0.37 -0.01 -0.10 -0.16 0.05 -0.20 0.24 -0.28 0.152783037 0.070927456 alcohol catabolic process;alcohol metabolic process;anatomical structure homeostasis;biological regulation;carbohydrate catabolic process;carbohydrate homeostasis;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular metabolic process;cellular process;chemical homeostasis;fructose 6-phosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose homeostasis;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;muscle cell homeostasis;positive regulation of biological process;positive regulation of cellular process;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of secretion;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;small molecule catabolic process;small molecule metabolic process "6-phosphofructokinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate binding;carbohydrate kinase activity;catalytic activity;cation binding;fructose binding;ion binding;kinase activity;metal ion binding;monosaccharide binding;nucleotide binding;phosphofructokinase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;sugar binding;transferase activity;transferase activity, transferring phosphorus-containing groups" 6-phosphofructokinase complex;apical plasma membrane;cell part;cytoplasmic part;cytosolic part;intracellular part;macromolecular complex;membrane part;plasma membrane part;protein complex Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Methane metabolism;Pentose phosphate pathway 4.99E-161 16 19 14 30.8

O75116;E9PF63;D6REE7;C9J5G3;Q13449;H3BLU2;F5H5G1 Rho-associated protein kinase 2 ROCK2 >sp|O75116|ROCK2_HUMAN Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4;>tr|E9PF63|E9PF63_HUMAN Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=2 SV=1 0.17 0.00 -0.01 -0.03 0.38 0.28 0.17 -0.19 0.401611771 -0.130325366 actin cytoskeleton organization;actin filament-based process;anatomical structure development;anatomical structure formation involved in morphogenesis;axon guidance;biological adhesion;biological regulation;cell adhesion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;centrosome duplication;centrosome organization;chemotaxis;cytokinesis;cytoskeleton organization;developmental process;intracellular signal transduction;locomotion;microtubule organizing center organization;multicellular organismal process;muscle contraction;muscle system process;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of developmental process;nervous system development;neural tube closure;organelle organization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of centrosome duplication;positive regulation of organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament bundle assembly;regulation of actin filament-based process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of cell adhesion;regulation of cell cycle;regulation of cell cycle process;regulation of cell differentiation;regulation of cell motility;regulation of cell-matrix adhesion;regulation of cell-substrate adhesion;regulation of cell-substrate junction assembly;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of centrosome cycle;regulation of centrosome duplication;regulation of cytoskeleton organization;regulation of developmental process;regulation of epidermal cell differentiation;regulation of epidermis development;regulation of epithelial cell differentiation;regulation of establishment of cell polarity;regulation of establishment or maintenance of cell polarity;regulation of focal adhesion assembly;regulation of keratinocyte differentiation;regulation of localization;regulation of locomotion;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of organelle organization;regulation of stress fiber assembly;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;smooth muscle contraction;system development;system process;taxis;tube closure;tube formation "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;kinase activity;lipid binding;metal ion binding;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural molecule activity;transferase activity;transferase activity, transferring phosphorus-containing groups" anchored to membrane;cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;spindle pole centrosome Axon guidance;Chemokine signaling pathway;Focal adhesion;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis;TGF-beta signaling pathway;Vascular smooth muscle contraction;Wnt signaling pathway 5.15E-117 7 19 14 19.6

O15020-2;O15020;E9PJZ2 "Spectrin beta chain, non-erythrocytic 2" SPTBN2 ">sp|O15020-2|SPTN2_HUMAN Isoform 2 of Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2;>sp|O15020|SPTN2_HUMAN Spectrin beta chain, non-erythrocytic 2 OS=Homo sapiens GN=SPTBN2 PE=1 SV=3" 0.19 0.08 0.62 0.06 -0.34 0.19 -0.04 -0.47 0.870379274 0.403300286 actin filament capping;adult behavior;anatomical structure morphogenesis;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;behavior;biological regulation;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cerebellar Purkinje cell layer morphogenesis;chemotaxis;death;developmental process;establishment of localization;growth;immune system process;locomotion;multicellular organism growth;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein

polymerization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;synapse assembly;synapse organization;taxis;transport;vesicle-mediated transport actin binding;binding;cytoskeletal protein binding;lipid binding;phospholipid binding;protein binding;structural constituent of cytoskeleton;structural molecule activity cell body;cell cortex part;cell part;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;neuronal cell body;organelle part;spectrin 9.47E-86 3 20 14 11.8
Q92973-2;Q92973;Q92973-3;B4DSC0;E7EW37;K7ENW1;K7ESC1 Transportin-1 TNPO1 >sp|Q92973-2|TNPO1_HUMAN Isoform 2 of Transportin-1 OS=Homo sapiens GN=TNPO1;>sp|Q92973|TNPO1_HUMAN Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2;>sp|Q92973-3|TNPO1_HUMAN Isoform 3 of Transportin-1 OS=Homo sapiens GN=TNPO1 -0.04 -0.05 -0.19 -0.01 0.14 0.06 0.03 -0.12 0.603092352 -0.096612517 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;gene expression;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mRNA metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein import into nucleus, translocation;protein transport;reproductive process;RNA metabolic process;transport;viral reproductive process;virus-host interaction" binding;nuclear localization sequence binding;peptide binding;protein transporter activity;signal sequence binding;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;nuclear part;nuclear pore;nucleus;organelle;organelle part;pore complex;protein complex 2.80E-86 7 20 14 30.8
O94973;O94973-2;O94973-3;E9PR62;H0YEG0;H0YDE9;E9PNC4 AP-2 complex subunit alpha-2 AP2A2 >sp|O94973|AP2A2_HUMAN AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2;>sp|O94973-2|AP2A2_HUMAN Isoform 2 of AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2;>sp|O94973-3|AP2A2_HUMAN Isoform 3 of AP-2 complex subunit alpha-2 OS=Homo sa -0.21 0.01 -0.16 0.11 0.29 0.32 0.01 0.16 1.056408146 -0.256401944 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;endocytosis;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;immune system process;intracellular protein transport;intracellular transport;locomotion;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of epidermal growth factor receptor signaling pathway;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;synaptic transmission;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport;viral reproduction binding;lipid binding;protein transporter activity;substrate-specific transporter activity;transporter activityAP-2 adaptor complex;AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;cytoplasmic part;cytoplasmic vesicle part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;plasma membrane part;protein complex Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease 3.60E-175 7 23 14 36.7
Q13310-2;Q13310-3;B1ANR0;Q13310;H0Y5F5;H0YCC8;H0YEU6;H0YEQ8;B1ANR1;H0Y6X6;H0YER0 Polyadenylate-binding protein 4 PABPC4 ">sp|Q13310-2|PABP4_HUMAN Isoform 2 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4;>sp|Q13310-3|PABP4_HUMAN Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4;>tr|B1ANR0|B1ANR0_HUMAN Poly(A) binding protein, cytoplasmic 4 (" 0.12 0.09 0.03 -0.11 -0.09 -0.49 -0.21 -0.66 1.163335742 0.395428197 biological regulation;biosynthetic process;blood coagulation;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;coagulation;hemostasis;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein metabolic process;regulation of biological quality;regulation of body fluid levels;RNA catabolic process;RNA metabolic process;RNA processing;translation binding;mRNA binding;nucleic acid binding;nucleotide binding;poly(A) RNA binding;poly(U) RNA binding;poly-purine tract binding;poly-pyrimidine tract binding;RNA binding;single-stranded RNA binding cell part;cytoplasm;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;ribonucleoprotein complex;RNA granule;stress granule mRNA surveillance pathway;RNA degradation;RNA transport 1.07E-270 11 26 14 41.2
Q9UG63;Q75MJ1;C9JHK9;C9JZV3 ATP-binding cassette sub-family F member 2 ABCF2 >sp|Q9UG63|ABCF2_HUMAN ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=1 SV=2;>tr|Q75MJ1|Q75MJ1_HUMAN ATP-binding cassette sub-family F member 2 OS=Homo sapiens GN=ABCF2 PE=2 SV=1;>tr|C9JHK9|C9JHK9_HUMAN ATP-binding cassette sub-fami 0.07 0.01 0.02 -0.10 0.01 -0.24 0.19 -0.09 0.110358459 0.030408929 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transporter activity" ATP-binding cassette (ABC) transporter complex;cell part;cytoplasmic part;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;mitochondrial envelope;mitochondrial part;mitochondrion;organelle;organelle envelope;organelle part;protein complex 1.15E-52 4 15 15 25
Q9BWD1;B7Z233 "Acetyl-CoA acetyltransferase, cytosolic" ACAT2 ">sp|Q9BWD1|THIC_HUMAN Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2;>tr|B7Z233|B7Z233_HUMAN Sterol O-acyltransferase 2 OS=Homo sapiens GN=ACAT2 PE=2 SV=1" 0.18 0.00 -0.07 -0.07 -0.38 -0.42 0.23 0.05 0.328885387 0.141924028 lipid metabolic process;metabolic process;primary metabolic process "acetyl-CoA C-acetyltransferase activity;acetyl-CoA C-acyltransferase activity;acetyltransferase activity;C-acetyltransferase activity;C-acyltransferase activity;catalytic activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part "Benzoate degradation;Butanoate metabolism;Carbon fixation pathways in prokaryotes;Fatty acid metabolism;Glyoxylate and dicarboxylate metabolism;Lysine degradation;Propanoate metabolism;Pyruvate metabolism;Synthesis and degradation of ketone bodies;Terpenoid backbone biosynthesis;Tryptophan metabolism;Two-component system;Valine, leucine and isoleucine degradation" 5.87E-200 2 15 15 50.1
P40121;P40121-2;E7ENU9;B8ZZL6;H7C0X8;REV__B8ZZL6;REV__E7ENU9;REV__P40121-2;REV__P40121 Macrophage-capping protein CAPG >sp|P40121|CAPG_HUMAN Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2;>sp|P40121-2|CAPG_HUMAN Isoform 2 of Macrophage-capping protein OS=Homo sapiens GN=CAPG;>tr|E7ENU9|E7ENU9_HUMAN Condensin complex subunit 3 (Fragment) OS=Homo sapiens GN=CAP -0.09 -0.26 0.27 0.13 0.33 0.14 0.39 -0.10 0.458501696 -0.179426527 actin filament capping;barbed-end actin filament capping;biological regulation;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of

cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;protein complex assembly;protein complex subunit organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;F-actin capping protein complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;nucleus;organelle;organelle membrane;organelle part;pigment granule;protein complex;vesicle 4.61E-156 9 15 15 52.6

P49589-3;P49589-2;B4DKY1;P49589;A8MVQ3;E9PLP0;C9JLN0;E9PRS8 "Cysteine--tRNA ligase, cytoplasmic" CARS ">sp|P49589-3|SYCC_HUMAN Isoform 3 of Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS;>sp|P49589-2|SYCC_HUMAN Isoform 2 of Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS;>tr|B4DKY1|B4DKY1_HUMAN Cysteine--tRNA ligase, cytoplasmic OS=Ho" -0.14 -0.17 0.13 0.00 0.15 -0.08 0.30 0.02 0.558237063 -0.143514151 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cysteinyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;cation binding;cysteine-tRNA ligase activity;identical protein binding;ion binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;metal ion binding;nucleic acid binding;nucleotide binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Aminoacyl-tRNA biosynthesis 3.42E-56 8 15 15 23.5

Q16543;K7EQA9;K7EKQ2;K7EL68;K7EIU0 Hsp90 co-chaperone Cdc37 CDC37 >sp|Q16543|CDC37_HUMAN Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1;>tr|K7EQA9|K7EQA9_HUMAN Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens GN=CDC37 PE=4 SV=1;>tr|K7EKQ2|K7EKQ2_HUMAN Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens GN 0.08 0.03 -0.09 -0.05 0.02 -0.03 0.23 0.01 0.394996155 -0.066531987 biological regulation;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein targeting;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-gamma-mediated signaling pathway;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of type I interferon-mediated signaling pathway;transport binding;protein binding;unfolded protein binding cell part;cell projection membrane;cell projection part;cytoplasmic part;cytosol;intracellular part;leading edge membrane;macromolecular complex;membrane part;plasma membrane part;protein complex;ruffle membrane 2.61E-198 5 15 15 41.5

Q13618-2;Q13618;Q13618-3;H7C1L6;H7C399 Cullin-3 CUL3 >sp|Q13618-2|CUL3_HUMAN Isoform 2 of Cullin-3 OS=Homo sapiens GN=CUL3;>sp|Q13618|CUL3_HUMAN Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2;>sp|Q13618-3|CUL3_HUMAN Isoform 3 of Cullin-3 OS=Homo sapiens GN=CUL3 0.20 0.15 -0.04 -0.06 0.17 0.13 0.23 -0.04 0.273361167 -0.062077577 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;anaphase;anatomical structure morphogenesis;biological regulation;catabolic process;cell cycle arrest;cell cycle phase;cell cycle process;cell division;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;COPII vesicle coating;cyclin catabolic process;cytokinesis;cytoskeleton organization;developmental process;embryonic cleavage;embryonic morphogenesis;G1/S transition of mitotic cell cycle;gastrulation;integrin-mediated signaling pathway;locomotion;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cellular process;negative regulation of Ras protein signal transduction;negative regulation of response to stimulus;negative regulation of Rho protein signal transduction;negative regulation of signal transduction;negative regulation of signaling;negative regulation of small GTPase mediated signal transduction;organelle organization;positive regulation of biological process;positive regulation of cell division;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of cytokinesis;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cell communication;regulation of cell cycle;regulation of cell division;regulation of cell proliferation;regulation of cellular process;regulation of cytokinesis;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;signal transduction;stem cell division;stress fiber assembly;trophectodermal cellular morphogenesis;ubiquitin-dependent protein catabolic process;vesicle coating;vesicle organization;Wnt receptor signaling pathway binding;POZ domain binding;protein binding;protein domain specific binding cell part;Cul3-RING ubiquitin ligase complex;cullin-RING ubiquitin ligase complex;cytoplasmic part;cytoskeletal part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;nucleus;organelle;organelle part;polar microtubule;protein complex;spindle microtubule;ubiquitin ligase complex Ubiquitin mediated proteolysis 2.79E-65 5 15 15 20.2

Q86XP3;Q86XP3-2;J3QRI2;J3KTK9;J3KRE3 ATP-dependent RNA helicase DDX42 DDX42 >sp|Q86XP3|DDX42_HUMAN ATP-dependent RNA helicase DDX42 OS=Homo sapiens GN=DDX42 PE=1 SV=1;>sp|Q86XP3-2|DDX42_HUMAN Isoform 2 of ATP-dependent RNA helicase DDX42 OS=Homo sapiens GN=DDX42 -0.01 0.13 0.04 0.06 0.11 -0.23 -0.61 -0.46 0.94138969 0.350112933 localization;macromolecule localization;protein localization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding" Cajal body;cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;nucleus;organelle;organelle part Spliceosome 1.38E-73 5 15 15 26.7

Q15056-2;Q15056;K7EJP0;Q9NYK1 Eukaryotic translation initiation factor 4H EIF4H >sp|Q15056-2|IF4H_HUMAN Isoform Short of Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H;>sp|Q15056|IF4H_HUMAN Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5 0.17 0.03 0.13 -0.08 0.14 -0.09 0.01 -0.07 0.345986095 0.064791207 activation of immune response;activation of innate immune response;biological regulation;cell activation;cell activation involved in immune response;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to abiotic stimulus;cellular response to external stimulus;cellular response to mechanical stimulus;cellular response to stimulus;defense response;defense response to virus;developmental growth;developmental process;growth;I-kappaB phosphorylation;immune effector process;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;inflammatory response;innate immune response;innate immune response-activating signal transduction;interaction with host;interspecies interaction between organisms;leukocyte activation;leukocyte activation involved in immune response;macromolecule metabolic process;macromolecule modification;macrophage activation;macrophage activation involved in immune response;metabolic process;microglial cell activation;microglial cell activation involved in immune response;modification by symbiont of host morphology or physiology;modification of morphology or physiology of other organism;modification of morphology or physiology of other organism involved in symbiotic interaction;modulation by organism of defense response of other organism involved in symbiotic interaction;modulation by organism of immune response of other organism involved in symbiotic interaction;modulation by organism of innate immunity in other organism involved in symbiotic interaction;modulation by symbiont of host defense response;modulation by symbiont of host immune response;modulation by symbiont of host innate immunity;multi-organism process;MyD88-dependent toll-like receptor signaling pathway;myeloid cell activation involved in immune response;myeloid leukocyte activation;pathogen-associated molecular pattern dependent induction by organism of innate immunity of other organism involved in symbiotic interaction;pathogen-associated molecular pattern dependent induction by symbiont of host innate immunity;pathogen-associated molecular pattern dependent modulation by organism of innate immunity in other organism involved in symbiotic interaction;pathogen-associated molecular pattern dependent modulation by symbiont of host innate immunity;pattern recognition receptor signaling pathway;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation by organism of defense response of other organism involved in symbiotic interaction;positive regulation by organism of immune response of other organism involved in symbiotic interaction;positive regulation by organism of innate immunity in other organism involved in symbiotic interaction;positive regulation by symbiont of host defense response;positive regulation by symbiont of host immune response;positive regulation by symbiont of host innate immunity;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of chemokine production;positive regulation of cytokine biosynthetic process;positive regulation of cytokine production;positive regulation of defense response;positive regulation of immune response;positive regulation of immune system process;positive regulation of inflammatory response;positive regulation of innate immune response;positive regulation of interferon-alpha biosynthetic process;positive regulation of interferon-beta biosynthetic process;positive regulation of interferon-gamma biosynthetic process;positive regulation of interleukin-6 production;positive regulation of interleukin-8 biosynthetic process;positive regulation of interleukin-8 production;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of NF-kappaB import into nucleus;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein metabolic process;positive regulation of protein transport;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of transcription factor import into nucleus;positive regulation of transmembrane transport;positive regulation of transport;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemokine production;regulation of cytokine biosynthetic process;regulation of cytokine production;regulation of defense response;regulation of establishment of protein localization;regulation of gene expression;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of innate immune response;regulation of interferon-alpha biosynthetic process;regulation of interferon-alpha production;regulation of interferon-beta biosynthetic process;regulation of interferon-beta production;regulation of interferon-gamma biosynthetic process;regulation of interferon-gamma production;regulation of interleukin-6 production;regulation of interleukin-8 biosynthetic process;regulation of interleukin-8 production;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of NF-kappaB import into nucleus;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of transcription factor import into nucleus;regulation of translation;regulation of translational initiation;regulation of transmembrane transport;regulation of transport;regulation of type I interferon production;reproduction;reproductive process;response to abiotic stimulus;response to biotic stimulus;response to chemical stimulus;response to defenses of other organism involved in symbiotic interaction;response to external stimulus;response to host;response to host defenses;response to host immune response;response to immune response of other organism involved in symbiotic interaction;response to mechanical stimulus;response to other organism;response to stimulus;response to stress;response to virus;response to wounding;sexual reproduction;signal transduction;toll-like receptor 7 signaling pathway;toll-like receptor 9 signaling pathway;toll-like receptor signaling pathway;viral reproductive process;virus-host interaction "binding;double-stranded RNA binding;drug binding;molecular transducer activity;nucleic acid binding;nucleotide binding;receptor activity;RNA binding;signal transducer activity;signaling receptor activity;single-stranded RNA binding;siRNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity;transmembrane signaling receptor activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;early phagosome;endocytic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;eukaryotic translation initiation factor 4F complex;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;phagocytic vesicle;plasma membrane;protein complex;vesicle Measles;Toll-like receptor signaling pathway 2.62E-137 4 15 15 61.8

P13804;P13804-2;H0YLU7;H0YK49;H0YL12;H0YNX6;H0YKF0;H0YL83;H0YM12;J3KN60 "Electron transfer flavoprotein subunit alpha, mitochondrial" ETFA ">sp|P13804|ETFA_HUMAN Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1;>sp|P13804-2|ETFA_HUMAN Isoform 2 of Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA;>tr|H0YLU7|H0YLU7_H" -0.33 -0.14 0.07 0.16 0.12 0.30 0.13 0.13 0.82872087 -0.22924751 cellular metabolic process;cellular process;electron transport chain;generation of precursor metabolites and energy;metabolic process;oxidation-reduction process;respiratory electron transport chain;small molecule metabolic process binding;catalytic activity;coenzyme binding;cofactor binding;electron carrier activity;flavin adenine dinucleotide binding;oxidoreductase activity cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part 4.36E-171 10 15 15 65.5

P30519;I3L430;I3L159;I3L1F5;I3L1Y2;I3L276;I3L4P8;I3L463Heme oxygenase 2 HMOX2 >sp|P30519|HMOX2_HUMAN Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2;>tr|I3L430|I3L430_HUMAN Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=2 SV=1;>tr|I3L159|I3L159_HUMAN Heme oxygenase 2 (Fragment) OS=Homo sapiens GN=HMOX2 PE=2 SV=1;>tr|I3L1F5|I3L1F5_-0.13 0.10 -0.12 0.02 -0.20 0.18 -0.09 0.14 0.151371859 -0.044607964 biological regulation;catabolic process;cation homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;cofactor catabolic process;cofactor metabolic process;establishment of localization;heme catabolic process;heme metabolic process;heme oxidation;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;ion homeostasis;iron ion homeostasis;metabolic process;metal ion homeostasis;nitrogen compound metabolic process;oxidation-reduction process;pigment catabolic process;pigment metabolic process;porphyrin-containing compound catabolic process;porphyrin-containing compound metabolic process;regulation of biological quality;response to chemical stimulus;response to hypoxia;response to oxidative stress;response to oxygen levels;response to stimulus;response to stress;small molecule metabolic process;tetrapyrrole catabolic process;tetrapyrrole metabolic process;transmembrane transport;transport "binding;catalytic activity;cation binding;heme oxygenase (decyclizing) activity;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;membrane;membrane part;organelle membrane;organelle part;plasma membrane Mineral absorption;Porphyrin and chlorophyll metabolism 4.69E-173 8 15 15 57.6

O14896;O14896-2;B1AJU4 Interferon regulatory factor 6 IRF6 >sp|O14896|IRF6_HUMAN Interferon regulatory factor 6 OS=Homo sapiens GN=IRF6 PE=1 SV=1;>sp|O14896-2|IRF6_HUMAN Isoform 2 of Interferon regulatory factor 6 OS=Homo sapiens GN=IRF6 0.36 0.07 0.22 -0.04 -1.23 -0.37 0.31 0.01 0.575472404 0.470379536 "anatomical structure development;biological regulation;biosynthetic process;cell cycle arrest;cell cycle process;cell development;cell differentiation;cell proliferation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cellular response to type I interferon;cytokine-mediated signaling pathway;developmental process;epidermal cell differentiation;epidermis development;epithelial cell differentiation;interferon-gamma-mediated signaling pathway;keratinocyte differentiation;keratinocyte proliferation;macromolecule biosynthetic process;macromolecule metabolic process;mammary gland epithelial cell differentiation;metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell proliferation;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;response to type I interferon;RNA biosynthetic process;RNA metabolic process;signal transduction;skin development;tissue development;transcription, DNA-dependent;type I interferon-mediated signaling pathway" binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding transcription factor activity cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.24E-157 3 15 15 39.8

P01130-3;P01130-6;P01130-4;P01130;J3KMZ9;P01130-2;P01130-5;H0YMD1;H0YM92;H0YMQ3;E9PP15;Q14114-2;Q14114-4;Q14114-3;Q14114 Low-density lipoprotein receptor LDLR >sp|P01130-3|LDLR_HUMAN Isoform 3 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR;>sp|P01130-6|LDLR_HUMAN Isoform 6 of Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR;>sp|P01130-4|LDLR_HUMAN Isoform 4 of Low-density lipoprotein recepto0.31 0.28 -0.20 0.09 -0.64 -0.08 0.00 0.14 0.523844713 0.260185578 "alcohol metabolic process;ammon gyrus development;anatomical structure development;anatomical structure formation involved in morphogenesis;biological regulation;blood coagulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cholesterol homeostasis;cholesterol import;cholesterol metabolic process;cholesterol transport;coagulation;cytokine-mediated signaling pathway;detection of abiotic stimulus;detection of external stimulus;detection of light stimulus;detection of stimulus;detection of visible light;developmental process;digestive system process;diterpenoid metabolic process;establishment of localization;hemostasis;homeostatic process;interaction with host;interspecies interaction between organisms;intestinal absorption;intestinal cholesterol absorption;isoprenoid metabolic process;layer formation in cerebral cortex;lipid homeostasis;lipid metabolic process;lipid transport;lipoprotein catabolic process;lipoprotein metabolic process;low-density lipoprotein particle clearance;macromolecule catabolic process;macromolecule metabolic process;metabolic process;multicellular organismal process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;organic substance transport;phospholipid transport;phototransduction;phototransduction, visible light;plasma lipoprotein particle clearance;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of CREB transcription factor activity;positive regulation of dendritic spine development;positive regulation of dendritic spine morphogenesis;positive regulation of developmental process;positive regulation of kinase activity;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of protein tyrosine kinase activity;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of transferase activity;positive regulation of triglyceride biosynthetic process;positive regulation of triglyceride metabolic process;primary metabolic process;protein metabolic process;proteolysis;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular amine metabolic process;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of dendritic spine development;regulation of dendritic spine morphogenesis;regulation of developmental process;regulation of gene expression;regulation of kinase activity;regulation of lipid biosynthetic process;regulation of lipid catabolic process;regulation of lipid metabolic process;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphatidylcholine catabolic process;regulation of phospholipid catabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein tyrosine kinase activity;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signaling;regulation of synaptic transmission;regulation of system process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of transmission of nerve impulse;regulation of triglyceride biosynthetic process;regulation of triglyceride metabolic process;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to light stimulus;response to organic substance;response to radiation;response to stimulus;retinoid metabolic process;signal transduction;small molecule metabolic process;steroid metabolic process;sterol homeostasis;sterol import;sterol metabolic process;sterol transmembrane transport;sterol transport;system process;terpenoid metabolic process;transmembrane transport;transport;viral reproductive process;virus-host interaction" apolipoprotein binding;binding;calcium ion binding;cargo receptor activity;cation binding;ion binding;lipoprotein particle binding;lipoprotein particle receptor activity;low-density lipoprotein particle binding;low-density lipoprotein receptor activity;metal ion binding;molecular transducer activity;protein binding;protein-lipid complex binding;receptor activity;reelin receptor activity;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity;very-low-density lipoprotein particle binding;very-low-density lipoprotein particle receptor activity caveola;cell part;clathrin coated vesicle membrane;clathrin-coated endocytic vesicle membrane;coated pit;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;early endosome;endocytic vesicle membrane;endosomal part;endosome;endosome membrane;external side of plasma membrane;extracellular region;extracellular region part;Golgi apparatus;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;late endosome;low-density lipoprotein particle;lysosome;lytic vacuole;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma lipoprotein particle;plasma membrane part;protein-lipid complex;vacuole;vesicle membrane Bile secretion;Endocytosis;Hepatitis C;Toxoplasmosis 3.87E-152 15 15 15 27.3

Q96AG4;I3L223 Leucine-rich repeat-containing protein 59 LRRC59 >sp|Q96AG4|LRC59_HUMAN Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 -0.01 -0.04 -0.15 0.06 0.40 0.08 -0.21 0.04 0.325501773 -0.108458883 cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleoid;organelle;organelle envelope;organelle membrane;organelle part 3.85E-111 2 15 15 42

Q16706 Alpha-mannosidase 2 MAN2A1 >sp|Q16706|MA2A1_HUMAN Alpha-mannosidase 2 OS=Homo sapiens GN=MAN2A1 PE=1 SV=2 0.08 0.24 -0.18 -0.03 0.56 0.78 -0.24 0.29 0.567677718 -0.318559546 alcohol metabolic process;anatomical structure development;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;glycosylation;hexose metabolic process;in utero embryonic development;liver development;lung alveolus development;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;mannose metabolic process;metabolic process;mitochondrion organization;monosaccharide metabolic process;multicellular organismal process;N-glycan processing;oligosaccharide metabolic process;organ development;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;respiratory gaseous exchange;small molecule metabolic process;vacuole organization "binding;carbohydrate binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing N-glycosyl compounds;hydrolase activity, hydrolyzing O-glycosyl compounds;ion binding;mannosidase activity;mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity;mannosyl-oligosaccharide mannosidase activity;metal ion binding;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part N-Glycan biosynthesis;Various types of N-glycan biosynthesis 6.56E-59 1 15 15 16.5

Q86UE4;E5RJU9;H0YB56;H0YBJ8 Protein LYRIC MTDH >sp|Q86UE4|LYRIC_HUMAN Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2;>tr|E5RJU9|E5RJU9_HUMAN Protein LYRIC OS=Homo sapiens GN=MTDH PE=2 SV=1 -0.60 0.01 0.01 0.07 0.37 0.23 -0.67 -0.10 0.113218944 -0.089346073 "biological regulation;cell junction assembly;cell junction organization;cell surface receptor linked signaling pathway;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to biotic stimulus;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to stimulus;lipopolysaccharide-mediated signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;positive regulation of angiogenesis;positive regulation of autophagy;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of developmental process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of protein kinase B signaling cascade;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of autophagy;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cell communication;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to biotic stimulus;response to chemical stimulus;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to stimulus;signal transduction;tight junction assembly" protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity apical plasma membrane;cell junction;cell part;cell-cell junction;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intercellular canaliculus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear membrane;nuclear part;nucleolus;nucleoplasm part;occluding junction;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;tight junction 2.28E-136 4 15 15 33.2

E7ESU4;Q9H0A0 N-acetyltransferase 10 NAT10 >tr|E7ESU4|E7ESU4_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=2 SV=1;>sp|Q9H0A0|NAT10_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2 -0.07 1.01 -0.12 0.85 -0.56 0.05 -1.20 0.21 0.776194025 0.794215211 "acetyltransferase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;N-acetyltransferase activity;N-acyltransferase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part Ribosome biogenesis in eukaryotes 2.50E-86 2 15 15 23

Q02818;H7BZI1;C9JKZ2;C9JBD3;C9J3C1 Nucleobindin-1 NUCB1 >sp|Q02818|NUCB1_HUMAN Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4;>tr|H7BZI1|H7BZI1_HUMAN Nucleobindin-1 (Fragment) OS=Homo sapiens GN=NUCB1 PE=4 SV=1;>tr|C9JKZ2|C9JKZ2_HUMAN Nucleobindin-1 (Fragment) OS=Homo sapiens GN=NUCB1 PE=2 SV=1 0.07 -0.04 -0.32 -0.01 0.65 0.29 0.21 -0.36 0.50309582 -0.273218923 binding;calcium ion binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding cell part;cytoplasmic part;cytoskeleton;endoplasmic reticulum-Golgi intermediate compartment;extracellular region part;extracellular space;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-bounded organelle;organelle 4.64E-65 5 15 15 37.5

O60313;E5KLJ6;O60313-2;E5KLJ5;E5KLK1;E5KLJ9;H7C321;C9JY58;H7C3G2;H7C141;C9JMB8 "Dynamin-like 120 kDa protein, mitochondrial;Dynamin-like 120 kDa protein, form S1" OPA1 ">sp|O60313|OPA1_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3;>tr|E5KLJ6|E5KLJ6_HUMAN Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=2 SV=1;>sp|O60313-2|OPA1_HUMAN Isoform 2 of Dynamin-like 120" -0.20 -0.11 0.18 0.08 0.03 0.10 0.00 0.26 0.431709384 -0.110831746 aging;anatomical structure formation involved in morphogenesis;apoptosis;axon cargo transport;axon transport of mitochondrion;biological regulation;catabolic process;cell aging;cell death;cellular catabolic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;cellular senescence;cytoskeleton-dependent intracellular transport;death;developmental process;establishment of localization;establishment of localization in cell;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;inner mitochondrial membrane organization;intracellular transport;membrane fusion;membrane organization;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrial fission;mitochondrial fusion;mitochondrial membrane organization;mitochondrion organization;multicellular organismal process;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of mitochondrion organization;negative regulation of organelle organization;negative regulation of release of cytochrome c from mitochondria;neural tube closure;neurological system process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle fission;organelle fusion;organelle organization;primary metabolic process;programmed cell death;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component organization;regulation of cellular process;regulation of mitochondrion organization;regulation of organelle organization;regulation of programmed cell death;regulation of release of cytochrome c from mitochondria;response to stimulus;response to stress;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;sensory perception;sensory perception of light stimulus;small molecule metabolic process;system process;transport;tube closure;tube formation;visual perception "binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;magnesium ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cell projection;cytoplasmic part;dendrite;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-enclosed lumen;mitochondrial crista;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial membrane;mitochondrial membrane part;mitochondrial outer membrane;mitochondrial part;neuron projection;organelle envelope lumen;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane 5.80E-51 11 15 15 23.3

Q14690 Protein RRP5 homolog PDCD11 >sp|Q14690|RRP5_HUMAN Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 -0.12 1.02 0.05 0.79 -0.52 0.00 -0.99 0.28 0.803668979 0.741947529 cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part 4.02E-67 1 15 15 12.8

O43175;Q5SZU1 D-3-phosphoglycerate dehydrogenase PHGDH >sp|O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4;>tr|Q5SZU1|Q5SZU1_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=2 SV=1 -0.34 -0.60 0.15 0.05 -0.22 -1.11 0.04 -1.03 0.48460268 0.391713404 amine biosynthetic process;amine metabolic process;anatomical structure development;aspartate family amino acid metabolic process;biological regulation;biosynthetic process;brain development;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cell cycle process;cell development;cell projection organization;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;developmental process;gamma-aminobutyric acid metabolic process;glial cell development;glutamine family amino acid metabolic process;glutamine metabolic process;glycine metabolic process;L-serine biosynthetic process;L-serine metabolic process;metabolic process;neural tube development;neuron projection development;nitrogen compound metabolic process;organ development;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of biological process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;serine family amino acid biosynthetic process;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule metabolic process;spinal cord development;sulfur compound metabolic process;taurine metabolic process;threonine metabolic process "binding;catalytic activity;coenzyme binding;cofactor binding;electron carrier activity;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;phosphoglycerate dehydrogenase activity" cell part;cytoplasmic part;cytosol;intracellular part "Glycine, serine and threonine metabolism;Methane metabolism" 1.02E-236 2 15 15 32.6

Q02809;B4DR87;Q5JXB9;Q5JXB8;Q5JXB7 "Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1" PLOD1 ">sp|Q02809|PLOD1_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2;>tr|B4DR87|B4DR87_HUMAN Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=2 SV=1" -0.42 0.02 -0.14 0.16 1.23 0.91 -0.10 0.66 1.049228407 -0.770614917 amine biosynthetic process;amine metabolic process;anatomical structure development;aspartate family amino acid biosynthetic process;aspartate family amino acid metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;hydroxylysine biosynthetic process;hydroxylysine metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;protein metabolic process;protein modification process;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;small molecule biosynthetic process;small molecule metabolic process;tissue development "binding;carboxylic acid binding;catalytic activity;cation binding;dioxygenase activity;identical protein binding;ion binding;iron ion binding;L-ascorbic acid binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptidyl-lysine 5-dioxygenase activity;procollagen-lysine 5-dioxygenase activity;protein binding;protein dimerization activity;protein homodimerization activity;transition metal ion binding;vitamin binding" cell part;collagen;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;extracellular matrix part;extracellular region part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;rough endoplasmic reticulum membrane Lysine degradation 5.66E-69 5 15 15 29.3

P30041 Peroxiredoxin-6 PRDX6 >sp|P30041|PRDX6_HUMAN Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 0.15 -0.10 -0.06 0.00 0.55 0.24 0.36 -0.07 0.821035164 -0.272560253 catabolic process;cellular catabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hydrogen peroxide;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;lipid catabolic process;lipid metabolic process;metabolic process;organophosphate metabolic process;phospholipid catabolic process;phospholipid metabolic process;primary metabolic process;reactive oxygen species metabolic process;response to chemical stimulus;response to hydrogen peroxide;response to inorganic substance;response to oxidative stress;response to reactive oxygen species;response to stimulus;response to stress "antioxidant activity;carboxylic ester hydrolase activity;catalytic activity;glutathione peroxidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on peroxide as acceptor;peroxidase activity;peroxiredoxin activity;phospholipase A2 activity;phospholipase activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lysosome;lytic vacuole;membrane-bounded organelle;membrane-bounded vesicle;organelle;vacuole;vesicle Methane metabolism;Phenylalanine metabolism;Phenylpropanoid biosynthesis 6.31E-210 1 15 15 62.9

P62826;B5MDF5;J3KQE5;F5H018;H0YFC6;B4DV51 GTP-binding nuclear protein Ran RAN >sp|P62826|RAN_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3;>tr|B5MDF5|B5MDF5_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=2 SV=1;>tr|J3KQE5|J3KQE5_HUMAN GTP-binding nuclear protein Ran (Fragment) OS=Homo sapien 0.03 -0.02 -0.21 -0.01 -0.29 -0.43 0.05 -0.21 0.612224383 0.163306077 "androgen receptor signaling pathway;biological regulation;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cytoskeleton organization;DNA metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;gene expression;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular signal transduction;intracellular transport;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitosis;mitotic spindle organization;nitrogen compound metabolic process;nuclear division;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;organelle fission;organelle organization;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein binding;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein export from nucleus;protein targeting;protein transport;regulation of binding;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein binding;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small GTPase mediated signal transduction;spindle organization;steroid hormone receptor signaling pathway;transport;viral infectious cycle;viral reproductive process" "androgen receptor binding;binding;catalytic activity;chromatin binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nuclear part;nuclear pore;nucleoplasm;organelle;organelle part;pigment granule;pore complex;protein complex;vesicle Ribosome biogenesis in eukaryotes;RNA transport 1.00E-97 6 15 15 58.3

P40429;M0QYS1;Q6NVV1;M0QZU1 60S ribosomal protein L13a RPL13A >sp|P40429|RL13A_HUMAN 60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2;>tr|M0QYS1|M0QYS1_HUMAN 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=4 SV=1 -0.11 0.03 0.90 -0.04 -0.65 -0.48 -0.30 -0.34 1.071536654 0.635792624 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 4.62E-60 4 15 15 52.2

P62081;B5MCP9 40S ribosomal protein S7 RPS7 >sp|P62081|RS7_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1;>tr|B5MCP9|B5MCP9_HUMAN 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=2 SV=1 0.02 0.03 -0.27 -0.03 -0.22 -0.48 -0.10 -0.34 0.868818456 0.22077283 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal small subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity 90S preribosome;cell part;cytoplasmic part;cytoskeletal part;cytosolic small ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;preribosome;ribonucleoprotein complex;ribosome;small ribosomal subunit;small-subunit processome Ribosome 1.60E-62 2 15 15 71.1

Q5JTH9-2;Q5JTH9-3;Q5JTH9;F5H456 RRP12-like protein RRP12 >sp|Q5JTH9-2|RRP12_HUMAN Isoform 2 of RRP12-like protein OS=Homo sapiens GN=RRP12;>sp|Q5JTH9-3|RRP12_HUMAN Isoform 3 of RRP12-like protein OS=Homo sapiens GN=RRP12;>sp|Q5JTH9|RRP12_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2;>tr|F5H456|F5H4 -0.04 0.74 0.13 0.70 -0.68 -0.12 -0.99 0.01 1.130152855 0.82717725 cell part;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;nucleolus;organelle;organelle membrane;organelle part 2.77E-211 4 15 15 15.6

O95171-2;O95171-3;O95171;F2Z2X8 Sciellin SCEL >sp|O95171-2|SCEL_HUMAN Isoform 2 of Sciellin OS=Homo sapiens GN=SCEL;>sp|O95171-3|SCEL_HUMAN Isoform 3 of Sciellin OS=Homo sapiens GN=SCEL;>sp|O95171|SCEL_HUMAN Sciellin OS=Homo sapiens GN=SCEL PE=1 SV=2 0.13 1.00 0.03 0.05 0.85 1.82 0.17 0.64 0.572350151 -0.568029117 cell differentiation;cellular developmental process;cellular process;developmental process;embryo development;epidermal cell differentiation;epithelial cell differentiation;keratinocyte differentiationbinding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;non-membrane-bounded organelle;organelle;plasma membrane 3.13E-67 4 15 15 27.2

Q13428;Q13428-3;Q13428-4;E9PHK9;Q13428-2;Q13428-8;J3KQ96;Q13428-6;Q13428-7;E7ETY2;Q13428-5;H0YA99 Treacle protein TCOF1 >sp|Q13428|TCOF_HUMAN Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3;>sp|Q13428-3|TCOF_HUMAN Isoform 3 of Treacle protein OS=Homo sapiens GN=TCOF1;>sp|Q13428-4|TCOF_HUMAN Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1;>tr|E9PHK9|E9PHK9_HUMAN Tre -0.42 0.85 -0.06 0.68 -0.41 -0.53 -1.47 -0.64 1.117703856 1.023031504 "anatomical structure development;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA biosynthetic process;RNA metabolic process;rRNA transcription;skeletal system development;system development;transcription from RNA polymerase I promoter;transcription of nuclear large rRNA transcript from RNA polymerase I promoter;transcription, DNA-dependent" transporter activity cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes 1.52E-68 12 15 15 13.3

Q86UY0;Q8NBS9;Q8NBS9-2 Thioredoxin domain-containing protein 5 TXNDC5>tr|Q86UY0|Q86UY0_HUMAN TXNDC5 protein OS=Homo sapiens GN=TXNDC5 PE=2 SV=1;>sp|Q8NBS9|TXND5_HUMAN Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2;>sp|Q8NBS9-2|TXND5_HUMAN Isoform 2 of Thioredoxin domain-containing protein 5 OS=H 0.01 -0.13 -0.18 -0.07 0.94 0.31 0.26 -0.03 0.943384754 -0.462932045 biological regulation;cell redox homeostasis;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;glycerol ether metabolic process;Golgi vesicle transport;homeostatic process;intracellular transport;membrane organization;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organic ether metabolic process;post-Golgi vesicle-mediated transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;regulation of programmed cell death;small molecule metabolic process;transport;vesicle-mediated transport "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide oxidoreductase activity" cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;lysosomal lumen;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;vacuolar lumen;vacuolar part Protein processing in endoplasmic reticulum 8.32E-83 3 15 15 45

P19971;C9JGI3;P19971-2 Thymidine phosphorylase TYMP >sp|P19971|TYPH_HUMAN Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2;>tr|C9JGI3|C9JGI3_HUMAN Thymidine phosphorylase (Fragment) OS=Homo sapiens GN=TYMP PE=2 SV=1;>sp|P19971-2|TYPH_HUMAN Isoform 2 of Thymidine phosphorylase OS=Homo sapiens GN=TYM -1.35 -0.94 -0.08 0.01 -0.26 0.33 1.06 0.79 1.03416233 -1.071682295 anatomical structure formation involved in morphogenesis;angiogenesis;biosynthetic process;catabolic process;cell differentiation;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic compound salvage;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;chemotaxis;developmental process;DNA metabolic process;DNA replication;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mitochondrial genome maintenance;mitochondrion organization;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside catabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside salvage;nucleotide metabolic process;organelle organization;primary metabolic process;pyrimidine base metabolic process;pyrimidine nucleoside biosynthetic process;pyrimidine nucleoside catabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside salvage;pyrimidine nucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;pyrimidine-containing compound salvage;response to chemical stimulus;response to external stimulus;response to stimulus;small molecule metabolic process;taxis "binding;catalytic activity;growth factor receptor binding;phosphorylase activity;platelet-derived growth factor receptor binding;protein binding;pyrimidine-nucleoside phosphorylase activity;receptor binding;thymidine phosphorylase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasmic part;cytosol;intracellular part Bladder cancer;Drug metabolism - other enzymes;Pyrimidine metabolism 1.70E-88 3 15 15 41.9

P22695;H3BRG4;H3BSJ9;H3BP04;H3BUE4;H3BUI9 "Cytochrome b-c1 complex subunit 2, mitochondrial" UQCRC2">sp|P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3;>tr|H3BRG4|H3BRG4_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=2 SV=1;>tr|H3BSJ9|H3BSJ9_HUMAN Cytochrome b-c1" -0.25

0.64 0.09 0.65 0.13 0.37 -1.40 -0.02 0.467188266 0.512998366 aerobic respiration;cellular metabolic process;cellular process;cellular respiration;electron transport chain;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;macromolecule metabolic process;metabolic process;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein metabolic process;proteolysis;respiratory electron transport chain;small molecule metabolic process "binding;catalytic activity;cation binding;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex III;organelle inner membrane;organelle membrane;organelle part;protein complex;respiratory chain complex III Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 1.96E-192 6 15 15 42.2

Q8IX12-2;Q8IX12;F5H2E6;F5H1H2;F5H3E1;F5H7M9;H0YFJ7 Cell division cycle and apoptosis regulator protein 1 CCAR1 >sp|Q8IX12-2|CCAR1_HUMAN Isoform 2 of Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1;>sp|Q8IX12|CCAR1_HUMAN Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2;>tr|F5H2E6|F5H2E6_HUMAN Cel -0.18 0.13 0.19 0.26 -0.11 -0.27 -0.75 -0.55 1.251436753 0.521379985 "apoptosis;biological regulation;biosynthetic process;cell cycle;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;programmed cell death;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;ligand-dependent nuclear receptor transcription coactivator activity;nucleic acid binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity cell part;cytoplasmic part;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part;perinuclear region of cytoplasm 5.89E-103 7 16 15 16.8

Q13283;F5H4D6;E5RIZ6;E5RI46;E5RIF8;E5RH42;Q5HYE9;E5RJU8;E5RH00 Ras GTPase-activating protein-binding protein 1 G3BP1 >sp|Q13283|G3BP1_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1;>tr|F5H4D6|F5H4D6_HUMAN Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=2 SV=1 0.19 0.18 -0.17 0.01 -0.11 -0.36 -0.28 -0.26 1.264870201 0.307534868 biological regulation;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;establishment of localization;intracellular signal transduction;metabolic process;negative regulation of biological process;negative regulation of canonical Wnt receptor signaling pathway;negative regulation of cell communication;negative regulation of cellular process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;primary metabolic process;Ras protein signal transduction;regulation of biological process;regulation of canonical Wnt receptor signaling pathway;regulation of cell communication;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of Wnt receptor signaling pathway;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;endonuclease activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;hydrolase activity, acting on ester bonds;mRNA binding;nuclease activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;plasma membrane;ribonucleoprotein complex;RNA granule;stress granule 6.95E-199 9 16 15 45.7

Q08379;Q08379-2;B7ZC06;REV__B7Z235;H0Y7B8;Q9UJT2-2;C9K0I0;Q8IXS0;Q9UJT2 Golgin subfamily A member 2 GOLGA2>sp|Q08379|GOGA2_HUMAN Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3;>sp|Q08379-2|GOGA2_HUMAN Isoform 2 of Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 -0.21 0.14 0.29 0.05 0.09 0.22 -0.73 -0.04 0.310679098 0.186172048 biological regulation;cell cycle phase;cell cycle process;cellular process;M phase;M phase of mitotic cell cycle;mitotic prophase;negative regulation of catalytic activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of phosphatase activity;prophase;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process cell part;centriole;cis-Golgi network;cytoplasmic part;cytoskeletal part;Golgi apparatus;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;microtubule organizing center part;non-membrane-bounded organelle;organelle;organelle membrane;organelle part 9.73E-83 9 16 15 21

Q08378-2;Q08378;Q08378-4 Golgin subfamily A member 3 GOLGA3 >sp|Q08378-2|GOGA3_HUMAN Isoform 2 of Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3;>sp|Q08378|GOGA3_HUMAN Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2;>sp|Q08378-4|GOGA3_HUMAN Isoform 3 of Golgin subfamily A member 3 OS=Homo sap -0.06 -0.01 0.26 0.04 0.46 -0.05 -0.30 -0.27 0.202092822 0.102128239 cellular process;establishment of localization;establishment of localization in cell;Golgi vesicle transport;intracellular transport;intra-Golgi vesicle-mediated transport;transport;vesicle-mediated transport transporter activity cell part;cytoplasmic part;endoplasmic reticulum-Golgi intermediate compartment;Golgi apparatus part;Golgi cisterna membrane;Golgi membrane;Golgi transport complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;protein complex 2.17E-102 3 16 15 15.3

Q96G03;F5H6V2;B4E0G8;E7ENQ8;E9PD70;H0Y921 Phosphoglucomutase-2 PGM2 >sp|Q96G03|PGM2_HUMAN Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4;>tr|F5H6V2|F5H6V2_HUMAN Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=2 SV=1 0.12 0.16 -0.04 0.04 0.19 0.37 0.37 -0.20 0.315147019 -0.112093841 alcohol catabolic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;deoxyribose phosphate catabolic process;deoxyribose phosphate metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;galactose catabolic process;galactose metabolic process;generation of precursor metabolites and energy;glucan biosynthetic process;glucan catabolic process;glucan metabolic process;glucose metabolic process;glycogen biosynthetic process;glycogen catabolic process;glycogen metabolic process;hexose catabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;organophosphate catabolic process;organophosphate metabolic process;oxidation-reduction process;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;intramolecular transferase activity;intramolecular transferase activity, phosphotransferases;ion binding;isomerase activity;magnesium ion binding;metal ion binding;phosphoglucomutase activity;phosphopentomutase activity" cell part;cytoplasmic part;cytosol;intracellular part Amino sugar and nucleotide sugar metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway;Purine metabolism;Starch and sucrose metabolism;Streptomycin biosynthesis 3.17E-65 6 16 15 32.2

P52306;P52306-2;P52306-4;P52306-5;P52306-6;P52306-3;H0Y8M2;D6RHH8;D6RHZ7;D6RF90;D6RB97;H0Y9J0;D6RBC6;D6REZ0;D6RC12;D6RE95 Rap1 GTPase-GDP dissociation stimulator 1RAP1GDS1 >sp|P52306|GDS1_HUMAN Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1 PE=1 SV=3;>sp|P52306-2|GDS1_HUMAN Isoform 2 of Rap1 GTPase-GDP dissociation stimulator 1 OS=Homo sapiens GN=RAP1GDS1;>sp|P52306-4|GDS1_HUMAN Isoform 4 of Rap1 GTPas 0.15 -0.25 0.08 -0.09 -0.21 -0.10 0.47 0.01 0.147233485 -0.070967856 enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity 5.34E-94 16 16 15 34.1

P47989 Xanthine dehydrogenase/oxidase;Xanthine dehydrogenase;Xanthine oxidase XDH >sp|P47989|XDH_HUMAN Xanthine dehydrogenase/oxidase OS=Homo sapiens GN=XDH PE=1 SV=4 -0.10 -0.04 0.36 0.02 -2.85 -2.07 0.64 0.01 0.566148297 1.12608004 activation of caspase activity;biological regulation;body fluid secretion;catabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;heterocycle catabolic process;heterocycle metabolic process;lactation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of endothelial cell differentiation;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell differentiation;negative regulation of epithelial cell proliferation;negative regulation of gene expression;negative regulation of intracellular protein kinase cascade;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein kinase B signaling cascade;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nitrogen compound metabolic process;nucleobase catabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;positive regulation of biological process;positive regulation of caspase activity;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of peptidase activity;positive regulation of reactive oxygen species metabolic process;primary metabolic process;purine base catabolic process;purine base metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of catalytic activity;regulation of cell communication;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of endothelial cell differentiation;regulation of endothelial cell proliferation;regulation of epithelial cell differentiation;regulation of epithelial cell proliferation;regulation of gene expression;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase B signaling cascade;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of reactive oxygen species metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;reproductive process;secretion;small molecule metabolic process;transport;xanthine catabolic process;xanthine metabolic process "2 iron, 2 sulfur cluster binding;binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;electron carrier activity;flavin adenine dinucleotide binding;ion binding;iron ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;molybdopterin cofactor binding;oxidoreductase activity;oxidoreductase activity, acting on CH or CH2 groups;oxidoreductase activity, acting on CH or CH2 groups, NAD or NADP as acceptor;oxidoreductase activity, acting on CH or CH2 groups, oxygen as acceptor;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transition metal ion binding;UDP-N-acetylmuramate dehydrogenase activity;xanthine dehydrogenase activity;xanthine oxidase activity" cell part;cytoplasmic part;cytosol;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microbody;organelle;peroxisome Caffeine metabolism;Drug metabolism - other enzymes;Peroxisome;Purine metabolism 1.26E-79 1 16 15 15.2

P29317 Ephrin type-A receptor 2 EPHA2 >sp|P29317|EPHA2_HUMAN Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 PE=1 SV=2 0.42 0.30 -0.12 -0.15 -1.15 -0.66 -0.46 -0.26 1.281109149 0.743928881 activation of Rac GTPase activity;activation of Ras GTPase activity;activation of Rho GTPase activity;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;apoptosis;axial mesoderm formation;biological adhesion;biological regulation;bone remodeling;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a tube;cell adhesion;cell chemotaxis;cell death;cell development;cell differentiation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;chemotaxis;death;developmental process;enzyme linked receptor protein signaling pathway;ephrin receptor signaling pathway;epidermal cell differentiation;epithelial cell differentiation;epithelial cell proliferation;formation of primary germ layer;intracellular protein kinase cascade;intracellular signal transduction;keratinocyte differentiation;lens fiber cell morphogenesis;leukocyte differentiation;locomotion;mammary gland epithelial cell proliferation;mesoderm formation;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;myeloid cell differentiation;myeloid leukocyte differentiation;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of intracellular protein kinase cascade;negative regulation of protein kinase B signaling cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;neural tube development;neuron differentiation;notochord cell development;notochord formation;osteoblast differentiation;osteoclast differentiation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of establishment of protein localization in plasma membrane;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Rac GTPase activity;positive regulation of Ras GTPase activity;positive regulation of Rho GTPase activity;programmed cell death;protein kinase B signaling cascade;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of blood vessel endothelial cell migration;regulation of catabolic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation of cell communication;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of endothelial cell migration;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of lamellipodium assembly;regulation of localization;regulation of locomotion;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to stimulus;regulation of Rho GTPase activity;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;signal transduction;skeletal system development;system development;taxis;tissue morphogenesis;tissue remodeling;transmembrane receptor protein tyrosine kinase signaling pathway;tube morphogenesis;vasculogenesis "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;ephrin receptor activity;kinase activity;molecular transducer activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;ribonucleotide binding;signal transducer activity;signaling receptor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity" adherens junction;anchoring junction;cell junction;cell part;cell projection membrane;cell projection part;cell-substrate adherens junction;cell-substrate junction;focal adhesion;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium membrane;leading edge membrane;membrane part;plasma membrane part;ruffle membrane Axon guidance 6.95E-78 1 17 15 19.7

P12830;Q9UII8;H3BNC6;J3QKP1;H3BVI7 Cadherin-1;E-Cad/CTF1;E-Cad/CTF2;E-Cad/CTF3 CDH1 ">sp|P12830|CADH1_HUMAN Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=3;>tr|Q9UII8|Q9UII8_HUMAN Cadherin 1, type 1, E-cadherin (Epithelial), isoform CRA_c OS=Homo sapiens GN=CDH1 PE=2 SV=1;>tr|H3BNC6|H3BNC6_HUMAN Fizzy-related protein homolog OS=Homo sapiens G" -0.14 0.15 0.19 0.21 -1.71 -0.67 -0.17 -0.21 0.918798781 0.792944115 "adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cellular response to acid;cellular response to amine stimulus;cellular response to amino acid stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to indole-3-methanol;cellular response to inorganic substance;cellular response to lithium ion;cellular response to metal ion;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cochlea development;developmental process;gland development;homeostatic process;homophilic cell adhesion;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;membrane organization;metabolic process;multicellular organismal process;multicellular organismal water homeostasis;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell-cell adhesion;negative regulation of cellular process;neurological system process;neuron projection development;organ development;pituitary gland development;plasma membrane organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of RNA metabolic process;positive regulation of transcription factor import into nucleus;positive regulation of transcription, DNA-dependent;positive regulation of transmembrane transport;positive regulation of transport;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein localization;protein localization in membrane;protein localization in plasma membrane;protein metabolic process;protein oligomerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of branching involved in salivary gland morphogenesis;regulation of catalytic activity;regulation of cell adhesion;regulation of cell-cell adhesion;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental process;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of gene expression;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organ morphogenesis;regulation of peptidase activity;regulation of primary metabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein localization at cell surface;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of water loss via skin;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to indole-3-methanol;response to inorganic substance;response to lithium ion;response to metal ion;response to organic nitrogen;response to organic substance;response to stimulus;response to toxin;salivary gland cavitation;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;synapse assembly;synapse organization;system process;tight junction assembly;trophectodermal cell differentiation;tube formation;tube lumen cavitation;water homeostasis" beta-catenin binding;binding;calcium ion binding;cation binding;cell adhesion molecule binding;ion binding;metal ion binding;protein binding actin cytoskeleton;adherens junction;aggresome;anchoring junction;apical junction complex;apical part of cell;axon part;axon terminus;basolateral plasma membrane;catenin complex;cell junction;cell part;cell projection part;cell surface;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;cytoplasm;cytoplasmic part;cytoskeleton;endosome;extrinsic to membrane;extrinsic to plasma membrane;focal adhesion;Golgi apparatus;Golgi apparatus part;inclusion body;integral to membrane;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lateral loop;lateral plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;neuron projection terminus;node of Ranvier;non-membrane-bounded organelle;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;Schmidt-Lanterman incisure;trans-Golgi network Adherens junction;Bacterial invasion of epithelial cells;Bladder cancer;Cell adhesion molecules (CAMs);Endometrial cancer;Melanoma;Pathogenic Escherichia coli infection;Pathways in cancer;Thyroid cancer 7.07E-255 5 18 15 26.6

Q9UJS0;Q9UJS0-2;F5GX33;R4GN64 Calcium-binding mitochondrial carrier protein Aralar2 SLC25A13 >sp|Q9UJS0|CMC2_HUMAN Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2;>sp|Q9UJS0-2|CMC2_HUMAN Isoform 2 of Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13;>tr|F5GX33|F5GX33_HUMAN -0.35 0.71 -0.25 0.64 0.27 1.27 -1.00 0.80 0.091365198 -0.148208126 alcohol biosynthetic process;alcohol metabolic process;ATP biosynthetic process;ATP metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;gluconeogenesis;glucose metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;hexose biosynthetic process;hexose metabolic process;intracellular transport;malate-aspartate shuttle;metabolic process;mitochondrial transport;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule biosynthetic process;small molecule metabolic process;transmembrane transport;transport acidic amino acid transmembrane transporter activity;active transmembrane transporter activity;amine transmembrane transporter activity;amino acid transmembrane transporter activity;binding;calcium ion binding;carboxylic acid transmembrane transporter activity;cation binding;ion binding;L-amino acid transmembrane transporter activity;L-aspartate transmembrane transporter activity;L-glutamate transmembrane transporter activity;metal ion binding;organic acid transmembrane transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;plasma membrane part 6.91E-138 4 19 15 40

P61981 "14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed" YWHAG >sp|P61981|1433G_HUMAN 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2 -0.19 0.00 -0.11 0.00 -0.01 0.36 0.31 0.53 1.250627548 -0.372306306 biological regulation;cell cycle process;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;G2/M transition of mitotic cell cycle;intracellular protein transport;intracellular transport;membrane organization;protein targeting;protein transport;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse;transport enzyme inhibitor activity;enzyme regulator activity;kinase inhibitor activity;kinase regulator activity;protein kinase C inhibitor activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis 0 1 22 15 68

Q6UWP8Suprabasin SBSN >sp|Q6UWP8|SBSN_HUMAN Suprabasin OS=Homo sapiens GN=SBSN PE=2 SV=2 -0.27 0.85 -0.18 0.09 2.04 2.67 0.32 0.19 0.754030179 -1.182750879 extracellular region 1.83E-294 1 26 15 74.7

P13798;C9JIF9;H7C393;H7C1U0;C9JLK2;H0YFE5;F8WEH5 Acylamino-acid-releasing enzyme APEH >sp|P13798|ACPH_HUMAN Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4;>tr|C9JIF9|C9JIF9_HUMAN Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=2 SV=1;>tr|H7C393|H7C393_HUMAN Acylamino-acid-releasing enzyme (Fragment) OS=Homo sap -0.09 -0.13 -0.12 -0.02 -0.38 -0.36 0.47 -0.14 0.023755107 0.014475763 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity" cell part;cytoplasm;intracellular organelle part;intracellular part;membrane;nuclear membrane;nuclear part;organelle membrane;organelle part 1.79E-112 7 16 16 25.1

Q92888;Q92888-3;M0QZR4;Q92888-2;Q6NX52;M0QYC1;M0QYS3;M0QZH8;M0R2C7 Rho guanine nucleotide exchange factor 1 ARHGEF1 >sp|Q92888|ARHG1_HUMAN Rho guanine nucleotide exchange factor 1 OS=Homo sapiens GN=ARHGEF1 PE=1 SV=2;>sp|Q92888-3|ARHG1_HUMAN Isoform 3 of Rho guanine nucleotide exchange factor 1 OS=Homo sapiens GN=ARHGEF1;>tr|M0QZR4|M0QZR4_HUMAN Rho guanine nucleotide ex 0.05 0.02 0.15 0.02 -0.27 -0.16 0.17 0.03 0.46342675 0.115382362 biological regulation;cell proliferation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;intracellular signal transduction;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental process;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of neurogenesis;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;Ras protein signal transduction;regulation of anatomical structure morphogenesis;regulation of axonogenesis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of G-protein coupled receptor protein signaling pathway;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;Rho protein signal transduction;signal transduction;small GTPase mediated signal transduction;termination of G-protein coupled receptor signaling pathway;termination of signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;lipid binding;nucleoside-triphosphatase regulator activity;phospholipid binding;Ras guanyl-nucleotide exchange factor activity;Rho guanyl-nucleotide exchange factor activity;small GTPase regulator activity cell part;cytoplasm;cytoplasmic part;cytosol;intracellular;intracellular part;membrane;plasma membrane ko05152;Regulation of actin cytoskeleton;Vascular smooth muscle contraction 2.57E-99 9 16 16 21.6

O15144;C9JTV5;G5E9J0;H7C3F9;G5E9S7 Actin-related protein 2/3 complex subunit 2 ARPC2 >sp|O15144|ARPC2_HUMAN Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 -0.21 0.09 -0.29 0.21 0.27 0.43 0.19 0.32 1.146497989 -0.352246866 biological regulation;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular process;defense response;immune response;immune system process;innate immune response;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to stimulus;response to stress structural constituent of cytoskeleton;structural molecule activity adherens junction;anchoring junction;Arp2/3 protein complex;cell junction;cell leading edge;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;endosome;focal adhesion;Golgi apparatus;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex Bacterial invasion of epithelial cells;Fc gamma R-mediated phagocytosis;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton;Shigellosis 1.44E-116 5 16 16 49.7

P08243-2;P08243;P08243-3;F8WEJ5;C9J057;C9JT45;C9JLN6;C9JM09 Asparagine synthetase [glutamine-hydrolyzing] ASNS >sp|P08243-2|ASNS_HUMAN Isoform 2 of Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS;>sp|P08243|ASNS_HUMAN Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens GN=ASNS PE=1 SV=4;>sp|P08243-3|ASNS_HUMAN Isoform 3 of Asparagine -0.54 -0.57 0.48 0.15 -0.22 -1.00 0.14 -0.72 0.365301314 0.33035114 activation of signaling protein activity involved in unfolded protein response;amine biosynthetic process;amine metabolic process;anatomical structure development;asparagine biosynthetic process;asparagine metabolic process;aspartate family amino acid biosynthetic process;aspartate family amino acid metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cell communication;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to hormone stimulus;cellular response to nutrient levels;cellular response to organic substance;cellular response to starvation;cellular response to stimulus;cellular response to stress;developmental process;glutamine family amino acid metabolic process;glutamine metabolic process;L-asparagine biosynthetic process;L-asparagine metabolic process;liver development;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;organ development;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle;positive regulation of cellular process;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of mitotic cell cycle;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to abiotic stimulus;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to follicle-stimulating hormone stimulus;response to gonadotropin stimulus;response to hormone stimulus;response to light stimulus;response to mechanical stimulus;response to methotrexate;response to nutrient levels;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to radiation;response to starvation;response to stimulus;response to stress;response to toxin;small molecule biosynthetic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;asparagine synthase (glutamine-hydrolyzing) activity;ATP binding;binding;carbon-nitrogen ligase activity, with glutamine as amido-N-donor;catalytic activity;cofactor binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part "Alanine, aspartate and glutamate metabolism;Nitrogen metabolism" 2.44E-124 8 16 16 36.3

Q9HB71;Q9HB71-3;B2ZWH1;Q9HB71-2 Calcyclin-binding protein CACYBP >sp|Q9HB71|CYBP_HUMAN Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2;>sp|Q9HB71-3|CYBP_HUMAN Isoform 3 of Calcyclin-binding protein OS=Homo sapiens GN=CACYBP 0.13 0.03 -0.06 -0.02 0.10 -0.47 -0.06 -0.49 0.686335356 0.246737273 aging;biological regulation;cardiac cell differentiation;cardiac muscle cell differentiation;cell differentiation;cellular developmental process;cellular process;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;developmental process;muscle cell differentiation;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of DNA metabolic process;regulation of DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to calcium ion;response to chemical stimulus;response to endogenous stimulus;response to growth hormone stimulus;response to hormone stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to peptide hormone stimulus;response to stimulus;striated muscle cell differentiation beta-catenin destruction complex;cell body;cell part;cell projection;cytoplasm;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane-enclosed lumen;neuron projection;nuclear envelope lumen;nuclear part;organelle envelope lumen;organelle part;protein complex Wnt signaling pathway 3.25E-149 4 16 16 71.9

B4DQ14;F8WAE5;Q9BY44;B4DF96;Q9BY44-2;C9IZE1;H7C5R5;H7C5Q3;F8WF18;F8WAT3 Eukaryotic translation initiation factor 2A EIF2A >tr|B4DQ14|B4DQ14_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2A PE=2 SV=1;>tr|F8WAE5|F8WAE5_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2A PE=2 SV=1;>sp|Q9BY44|EIF2A_HUMAN Eukaryoti 0.27 0.09 -0.34 -0.17 -0.01 -0.33 0.21 -0.35 0.149211911 0.078632803 biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;ER-nucleus signaling pathway;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;organelle assembly;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of translation;response to stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;signal transduction;SREBP-mediated signaling pathway "binding;nucleic acid binding;ribonucleoprotein binding;ribosome binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity;tRNA binding" cell part;cytoplasmic part;eukaryotic translation initiation factor 2 complex;intracellular part;macromolecular complex;protein complex 3.01E-123 10 16 16 42.7

P23588;E7EX17;B4DS13;F8W0K0;F8VSC7;F8VP89;F8VX11;F8VRU1;F8VYE9 Eukaryotic translation initiation factor 4B EIF4B >sp|P23588|IF4B_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2;>tr|E7EX17|E7EX17_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=2 SV=1;>tr|B4DS13|B4DS13_HUMAN Eukaryotic translation initi -0.08 0.03 0.09 0.06 -0.11 -0.27 -0.06 -0.49 1.041512979 0.257095287 biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;enzyme linked receptor protein signaling pathway;insulin receptor signaling pathway;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway"binding;nucleic acid binding;nucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex mTOR signaling pathway;RNA transport 3.37E-107 9 16 16 35

P12081-4;P12081;B4DDD8;B3KWE1;P12081-3;P12081-2;B4E1C5;E7ETE2;C9JWK3;C9JV49;B4DDY8;P49590;B4DQ67;C9JHI8;E9PG66;D6RF05;D6RJE6 "Histidine--tRNA ligase, cytoplasmic" HARS ">sp|P12081-4|SYHC_HUMAN Isoform 4 of Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS;>sp|P12081|SYHC_HUMAN Histidine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=HARS PE=1 SV=2;>tr|B4DDD8|B4DDD8_HUMAN Histidine--tRNA ligase, cytoplasmic OS=Homo" 0.13 -0.06 0.06 -0.07 -0.02 -0.24 0.38 -0.09 0.020834298 0.009003811 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;histidyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;histidine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part Aminoacyl-tRNA biosynthesis 5.25E-151 17 16 16 37.2

Q8TEX9;Q8TEX9-2;H0YN14;H0YMR4;H0YN07;H0YLV0;H0YL92;H0YK93;H0YKG5 Importin-4 IPO4 >sp|Q8TEX9|IPO4_HUMAN Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2;>sp|Q8TEX9-2|IPO4_HUMAN Isoform 2 of Importin-4 OS=Homo sapiens GN=IPO4;>tr|H0YN14|H0YN14_HUMAN Importin-4 OS=Homo sapiens GN=IPO4 PE=2 SV=1 0.18 -0.10 0.13 0.01 -0.21 -0.49 0.04 -0.34 1.014330867 0.305769493 establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;transport protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;organelle part;pore complex;protein complex 3.48E-205 9 16 16 21.5

Q2M389;Q2M389-2;F8VYH7;F8W1W1;F8VNZ5 WASH complex subunit 7 KIAA1033 >sp|Q2M389|WASH7_HUMAN WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 PE=1 SV=2;>sp|Q2M389-2|WASH7_HUMAN Isoform 2 of WASH complex subunit 7 OS=Homo sapiens GN=KIAA1033 0.06 0.00 0.05 -0.03 -0.18 -0.10 0.31 -0.18 0.186673137 0.059866437 cellular process;endosome transport;establishment of localization;establishment of localization in cell;intracellular transport;transport;vesicle-mediated transport cell part;cytoplasmic part;endosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;organelle;protein complex;WASH complex 1.29E-86 5 16 16 18.5

Q969V3-2;Q969V3;K7EMW4;K7ELZ9;K7ENM2;K7EQ66;K7EN96 Nicalin NCLN >sp|Q969V3-2|NCLN_HUMAN Isoform 2 of Nicalin OS=Homo sapiens GN=NCLN;>sp|Q969V3|NCLN_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2;>tr|K7EMW4|K7EMW4_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=4 SV=1 0.07 -0.03 -0.04 -0.10 0.45 0.30 -0.17 -0.06 0.425752016 -0.1556867 biological regulation;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling catalytic activity;hydrolase activity;peptidase activity cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part 5.09E-143 7 16 16 37

Q92621;F2Z2D0 Nuclear pore complex protein Nup205 NUP205 >sp|Q92621|NU205_HUMAN Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 0.21 0.49 0.09 0.42 0.05 -0.01 -0.65 -0.30 1.1868519 0.528582466 "biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of RNA localization;glucose transport;hexose transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide transport;mRNA transport;nuclear pore complex assembly;nuclear pore organization;nucleic acid transport;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein import into nucleus, docking;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process" structural constituent of nuclear pore;structural molecule activity cell part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;organelle membrane;organelle part;pore complex;protein complex RNA transport 5.24E-101 2 16 16 11.5

P35658-2;P35658-4;P35658;P35658-3;P35658-5;H0YF36;H0Y837;E9PKD2;B7ZAV2 Nuclear pore complex protein Nup214 NUP214 >sp|P35658-2|NU214_HUMAN Isoform 2 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214;>sp|P35658-4|NU214_HUMAN Isoform 4 of Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214;>sp|P35658|NU214_HUMAN Nuclear pore complex protein Nup2 0.03 0.31 -0.04 0.12 -0.03 -0.18 -0.44 -0.30 1.214934851 0.34230603 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;gene expression;glucose transport;hexose transport;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;monosaccharide transport;mRNA export from nucleus;mRNA metabolic process;mRNA transport;nitrogen compound metabolic process;nuclear export;nuclear import;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;organic substance transport;primary metabolic process;protein export from nucleus;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cell cycle;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA metabolic process;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process nucleocytoplasmic transporter activity;transporter activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane part;nuclear part;nuclear pore;nucleoplasm;organelle part;pore complex;protein complex RNA transport 5.74E-110 9 16 16 13.3

Q460N5-4;Q460N5-1;Q460N5;H7C5R8;Q460N5-3;Q460N5-5;H7C4Y3 Poly [ADP-ribose] polymerase 14 PARP14 >sp|Q460N5-4|PAR14_HUMAN Isoform 4 of Poly [ADP-ribose] polymerase 14 OS=Homo sapiens GN=PARP14;>sp|Q460N5-1|PAR14_HUMAN Isoform 1 of Poly [ADP-ribose] polymerase 14 OS=Homo sapiens GN=PARP14;>sp|Q460N5|PAR14_HUMAN Poly [ADP-ribose] polymerase 14 OS=Homo s 0.27 -0.09 0.16 -0.09 -0.88 -0.90 0.06 -0.11 0.82091127 0.516886428 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "catalytic activity;NAD+ ADP-ribosyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 7.11E-120 7 16 16 15.3

Q16822;B4DW73;H0YML5;H0YM31;Q16822-2;H0YMU6;H0YNG4;H0YMA5;F5GZM4;P35558 "Phosphoenolpyruvate carboxykinase [GTP], mitochondrial" PCK2 ">sp|Q16822|PCKGM_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3;>tr|B4DW73|B4DW73_HUMAN Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=2 SV=1;>tr|H0YML5|H0YML5_HUMAN Phospho" -1.68 -1.40 0.57 0.40 0.00 -0.32 0.47 -0.44 0.284715957 -0.453293272 alcohol biosynthetic process;alcohol metabolic process;alditol biosynthetic process;alditol metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate homeostasis;carbohydrate metabolic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chemical homeostasis;dicarboxylic acid metabolic process;drug metabolic process;gluconeogenesis;glucose homeostasis;glucose metabolic process;glycerol biosynthetic process;glycerol biosynthetic process from pyruvate;glycerol metabolic process;hexose biosynthetic process;hexose metabolic process;homeostatic process;internal protein amino acid acetylation;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;organic acid metabolic process;oxaloacetate metabolic process;oxoacid metabolic process;polyol biosynthetic process;polyol metabolic process;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;pyruvate metabolic process;regulation of biological quality;response to activity;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;small molecule biosynthetic process;small molecule metabolic process "binding;carbon-carbon lyase activity;carboxylic acid binding;carboxy-lyase activity;catalytic activity;cation binding;GDP binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ion binding;kinase activity;lyase activity;magnesium ion binding;manganese ion binding;metal ion binding;nucleotide binding;phosphoenolpyruvate carboxykinase (GTP) activity;phosphoenolpyruvate carboxykinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part Adipocytokine signaling pathway;Citrate cycle (TCA cycle);Glycolysis / Gluconeogenesis;Insulin signaling pathway;PPAR signaling pathway;Proximal tubule bicarbonate reclamation;Pyruvate metabolism 1.60E-120 10 16 16 30.9

P35232;C9JW96;C9JZ20;E7ESE2;E9PCW0;B4DY47;D6RBK0 Prohibitin PHB >sp|P35232|PHB_HUMAN Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1;>tr|C9JW96|C9JW96_HUMAN Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=2 SV=2;>tr|C9JZ20|C9JZ20_HUMAN Prohibitin (Fragment) OS=Homo sapiens GN=PHB PE=2 SV=1;>tr|E7ESE2|E7ESE2_HUMAN Prohibiti -0.38 0.11 0.08 0.22 0.36 0.13 -1.20 -0.18 0.24020669 0.231749546 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interleukin-6;cellular response to organic substance;cellular response to stimulus;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;DNA biosynthetic process;DNA metabolic process;DNA replication;histone deacetylation;histone modification;intracellular receptor mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of androgen receptor signaling pathway;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of glucocorticoid receptor signaling pathway;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription by competitive promoter binding;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;progesterone receptor signaling pathway;protein deacetylation;protein deacylation;protein metabolic process;protein modification process;regulation of androgen receptor signaling pathway;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of glucocorticoid receptor signaling pathway;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to cytokine stimulus;response to interleukin-6;response to organic substance;response to stimulus;signal transduction;steroid hormone receptor signaling pathway" binding;DNA binding;nucleic acid binding;nucleic acid binding transcription factor activity;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription regulatory region DNA binding cell part;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;nuclear part;nucleoplasm;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part;plasma membrane part 9.80E-258 7 16 16 75

P16435;H0Y4R2;E7EMD0;F5H468;E7EVY7;E7EPN3;E7EWU0;C9JU80 NADPH--cytochrome P450 reductase POR>sp|P16435|NCPR_HUMAN NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2;>tr|H0Y4R2|H0Y4R2_HUMAN NADPH--cytochrome P450 reductase (Fragment) OS=Homo sapiens GN=POR PE=4 SV=1;>tr|E7EMD0|E7EMD0_HUMAN NADPH--cytochrome P450 reductase OS=Homo sa -0.08 -0.01 0.27 0.07 0.38 0.32 -0.35 -0.18 0.033262615 0.01983551 amine metabolic process;betaine metabolic process;biological regulation;carboxylic acid metabolic process;carnitine metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular organofluorine metabolic process;cellular organohalogen metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to follicle-stimulating hormone stimulus;cellular response to gonadotropin stimulus;cellular response to hormone stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;demethylation;fatty acid metabolic process;fatty acid oxidation;flavonoid metabolic process;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;lipid metabolic process;lipid modification;lipid oxidation;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of lipase activity;negative regulation of molecular function;negative regulation of peptidase activity;negative regulation of programmed cell death;nitrate catabolic process;nitrate metabolic process;nitric oxide catabolic process;nitric oxide metabolic process;nitrogen compound metabolic process;one-carbon metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;phenylpropanoid metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cholesterol biosynthetic process;positive regulation of cholesterol metabolic process;positive regulation of chondrocyte differentiation;positive regulation of developmental process;positive regulation of hormone biosynthetic process;positive regulation of hormone metabolic process;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of monooxygenase activity;positive regulation of oxidoreductase activity;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smoothened signaling pathway;positive regulation of steroid biosynthetic process;positive regulation of steroid hormone biosynthetic process;positive regulation of steroid metabolic process;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cartilage development;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cholesterol biosynthetic process;regulation of cholesterol metabolic process;regulation of chondrocyte differentiation;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of developmental growth;regulation of developmental process;regulation of endopeptidase activity;regulation of growth;regulation of growth plate cartilage chondrocyte proliferation;regulation of hormone biosynthetic process;regulation of hormone metabolic process;regulation of hydrolase activity;regulation of lipase activity;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of organ morphogenesis;regulation of oxidoreductase activity;regulation of peptidase activity;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of smoothened signaling pathway;regulation of steroid biosynthetic process;regulation of steroid hormone biosynthetic process;regulation of steroid metabolic process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to follicle-stimulating hormone stimulus;response to gonadotropin stimulus;response to hormone stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to peptide hormone stimulus;response to stimulus;secondary metabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;cytochrome-b5 reductase activity;electron carrier activity;flavin adenine dinucleotide binding;FMN binding;hydrolase activity;ion binding;iron ion binding;iron-cytochrome-c reductase activity;metal ion binding;monooxygenase activity;NADP binding;NADPH-hemoprotein reductase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on a heme group of donors;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, heme protein as acceptor;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen;transition metal ion binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane-bounded organelle;mitochondrion;organelle;organelle membrane;organelle part 3.22E-113 8 16 16 30.6

P39023;G5E9G0;H7C422;H7C3M2;B5MCW2;F8WCR1;Q92901 60S ribosomal protein L3 RPL3 >sp|P39023|RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2;>tr|G5E9G0|G5E9G0_HUMAN 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=2 SV=1;>tr|H7C422|H7C422_HUMAN 60S ribosomal protein L3 (Fragment) OS=Homo sapiens GN=RPL3 PE=2 SV=1 -0.28 0.05 -0.09 0.01 -0.05 -0.64 -0.53 -0.63 1.032615676 0.384266318 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasm;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 5.00E-110 7 16 16 41.2

P04844;P04844-2;Q5JYR7;Q5JYR4;F2Z3K5;Q5JYR3;H0Y5M1 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 RPN2 >sp|P04844|RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3;>sp|P04844-2|RPN2_HUMAN Isoform 2 of Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens G 0.00 0.12 -0.48 -0.34 1.04 0.83 -0.28 0.07 0.739164879 -0.590796459 aging;biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glycosylation;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to drug;response to stimulus;SRP-dependent cotranslational protein targeting to membrane;translation;transport "binding;catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;ribonucleoprotein binding;ribosome binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" autophagic vacuole membrane;cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nucleus;oligosaccharyltransferase complex;organelle;organelle membrane;organelle part;protein complex;rough endoplasmic reticulum;vacuolar membrane;vacuolar part N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis 1.43E-214 7 16 16 38.8

Q5K651;C9JKF1 Sterile alpha motif domain-containing protein 9 SAMD9 >sp|Q5K651|SAMD9_HUMAN Sterile alpha motif domain-containing protein 9 OS=Homo sapiens GN=SAMD9 PE=1 SV=1;>tr|C9JKF1|C9JKF1_HUMAN Sterile alpha motif domain-containing protein 9 (Fragment) OS=Homo sapiens GN=SAMD9 PE=2 SV=1 0.37 0.35 -0.22 -0.14 -0.10 0.78 0.60 0.45 0.580240787 -0.341255885 cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;organelle 3.08E-97 2 16 16 13.5

P08240;P08240-2 Signal recognition particle receptor subunit alpha SRPR >sp|P08240|SRPR_HUMAN Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2;>sp|P08240-2|SRPR_HUMAN Isoform 2 of Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR 0.31 0.10 -0.34 -0.17 0.47 0.00 -0.23 -0.20 0.054609787 -0.035049184 activation of signaling protein activity involved in unfolded protein response;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;SRP-dependent cotranslational protein targeting to membrane;translation;transport "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleoprotein binding;ribonucleotide binding;signal recognition particle binding" cell part;cytoplasmic part;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;organelle part;protein complex;receptor complex;signal recognition particle receptor complex Protein export 4.35E-58 2 16 16 35

Q9Y3F4;B4DNJ6;B0AZV0;H0YH33 Serine-threonine kinase receptor-associated protein STRAP >sp|Q9Y3F4|STRAP_HUMAN Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1;>tr|B4DNJ6|B4DNJ6_HUMAN Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=2 SV=1;>tr|B0AZV0|B0AZV0_HUMAN Serine-thre 0.13 0.03 -0.07 -0.05 0.00 -0.11 0.18 -0.23 0.185829312 0.049638659 "biological regulation;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;enzyme linked receptor protein signaling pathway;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;response to stimulus;RNA metabolic process;RNA processing;RNA splicing;signal transduction;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway" "catalytic activity;kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell junction;cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;nuclear part;nucleus;organelle;organelle part;plasma membrane;ribonucleoprotein complex;spliceosomal complex RNA transport 7.38E-164 4 16 16 64.9

Q9UGI8;Q9UGI8-2;F8W7T0;B7Z6L5;F8WDI4;H7BYK1 Testin TES >sp|Q9UGI8|TES_HUMAN Testin OS=Homo sapiens GN=TES PE=1 SV=1;>sp|Q9UGI8-2|TES_HUMAN Isoform 2 of Testin OS=Homo sapiens GN=TES 0.11 -0.11 0.23 -0.09 -0.84 -0.50 0.48 -0.08 0.368347717 0.270865969 biological regulation;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;regulation of biological process;regulation of cell proliferation;regulation of cellular process binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding adherens junction;anchoring junction;cell junction;cell part;cell-substrate adherens junction;cell-substrate junction;cytoplasm;focal adhesion;intracellular part;macromolecular complex;membrane;plasma membrane;protein complex 1.24E-79 6 16 16 39.7

O94826 Mitochondrial import receptor subunit TOM70 TOMM70A >sp|O94826|TOM70_HUMAN Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70A PE=1 SV=1 -0.39 0.31 0.07 0.36 0.03 0.38 -0.94 0.01 0.253672681 0.217618274 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule metabolic process;metabolic process;mitochondrial transport;primary metabolic process;protein import;protein metabolic process;protein targeting;protein targeting to mitochondrion;protein transport;transport macromolecule transmembrane transporter activity;protein transmembrane transporter activity;protein transporter activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial outer membrane translocase complex;mitochondrial part;organelle part;protein complex 1.92E-126 1 16 16 35.2

Q14166 Tubulin--tyrosine ligase-like protein 12 TTLL12 >sp|Q14166|TTL12_HUMAN Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2 0.22 -0.09 0.23 0.04 -0.66 -0.82 0.07 -0.50 1.153422158 0.576164628 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification process "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;tubulin-tyrosine ligase activity" 2.17E-126 1 16 16 35.7

P46937-2;F5H202;P46937;E9PRV2;P46937-3;P46937-4;H0YCI3;H7C4S7;F5GWK7;F5GWH1;H7C5T8;Q8IX03;Q8IX03-2;H7C4U7;H7C535;Q96QZ7-4;Q96QZ7-3;E7EWI0;Q96QZ7-5;Q96QZ7-7;Q86UL8-2;Q96QZ7-6;Q86UL8;Q96QZ7-2;Q96QZ7 Yorkie homolog YAP1 >sp|P46937-2|YAP1_HUMAN Isoform 2 of Yorkie homolog OS=Homo sapiens GN=YAP1;>tr|F5H202|F5H202_HUMAN Yorkie homolog OS=Homo sapiens GN=YAP1 PE=2 SV=1;>sp|P46937|YAP1_HUMAN Yorkie homolog OS=Homo sapiens GN=YAP1 PE=1 SV=2;>tr|E9PRV2|E9PRV2_HUMAN Yorkie homol 0.01 -0.19 0.04 0.02 -0.02 -0.17 0.14 -0.26 0.167691781 0.046334358 "anatomical structure development;anatomical structure morphogenesis;biological adhesion;biological regulation;biosynthetic process;cell adhesion;cell cycle arrest;cell cycle process;cell development;cell differentiation;cell migration;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component assembly;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular response to abiotic stimulus;cellular response to gamma radiation;cellular response to ionizing radiation;cellular response to radiation;cellular response to stimulus;cellular response to stress;contact inhibition;developmental process;embryonic heart tube morphogenesis;embryonic morphogenesis;embryonic organ development;epidermal cell differentiation;epithelial cell development;epithelial cell differentiation;epithelial tube morphogenesis;glomerular epithelial cell development;glomerular visceral epithelial cell development;hippo signaling cascade;intracellular signal transduction;keratinocyte differentiation;lateral mesoderm development;localization;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;membrane organization;mesoderm development;metabolic process;mitotic cell cycle arrest;morphogenesis of an epithelium;negative regulation of activin receptor signaling pathway;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell death;negative regulation of cell differentiation;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell proliferation;negative regulation of cellular component movement;negative regulation of cellular process;negative regulation of developmental process;negative regulation of epithelial cell differentiation;negative regulation of intracellular protein kinase cascade;negative regulation of locomotion;negative regulation of programmed cell death;negative regulation of protein kinase B signaling cascade;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;nitrogen compound metabolic process;non-canonical Wnt receptor signaling pathway;notochord development;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;paraxial mesoderm development;planar cell polarity pathway involved in axis elongation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of gene expression;positive regulation of growth;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of organ growth;positive regulation of phosphatase activity;positive regulation of phosphoprotein phosphatase activity;positive regulation of receptor internalization;positive regulation of receptor-mediated endocytosis;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;positive regulation of transport;positive regulation of Wnt receptor signaling pathway;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein localization;protein localization in membrane;protein oligomerization;receptor clustering;regulation of activin receptor signaling pathway;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of developmental process;regulation of endocytosis;regulation of epithelial cell differentiation;regulation of establishment of planar polarity;regulation of gene expression;regulation of growth;regulation of hippo signaling cascade;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of keratinocyte proliferation;regulation of lipase activity;regulation of lipoprotein lipase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ growth;regulation of organ morphogenesis;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase B signaling cascade;regulation of receptor internalization;regulation of receptor-mediated endocytosis;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of stem cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transport;regulation of vesicle-mediated transport;regulation of Wnt receptor signaling pathway;response to abiotic stimulus;response to DNA damage stimulus;response to gamma radiation;response to ionizing radiation;response to radiation;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;SMAD protein signal transduction;somatic stem cell maintenance;stem cell maintenance;tissue development;tissue morphogenesis;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transcription, DNA-dependent;tube morphogenesis;vasculogenesis;Wnt receptor signaling pathway;Wnt receptor signaling pathway, planar cell polarity pathway" activin receptor binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;chromatin binding;DNA binding;molecular transducer activity;nucleic acid binding;nucleotide binding;protein binding;protein binding transcription factor activity;protein complex scaffold;protein C-terminus binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;receptor serine/threonine kinase binding;receptor signaling complex scaffold activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA polymerase II transcription factor binding transcription factor activity;signal transducer activity;SMAD binding;structural molecule activity;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transcription regulatory region DNA binding;transmembrane receptor protein serine/threonine kinase binding;type II activin receptor binding cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell junction;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nuclear part;nucleoplasm;nucleoplasm part;nucleus;occluding junction;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;postsynaptic density;protein complex;ruffle membrane;synapse part;tight junction;transcription factor complex Tight junction 7.74E-125 25 16 16 60

Q16181-2;E7ES33;E7EPK1;Q16181;G3V1Q4;H0Y3Y4;H0YFF6;F5GZE5;Q5JXL7;Q6ZU15 Septin-7 07-Sep >sp|Q16181-2|SEPT7_HUMAN Isoform 2 of Septin-7 OS=Homo sapiens GN=SEPT7;>tr|E7ES33|E7ES33_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=2 SV=2;>tr|E7EPK1|E7EPK1_HUMAN Septin-7 OS=Homo sapiens GN=SEPT7 PE=2 SV=1;>sp|Q16181|SEPT7_HUMAN Septin-7 OS=Homo sapiens -0.17 0.00 -0.10 0.06 0.31 0.17 -0.21 -0.13 0.257423684 -0.088802964 anatomical structure morphogenesis;biological regulation;cell cycle;cell cycle phase;cell cycle process;cell division;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cilium morphogenesis;cytokinesis;developmental process;macromolecular complex assembly;macromolecular complex subunit organization;mitosis;nuclear division;organelle fission;organelle organization;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of embryonic cell shape;regulation of embryonic development;regulation of multicellular organismal development;regulation of multicellular organismal process binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;structural molecule activity actin cytoskeleton;actin filament bundle;actomyosin;axon part;axon terminus;axoneme;cell cortex;cell cortex part;cell division site part;cell part;cell projection part;chromosomal part;cilium axoneme;cilium part;cleavage furrow;condensed chromosome kinetochore;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;microtubule cytoskeleton;midbody;neuron projection terminus;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;protein complex;septin complex;spindle;stress fiber;synapse 1.93E-126 10 17 16 44.5

P62937;F8WE65;C9J5S7;Q567Q0;Q9Y536;F5H284;A2BFH1;A6NM32;E5RIZ5 Peptidyl-prolyl cis-trans isomerase A;Peptidyl-prolyl cis-trans isomerase PPIA >sp|P62937|PPIA_HUMAN Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2;>tr|F8WE65|F8WE65_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens GN=PPIA PE=2 SV=1;>tr|C9J5S7|C9J5S7_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo 0.06 -0.08 -0.42 -0.04 -0.17 -0.06 0.42 0.00 0.412416808 -0.166935735 biological regulation;biosynthetic process;cell activation;cell migration;cell motility;cellular biosynthetic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;DNA metabolic process;DNA replication;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;establishment of localization;establishment of localization in cell;exocytosis;immune system process;interaction with host;interspecies interaction between organisms;leukocyte migration;lipid particle organization;locomotion;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;movement in environment of other organism involved in symbiotic interaction;movement in host environment;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-proline modification;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cellular process;positive regulation of protein secretion;positive regulation of protein transport;positive regulation of reproductive process;positive regulation of secretion;positive regulation of transport;positive regulation of viral genome replication;positive regulation of viral reproduction;primary metabolic process;protein folding;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of localization;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of reproductive process;regulation of secretion;regulation of transport;regulation of viral genome replication;regulation of viral reproduction;release of virus from host;reproductive process;RNA-dependent DNA replication;secretion;secretion by cell;transport;uncoating of virus;vesicle-mediated transport;viral reproductive process binding;catalytic activity;cis-trans isomerase activity;isomerase activity;peptide binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;unfolded protein binding;virion binding cell part;cytoplasm;cytoplasmic part;cytosol;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 0 9 17 16 89.1

K7ENL3;P40763-2;P40763;G8JLH9;K7EP08 Signal transducer and activator of transcription 3 STAT3 >tr|K7ENL3|K7ENL3_HUMAN Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=4 SV=1;>sp|P40763-2|STAT3_HUMAN Isoform Del-701 of Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3;>sp|P40763|STAT3_HUMAN Sig 0.09 -0.10 -0.02 -0.20 -0.69 -0.22 0.55 0.33 0.063470983 -0.053192257 "acute inflammatory response;acute-phase response;astrocyte differentiation;behavior;biological regulation;carbohydrate homeostasis;cell differentiation;cell proliferation;cell surface receptor linked signaling pathway;cellular component movement;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interleukin-6;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;cytokine-mediated signaling pathway;defense response;developmental process;eating behavior;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;eye photoreceptor cell differentiation;feeding behavior;glial cell differentiation;glucose homeostasis;homeostatic process;inflammatory response;interaction with host;interleukin-6-mediated signaling pathway;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular protein transport;intracellular signal transduction;intracellular transport;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;multicellular organismal homeostasis;multicellular organismal process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nerve growth factor receptor signaling pathway;neuron differentiation;nuclear import;nuclear transport;nucleocytoplasmic transport;photoreceptor cell differentiation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of Notch signaling pathway;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;protein import;protein import into nucleus;protein targeting;protein transport;radial glial cell differentiation;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organism growth;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of Notch signaling pathway;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproduction;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to ethanol;response to hormone stimulus;response to interleukin-6;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;sexual reproduction;signal transduction;stem cell maintenance;temperature homeostasis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;viral reproductive process;virus-host interaction" binding;calcium ion binding;cation binding;DNA binding;enzyme binding;ion binding;kinase binding;ligand-dependent nuclear receptor activity;metal ion binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein dimerization activity;protein kinase binding;receptor activity;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;signal transducer activity;signaling receptor activity;transcription regulatory region DNA bindingcell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;plasma membrane   Acute myeloid leukemia;Adipocytokine signaling pathway;Chemokine signaling pathway;Hepatitis C;Jak-STAT signaling pathway;ko05152;Measles;Pancreatic cancer;Pathways in cancer;Toxoplasmosis 6.82E-123 5 17 16 36.8

B4DDF4;Q99439;B4DUT8;Q99439-2;H3BTZ5;H3BVI6;K7ES69;H3BQH0;H3BQR6;K7EQ72;K7ER02;B7Z7E1;B4DUX6;P51911 Calponin-2 CNN2 >tr|B4DDF4|B4DDF4_HUMAN Calponin-2 OS=Homo sapiens GN=CNN2 PE=2 SV=1;>sp|Q99439|CNN2_HUMAN Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4;>tr|B4DUT8|B4DUT8_HUMAN Calponin-2 OS=Homo sapiens GN=CNN2 PE=2 SV=1;>sp|Q99439-2|CNN2_HUMAN Isoform 2 of Calponin-2 OS= -0.06 -0.14 -0.29 -0.15 -0.18 -0.14 0.59 0.47 0.72527752 -0.349351848 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;anatomical structure development;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to abiotic stimulus;cellular response to external stimulus;cellular response to mechanical stimulus;cellular response to stimulus;cytoskeleton organization;developmental process;hemopoiesis;hemopoietic or lymphoid organ development;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of endocytosis;negative regulation of locomotion;negative regulation of phagocytosis;negative regulation of transport;organ development;organelle organization;positive regulation of biological process;positive regulation of gene expression;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;regulation of actin filament-based process;regulation of biological process;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of gene expression;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of phagocytosis;regulation of smooth muscle contraction;regulation of system process;regulation of transport;regulation of vesicle-mediated transport;response to abiotic stimulus;response to external stimulus;response to mechanical stimulus;response to stimulus;response to stress;response to wounding;wound healing actin binding;binding;cytoskeletal protein binding;protein binding   actin filament bundle;actomyosin;cell junction;cell part;cell-cell junction;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;organelle;organelle part;stress fiber 6.67E-219 14 18 16 73.2

Q14103-3;Q14103;H0Y8G5;H0YA96;Q14103-4;B4DTC3;Q14103-2;D6RAF8;D6RF44;D6RBQ9;D6RD83;F5H6R6 Heterogeneous nuclear ribonucleoprotein D0 HNRNPD >sp|Q14103-3|HNRPD_HUMAN Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD;>sp|Q14103|HNRPD_HUMAN Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1;>tr|H0Y8G5|H0Y8G5_HUMAN Heterogeneous nuclear r -0.21 0.39 -0.26 0.45 -0.03 -0.30 -1.20 -0.25 0.712153434 0.533380562 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;sequence-specific DNA binding;telomeric DNA binding cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex 1.44E-144 12 18 16 47.1

P16152;B4DFK7;E9PQ63;A8MTM1 Carbonyl reductase [NADPH] 1 CBR1 >sp|P16152|CBR1_HUMAN Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 -0.06 -0.26 0.11 0.04 0.02 -0.03 0.49 -0.06 0.392701181 -0.148450857 arachidonic acid metabolic process;carboxylic acid metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cofactor metabolic process;cyclooxygenase pathway;drug metabolic process;fat-soluble vitamin metabolic process;fatty acid metabolic process;icosanoid metabolic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;quinone cofactor metabolic process;small molecule metabolic process;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process;vitamin K metabolic process;vitamin metabolic process"15-hydroxyprostaglandin dehydrogenase (NADP+) activity;carbonyl reductase (NADPH) activity;catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;prostaglandin-E2 9-reductase activity" cell part;cytoplasmic part;cytosol;intracellular part Arachidonic acid metabolism 0 4 19 16 78

O43390;O43390-2;O43390-3;E7ETM7 Heterogeneous nuclear ribonucleoprotein R HNRNPR >sp|O43390|HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1;>sp|O43390-2|HNRPR_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR;>sp|O43390-3|HNRPR_HUMAN Isoform 3 of Heterogeneo -0.30 1.04 -0.02 1.09 -0.24 0.27 -1.39 0.25 0.581462335 0.729420612 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;spliceosomal complex 4.77E-175 4 23 16 37.8

O60264 SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 SMARCA5 >sp|O60264|SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1 -0.04 0.98 -0.13 0.74 -0.47 -0.03 -1.06 0.12 0.837880494 0.748502329 "ATP-dependent chromatin remodeling;biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;chromatin assembly;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromatin silencing;chromatin silencing at rDNA;chromosome organization;developmental process;DNA metabolic process;DNA repair;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;double-strand break repair;embryo development;gene silencing;histone exchange;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of gene expression, epigenetic;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;nucleosome positioning;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of gene expression, epigenetic;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription initiation, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;chromatin binding;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleosome binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromatin remodeling complex;chromatin silencing complex;chromosome;condensed chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ISWI complex;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;NURF complex;organelle;organelle part;protein complex;RSF complex 1.28E-161 1 27 16 26.1

Q5VTE0;P68104;A6PW80;Q5JR01 Putative elongation factor 1-alpha-like 3;Elongation factor 1-alpha 1 EEF1A1P5;EEF1A1 >sp|Q5VTE0|EF1A3_HUMAN Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1;>sp|P68104|EF1A1_HUMAN Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 -0.08 -0.03 -0.21 0.01 -0.46 -0.30 0.08 -0.36 0.61333835 0.182765611 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;transcription, DNA-dependent" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex RNA transport 6.86E-214 4 28 16 53.9

P60842;J3KT12;P60842-2;J3QS69;J3KTB5;J3QL43;J3KSZ0;J3QR64;J3QLN6;J3KS25;J3KTN0;J3QKZ9;J3QL52;B4E102;J3KS93 Eukaryotic initiation factor 4A-I EIF4A1 >sp|P60842|IF4A1_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1;>tr|J3KT12|J3KT12_HUMAN Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=3 SV=1;>sp|P60842-2|IF4A1_HUMAN Isoform 2 of Eukaryotic initiation factor 4A 0.14 -0.02 -0.18 -0.07 -0.08 -0.39 0.11 -0.38 0.445383328 0.152296985 biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cellular process;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;signal transduction;translational initiation;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mRNA binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA cap binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex RNA transport 0 15 29 16 69.5

Q15019;Q15019-2;B5MCX3;H7C2Y0;C9J2Q4;C9J938;C9JB25;C9IZU3;C9IY94;H7C310;C9JZI2;C9JQJ4;C9JFT1;F8WB65;B5MD47;C9JT15;C9JSE7;H7C1T1 Septin-2 02-Sep >sp|Q15019|SEPT2_HUMAN Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1;>sp|Q15019-2|SEPT2_HUMAN Isoform 2 of Septin-2 OS=Homo sapiens GN=SEPT2;>tr|B5MCX3|B5MCX3_HUMAN Septin-2 OS=Homo sapiens GN=SEPT2 PE=2 SV=1;>tr|H7C2Y0|H7C2Y0_HUMAN Septin-2 (Fragment) OS=Ho -0.12 -0.03 -0.11 0.08 0.27 0.06 -0.09 0.08 0.592487654 -0.121283671 anatomical structure formation involved in morphogenesis;biological regulation;cell cycle;cell cycle phase;cell cycle process;cell division;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;cilium assembly;developmental process;mitosis;neuron projection development;nuclear division;organelle fission;organelle organization;regulation of amine transport;regulation of amino acid transport;regulation of anion transport;regulation of biological process;regulation of cellular process;regulation of ion transport;regulation of L-glutamate transport;regulation of localization;regulation of organic acid transport;regulation of protein localization;regulation of transport;response to stimulus;signal transduction;smoothened signaling pathway binding;enzyme regulator activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding actin cytoskeleton;cell cortex part;cell division site part;cell part;cell projection membrane;cell projection part;cell surface;chromosomal part;cilium membrane;cilium part;cleavage furrow;condensed chromosome kinetochore;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;exocyst;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane part;midbody;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane part;protein complex;septin complex;spindle;synapse 2.43E-208 18 17 17 57.6

P24752;G3XAB4;H0YEL7;E9PRQ6;E9PKF3 "Acetyl-CoA acetyltransferase, mitochondrial" ACAT1 ">sp|P24752|THIL_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1" 0.10 0.00 -0.05 -0.01 0.35 -0.04 -0.10 -0.27 0.063567971 0.024959888 adipose tissue development;amine catabolic process;amine metabolic process;anatomical structure development;biosynthetic process;brain development;branched chain family amino acid catabolic process;branched chain family amino acid metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone body metabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;ketone body biosynthetic process;ketone body catabolic process;lipid metabolic process;liver development;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;metanephric proximal convoluted tubule development;nitrogen compound metabolic process;organ development;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;proximal convoluted tubule development;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to nutrient levels;response to organic cyclic compound;response to organic substance;response to starvation;response to stimulus;response to stress;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;tissue development "acetyl-CoA C-acetyltransferase activity;acetyl-CoA C-acyltransferase activity;acetyltransferase activity;binding;C-acetyltransferase activity;C-acyltransferase activity;catalytic activity;cation binding;coenzyme binding;cofactor binding;ion binding;metal ion binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part "Benzoate degradation;Butanoate metabolism;Carbon fixation pathways in prokaryotes;Fatty acid metabolism;Glyoxylate and dicarboxylate metabolism;Lysine degradation;Propanoate metabolism;Pyruvate metabolism;Synthesis and degradation of ketone bodies;Terpenoid backbone biosynthesis;Tryptophan metabolism;Two-component system;Valine, leucine and isoleucine degradation" 1.31E-168 5 17 17 51.3

P46379-2;B0UX83;P46379;P46379-3;P46379-4;P46379-5;F6S6P2;H0Y4L1;F6UR09;F6U1F2;F6XTU0;H0Y710;F6RG75;F6WML8;F6VEM6;F6X9W3;F6U341;F6TC96 Large proline-rich protein BAG6 BAG6 ">sp|P46379-2|BAG6_HUMAN Isoform 2 of Large proline-rich protein BAG6 OS=Homo sapiens GN=BAG6;>tr|B0UX83|B0UX83_HUMAN HLA-B associated transcript 3, isoform CRA_a OS=Homo sapiens GN=BAG6 PE=2 SV=1;>sp|P46379|BAG6_HUMAN Large proline-rich protein BAG6 OS=Hom" 0.35 -0.04 0.17 -0.18 -0.06 -0.05 0.31 -0.33 0.229086635 0.106057824 "anatomical structure development;apoptosis;apoptosis in response to endoplasmic reticulum stress;biological regulation;brain development;catabolic process;cell cycle process;cell death;cell differentiation;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule catabolic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromosome organization;chromosome organization involved in meiosis;death;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis;DNA damage response, signal transduction resulting in induction of apoptosis;embryo development;establishment of localization;gamete generation;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;intracellular signal transduction;kidney development;localization;localization within membrane;lung development;macromolecule catabolic process;macromolecule localization;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of proteasomal ubiquitin-dependent protein catabolic process;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;organ development;organelle organization;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein acetylation;protein acylation;protein insertion into ER membrane;protein insertion into membrane;protein localization;protein localization to organelle;protein metabolic process;protein modification process;protein stabilization;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of cell death;regulation of cell proliferation;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein stability;regulation of proteolysis;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;signal transduction in response to DNA damage;spermatogenesis;synaptonemal complex assembly;synaptonemal complex organization;tail-anchored membrane protein insertion into ER membrane;transport;ubiquitin-dependent protein catabolic process" binding;polyubiquitin binding;proteasome binding;protein binding;protein complex binding;ribonucleoprotein binding;ribosome binding;small conjugating protein binding;ubiquitin binding BAT3 complex;cell part;cytoplasm;cytoplasmic part;cytosolic part;ER membrane insertion complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex 3.40E-88 18 17 17 23.3

Q6YHK3-4;Q6YHK3;Q6YHK3-2;Q6YHK3-3 CD109 antigen CD109 >sp|Q6YHK3-4|CD109_HUMAN Isoform 4 of CD109 antigen OS=Homo sapiens GN=CD109;>sp|Q6YHK3|CD109_HUMAN CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2;>sp|Q6YHK3-2|CD109_HUMAN Isoform 2 of CD109 antigen OS=Homo sapiens GN=CD109;>sp|Q6YHK3-3|CD109_HUMAN Isofo -0.42 0.14 -0.37 0.56 1.76 1.55 -0.48 0.09 0.528867255 -0.752990438 biological regulation;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity anchored to membrane;cell part;extracellular region part;extracellular space;intrinsic to membrane;membrane;membrane part;plasma membrane 4.36E-94 4 17 17 16.5

Q8NBJ5;M0QX72;M0QYH0;Q5SXQ3;F5H3T5;Q8IYK4 Procollagen galactosyltransferase 1 COLGALT1 >sp|Q8NBJ5|GT251_HUMAN Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1 -0.30 -0.17 -0.07 0.12 0.76 0.59 -0.15 -0.05 0.679268406 -0.39039277 biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide metabolic process;cellular process;extracellular matrix organization;extracellular structure organization;lipid biosynthetic process;lipid metabolic process;lipopolysaccharide biosynthetic process;lipopolysaccharide metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;polysaccharide biosynthetic process;polysaccharide metabolic process;primary metabolic process "catalytic activity;galactosyltransferase activity;procollagen galactosyltransferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;UDP-galactosyltransferase activity;UDP-glycosyltransferase activity" cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Lysine degradation;Other types of O-glycan biosynthesis 9.67E-70 6 17 17 25.6

P17812;B4DR64;B7Z9C4;Q9NRF8 CTP synthase 1 CTPS1 >sp|P17812|PYRG1_HUMAN CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2;>tr|B4DR64|B4DR64_HUMAN CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=2 SV=1 0.19 -0.17 0.00 -0.08 -0.01 -0.18 0.40 0.00 0.174176413 -0.068495388 amine metabolic process;biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;CTP biosynthetic process;CTP metabolic process;'de novo' CTP biosynthetic process;glutamine family amino acid metabolic process;glutamine metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;response to chemical stimulus;response to drug;response to stimulus;ribonucleoside metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;CTP synthase activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Pyrimidine metabolism 3.37E-153 4 17 17 37.6

P07339;H7C469;C9JH19;F8WD96;H7C1V0;F8W787Cathepsin D;Cathepsin D light chain;Cathepsin D heavy chain CTSD >sp|P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1;>tr|H7C469|H7C469_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=3 SV=1;>tr|C9JH19|C9JH19_HUMAN Cathepsin D light chain (Fragment) OS=Homo sapiens GN=CTSD PE=2 SV=1;>tr|F8WD96 -0.61 -0.40 0.13 0.31 0.44 0.52 0.25 0.25 0.954876206 -0.508477721 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;autophagic vacuole assembly;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;collagen catabolic process;collagen metabolic process;death;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;immune system process;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;organelle assembly;organelle organization;primary metabolic process;protein metabolic process;proteolysis;response to biotic stimulus;response to stimulus;vacuole organization "aspartic-type endopeptidase activity;aspartic-type peptidase activity;catalytic activity;endopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;extracellular region part;extracellular space;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal lumen;lysosome;lytic vacuole;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrion;organelle;organelle lumen;organelle part;pigment granule;vacuolar lumen;vacuolar part;vacuole;vesicle ko05152;Lysosome 6.77E-201 6 17 17 45.9

Q13561;Q13561-3;Q13561-2;F5H2S7;F5H223;F8W1I6;H0YI98;F8VW18;F8VRV7;F8VX93;H0YHL1;F8W0U6 Dynactin subunit 2 DCTN2 >sp|Q13561|DCTN2_HUMAN Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4;>sp|Q13561-3|DCTN2_HUMAN Isoform 3 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2;>sp|Q13561-2|DCTN2_HUMAN Isoform 2 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2;>tr|F5H2S7|F5H2 -0.04 -0.04 -0.10 0.04 0.24 0.21 0.08 -0.08 0.822289881 -0.15238215 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;cell cycle phase;cell cycle process;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;G2/M transition of mitotic cell cycle;immune system process;microtubule cytoskeleton organization;microtubule-based process;mitosis;mitotic spindle organization;nuclear division;organelle fission;organelle organization;spindle organization "catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;pyrophosphatase activity" cell part;cell projection part;centrosome;chromosomal part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;dynactin complex;dynein complex;growth cone;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;microtubule;microtubule associated complex;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex;site of polarized growth;vesicle Huntington's disease;Vasopressin-regulated water reabsorption 8.55E-243 12 17 17 46.1

Q7Z478;H0Y8L1 ATP-dependent RNA helicase DHX29 DHX29 >sp|Q7Z478|DHX29_HUMAN ATP-dependent RNA helicase DHX29 OS=Homo sapiens GN=DHX29 PE=1 SV=2 0.16 -0.02 0.00 -0.13 0.17 0.23 0.33 -0.01 0.797042053 -0.173156751 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 3.25E-109 2 17 17 18.3

Q7L2E3-3;H7BXY3;Q7L2E3;Q7L2E3-2 Putative ATP-dependent RNA helicase DHX30 DHX30 >sp|Q7L2E3-3|DHX30_HUMAN Isoform 3 of Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30;>tr|H7BXY3|H7BXY3_HUMAN Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=2 SV=1;>sp|Q7L2E3|DHX30_HUMAN Putative ATP-dependent RNA -0.11 0.21 0.16 0.28 0.01 -0.32 -0.73 -0.60 1.217726859 0.542477696 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;chromatin binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding" cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle part 3.16E-86 4 17 17 18.6

P60228;E5RGA2;H0YBR5;E5RIT4;E5RHS5;H0YAW4;E5RII3;E5RIP5;E5RJ25;H0YBP5 Eukaryotic translation initiation factor 3 subunit E EIF3E >sp|P60228|EIF3E_HUMAN Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1;>tr|E5RGA2|E5RGA2_HUMAN Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=2 SV=10.14 0.04 -0.09 -0.09 -0.20 -0.43 -0.04 -0.47 1.031584516 0.285518023 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;negative regulation of translational initiation;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;RNA catabolic process;RNA metabolic process;translational initiation" "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;PML body;protein complex Hepatitis C;RNA transport 1.49E-195 10 17 17 42.5

Q9H6S3;B7ZKL3;Q9H6S3-2;H0YD62;H0YF37;E9PN68;E9PLN2;E9PNT0;E9PLH1 Epidermal growth factor receptor kinase substrate 8-like protein 2 EPS8L2 >sp|Q9H6S3|ES8L2_HUMAN Epidermal growth factor receptor kinase substrate 8-like protein 2 OS=Homo sapiens GN=EPS8L2 PE=1 SV=2;>tr|B7ZKL3|B7ZKL3_HUMAN EPS8L2 protein OS=Homo sapiens GN=EPS8L2 PE=2 SV=1;>sp|Q9H6S3-2|ES8L2_HUMAN Isoform 2 of Epidermal growth -0.40 -0.42 0.26 0.08 -0.98 -0.17 0.75 0.25 0.070752271 -0.083406413 cell part;cytoplasm;intracellular part;membrane;plasma membrane 3.44E-143 9 17 17 36.6

Q5SNT6;F8W7U3;Q641Q2;J3KP36;Q9Y4E1-3;E7ESD2;Q9Y4E1-6;Q9Y4E1-2;Q9Y4E1;Q641Q2-2;Q9Y4E1-4;Q9Y4E1-5;F5GY39;Q5SRD0;B1AP61 WASH complex subunit FAM21B;WASH complex subunit FAM21A;WASH complex subunit FAM21C FAM21B;FAM21A;FAM21C >sp|Q5SNT6|FA21B_HUMAN WASH complex subunit FAM21B OS=Homo sapiens GN=FAM21B PE=2 SV=2;>tr|F8W7U3|F8W7U3_HUMAN WASH complex subunit FAM21A OS=Homo sapiens GN=FAM21A PE=2 SV=1;>sp|Q641Q2|FA21A_HUMAN WASH complex subunit FAM21A OS=Homo sapiens GN=FAM21A PE=2 -0.05 0.03 0.05 -0.27 -0.11 -0.34 0.05 0.03 0.101400716 0.033434506 "cellular process;endosome transport;establishment of localization;establishment of localization in cell;intracellular transport;retrograde transport, endosome to Golgi;transport;vesicle-mediated transport" cell part;cytoplasmic part;early endosome;early endosome membrane;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane;protein complex;WASH complex 1.36E-200 15 17 17 27.9

Q9Y285;K7ER00;B4E363;K7ER16;K7EPH2;K7EK06;K7ERS0;REV__Q96P70 Phenylalanine--tRNA ligase alpha subunit FARSA >sp|Q9Y285|SYFA_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3;>tr|K7ER00|K7ER00_HUMAN Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=3 SV=1;>tr|B4E363|B4E363_HUMAN Phenylalanine--tRNA ligase alpha s 0.20 -0.10 0.21 -0.12 0.07 -0.20 0.23 -0.38 0.274319886 0.116339769 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;phenylalanyl-tRNA aminoacylation;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;phenylalanine-tRNA ligase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Aminoacyl-tRNA biosynthesis 9.52E-147 8 17 17 43.5

O95373;E9PLB2;E9PLJ0 Importin-7 IPO7 >sp|O95373|IPO7_HUMAN Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 0.19 -0.02 0.09 -0.05 -0.11 -0.08 0.16 -0.26 0.505276825 0.124753891 biological regulation;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;multi-organism process;nuclear import;nuclear transport;nucleocytoplasmic transport;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular process;reproductive process;response to stimulus;signal transduction;transport;viral reproductive process;virus-host interaction binding;enzyme binding;enzyme regulator activity;GTPase binding;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;protein transporter activity;Ran GTPase binding;Ras GTPase binding;small GTPase binding;small GTPase regulator activity;substrate-specific transporter activity;transporter activity cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;nuclear part;nuclear pore;organelle;organelle part;pore complex;protein complex 2.94E-128 3 17 17 19.4

E9PEM5;P50851-2;F5H1X8;P50851;H0YAC6;H0Y9N9;Q5T321;Q8NFP9;F5GXV7 Lipopolysaccharide-responsive and beige-like anchor protein LRBA >tr|E9PEM5|E9PEM5_HUMAN Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=2 SV=1;>sp|P50851-2|LRBA_HUMAN Isoform 2 of Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA;>tr|F5H1X8|F5H1X8 0.30 -0.11 -0.19 -0.26 -0.38 0.06 0.80 0.05 0.2822136 -0.198510241 localization;macromolecule localization;protein localization cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endomembrane system;endoplasmic reticulum;Golgi apparatus;Golgi apparatus part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lysosome;lytic vacuole;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle part;plasma membrane;trans-Golgi network;vacuole;vesicle 1.86E-93 9 17 17 8.7

P49736;H0Y8E6 DNA replication licensing factor MCM2 MCM2 >sp|P49736|MCM2_HUMAN DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4;>tr|H0Y8E6|H0Y8E6_HUMAN DNA replication licensing factor MCM2 (Fragment) OS=Homo sapiens GN=MCM2 PE=3 SV=1 0.02 -0.01 -0.08 0.13 0.28 -0.39 -0.89 -0.93 0.743487815 0.497071479 biological regulation;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin organization;chromosome organization;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA unwinding involved in replication;DNA-dependent DNA replication initiation;G1/S transition of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome assembly;nucleosome organization;organelle organization;primary metabolic process;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;S phase;S phase of mitotic cell cycle "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;DNA binding;DNA helicase activity;DNA replication origin binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;sequence-specific DNA binding" cell part;chromatin;chromosomal part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;MCM complex;membrane-bounded organelle;nuclear chromosome part;nuclear origin of replication recognition complex;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;origin recognition complex;protein complex Cell cycle;Cell cycle - yeast;DNA replication;Meiosis - yeast 2.10E-106 2 17 17 24.9

Q9Y2A7;Q9Y2A7-2;F8W050;P55160 Nck-associated protein 1NCKAP1>sp|Q9Y2A7|NCKP1_HUMAN Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1;>sp|Q9Y2A7-2|NCKP1_HUMAN Isoform 2 of Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 0.11 -0.16 -0.12 0.00 0.02 0.21 0.20 0.01 0.807198381 -0.151618541 "actin cytoskeleton organization;actin filament-based process;actin polymerization-dependent cell motility;activation of immune response;ameboidal cell migration;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;anterior/posterior axis specification;anterior/posterior axis specification, embryo;anterior/posterior pattern specification;antigen receptor-mediated signaling pathway;apical protein localization;apoptosis;asymmetric protein localization;axis specification;B cell homeostasis;B cell receptor signaling pathway;basal protein localization;biological regulation;body morphogenesis;cell chemotaxis;cell death;cell development;cell migration;cell migration involved in gastrulation;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to stimulus;central nervous system development;chemotaxis;chordate embryonic development;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;death;defense response;developmental process;embryo development;embryo development ending in birth or egg hatching;embryonic axis specification;embryonic body morphogenesis;embryonic foregut morphogenesis;embryonic heart tube development;embryonic morphogenesis;embryonic organ morphogenesis;embryonic pattern specification;endoderm development;erythrocyte development;establishment or maintenance of actin cytoskeleton polarity;establishment or maintenance of cell polarity;establishment or maintenance of cytoskeleton polarity;homeostasis of number of cells;homeostatic process;immune response;immune response-activating cell surface receptor signaling pathway;immune response-activating signal transduction;immune response-regulating cell surface receptor signaling pathway;immune response-regulating signaling pathway;immune system process;in utero embryonic development;innate immune response;lamellipodium assembly;leukocyte chemotaxis;leukocyte homeostasis;leukocyte migration;localization;locomotion;lymphocyte homeostasis;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;maintenance of cell polarity;mesoderm morphogenesis;mesodermal cell migration;myeloid cell homeostasis;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of cytokine production;negative regulation of hydrolase activity;negative regulation of interleukin-17 production;negative regulation of interleukin-6 production;negative regulation of molecular function;negative regulation of multicellular organismal process;negative regulation of myosin-light-chain-phosphatase activity;negative regulation of phosphatase activity;negative regulation of phosphoprotein phosphatase activity;negative regulation of programmed cell death;neural tube closure;neutrophil chemotaxis;notochord morphogenesis;organ morphogenesis;organelle organization;paraxial mesoderm morphogenesis;pattern specification process;positive regulation of actin filament polymerization;positive regulation of alpha-beta T cell activation;positive regulation of alpha-beta T cell differentiation;positive regulation of B cell activation;positive regulation of B cell differentiation;positive regulation of B cell proliferation;positive regulation of behavior;positive regulation of biological process;positive regulation of CD4-positive, alpha-beta T cell activation;positive regulation of CD4-positive, alpha-beta T cell differentiation;positive regulation of CD8-positive, alpha-beta T cell differentiation;positive regulation of cell activation;positive regulation of cell adhesion;positive regulation of cell adhesion mediated by integrin;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of cytoskeleton organization;positive regulation of developmental process;positive regulation of endocytosis;positive regulation of erythrocyte differentiation;positive regulation of gamma-delta T cell activation;positive regulation of gamma-delta T cell differentiation;positive regulation of immune response;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of leukocyte proliferation;positive regulation of locomotion;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of lymphocyte proliferation;positive regulation of mononuclear cell proliferation;positive regulation of myeloid cell differentiation;positive regulation of neutrophil chemotaxis;positive regulation of organelle organization;positive regulation of phagocytosis;positive regulation of phagocytosis, engulfment;positive regulation of protein complex assembly;positive regulation of protein polymerization;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of T cell activation;positive regulation of T cell differentiation;positive regulation of T cell proliferation;positive regulation of transport;posttranscriptional regulation of gene expression;programmed cell death;protein complex assembly;protein complex subunit organization;protein localization;protein stabilization;regionalization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of alpha-beta T cell activation;regulation of alpha-beta T cell differentiation;regulation of anatomical structure size;regulation of apoptosis;regulation of B cell activation;regulation of B cell differentiation;regulation of B cell proliferation;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of CD4-positive, alpha-beta T cell activation;regulation of CD4-positive, alpha-beta T cell differentiation;regulation of CD8-positive, alpha-beta T cell differentiation;regulation of cell activation;regulation of cell adhesion;regulation of cell adhesion mediated by integrin;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular component size;regulation of cellular metabolic process;regulation of cellular process;regulation of chemotaxis;regulation of cytokine production;regulation of cytoskeleton organization;regulation of dephosphorylation;regulation of developmental process;regulation of endocytosis;regulation of erythrocyte differentiation;regulation of gamma-delta T cell activation;regulation of gamma-delta T cell differentiation;regulation of gene expression;regulation of homeostatic process;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of interleukin-17 production;regulation of interleukin-6 production;regulation of leukocyte activation;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of leukocyte proliferation;regulation of lipase activity;regulation of lipoprotein lipase activity;regulation of localization;regulation of locomotion;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of lymphocyte proliferation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of myosin-light-chain-phosphatase activity;regulation of neutrophil chemotaxis;regulation of organelle organization;regulation of phagocytosis;regulation of phagocytosis, engulfment;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of protein localization;regulation of protein polymerization;regulation of protein stability;regulation of response to external stimulus;regulation of response to stimulus;regulation of T cell activation;regulation of T cell differentiation;regulation of T cell proliferation;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to drug;response to external stimulus;response to stimulus;response to stress;segmentation;signal transduction;somitogenesis;system development;T cell homeostasis;taxis;tissue development;tissue morphogenesis;tube closure;tube development;tube formation;zygotic determination of anterior/posterior axis, embryo" binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;kinase activator activity;kinase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;protein complex binding;protein kinase activator activity;protein kinase regulator activity;Rac GTPase activator activity;Ras GTPase activator activity;Rho GTPase activator activity;small GTPase regulator activity cell part;cell projection membrane;cell projection part;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;lamellipodium membrane;leading edge membrane;macromolecular complex;membrane part;plasma membrane part;protein complex;SCAR complex Regulation of actin cytoskeleton 4.28E-72 4 17 17 16.5

P49790;F6QR24 Nuclear pore complex protein Nup153 NUP153 >sp|P49790|NU153_HUMAN Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2;>tr|F6QR24|F6QR24_HUMAN Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=2 SV=1 -0.42 0.66 0.06 0.73 0.15 -0.01 -1.03 0.05 0.500704918 0.465316547 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;entry into cell of other organism involved in symbiotic interaction;entry into host;entry into host cell;entry into other organism involved in symbiotic interaction;entry of virus into host cell;establishment of localization;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;interaction with host;interspecies interaction between organisms;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide transport;movement in environment of other organism involved in symbiotic interaction;movement in host environment;mRNA transport;multi-organism process;negative regulation of biological process;negative regulation of intracellular transport;negative regulation of nucleobase-containing compound transport;negative regulation of nucleocytoplasmic transport;negative regulation of RNA export from nucleus;negative regulation of transport;nuclear pore complex assembly;nuclear pore organization;nucleic acid transport;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of glucose transport;regulation of intracellular transport;regulation of localization;regulation of nucleobase-containing compound transport;regulation of nucleocytoplasmic transport;regulation of RNA export from nucleus;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process binding;cation binding;DNA binding;ion binding;metal ion binding;nucleic acid binding;nucleocytoplasmic transporter activity;protein anchor;protein binding;structural constituent of nuclear pore;structural molecule activity;transition metal ion binding;transporter activity;zinc ion binding cell part;cytoplasm;inclusion body;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;nuclear inclusion body;nuclear membrane;nuclear part;nuclear periphery;nucleolus;nucleoplasm;organelle;organelle membrane;organelle part RNA transport 4.89E-114 2 17 17 18.4

O00151 PDZ and LIM domain protein 1 PDLIM1 >sp|O00151|PDLI1_HUMAN PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4 0.00 -0.09 -0.15 -0.05 -0.68 -0.12 0.29 0.25 0.01105363 -0.007762377 "biological regulation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to chemical stimulus;response to hypoxia;response to oxidative stress;response to oxygen levels;response to stimulus;response to stress" binding;cation binding;ion binding;metal ion binding;protein binding transcription factor activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleoplasm part;organelle;organelle part;protein complex;transcription factor complex 8.02E-228 1 17 17 67.5

P25786;P25786-2;F5GX11;B4DEV8;F5H112 Proteasome subunit alpha type-1 PSMA1 >sp|P25786|PSA1_HUMAN Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1;>sp|P25786-2|PSA1_HUMAN Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1;>tr|F5GX11|F5GX11_HUMAN Proteasome subunit alpha type-1 OS=Homo sapien -0.05 0.05 -0.07 -0.01 0.05 -0.08 -0.15 -0.13 0.441127239 0.056833741 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of defense response;negative regulation of immune response;negative regulation of immune system process;negative regulation of inflammatory response;negative regulation of inflammatory response to antigenic stimulus;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of inflammatory response;regulation of inflammatory response to antigenic stimulus;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" "binding;catalytic activity;endopeptidase activity;hydrolase activity;lipopolysaccharide binding;nucleic acid binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;RNA binding;threonine-type endopeptidase activity;threonine-type peptidase activity" "cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;polysome;proteasome core complex;proteasome core complex, alpha-subunit complex;protein complex;ribonucleoprotein complex" Proteasome 9.56E-86 5 17 17 51

Q9P2B2 Prostaglandin F2 receptor negative regulator PTGFRN >sp|Q9P2B2|FPRP_HUMAN Prostaglandin F2 receptor negative regulator OS=Homo sapiens GN=PTGFRN PE=1 SV=2 0.02 -0.02 0.09 -0.02 0.11 0.30 0.03 -0.04 0.42573518 -0.082931499 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;lipid particle organization;organelle organization cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 5.55E-62 1 17 17 22.4

Q6NZI2;Q6NZI2-2;Q6NZI2-3 Polymerase I and transcript release factor PTRF >sp|Q6NZI2|PTRF_HUMAN Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1;>sp|Q6NZI2-2|PTRF_HUMAN Isoform 2 of Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF -0.21 0.28 -0.38 0.32 0.93 0.55 -0.91 0.01 0.115313529 -0.141319597 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;termination of RNA polymerase I transcription;transcription initiation from RNA polymerase I promoter;transcription initiation, DNA-dependent;transcription termination, DNA-dependent" binding;nucleic acid binding;RNA binding;rRNA binding;rRNA primary transcript binding caveola;cell part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane part;membrane raft;membrane-bounded organelle;mitochondrion;nuclear part;nucleoplasm;organelle;organelle part;plasma membrane part 0 3 17 17 40.3

P38159;P38159-2;H0Y6E7;H3BT71;Q96E39;B3KRG5;H3BUY5;H3BR27;P38159-3;H3BNC1;O75526;Q8N7X1 "RNA-binding motif protein, X chromosome;RNA-binding motif protein, X chromosome, N-terminally processed;RNA binding motif protein, X-linked-like-1" RBMX;RBMXL1 ">sp|P38159|RBMX_HUMAN RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3;>sp|P38159-2|RBMX_HUMAN Isoform 2 of RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX;>tr|H0Y6E7|H0Y6E7_HUMAN RNA-binding motif protein, X chromo" -0.27 1.14 0.17 1.12 -0.07 0.20 -1.46 0.18 0.664240387 0.827332139 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interleukin-1;cellular response to organic substance;cellular response to stimulus;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;membrane protein ectodomain proteolysis;membrane protein proteolysis;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein oligomerization;proteolysis;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to cytokine stimulus;response to interleukin-1;response to organic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;chromatin binding;core promoter binding;DNA binding;mRNA binding;nucleic acid binding;nucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;transcription regulatory region DNA binding catalytic step 2 spliceosome;cell part;chromatin;chromosomal part;euchromatin;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex;vesicle Spliceosome 8.21E-102 12 17 17 42.5

P62753;A2A3R5;A2A3R7;REV__Q9Y5R4;Q9Y253-2;B4DG64;Q9Y253 40S ribosomal protein S6 RPS6 >sp|P62753|RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1;>tr|A2A3R5|A2A3R5_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=2 SV=1 -0.06 0.04 -0.08 0.02 -0.01 -0.48 -0.27 -0.39 1.071187277 0.270675473 "biological regulation;biosynthetic process;carbohydrate homeostasis;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chemical homeostasis;cotranslational protein targeting to membrane;DNA biosynthetic process;DNA metabolic process;DNA repair;DNA replication;DNA synthesis involved in DNA repair;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glucose homeostasis;homeostatic process;insulin receptor signaling pathway;intracellular protein transport;intracellular signal transduction;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;postreplication repair;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;pyrimidine dimer repair;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to light stimulus;response to organic substance;response to peptide hormone stimulus;response to radiation;response to stimulus;response to stress;response to UV;response to UV-C;ribonucleoprotein complex assembly;ribonucleoprotein complex biogenesis;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;ribosomal small subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;signal transduction;SRP-dependent cotranslational protein targeting to membrane;TOR signaling cascade;translation;translational elongation;translational initiation;translational termination;transmembrane receptor protein tyrosine kinase signaling pathway;transport;viral transcription" "binding;catalytic activity;cation binding;damaged DNA binding;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;ion binding;metal ion binding;nucleic acid binding;nucleotidyltransferase activity;structural constituent of ribosome;structural molecule activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome;small ribosomal subunit Insulin signaling pathway;mTOR signaling pathway;Ribosome 9.76E-175 7 17 17 48.2

C9J9K3;P08865;A6NE09;C9JQR9 40S ribosomal protein SA RPSA;RPSAP58 >tr|C9J9K3|C9J9K3_HUMAN 40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=2 SV=1;>sp|P08865|RSSA_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4;>tr|A6NE09|A6NE09_HUMAN 40S ribosomal protein SA OS=Homo sapiens GN=RPSAP58 PE=2 0.11 -0.03 -0.10 -0.01 -0.11 -0.33 0.06 -0.14 0.570059192 0.122898492 "biological adhesion;biosynthetic process;catabolic process;cell adhesion;cellular biosynthetic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cleavage involved in rRNA processing;cotranslational protein targeting to membrane;endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage involved in rRNA processing;endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA);endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA);establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;establishment of RNA localization;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA 3'-end processing;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosomal small subunit assembly;RNA 3'-end processing;RNA biosynthetic process;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA processing;RNA transport;rRNA 3'-end processing;rRNA export from nucleus;rRNA metabolic process;rRNA processing;rRNA transport;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;laminin receptor activity;receptor activity;ribonucleoprotein binding;ribosome binding;structural constituent of ribosome;structural molecule activity 90S preribosome;cell part;cytosolic small ribosomal subunit;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;preribosome;ribonucleoprotein complex;small ribosomal subunit Ribosome 0 4 17 17 66.3

E7EP00;P53992;G5EA31;B4DZT4;F6RFB3;REV__Q8NEG5 Protein transport protein Sec24C SEC24C >tr|E7EP00|E7EP00_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=2 SV=2;>sp|P53992|SC24C_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3;>tr|G5EA31|G5EA31_HUMAN Protein transport protein Sec24C OS=Homo sapien -0.10 -0.10 0.10 -0.18 0.32 0.29 0.20 0.02 1.26194514 -0.279169866 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;COPII vesicle coating;ER to Golgi vesicle-mediated transport;establishment of localization;establishment of localization in cell;establishment of protein localization;glycosylation;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;organelle organization;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein transport;small molecule metabolic process;transport;vesicle coating;vesicle organization;vesicle-mediated transport binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;COPII vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;protein complex;vesicle coat Protein processing in endoplasmic reticulum 3.31E-80 6 17 17 24.1

F5GZ12;Q9UBC9;B1AN48 Small proline-rich protein 3 SPRR3 >tr|F5GZ12|F5GZ12_HUMAN Small proline-rich protein 3 OS=Homo sapiens GN=SPRR3 PE=2 SV=1;>sp|Q9UBC9|SPRR3_HUMAN Small proline-rich protein 3 OS=Homo sapiens GN=SPRR3 PE=1 SV=2;>tr|B1AN48|B1AN48_HUMAN Small proline-rich protein 3 (Fragment) OS=Homo sapiens G 0.23 1.38 -1.20 -0.47 1.84 2.86 0.93 0.79 0.950238042 -1.62040212 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process;response to stimulus;response to stress;response to wounding;wound healing structural molecule activity cell part;cytoplasm;intracellular part 6.96E-105 3 17 17 89.4

P60174-1;P60174;P60174-4 Triosephosphate isomerase TPI1 >sp|P60174-1|TPIS_HUMAN Isoform 2 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1;>sp|P60174|TPIS_HUMAN Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3;>sp|P60174-4|TPIS_HUMAN Isoform 4 of Triosephosphate isomerase OS=Homo sapiens GN=TPI1 0.00 -0.13 -0.30 0.01 0.11 0.00 0.34 0.03 0.90681755 -0.222279659 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular aldehyde metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;developmental process;embryo development;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glyceraldehyde-3-phosphate metabolic process;glycolysis;heterocycle metabolic process;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;NADP metabolic process;NADPH regeneration;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organophosphate metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;pentose-phosphate shunt;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "catalytic activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting aldoses and ketoses;isomerase activity;triose-phosphate isomerase activity" cell part;cytoplasmic part;cytosol;intracellular part Carbon fixation in photosynthetic organisms;Fructose and mannose metabolism;Glycolysis /

Gluconeogenesis;Inositol phosphate metabolism 0 3 17 17 77.9
Q6PGP7;D6RCE2;D6RDA0 Tetratricopeptide repeat protein 37 TTC37 >sp|Q6PGP7|TTC37_HUMAN Tetratricopeptide repeat protein 37 OS=Homo sapiens GN=TTC37 PE=1 SV=1 -0.06 0.00 -0.21 -0.14 -0.02 -0.03 0.51 0.13 0.794051265 -0.24837646 cell part;chromatin;chromosomal part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;Ski complex;transcriptionally active chromatin RNA degradation 3.74E-126 3 17 17 15.9
Q16222-3;Q16222;Q16222-2;B1AR80;Q3KQV9 UDP-N-acetylhexosamine pyrophosphorylase;UDP-N-acetylgalactosamine pyrophosphorylase;UDP-N-acetylglucosamine pyrophosphorylase UAP1 >sp|Q16222-3|UAP1_HUMAN Isoform 3 of UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1;>sp|Q16222|UAP1_HUMAN UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3;>sp|Q16222-2|UAP1_HUMAN Isoform AGX1 of UDP-N-acetylhexos 0.91 0.29 -0.17 -0.26 -0.14 -0.27 -0.20 -0.29 0.659899638 0.417973753 alcohol biosynthetic process;alcohol metabolic process;amino sugar biosynthetic process;amino sugar metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;dolichol-linked oligosaccharide biosynthetic process;glucosamine biosynthetic process;glucosamine metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;N-acetylglucosamine biosynthetic process;N-acetylglucosamine metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleotide-sugar metabolic process;oligosaccharide biosynthetic process;oligosaccharide metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;small molecule biosynthetic process;small molecule metabolic process;UDP-N-acetylglucosamine biosynthetic process;UDP-N-acetylglucosamine metabolic process "binding;carbohydrate binding;catalytic activity;nucleotidyltransferase activity;transferase activity;transferase activity, transferring phosphorus-containing groups;UDP-N-acetylglucosamine diphosphorylase activity;uridylyltransferase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane Amino sugar and nucleotide sugar metabolism 4.63E-213 5 17 17 41.7
O94874;O94874-2;O94874-3 E3 UFM1-protein ligase 1 UFL1 >sp|O94874|UFL1_HUMAN E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 PE=1 SV=2;>sp|O94874-2|UFL1_HUMAN Isoform 2 of E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1;>sp|O94874-3|UFL1_HUMAN Isoform 3 of E3 UFM1-protein ligase 1 OS=Homo sapiens GN=UFL1 -0.28 0.29 0.24 0.12 0.32 0.31 -0.53 -0.07 0.124246881 0.083547758 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of sequence-specific DNA binding transcription factor activity;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ufmylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent" "acid-amino acid ligase activity;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;small conjugating protein ligase activity;UFM1 conjugating enzyme activity" cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.90E-54 3 17 17 26.8
P62195;P62195-2;J3QQM1;J3QSA9;J3KRP2;J3QLH6;J3QSE0;J3QRW1;J3QRR3;J3KTQ9 26S protease regulatory subunit 8 PSMC5 >sp|P62195|PRS8_HUMAN 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1;>sp|P62195-2|PRS8_HUMAN Isoform 2 of 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5;>tr|J3QQM1|J3QQM1_HUMAN 26S protease regulatory subunit 8 (Fragment) -0.02 0.07 -0.03 -0.04 -0.02 -0.13 -0.11 -0.27 0.91659728 0.123239295 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;biosynthetic process;catabolic process;cell cycle phase;cell cycle process;cell death;cellular biosynthetic process;cellular catabolic process;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of ligase activity;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of ligase activity;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular biosynthetic process;regulation of cellular ketone metabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of ligase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;transcription from RNA polymerase II promoter;transcription, DNA-dependent;ubiquitin-dependent protein catabolic process;viral reproduction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;protein binding

transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transcription cofactor activity;transcription factor binding transcription factor activity"	cell part;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nuclear proteasome complex;nucleoplasm;organelle;organelle part;proteasome accessory complex;proteasome complex;protein complex;vesicle Proteasome	9.35E-192	10	18	17	57.1
O00232;O00232-2;F8VU88;F8VWR9;O75334-2;J3KNM3;O75334-4;G3V200;O75334-3;O75334 26S proteasome non-ATPase regulatory subunit 12	PSMD12 >sp|O00232|PSD12_HUMAN 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3;>sp|O00232-2|PSD12_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12	0.06 0.00 -0.09
-0.09	-0.05	-0.15	0.11 -0.18		0.186839197	0.037132679	"anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological adhesion;biological regulation;catabolic process;cell adhesion;cell cycle phase;cell cycle process;cell death;cell-matrix adhesion;cell-substrate adhesion;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction"		cell part;cell surface;cytoplasm;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome regulatory particle;protein complex;synapse Proteasome	6.08E-97 10	18	17	42.1
P34897-3;P34897;P34897-2;B4DLV4;H0YIZ0;G3V2Y4;G3V5L0;G3V4W5;G3V540;G3V241;G3V3Y8;G3V4T0;G3V4X0;G3V2W0;G3V2E4;G3V2D2;G3V2Y1;G3V3C6"Serine hydroxymethyltransferase, mitochondrial;Serine hydroxymethyltransferase"	SHMT2	">sp|P34897-3|GLYM_HUMAN Isoform 3 of Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2;>sp|P34897|GLYM_HUMAN Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3;>sp|P34897-2|GLYM_HUMAN Isoform 2 of Serine"	-0.05	-0.28	0.18 0.06 -0.13	-0.80	-0.13	-0.71
0.872749204	0.420908868	amine biosynthetic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;folic acid-containing compound metabolic process;glycine biosynthetic process;glycine biosynthetic process from serine;glycine metabolic process;heterocycle metabolic process;L-serine biosynthetic process;L-serine metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;nitrogen compound metabolic process;one-carbon metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;pteridine-containing compound metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;serine family amino acid biosynthetic process;serine family amino acid metabolic process;small molecule biosynthetic process;small molecule metabolic process;tetrahydrofolate interconversion;tetrahydrofolate metabolic process	"aldehyde-lyase activity;amine binding;amino acid binding;binding;carbon-carbon lyase activity;carboxylic acid binding;catalytic activity;chromatin binding;cofactor binding;glycine hydroxymethyltransferase activity;hydroxymethyl-, formyl- and related transferase activity;L-allo-threonine aldolase activity;lyase activity;methyltransferase activity;pyridoxal phosphate binding;threonine aldolase activity;transferase activity;transferase activity, transferring one-carbon groups;vitamin B6 binding;vitamin binding"	cell part;cytoplasmic part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microtubule cytoskeleton;mitochondrial inner membrane;mitochondrial intermembrane space;mitochondrial matrix;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle envelope lumen;organelle inner membrane;organelle lumen;organelle membrane;organelle part"Cyanoamino acid metabolism;Glycine, serine and threonine metabolism;Methane metabolism;One carbon pool by folate"	1.20E-127	18	18	17	46.8
P31930;REV__A2RU56"Cytochrome b-c1 complex subunit 1, mitochondrial"	UQCRC1">sp|P31930|QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3"
-0.15	0.51 0.14 0.62 0.24 0.34 -1.20	-0.15		0.498161698	0.471503165	"aerobic respiration;cellular metabolic process;cellular process;cellular respiration;electron transport chain;energy derivation by oxidation of organic compounds;generation of precursor metabolites and energy;metabolic process;mitochondrial electron transport, ubiquinol to cytochrome c;oxidation-reduction process;oxidative phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;respiratory electron transport chain;response to activity;response to alkaloid;response to chemical stimulus;response to organic substance;response to stimulus;small molecule metabolic process"	"binding;catalytic activity;cation binding;cation transmembrane transporter activity;hydrogen ion transmembrane transporter activity;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;monovalent inorganic cation transmembrane transporter activity;oxidoreductase activity;oxidoreductase activity, acting on diphenols and related substances as donors;oxidoreductase activity, acting on diphenols and related substances as donors, cytochrome as acceptor;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;ubiquinol-cytochrome-c reductase activity"	cell part;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane part;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain;mitochondrial respiratory chain complex III;organelle part;protein complex;respiratory chain;respiratory chain complex III Alzheimer's disease;Cardiac muscle contraction;Huntington's disease;Oxidative phosphorylation;Parkinson's disease	3.48E-120	2	18	17	43.8
P54578;P54578-2;A6NJA2;B7Z4N8;J3QQT6;J3KS55	Ubiquitin carboxyl-terminal hydrolase 14;Ubiquitin carboxyl-terminal hydrolase	USP14	>sp|P54578|UBP14_HUMAN Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14 PE=1 SV=3;>sp|P54578-2|UBP14_HUMAN Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens GN=USP14;>tr|A6NJA2|A6NJA2_HUMAN Ubiquitin carboxyl-terminal h
0.01 -0.13	-0.04	0.03 -0.12	-0.14	0.35 -0.14		0.053880004	-0.020002831	biological regulation;catabolic process;cell communication;cell-cell signaling;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of behavior;regulation of biological process;regulation of catabolic process;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of locomotion;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of proteasomal protein catabolic

process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of proteolysis;regulation of response to external stimulus;regulation of response to stimulus;signaling;synaptic transmission;ubiquitin-dependent protein catabolic process "binding;catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;guanylyltransferase activity;hydrolase activity;hydrolase activity, acting on ester bonds;nucleotidyltransferase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;peptidase inhibitor activity;peptidase regulator activity;proteasome binding;protein binding;protein complex binding;RNA guanylyltransferase activity;small conjugating protein-specific protease activity;thiolester hydrolase activity;transferase activity;transferase activity, transferring phosphorus-containing groups;tRNA guanylyltransferase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity" cell part;cell surface;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;proteasome complex;protein complex;synapse;vesicle 1.22E-173 6 18 17 45.1

E9PB90;P52789 Hexokinase-2 HK2>tr|E9PB90|E9PB90_HUMAN Hexokinase-2 OS=Homo sapiens GN=HK2 PE=2 SV=1;>sp|P52789|HXK2_HUMAN Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2 0.36 0.35 -0.09 0.02 0.00 0.25 -0.31 -0.20 0.552282851 0.221994207 alcohol catabolic process;alcohol metabolic process;apoptotic mitochondrial changes;biological regulation;body fluid secretion;carbohydrate catabolic process;carbohydrate homeostasis;carbohydrate metabolic process;carbohydrate transport;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular glucose homeostasis;cellular homeostasis;cellular metabolic process;cellular process;chemical homeostasis;establishment of localization;generation of precursor metabolites and energy;glucose catabolic process;glucose homeostasis;glucose metabolic process;glucose transport;glycolysis;hexose catabolic process;hexose metabolic process;hexose transport;homeostatic process;lactation;metabolic process;mitochondrion organization;monosaccharide catabolic process;monosaccharide metabolic process;monosaccharide transport;multicellular organismal process;multicellular organismal reproductive process;organelle organization;organic substance transport;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of glucose import;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;secretion;small molecule catabolic process;small molecule metabolic process;transmembrane transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate binding;carbohydrate kinase activity;catalytic activity;fructokinase activity;glucokinase activity;glucose binding;hexokinase activity;kinase activity;mannokinase activity;monosaccharide binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;sugar binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane Amino sugar and nucleotide sugar metabolism;Butirosin and neomycin biosynthesis;Carbohydrate digestion and absorption;Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Insulin signaling pathway;Starch and sucrose metabolism;Streptomycin biosynthesis;Type II diabetes mellitus 7.36E-76 2 21 17 26.9

P50395;E7EU23;P50395-2;Q5SX87;Q5SX90;Q5SX86;Q5SX91 Rab GDP dissociation inhibitor beta GDI2 >sp|P50395|GDIB_HUMAN Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2;>tr|E7EU23|E7EU23_HUMAN Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=2 SV=1;>sp|P50395-2|GDIB_HUMAN Isoform 2 of Rab GDP dissociation inhibitor be 0.15 -0.09 -0.13 -0.08 0.11 -0.06 0.44 -0.05 0.450859154 -0.146470034 biological regulation;cellular process;cellular response to stimulus;establishment of localization;establishment of protein localization;intracellular signal transduction;protein transport;regulation of biological process;regulation of cellular process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport enzyme activator activity;enzyme regulator activity;GDP-dissociation inhibitor activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Rab GDP-dissociation inhibitor activity;Rab GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;cell surface;cytoplasmic part;cytosol;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;organelle 0 7 26 17 63.8

P14866;M0QXS5;P14866-2;M0R1W6;B4DVF8;M0QYL7 Heterogeneous nuclear ribonucleoprotein L HNRNPL >sp|P14866|HNRPL_HUMAN Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2;>tr|M0QXS5|M0QXS5_HUMAN Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=4 SV=1;>sp|P14866-2|HNRPL_HUMAN Isoform 2 of Hete -0.06 0.45 -0.06 0.52 -0.03 -0.01 -1.00 -0.22 0.797342572 0.527819379 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;DNA binding;nucleic acid binding;nucleotide binding;regulatory region DNA binding;regulatory region nucleic acid binding;RNA binding;transcription regulatory region DNA binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex 2.23E-230 6 26 17 64.3

Q10567-3;Q10567-2;Q10567;Q10567-4;C9J1E7;K7EJX1;H7C034;K7ERE4;K7EKZ5;K7EJ01 AP-1 complex subunit beta-1 AP1B1 >sp|Q10567-3|AP1B1_HUMAN Isoform C of AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1;>sp|Q10567-2|AP1B1_HUMAN Isoform B of AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1;>sp|Q10567|AP1B1_HUMAN AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B -0.13 -0.08 0.01 0.03 -0.14 0.03 0.26 0.00 0.359381981 -0.080946524 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;membrane invagination;membrane organization;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;transport;vesicle-mediated transport;viral reproduction protein transporter activity;substrate-specific transporter activity;transporter activity AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;clathrin coated vesicle membrane;coated vesicle membrane;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;lysosomal membrane;macromolecular complex;membrane;membrane coat;membrane part;organelle membrane;organelle part;protein complex;trans-Golgi network membrane;vacuolar membrane;vacuolar part;vesicle membrane Lysosome 1.81E-217 10 32 17 35.5

P61158;B4DXW1;F5H3P5;Q9P1U1-2;Q9P1U1;Q9P1U1-3;F8WEW2;F8WE84;H7C4J1;Q9C0K3;C9IZN3 Actin-related protein 3 ACTR3 >sp|P61158|ARP3_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3;>tr|B4DXW1|B4DXW1_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=2 SV=1;>tr|F5H3P5|F5H3P5_HUMAN Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=2 SV=1 -0.07 0.07 -0.19 0.32 0.17 0.37 0.21 0.37 0.875564582 -0.24708136 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin nucleation;anatomical structure morphogenesis;Arp2/3 complex-mediated actin nucleation;asymmetric cell division;biological regulation;cell cycle;cell cycle cytokinesis;cell cycle process;cell division;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular process;cilium morphogenesis;cytokinesis;cytokinesis after meiosis;cytoskeleton organization;defense response;developmental process;establishment or maintenance of cell polarity;immune response;immune system process;innate immune response;localization;meiotic cell cycle;organelle localization;organelle organization;positive regulation of actin filament polymerization;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of dendrite morphogenesis;positive regulation of developmental process;positive regulation of filopodium assembly;positive regulation of lamellipodium assembly;positive regulation of neurogenesis;positive regulation of neuron differentiation;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of filopodium assembly;regulation of lamellipodium assembly;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myosin II filament organization;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;response to antibiotic;response to carbohydrate stimulus;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;spindle localization adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding Arp2/3 protein complex;cell junction;cell part;cell projection;cell-substrate junction;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;excitatory synapse;Golgi apparatus part;Golgi membrane;hemidesmosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;podosome;protein complex;synapse 2.28E-170 11 18 18 54.8

P35573;P35573-2;P35573-3 "Glycogen debranching enzyme;4-alpha-glucanotransferase;Amylo-alpha-1,6-glucosidase" AGL >sp|P35573|GDE_HUMAN Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3;>sp|P35573-2|GDE_HUMAN Isoform 5 of Glycogen debranching enzyme OS=Homo sapiens GN=AGL;>sp|P35573-3|GDE_HUMAN Isoform 6 of Glycogen debranching enzyme OS=Homo sapiens GN=AGL -0.30 -0.22 0.06 -0.01 -0.54 0.00 0.56 0.07 0.222332163 -0.141659877 alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan biosynthetic process;glucan catabolic process;glucan metabolic process;glucose metabolic process;glycogen biosynthetic process;glycogen catabolic process;glycogen metabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;oxidation-reduction process;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;response to chemical stimulus;response to corticosteroid stimulus;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to nutrient;response to nutrient levels;response to organic substance;response to steroid hormone stimulus;response to stimulus;small molecule metabolic process "4-alpha-glucanotransferase activity;alpha-glucosidase activity;amylo-alpha-1,6-glucosidase activity;binding;carbohydrate binding;catalytic activity;glucosidase activity;glycogen debranching enzyme activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;pattern binding;polysaccharide binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic part;cytosol;endoplasmic reticulum;inclusion body;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;isoamylase complex;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;sarcoplasmic reticulum Starch and sucrose metabolism 8.68E-108 3 18 18 16.3

Q99459 Cell division cycle 5-like protein CDC5L >sp|Q99459|CDC5L_HUMAN Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2 0.01 0.21 0.27 0.35 0.00 -0.23 -1.05 -0.21 1.017872658 0.580848956 "biological regulation;biosynthetic process;cell cycle;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;chromatin binding;DNA binding;nucleic acid binding;protein binding;protein domain specific binding;RNA binding;WD40-repeat domain binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;protein complex;Prp19 complex;ribonucleoprotein complex;spliceosomal complex Spliceosome 7.74E-160 1 18 18 33.3

Q9ULV4;A7MAP0;A7MAP1;B4E3S0;H0YHL7;F8W1H8;F8VUX3;F8VSA4;F8VRE9;F8VTT6;F8VVB7;F8VV53;REV__K7EL62;REV__P29992 Coronin-1C;Coronin CORO1C>sp|Q9ULV4|COR1C_HUMAN Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1;>tr|A7MAP0|A7MAP0_HUMAN Coronin OS=Homo sapiens GN=CORO1C PE=2 SV=1;>tr|A7MAP1|A7MAP1_HUMAN Coronin OS=Homo sapiens GN=CORO1C PE=2 SV=1;>tr|B4E3S0|B4E3S0_HUMAN Coronin OS=Homo sapiens GN 0.04 0.59 -0.31 0.40 0.57 0.49 -0.50 0.05 0.029796094 0.028523846 actin cytoskeleton organization;actin filament-based process;biological regulation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cellular response to stimulus;cytoskeleton organization;endocytosis;establishment of localization;membrane invagination;membrane organization;organelle organization;phagocytosis;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction;transport;vesicle-mediated transport actin binding;actin filament binding;binding;cytoskeletal protein binding;protein binding actin cytoskeleton;cell part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 5.22E-125 14 18 18 39.5

P23743;G3V4E1;H0YJH4;Q3ZE25;G3V327;C9JM35;P23743-2;F8W1M3;F8W1H7;G3V4I3;F8VNZ9;F8VWX8;G3V312;H0YJE7;Q9Y6T7-2;C9JTC0;B5MCD5;B5MBY2;Q9Y6T7;F8WD28 Diacylglycerol kinase alpha DGKA >sp|P23743|DGKA_HUMAN Diacylglycerol kinase alpha OS=Homo sapiens GN=DGKA PE=1 SV=3;>tr|G3V4E1|G3V4E1_HUMAN Diacylglycerol kinase alpha (Fragment) OS=Homo sapiens GN=DGKA PE=2 SV=1 0.06 -0.08 0.03 0.03 -0.80 -0.27 0.37 0.05 0.271103924 0.175617963 activation of protein kinase activity;activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway;biological regulation;cell activation;cell surface receptor linked signaling pathway;cellular process;cellular response to stimulus;G-protein coupled receptor protein signaling pathway;intracellular signal transduction;platelet activation;positive regulation of catalytic activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of protein kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to stimulus;signal transduction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;diacylglycerol kinase activity;ion binding;kinase activity;lipid binding;metal ion binding;nucleotide binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Glycerolipid metabolism;Glycerophospholipid metabolism;Phosphatidylinositol signaling system 7.47E-134 20 18 18 28.7

Q9NY33-4;Q9NY33;G3V1D3;G3V180;E9PQ14;Q9NY33-2;E9PNX5;E9PKK8;E9PPK9 Dipeptidyl peptidase 3 DPP3 >sp|Q9NY33-4|DPP3_HUMAN Isoform 4 of Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3;>sp|Q9NY33|DPP3_HUMAN Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=1 SV=2;>tr|G3V1D3|G3V1D3_HUMAN Dipeptidyl peptidase 3 OS=Homo sapiens GN=DPP3 PE=2 SV=1;>tr|G3V180|G 0.03 -0.07 0.06 -0.09 -0.10 0.18 0.63 0.11 0.593989235 -0.222514492 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "aminopeptidase activity;binding;catalytic activity;cation binding;dipeptidyl-peptidase activity;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding;zinc ion binding" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;plasma membrane 0 9 18 18 38.6

Q15717;B4DVB8;M0QZR9;M0R055;B1AM48;Q12926-2;Q12926;P26378-4;P26378-2;P26378-5;B1APY9;P26378;P26378-3;B1APY8;B1AM49 ELAV-like protein 1 ELAVL1 >sp|Q15717|ELAV1_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2;>tr|B4DVB8|B4DVB8_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1;>tr|M0QZR9|M0QZR9_HUMAN ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=4 SV=1 0.07 0.50 0.02 0.59 0.10 0.13 -1.04 -0.05 0.688124012 0.507456352 "3'-UTR-mediated mRNA stabilization;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;gene expression;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;multicellular organismal development;multicellular organismal process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of protein metabolic process;positive regulation of translation;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of RNA stability;regulation of transcription, DNA-dependent;regulation of translation;RNA metabolic process;RNA processing;RNA stabilization"AU-rich element binding;binding;mRNA 3'-UTR AU-rich region binding;mRNA 3'-UTR binding;mRNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part 2.05E-191 15 18 18 58.6

Q01581;D6RIW1;P54868-3;P54868-2;P54868 "Hydroxymethylglutaryl-CoA synthase, cytoplasmic" HMGCS1 ">sp|Q01581|HMCS1_HUMAN Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2" 0.42 0.18 -0.49 -0.22 -0.71 -0.88 0.26 -0.29 0.482254172 0.376688901 alcohol metabolic process;anatomical structure development;biosynthetic process;brain development;cellular biosynthetic process;cellular ketone body metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cholesterol;cellular response to endogenous stimulus;cellular response to follicle-stimulating hormone stimulus;cellular response to gonadotropin stimulus;cellular response to hormone stimulus;cellular response to lipid;cellular response to organic substance;cellular response to stimulus;cholesterol biosynthetic process;cholesterol metabolic process;developmental process;developmental process involved in reproduction;gonad development;isoprenoid biosynthetic process;isoprenoid metabolic process;ketone body biosynthetic process;lipid biosynthetic process;lipid metabolic process;liver development;male gonad development;metabolic process;organ development;primary metabolic process;reproductive process;reproductive structure development;response to abiotic stimulus;response to acid;response to chemical stimulus;response to cholesterol;response to drug;response to endogenous stimulus;response to external stimulus;response to extracellular stimulus;response to follicle-stimulating hormone stimulus;response to gonadotropin stimulus;response to hormone stimulus;response to inorganic substance;response to light intensity;response to light stimulus;response to lipid;response to lipoprotein stimulus;response to low light intensity stimulus;response to metal ion;response to nutrient;response to nutrient levels;response to organic cyclic compound;response to organic substance;response to purine-containing compound;response to radiation;response to stimulus;response to tellurium ion;response to vitamin;response to vitamin E;small molecule biosynthetic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process "binding;catalytic activity;drug binding;hydroxymethylglutaryl-CoA synthase activity;isomerase activity;organic acid binding;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;nucleus;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane "Butanoate metabolism;Synthesis and degradation of ketone bodies;Terpenoid backbone biosynthesis;Valine, leucine and isoleucine degradation" 7.63E-281 5 18 18 45

Q8N3F8;H0Y6J8;Q68D58;B0QY91 MICAL-like protein 1 MICALL1 >sp|Q8N3F8|MILK1_HUMAN MICAL-like protein 1 OS=Homo sapiens GN=MICALL1 PE=1 SV=2;>tr|H0Y6J8|H0Y6J8_HUMAN MICAL-like protein 1 (Fragment) OS=Homo sapiens GN=MICALL1 PE=4 SV=1 -0.09 0.10 0.24 -0.01 -1.15 -0.43 0.24 -0.19 0.625805198 0.443047186 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 1.02E-81 4 18 18 34.6

Q13724-2;Q13724;C9J8D4;C9JDQ1;B8ZZE2 Mannosyl-oligosaccharide glucosidase MOGS >sp|Q13724-2|MOGS_HUMAN Isoform 2 of Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS;>sp|Q13724|MOGS_HUMAN Mannosyl-oligosaccharide glucosidase OS=Homo sapiens GN=MOGS PE=1 SV=5;>tr|C9J8D4|C9J8D4_HUMAN Mannosyl-oligosaccharide glucosidase (Fra -0.31 -0.10 0.13 0.18 -0.20 0.32 0.05 0.45 0.392891949 -0.178587149 carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;glycosylation;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;oligosaccharide metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine"catalytic activity;glucosidase activity;hydrolase activity;hydrolase activity, acting on glycosyl bonds;hydrolase activity, hydrolyzing O-glycosyl compounds;mannosyl-oligosaccharide glucosidase activity" cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;organelle membrane;organelle part N-Glycan biosynthesis;Protein processing in endoplasmic reticulum 2.53E-63 5 18 18 37.3

P46087;P46087-4;P46087-2;P46087-3;F5GWB7;F5H709;F5H5X6;F5GYR3;F5H359;F5H8G6 Putative ribosomal RNA methyltransferase NOP2NOP2 >sp|P46087|NOP2_HUMAN Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2 PE=1 SV=2;>sp|P46087-4|NOP2_HUMAN Isoform 4 of Putative ribosomal RNA methyltransferase NOP2 OS=Homo sapiens GN=NOP2;>sp|P46087-2|NOP2_HUMAN Isoform 2 of Putative r -0.28 0.99 0.21 0.99 -0.46 0.07 -1.37 0.12 0.817958238 0.888015002 biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;methylation;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;small molecule metabolic process "binding;catalytic activity;methyltransferase activity;nucleic acid binding;RNA binding;S-adenosylmethionine-dependent methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part 8.46E-145 10 18 18 28.8

P21589-2;P21589;Q96B60;H0Y7R7;H0Y3X5 5-nucleotidase NT5E >sp|P21589-2|5NTD_HUMAN Isoform 2 of 5-nucleotidase OS=Homo sapiens GN=NT5E;>sp|P21589|5NTD_HUMAN 5-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1;>tr|Q96B60|Q96B60_HUMAN 5-nucleotidase OS=Homo sapiens GN=NT5E PE=2 SV=1 -0.02 1.03 -0.14 0.71 0.79 0.75 -1.90 -0.08 0.285638834 0.503407803 adenosine biosynthetic process;adenosine metabolic process;AMP catabolic process;AMP metabolic process;biological regulation;biosynthetic process;catabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;DNA metabolic process;heterocycle biosynthetic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of response to external stimulus;negative regulation of response to stimulus;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside catabolic process;nucleoside metabolic process;nucleoside monophosphate catabolic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine base metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine nucleoside monophosphate catabolic process;purine nucleoside monophosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine ribonucleoside monophosphate catabolic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound catabolic process;purine-containing compound metabolic process;pyrimidine base metabolic process;pyrimidine nucleoside catabolic process;pyrimidine nucleoside metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of defense response;regulation of inflammatory response;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;ribonucleoside biosynthetic process;ribonucleoside metabolic process;ribonucleoside monophosphate catabolic process;ribonucleoside monophosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "5'-nucleotidase activity;binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nucleotidase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity" anchored to membrane;cell part;cytoplasm;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;organelle;plasma membrane;vesicle Nicotinate and nicotinamide metabolism;Purine metabolism;Pyrimidine metabolism 4.08E-116 5 18 18 48.3

Q99623;J3KPX7;F5GY37;Q99623-2;F5GWA7;B4DW05;F5H3X6;F5H2D2;F5H0C5;F5H0S4 Prohibitin-2 PHB2 >sp|Q99623|PHB2_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2;>tr|J3KPX7|J3KPX7_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=4 SV=1;>tr|F5GY37|F5GY37_HUMAN Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=2 SV=1;>sp|Q99623-2|PHB2_HUMAN Isoform 2 of Prohibit -0.33 0.11 0.10 0.19 0.41 0.09 -1.14 -0.29 0.267612656 0.244272266 "anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;branching involved in mammary gland duct morphogenesis;branching morphogenesis of a tube;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;developmental process involved in reproduction;macromolecule biosynthetic process;macromolecule metabolic process;mammary gland alveolus development;mammary gland branching involved in thelarche;metabolic process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an epithelium;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of epithelial cell proliferation;negative regulation of estrogen receptor signaling pathway;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of mammary gland epithelial cell proliferation;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biosynthetic process;regulation of branching involved in mammary gland duct morphogenesis;regulation of cell communication;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of epithelial cell proliferation;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of mammary gland epithelial cell proliferation;regulation of metabolic process;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA metabolic process;tissue morphogenesis;transcription, DNA-dependent;tube morphogenesis" binding;estrogen receptor binding;hormone receptor binding;nuclear hormone receptor binding;protein binding;receptor binding;steroid hormone receptor binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part 2.61E-167 10 18 18 61.5

O14744;O14744-2;G3V5W5;B4DX49;B4DV00;A8MTP3;G3V580;H0YJX6;G3V5L5;G3V2L6;G3V2X6;C9JSX3;H0YJ77;H7BZ44;G3V5T6;H0YJD3;G3V507;G3V2F5 "Protein arginine N-methyltransferase 5;Protein arginine N-methyltransferase 5, N-terminally processed" PRMT5 >sp|O14744|ANM5_HUMAN Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4;>sp|O14744-2|ANM5_HUMAN Isoform 2 of Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5;>tr|G3V5W5|G3V5W5_HUMAN Protein arginine N-methyltransferas 0.19 0.05 -0.20 -0.14 -0.14 -0.35 0.15 -0.42 0.429605336 0.163649587 "biological regulation;biosynthetic process;cell activation;cell proliferation;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;endothelial cell activation;histone arginine methylation;histone H4-R3 methylation;histone methylation;histone modification;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;ncRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;one-carbon metabolic process;organelle organization;primary metabolic process;protein alkylation;protein metabolic process;protein methylation;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitosis;regulation of mitotic cell cycle;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA biosynthetic process;RNA metabolic process;small molecule metabolic process;spliceosomal snRNP assembly;transcription, DNA-dependent" "arginine N-methyltransferase activity;binding;catalytic activity;chromatin binding;histone methyltransferase activity;histone-arginine N-methyltransferase activity;methyltransferase activity;N-methyltransferase activity;protein methyltransferase activity;protein-arginine N-methyltransferase activity;protein-arginine omega-N symmetric methyltransferase activity;ribonucleoprotein binding;S-adenosylmethionine-dependent methyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex Cell cycle - yeast;RNA transport 3.51E-96 18 18 18 30.8

O00231;O00231-2;J3QRY4;J3KSW3;J3QS13 26S proteasome non-ATPase regulatory subunit 11 PSMD11 >sp|O00231|PSD11_HUMAN 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3;>sp|O00231-2|PSD11_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 0.07 0.02 -0.16 -0.09 -0.09 -0.20 0.00 -0.16 0.452657998 0.074273079 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cell differentiation;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;proteasome assembly;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;stem cell differentiation;ubiquitin-dependent protein catabolic process;viral reproduction" cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;protein complex Proteasome 8.14E-215 5 18 18 46

Q92878;Q92878-2;Q92878-3;E7ESD9;E7EN38;H7C0P8;E9PM98;H7C0V2 DNA repair protein RAD50 RAD50 >sp|Q92878|RAD50_HUMAN DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1;>sp|Q92878-2|RAD50_HUMAN Isoform 2 of DNA repair protein RAD50 OS=Homo sapiens GN=RAD50;>sp|Q92878-3|RAD50_HUMAN Isoform 3 of DNA repair protein RAD50 OS=Homo sapiens GN=RAD -0.26 0.12 0.15 0.16 -0.24 -0.38 -0.89 -0.47 1.2825315 0.538827091 anatomical structure homeostasis;biological regulation;biosynthetic process;cell cycle process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA recombination;DNA repair;DNA replication;double-strand break repair;double-strand break repair via homologous recombination;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;organelle organization;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of kinase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein autophosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of transferase activity;primary metabolic process;reciprocal DNA recombination;reciprocal meiotic recombination;recombinational repair;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of DNA metabolic process;regulation of DNA recombination;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic recombination;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein autophosphorylation;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;response to DNA damage stimulus;response to stimulus;response to stress;RNA-dependent DNA replication;telomere maintenance;telomere maintenance via telomerase;telomere maintenance via telomere lengthening;telomere organization "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;binding, bridging;catalytic activity;cation binding;DNA binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nuclease activity;nucleic acid binding;nucleotide binding;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transition metal ion binding;zinc ion binding" "cell part;chromosomal part;chromosome, telomeric region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;Mre11 complex;nuclear chromosome part;nuclear chromosome, telomeric region;nuclear part;nucleoplasm;nucleus;organelle;organelle part;pronucleus;protein complex" Homologous recombination;Non-homologous end-joining 2.01E-107 8 18 18 16.4

P62917;E9PKZ0;G3V1A1;E9PKU4;E9PP36 60S ribosomal protein L8 RPL8 >sp|P62917|RL8_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2;>tr|E9PKZ0|E9PKZ0_HUMAN 60S ribosomal protein L8 (Fragment) OS=Homo sapiens GN=RPL8 PE=2 SV=1;>tr|G3V1A1|G3V1A1_HUMAN 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=2 SV=1 -0.13 0.00 0.14 0.06 -0.06 -0.54 -0.37 -0.40 1.286358038 0.361825032 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 1.79E-97 5 18 18 48.6

Q14683;G8JLG1;H0Y7K8 Structural maintenance of chromosomes protein 1A SMC1A >sp|Q14683|SMC1A_HUMAN Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2 0.02 0.50 0.05 0.50 0.01 -0.12 -0.94 -0.33 1.038061492 0.610297065 "anaphase;biological regulation;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome condensation;chromosome organization;cytokinesis;cytoskeleton organization;developmental process;DNA conformation change;DNA metabolic process;DNA packaging;DNA recombination;DNA repair;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;meiosis;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;mitotic sister chromatid cohesion;mitotic spindle organization;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA endoreduplication;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA endoreduplication;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to abiotic stimulus;response to DNA damage stimulus;response to radiation;response to stimulus;response to stress;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction in response to DNA damage;sister chromatid cohesion;spindle organization;stem cell maintenance" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;chromatin binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromosomal part;chromosome;cohesin complex;cohesin core heterodimer;condensed chromosome;condensed chromosome kinetochore;condensed nuclear chromosome;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;meiotic cohesin complex;non-membrane-bounded organelle;nuclear chromosome;nuclear part;nucleoplasm;organelle;organelle part;protein complex Cell cycle;Cell cycle - yeast;Meiosis - yeast;Oocyte meiosis 1.78E-70 3 18 18 19.1

Q08945;E9PPZ7;E9PMD4 FACT complex subunit SSRP1 SSRP1 >sp|Q08945|SSRP1_HUMAN FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 0.09 0.11 0.07 0.10 -0.13 -0.64 -0.60 -0.08 1.257313976 0.455369378 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA repair;DNA replication;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;viral reproductive process" binding;chromatin binding;DNA binding;nucleic acid binding cell part;chromosome;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part 3.05E-112 3 18 18 29.9

Q14258 E3 ubiquitin/ISG15 ligase TRIM25 TRIM25 >sp|Q14258|TRI25_HUMAN E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2 0.29 -0.10 -0.25 -0.37 -0.37 -0.28 0.39 0.02 0.069623413 -0.045439598 biological regulation;defense response;defense response to virus;immune effector process;immune response;immune system process;innate immune response;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of cytokine production;negative regulation of multicellular organismal process;negative regulation of type I interferon production;regulation of biological process;regulation of cytokine production;regulation of multicellular organismal process;regulation of type I interferon production;reproductive process;response to biotic stimulus;response to other organism;response to stimulus;response to stress;response to virus;viral reproductive process;virus-host interaction "acid-amino acid ligase activity;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell junction;cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle RIG-I-like receptor signaling pathway 3.77E-132 1 18 18 36

Q15181;Q5SQT6 Inorganic pyrophosphatase PPA1 >sp|Q15181|IPYR_HUMAN Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2;>tr|Q5SQT6|Q5SQT6_HUMAN Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=2 SV=1 -0.01 -0.07 0.04 0.05 -0.20 -0.18 0.24 -0.31 0.377735689 0.114910097 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;diphosphate metabolic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic diphosphatase activity;ion binding;magnesium ion binding;metal ion binding;pyrophosphatase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Oxidative phosphorylation 5.16E-249 2 19 18 71.6

P21796;C9JI87 Voltage-dependent anion-selective channel protein 1 VDAC1 >sp|P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2;>tr|C9JI87|C9JI87_HUMAN Voltage-dependent anion-selective channel protein 1 (Fragment) OS=Homo sapiens GN=VDAC1 PE=2 SV=1 -0.38 0.80 -0.04 0.83 0.47 0.97 -1.24 0.63 0.057122367 0.097895849 apoptosis;behavior;behavioral defense response;behavioral fear response;cell communication;cell death;cell-cell signaling;cellular process;cognition;death;defense response;fear response;interaction with host;interspecies interaction between organisms;learning;learning or memory;multicellular organismal process;multicellular organismal response to stress;multi-organism process;neurological system process;neuron-neuron synaptic transmission;programmed cell death;reproductive process;response to stimulus;response to stress;signaling;synaptic transmission;system process;viral reproductive process;virus-host interaction anion channel activity;anion transmembrane transporter activity;channel activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;passive transmembrane transporter activity;porin activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity;voltage-gated anion channel activity;voltage-gated channel activity;voltage-gated ion channel activity;wide pore channel activity cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial outer membrane;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;plasma membrane;pore complex;protein complex Calcium signaling pathway;Huntington's disease;Parkinson's disease 0 2 19 18 79.2

Q32MZ4-3;Q32MZ4-2;Q32MZ4;C9JTC6 Leucine-rich repeat flightless-interacting protein 1 LRRFIP1 >sp|Q32MZ4-3|LRRF1_HUMAN Isoform 3 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1;>sp|Q32MZ4-2|LRRF1_HUMAN Isoform 2 of Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1;>sp|Q32MZ4|LRRF1_HUM 0.04 0.11 -0.03 -0.14 -0.32 -0.13 0.16 -0.13 0.367299181 0.101787655 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;double-stranded RNA binding;nucleic acid binding;RNA binding cell part;cytoplasm;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 0 4 22 18 39.2

Q9H223 EH domain-containing protein 4 EHD4 >sp|Q9H223|EHD4_HUMAN EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1 0.19 0.02 -0.11 -0.12 0.80 0.33 0.04 -0.48 0.250540567 -0.181185239 biological regulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;endocytic recycling;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;membrane invagination;membrane organization;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;pinocytosis;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of endocytosis;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;early endosome membrane;endoplasmic reticulum;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;recycling endosome membrane Endocytosis 1.71E-204 1 25 18 48.6

P27348;E9PG15;REV__Q8IWB1 14-3-3 protein theta YWHAQ >sp|P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1;>tr|E9PG15|E9PG15_HUMAN 14-3-3 protein theta (Fragment) OS=Homo sapiens GN=YWHAQ PE=2 SV=1 -0.03 0.06 -0.36 -0.03 0.24 0.20 0.16 0.22 1.283017725 -0.295052032 "biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular signal transduction;intracellular transport;membrane organization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;protein targeting;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to stimulus;signal transduction;small GTPase mediated signal transduction;transport" cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;intracellular organelle part;intracellular part;membrane;organelle membrane;organelle part;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis 0 3 26 18 74.3

Q7L576;Q7L576-2;Q7L576-3;H0YLJ5;H0YL39;H0YL50;H0YN93 Cytoplasmic FMR1-interacting protein 1 CYFIP1 >sp|Q7L576|CYFP1_HUMAN Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1 0.16 -0.08 0.18 -0.06 0.05 0.15 0.39 -0.01 0.332616926 -0.094290426 axon extension;biological regulation;cell growth;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental cell growth;developmental growth;developmental growth involved in morphogenesis;developmental process;growth;lamellipodium assembly;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;ruffle organization actin binding;actin filament binding;binding;cytoskeletal protein binding;enzyme binding;GTPase binding;protein binding;Rac GTPase binding;Ras GTPase binding;Rho GTPase binding;small GTPase binding cell junction;cell part;cell projection;cytoplasmic part;intracellular part;lamellipodium;macromolecular complex;mRNA cap binding complex;neuron projection;perinuclear region of cytoplasm;protein complex;RNA cap binding complex;ruffle;synapse Regulation of actin cytoskeleton 2.67E-206 7 34 18 28.2

Q9Y3I0;E7EQS9 tRNA-splicing ligase RtcB homolog C22orf28 >sp|Q9Y3I0|RTCB_HUMAN tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=C22orf28 PE=1 SV=1 0.07 0.02 -0.02 0.05 0.11 -0.01 -0.03 -0.19 0.363872221 0.058480833 "anatomical structure development;anatomical structure morphogenesis;biological adhesion;cell adhesion;cell morphogenesis;cell morphogenesis involved in differentiation;cell-matrix adhesion;cell-substrate adhesion;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;in utero embryonic development;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;placenta development;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via endonucleolytic cleavage and ligation;substrate adhesion-dependent cell spreading;tRNA metabolic process;tRNA processing;tRNA splicing, via endonucleolytic cleavage and ligation" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming phosphoric ester bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA ligase (ATP) activity;RNA ligase activity" cell part;cytoplasm;intracellular part;macromolecular complex;protein complex;tRNA-splicing ligase complex 5.80E-113 2 19 19 44.6

Q96HE7;G3V3E6;G3V5B3;G3V2H0;G3V503;Q5TAE8;Q86YB8;Q7Z6L1-3;Q7Z6L1;Q7Z6L1-2;Q7Z6L1-4 ERO1-like protein alpha ERO1L >sp|Q96HE7|ERO1A_HUMAN ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 0.18 -0.15 -0.12 -0.21 0.10 0.05 0.56 0.34 0.97433263 -0.335893646 apoptosis;apoptosis in response to endoplasmic reticulum stress;autophagic vacuole fusion;biological regulation;brown fat cell differentiation;calcium ion homeostasis;calcium ion transport;calcium ion transport into cytosol;cation homeostasis;cation transport;cell death;cell differentiation;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule metabolic process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cellular response to topologically incorrect protein;cellular response to unfolded protein;chaperone mediated protein folding requiring cofactor;chaperone-mediated protein folding;chemical homeostasis;cytosolic calcium ion homeostasis;cytosolic calcium ion transport;'de novo' posttranslational protein folding;'de novo' protein folding;death;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;electron transport chain;elevation of cytosolic calcium ion concentration;endoplasmic reticulum unfolded protein response;ER-nucleus signaling pathway;establishment of localization;fat cell differentiation;generation of precursor metabolites and energy;homeostatic process;ion homeostasis;ion transport;macromolecule metabolic process;macromolecule modification;membrane fusion;membrane organization;metabolic process;metal ion homeostasis;metal ion transport;negative regulation of biological process;negative regulation of sequestering of calcium ion;organelle fusion;organelle membrane fusion;organelle organization;oxidation-reduction process;primary metabolic process;programmed cell death;protein folding;protein metabolic process;protein modification process;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of homeostatic process;regulation of ion homeostasis;regulation of localization;regulation of sequestering of calcium ion;release of sequestered calcium ion into cytosol;response to abiotic stimulus;response to chemical stimulus;response to endoplasmic reticulum stress;response to organic substance;response to stimulus;response to stress;response to temperature stimulus;response to topologically incorrect protein;response to unfolded protein;signal transduction;transport "binding;catalytic activity;coenzyme binding;cofactor binding;flavin adenine dinucleotide binding;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;lipid binding;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor;phosphatidylinositol binding;phosphatidylinositol-3-phosphate binding;phospholipid binding;protein binding;protein disulfide isomerase activity;unfolded protein binding" autophagic vacuole membrane;cell part;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;lysosomal membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part;vacuolar membrane;vacuolar part;vesicle Protein processing in endoplasmic reticulum;Vibrio cholerae infection 6.54E-159 11 19 19 53.4

P15170-2;P15170-3;H3BR35;P15170;Q8IYD1;H3BSV8 Eukaryotic peptide chain release factor GTP-binding subunit ERF3A;Eukaryotic peptide chain release factor GTP-binding subunit ERF3B GSPT1;GSPT2 >sp|P15170-2|ERF3A_HUMAN Isoform 2 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1;>sp|P15170-3|ERF3A_HUMAN Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT 0.10 -0.10 -0.01 -0.05 0.10 -0.04 0.42 -0.25 0.177116198 -0.069688394 "catabolic process;cell cycle;cell cycle process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex disassembly;cellular protein metabolic process;G1/S transition of mitotic cell cycle;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule methylation;macromolecule modification;metabolic process;methylation;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;one-carbon metabolic process;primary metabolic process;protein alkylation;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein methylation;protein modification process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;RNA catabolic process;RNA metabolic process;small molecule metabolic process;translational termination""binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation release factor activity;translation termination factor activity" cell part;cytoplasmic part;cytosol;intracellular;intracellular part mRNA surveillance pathway 1.17E-87 6 19 19 35.5

B4E2W0;P55084;F5GZQ3;B5MD38;C9JEY0;C9JE81;C9K0M0 "Trifunctional enzyme subunit beta, mitochondrial;3-ketoacyl-CoA thiolase" HADHB ">tr|B4E2W0|B4E2W0_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=HADHB PE=2 SV=1;>sp|P55084|ECHB_HUMAN Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3;>tr|F5GZQ3|F5GZQ3_HUMAN 3-ketoacyl-CoA thiolase OS=Homo sapiens GN=" -0.48 -0.18 0.10 0.11 0.22 0.10 -0.40 -0.05 0.155156083 -0.082345619 biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;cardiolipin acyl-chain remodeling;cardiolipin metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;organophosphate metabolic process;oxidation-reduction process;oxoacid metabolic process;phosphatidylglycerol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "3-hydroxyacyl-CoA dehydrogenase activity;acetyl-CoA C-acyltransferase activity;binding;C-acyltransferase activity;carbon-oxygen lyase activity;carboxylic acid binding;catalytic activity;coenzyme binding;cofactor binding;enoyl-CoA hydratase activity;fatty acid binding;fatty-acyl-CoA binding;hydro-lyase activity;lipid binding;long-chain-3-hydroxyacyl-CoA dehydrogenase activity;long-chain-enoyl-CoA hydratase activity;lyase activity;monocarboxylic acid binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;endoplasmic reticulum;fatty acid beta-oxidation multienzyme complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial outer membrane;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;protein complex "Benzoate degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Valine, leucine and isoleucine degradation" 1.17E-85 7 19 19 36.1

O95163;F5H2T0;H0YDF3 Elongator complex protein 1 IKBKAP >sp|O95163|ELP1_HUMAN Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3;>tr|F5H2T0|F5H2T0_HUMAN Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=2 SV=1 0.31 0.03 0.03 -0.14 -0.37 -0.40 0.15 -0.55 0.835710524 0.349558217 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;immune response;immune system process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;primary metabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA metabolic process;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent" enzyme regulator activity;kinase regulator activity;molecular transducer activity;phosphorylase kinase regulator activity;protein kinase regulator activity;signal transducer activity "cell part;cytoplasm;DNA-directed RNA polymerase II, holoenzyme;Elongator holoenzyme complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;organelle;organelle part;protein complex;transcription elongation factor complex" 1.04E-117 3 19 19 20.3

O95202;O95202-2;O95202-3 "LETM1 and EF-hand domain-containing protein 1, mitochondrial" LETM1 ">sp|O95202|LETM1_HUMAN LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1" -0.59 0.15 0.07 0.24 0.14 0.52 -1.03 0.20 0.009174725 0.011082562 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;cristae formation;inner mitochondrial membrane organization;membrane organization;mitochondrial membrane organization;mitochondrion organization;organelle organization binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 1.24E-114 3 19 19 33.2

P04181;P04181-2 "Ornithine aminotransferase, mitochondrial;Ornithine aminotransferase, hepatic form;Ornithine aminotransferase, renal form" OAT ">sp|P04181|OAT_HUMAN Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1;>sp|P04181-2|OAT_HUMAN Isoform 2 of Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT" 0.23 -0.06 -0.05 -0.03 -0.96 -0.51 0.02 0.17 0.538677687 0.341871862 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutamine family amino acid biosynthetic process;glutamine family amino acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;L-proline biosynthetic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;multicellular organismal process;neurological system process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;proline biosynthetic process;proline metabolic process;protein complex assembly;protein complex subunit organization;protein hexamerization;protein oligomerization;sensory perception;sensory perception of light stimulus;small molecule biosynthetic process;small molecule metabolic process;system process;visual perception "binding;catalytic activity;cofactor binding;ornithine-oxo-acid transaminase activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part Arginine and proline metabolism 4.05E-152 2 19 19 45.1

Q9Y520-3;Q9Y520-4;E7EPN9;Q9Y520-5;Q9Y520;Q9Y520-7;Q9Y520-6;Q9Y520-2;H7C5N8 Protein PRRC2C PRRC2C >sp|Q9Y520-3|PRC2C_HUMAN Isoform 3 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C;>sp|Q9Y520-4|PRC2C_HUMAN Isoform 4 of Protein PRRC2C OS=Homo sapiens GN=PRRC2C;>tr|E7EPN9|E7EPN9_HUMAN Protein PRRC2C OS=Homo sapiens GN=PRRC2C PE=2 SV=1;>sp|Q9Y520-5|PRC2C_HUMA 0.29 0.05 -0.02 -0.15 -0.09 -0.56 -0.05 -0.48 0.899339054 0.338772723 6.91E-106 9 19 19 13

P43686;P43686-2 26S protease regulatory subunit 6B PSMC4 >sp|P43686|PRS6B_HUMAN 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2;>sp|P43686-2|PRS6B_HUMAN Isoform 2 of 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 0.03 0.07 -0.07 -0.05 -0.03 -0.24 -0.03 -0.29 0.799479313 0.144251103 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;blastocyst development;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nuclear part;nucleoplasm;organelle;organelle part;proteasome accessory complex;protein complex Proteasome 1.87E-143 2 19 19 57.7

P46060;F8W7I9;H0Y4Q3;B0QYT5;B0QYT4;B0QYT6 Ran GTPase-activating protein 1 RANGAP1 >sp|P46060|RAGP1_HUMAN Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1;>tr|F8W7I9|F8W7I9_HUMAN Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=2 SV=1 0.24 0.19 -0.38 -0.08 -0.29 -0.18 0.00 0.07 0.219754407 0.094969299 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular process;cellular response to stimulus;M phase;M phase of mitotic cell cycle;mitotic anaphase;mitotic prometaphase;negative regulation of biological process;negative regulation of intracellular protein transport;negative regulation of intracellular transport;negative regulation of nucleocytoplasmic transport;negative regulation of protein export from nucleus;negative regulation of protein transport;negative regulation of transport;positive regulation of catalytic activity;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of molecular function;positive regulation of Ran GTPase activity;positive regulation of Ras GTPase activity;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of establishment of protein localization;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein localization;regulation of protein transport;regulation of purine nucleotide catabolic process;regulation of Ran GTPase activity;regulation of Ras GTPase activity;regulation of transport;response to stimulus;signal transduction enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;Ran GTPase activator activity;Ras GTPase activator activity;small GTPase regulator activity cell part;chromosomal part;condensed chromosome kinetochore;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;nuclear membrane;nuclear part;nuclear pore;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;pore complex;protein complex;spindle pole RNA transport 1.34E-255 6 19 19 46.3

P37837;F2Z393;E9PM01;E9PKI8 Transaldolase TALDO1 >sp|P37837|TALDO_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2;>tr|F2Z393|F2Z393_HUMAN Transaldolase OS=Homo sapiens GN=TALDO1 PE=2 SV=1 0.09 -0.01 -0.05 -0.09 0.39 0.12 0.18 -0.12 0.598639991 -0.15757625 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;NADP metabolic process;NADPH regeneration;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;pentose biosynthetic process;pentose metabolic process;pentose-phosphate shunt;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;xylulose biosynthetic process;xylulose metabolic process "catalytic activity;sedoheptulose-7-phosphate:D-glyceraldehyde-3-phosphate glyceronetransferase activity;transferase activity;transferase activity, transferring aldehyde or ketonic groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Pentose phosphate pathway 2.28E-114 4 19 19 50.1

E9PIR7;B2R5P6;Q16881-5;E2QRB9;Q16881-2;B7Z2S5;Q16881-4;E9PNQ6;E7ESI6;Q16881-3;E7EW10;Q16881-6;B7Z904;Q16881;F5H780;E9PMY9;E9PKD3;E9PIZ5;E9PLT3;E9PKI4;E9PQI3;E9PRI8;E9PJU2;E7EWK1;F5H1L4;E7ENA2;Q9NNW7-2;D3YTF8;F5H2V0;D3YTF9;Q9NNW7 "Thioredoxin reductase 1, cytoplasmic" TXNRD1">tr|E9PIR7|E9PIR7_HUMAN Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=2 SV=1;>tr|B2R5P6|B2R5P6_HUMAN Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=2 SV=1;>sp|Q16881-5|TRXR1_HUMAN Isoform 5 of Thioredoxin reductase 1," 0.72 -0.17 -0.71 -0.53 1.87 1.28 0.87 0.58 1.282124489 -1.325591121 amine metabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;benzene-containing compound metabolic process;biological regulation;carboxylic acid metabolic process;catabolic process;cell proliferation;cell redox homeostasis;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to copper ion;cellular response to hydrogen peroxide;cellular response to hyperoxia;cellular response to inorganic substance;cellular response to metal ion;cellular response to oxidative stress;cellular response to oxygen levels;cellular response to reactive oxygen species;cellular response to stimulus;cellular response to stress;coenzyme metabolic process;cofactor metabolic process;developmental process;electron transport chain;formation of primary germ layer;generation of precursor metabolites and energy;glutathione metabolic process;halogen metabolic process;heart development;hemopoiesis;hemopoietic or lymphoid organ development;heterocycle metabolic process;homeostatic process;hydrogen peroxide catabolic process;hydrogen peroxide metabolic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;mesoderm formation;metabolic process;methylmercury metabolic process;NADP metabolic process;NADPH oxidation;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule interconversion;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organ development;organic acid metabolic process;organomercury metabolic process;organometal metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;peptide metabolic process;placenta development;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein tetramerization;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;reactive oxygen species metabolic process;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;response to axon injury;response to chemical stimulus;response to copper ion;response to drug;response to hydrogen peroxide;response to hyperoxia;response to inorganic substance;response to metal ion;response to oxidative stress;response to oxygen levels;response to oxygen radical;response to reactive oxygen species;response to selenium ion;response to stimulus;response to stress;response to wounding;selenium compound metabolic process;selenocysteine metabolic process;serine family amino acid metabolic process;signal transduction;small molecule metabolic process;sulfur compound metabolic process "antioxidant activity;binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;disulfide oxidoreductase activity;electron carrier activity;flavin adenine dinucleotide binding;ion binding;mercury ion binding;metal ion binding;NAD(P)H oxidase activity;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, oxygen as acceptor;protein disulfide oxidoreductase activity;selenate reductase activity;thioredoxin-disulfide reductase activity;transition metal ion binding" cell body;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;neuronal cell body;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle partPyrimidine metabolism;Selenocompound metabolism 8.51E-142 31 19 19 49

Q93009;F5H8E5;B7Z815;H3BND8;F5H2X1;H3BMF6 Ubiquitin carboxyl-terminal hydrolase 7;Ubiquitin carboxyl-terminal hydrolase USP7 >sp|Q93009|UBP7_HUMAN Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2;>tr|F5H8E5|F5H8E5_HUMAN Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP7 PE=2 SV=1;>tr|B7Z815|B7Z815_HUMAN Ubiquitin carboxyl-terminal hydrolase OS 0.07 0.06 0.05 -0.01 0.09 -0.23 -0.15 -0.54 0.820676357 0.249479618 "biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;DNA repair;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;maintenance of DNA methylation;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multicellular organismal development;multicellular organismal process;multi-organism process;negative regulation of molecular function;negative regulation of NF-kappaB transcription factor activity;negative regulation of sequence-specific DNA binding transcription factor activity;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair;primary metabolic process;protein deubiquitination;protein metabolic process;protein modification by small protein conjugation or removal;protein modification by small protein removal;protein modification process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;transcription-coupled nucleotide-excision repair;ubiquitin-dependent protein catabolic process;viral reproductive process;virus-host interaction" "binding;catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;p53 binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding;small conjugating protein-specific protease activity;thiolester hydrolase activity;ubiquitin thiolesterase activity;ubiquitin-specific protease activity"cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;PML body 1.20E-127 6 19 19 22.1

Q9H0D6;Q9H0D6-2;B4DZC3 5-3 exoribonuclease 2 XRN2 >sp|Q9H0D6|XRN2_HUMAN 5-3 exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1;>sp|Q9H0D6-2|XRN2_HUMAN Isoform 2 of 5-3 exoribonuclease 2 OS=Homo sapiens GN=XRN2;>tr|B4DZC3|B4DZC3_HUMAN 5-3 exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=2 SV=1 0.01 0.44 0.07 0.50 -0.27 -0.14 -1.03 -0.17 1.116570898 0.656177234 "biological regulation;biosynthetic process;catabolic process;cell growth;cellular biosynthetic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA catabolic process;DNA catabolic process, exonucleolytic;DNA metabolic process;gamete generation;growth;macromolecule catabolic process;macromolecule metabolic process;male gamete generation;metabolic process;mRNA metabolic process;mRNA processing;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;spermatogenesis;transcription termination, DNA-dependent" "5'-3' exonuclease activity;5'-3' exoribonuclease activity;binding;catalytic activity;cation binding;exonuclease activity;exonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;exoribonuclease activity;exoribonuclease activity, producing 5'-phosphomonoesters;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;metal ion binding;nuclease activity;nucleic acid binding;ribonuclease activity;transition metal ion binding;zinc ion binding" aggresome;cell part;inclusion body;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part Ribosome biogenesis in eukaryotes;RNA degradation 7.40E-109 3 19 19 29.7

Q6Y7W6-4;Q6Y7W6;Q6Y7W6-3;I1E4Y6;E7ESB6;C9JHW1;E9PC50;C9JH18;F8WCD5;C9JPV7;C9JXQ0;C9J0V6;C9JHT0;C9JRZ2;C9JW88;C9JH78;C9IYH5 PERQ amino acid-rich with GYF domain-containing protein 2 GIGYF2 >sp|Q6Y7W6-4|PERQ2_HUMAN Isoform 3 of PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2;>sp|Q6Y7W6|PERQ2_HUMAN PERQ amino acid-rich with GYF domain-containing protein 2 OS=Homo sapiens GN=GIGYF2 PE=1 SV=1;>sp|Q6Y7W6-3|PERQ 0.11 0.06 0.14 -0.06 -0.07 -0.19 0.01 -0.24 1.104130056 0.184645517 adult behavior;adult locomotory behavior;anatomical structure homeostasis;behavior;biological regulation;cell cycle phase;cell cycle process;cell death;cell differentiation;cell differentiation in spinal cord;cell surface receptor linked signaling pathway;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;central nervous system neuron differentiation;death;developmental process;enzyme linked receptor protein signaling pathway;feeding behavior;growth;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;insulin-like growth factor receptor signaling pathway;locomotory behavior;macromolecule metabolic process;metabolic process;multicellular organism growth;multicellular organismal movement;multicellular organismal process;musculoskeletal movement;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron differentiation;post-embryonic development;posttranscriptional regulation of gene expression;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;response to stimulus;S phase;S phase of mitotic cell cycle;signal transduction;spinal cord motor neuron differentiation;system process;tissue homeostasis;transmembrane receptor protein tyrosine kinase signaling pathway 1.85E-214 17 20 19 22.3

Q6UB35;H0Y327;Q4VXM0;Q5JYA3;Q5JYA8;Q6UB35-2;Q4VXM1;Q5JYA5;Q5JYA4;H0Y2S0 "Monofunctional C1-tetrahydrofolate synthase, mitochondrial" MTHFD1L ">sp|Q6UB35|C1TM_HUMAN Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1" 0.01 -0.10 0.08 0.04 -0.26 -0.44 -0.07 -0.23 1.248938605 0.258161824 aromatic compound biosynthetic process;biosynthetic process;carboxylic acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;folic acid-containing compound biosynthetic process;folic acid-containing compound metabolic process;formate metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;monocarboxylic acid metabolic process;nitrogen compound metabolic process;one-carbon metabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;pteridine-containing compound biosynthetic process;pteridine-containing compound metabolic process;small molecule metabolic process;tetrahydrofolate interconversion;tetrahydrofolate metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;formate-tetrahydrofolate ligase activity;identical protein binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;methylenetetrahydrofolate dehydrogenase (NADP+) activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH group of donors;oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle One carbon pool by folate 1.41E-122 10 20 19 23.8

P07195;A8MW50;C9J7H8;F5H793;F5H5G7;F5H155;G3XAP5;F5H245;Q6ZMR3;P07864 L-lactate dehydrogenase B chain;L-lactate dehydrogenase LDHB >sp|P07195|LDHB_HUMAN L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2;>tr|A8MW50|A8MW50_HUMAN L-lactate dehydrogenase (Fragment) OS=Homo sapiens GN=LDHB PE=2 SV=1;>tr|C9J7H8|C9J7H8_HUMAN L-lactate dehydrogenase B chain (Fragment) OS=Homo 0.13 -0.01 -0.12 -0.06 -0.12 -0.37 0.17 -0.42 0.483074826 0.169536431 alcohol catabolic process;alcohol metabolic process;ATP biosynthetic process;ATP metabolic process;biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;catabolic process;cell motility;cellular biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component movement;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle biosynthetic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;lactate biosynthetic process;lactate biosynthetic process from pyruvate;lactate metabolic process;lactate oxidation;locomotion;metabolic process;monocarboxylic acid metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;NAD metabolic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;pyruvate metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;sperm motility "binding;catalytic activity;coenzyme binding;cofactor binding;lactate dehydrogenase activity;L-lactate dehydrogenase activity;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Cysteine and methionine metabolism;Glycolysis / Gluconeogenesis;Propanoate metabolism;Pyruvate metabolism 2.22E-272 10 21 19 56.3

P61221;D6R9I9;D6RGF4;H0Y990 ATP-binding cassette sub-family E member 1 ABCE1 >sp|P61221|ABCE1_HUMAN ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1;>tr|D6R9I9|D6R9I9_HUMAN ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=2 SV=1 0.16 0.05 -0.25 -0.10 -0.16 -0.29 0.31 -0.27 0.151951376 0.069346974 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;heterocycle catabolic process;heterocycle metabolic process;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;reproductive process;response to biotic stimulus;response to other organism;response to stimulus;response to virus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;RNA catabolic process;RNA metabolic process;small molecule metabolic process;viral reproductive process;virus-host interaction "4 iron, 4 sulfur cluster binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;cation binding;electron carrier activity;enzyme inhibitor activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonuclease inhibitor activity;ribonucleotide binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 2.73E-199 4 20 20 41.2

Q8NE71-2;Q8NE71;H0YGW7;Q5STZ8;Q5STZ7;F5GYK6 ATP-binding cassette sub-family F member 1 ABCF1 >sp|Q8NE71-2|ABCF1_HUMAN Isoform 2 of ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1;>sp|Q8NE71|ABCF1_HUMAN ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2;>tr|H0YGW7|H0YGW7_HUMAN ATP-binding cassette sub--0.21 -0.05 0.03 0.00 0.25 0.17 0.01 0.09 1.082785647 -0.190184365 ATP catabolic process;ATP metabolic process;catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;defense response;heterocycle catabolic process;heterocycle metabolic process;inflammatory response;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;response to stimulus;response to stress;response to wounding;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;translational initiation "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleoprotein binding;ribonucleotide binding;ribosome binding;RNA binding;translation activator activity;translation factor activity, nucleic acid binding;translation regulator activity;translation regulator activity, nucleic acid binding" cell part;cytoplasmic part;envelope;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleoplasm;organelle;organelle envelope;organelle part;polysomal ribosome;ribonucleoprotein complex;ribosome 2.83E-198 6 20 20 33.2

Q12797;Q12797-10;E5RHJ2;E5RHK2;Q12797-7;Q12797-6;Q12797-2;E5RG56;G3XAN5;E5RG29;Q12797-4;Q12797-3;Q12797-9;Q12797-5;Q12797-8 Aspartyl/asparaginyl beta-hydroxylase ASPH >sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3;>sp|Q12797-10|ASPH_HUMAN Isoform 10 of Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH -0.28 -0.20 0.06 -0.01 1.43 0.73 -0.42 -0.08 0.514767767 -0.521554105 "activation of store-operated calcium channel activity;anatomical structure development;anatomical structure morphogenesis;appendage morphogenesis;biological regulation;calcium ion transmembrane transport;calcium ion transport;calcium-mediated signaling;cation transport;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to calcium ion;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to metal ion;cellular response to stimulus;detection of calcium ion;detection of chemical stimulus;detection of stimulus;developmental process;divalent inorganic cation transport;divalent metal ion transport;establishment of localization;face morphogenesis;intracellular signal transduction;ion transmembrane transport;ion transport;limb morphogenesis;macromolecule metabolic process;macromolecule modification;metabolic process;metal ion transport;multicellular organismal process;muscle contraction;muscle system process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;palate development;pattern specification process;peptidyl-amino acid modification;peptidyl-aspartic acid hydroxylation;peptidyl-aspartic acid modification;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of calcium ion transport;positive regulation of calcium ion transport into cytosol;positive regulation of calcium ion transport via store-operated calcium channel activity;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of gene expression;positive regulation of homeostatic process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of ion transmembrane transporter activity;positive regulation of ion transport;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of protein metabolic process;positive regulation of protein transport;positive regulation of proteolysis;positive regulation of RNA metabolic process;positive regulation of ryanodine-sensitive calcium-release channel activity;positive regulation of transcription, DNA-dependent;positive regulation of transport;positive regulation of transporter activity;primary metabolic process;protein hydroxylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of calcium ion transport via store-operated calcium channel activity;regulation of cardiac muscle contraction;regulation of cardiac muscle contraction by calcium ion signaling;regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion;regulation of cell communication;regulation of cell communication by electrical coupling;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of establishment of protein localization;regulation of gene expression;regulation of heart contraction;regulation of homeostatic process;regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of metal ion transport;regulation of molecular function;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of proteolysis;regulation of receptor activity;regulation of release of sequestered calcium ion into cytosol;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of response to stimulus;regulation of RNA metabolic process;regulation of ryanodine-sensitive calcium-release channel activity;regulation of signal transduction;regulation of signaling;regulation of striated muscle contraction;regulation of system process;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;response to ATP;response to calcium ion;response to chemical stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to stimulus;second-messenger-mediated signaling;signal transduction;system process;transmembrane transport;transport" "binding;calcium ion binding;catalytic activity;cation binding;dioxygenase activity;electron carrier activity;ion binding;ion channel binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen;oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen;peptide-aspartate beta-dioxygenase activity;protein binding;structural constituent of muscle;structural molecule activity" calcium channel complex;cation channel complex;cell cortex part;cell part;cortical endoplasmic reticulum;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;ion channel complex;junctional sarcoplasmic reticulum membrane;macromolecular complex;membrane;membrane part;membrane-enclosed lumen;organelle lumen;organelle membrane;organelle part;plasma membrane;protein complex;sarcoplasmic reticulum lumen;sarcoplasmic reticulum membrane 7.68E-107 15 20 20 33.2

Q8WWM7-6;Q8WWM7-8;Q8WWM7-5;Q8WWM7-4;Q8WWM7-9;Q8WWM7-2;Q8WWM7;Q8WWM7-3;H3BUF6;Q8WWM7-7;H3BSK9;H3BUE3;H3BSQ5 Ataxin-2-like protein ATXN2L >sp|Q8WWM7-6|ATX2L_HUMAN Isoform 6 of Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L;>sp|Q8WWM7-8|ATX2L_HUMAN Isoform 8 of Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L;>sp|Q8WWM7-5|ATX2L_HUMAN Isoform 5 of Ataxin-2-like protein OS=Homo sapiens GN=ATXN2 -0.02 -0.08 0.18 -0.13 0.15 -0.19 -0.12 -0.44 0.414751774 0.140180004 biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of cytoplasmic mRNA processing body assembly;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;stress granule assembly cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part;ribonucleoprotein complex;RNA granule;stress granule 1.04E-103 13 20 20 26.9

O95817;C9JFK9 BAG family molecular chaperone regulator 3 BAG3 >sp|O95817|BAG3_HUMAN BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3;>tr|C9JFK9|C9JFK9_HUMAN BAG family molecular chaperone regulator 3 (Fragment) OS=Homo sapiens GN=BAG3 PE=2 SV=1 0.00 -0.06 0.13 0.01 -0.53 -0.01 0.39 0.12 0.040491879 0.023929841 anatomical structure development;apoptosis;biological regulation;brain development;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;developmental process;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organ development;primary metabolic process;programmed cell death;protein folding;protein metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;spinal cord development cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;neuron projection;plasma membrane 3.11E-134 2 20 20 54.6

Q9NYF8-2;Q9NYF8;Q9NYF8-3;E9PK91;E9PK09;E9PQN2;E9PKI6;Q9NYF8-4;E9PJA7;H0YF00;B0AZU3;H0YF14;H0YF63 Bcl-2-associated transcription factor 1 BCLAF1 >sp|Q9NYF8-2|BCLF1_HUMAN Isoform 2 of Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1;>sp|Q9NYF8|BCLF1_HUMAN Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2;>sp|Q9NYF8-3|BCLF1_HUMAN Isoform 3 of Bcl-2-associate -0.37 0.18 0.08 0.34 0.07 -0.12 -0.99 -0.63 0.705075363 0.47437915 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;induction of apoptosis;induction of programmed cell death;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of protein complex assembly;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription initiation, DNA-dependent;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA-dependent transcription in response to stress;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein complex assembly;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription initiation, DNA-dependent;regulation of transcription, DNA-dependent;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part 2.42E-67 13 20 20 26.5

P30622-2;P30622-1;P30622;J3KP58;F5H0N7;F5H6A0;F5H1T5;F6VGP8;F5H367;F5H270 CAP-Gly domain-containing linker protein 1CLIP1 >sp|P30622-2|CLIP1_HUMAN Isoform 3 of CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1;>sp|P30622-1|CLIP1_HUMAN Isoform 2 of CAP-Gly domain-containing linker protein 1 OS=Homo sapiens GN=CLIP1;>sp|P30622|CLIP1_HUMAN CAP-Gly domain-contai -0.07 0.07 0.12 -0.01 0.25 0.66 0.40 0.11 1.090406072 -0.328402122 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;M phase;M phase of mitotic cell cycle;microtubule bundle formation;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;organelle organization;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of cytoskeleton organization;positive regulation of microtubule polymerization;positive regulation of microtubule polymerization or depolymerization;positive regulation of organelle organization;positive regulation of protein complex assembly;positive regulation of protein polymerization;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;transport binding;cation binding;cytoskeletal protein binding;identical protein binding;ion binding;metal ion binding;microtubule binding;microtubule plus-end binding;nucleic acid binding;protein binding;protein dimerization activity;protein homodimerization activity;transition metal ion binding;tubulin binding;zinc ion binding cell part;cell projection;centrosome;chromosomal part;cytoplasm;cytoplasmic microtubule;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;endosome;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane-bounded organelle;microtubule;microtubule organizing center;microtubule plus end;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;protein complex;ruffle;vesicle membrane 4.29E-151 10 20 20 18.8

Q96KP4;Q96KP4-2;J3QKT2;J3KSV5;J3QQN6;J3QR27;J3QLU1;J3QKQ0;J3QRD0;J3QL02;J3QRA8;J3KSS4;J3KRD5;J3QRP4;J3QRH4 Cytosolic non-specific dipeptidase CNDP2 >sp|Q96KP4|CNDP2_HUMAN Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2 PE=1 SV=2;>sp|Q96KP4-2|CNDP2_HUMAN Isoform 2 of Cytosolic non-specific dipeptidase OS=Homo sapiens GN=CNDP2;>tr|J3QKT2|J3QKT2_HUMAN Cytosolic non-specific dipeptidase (Fragm 0.02 -0.09 -0.15 0.02 -0.62 -0.33 0.50 -0.05 0.110312196 0.075306112 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutathione biosynthetic process;glutathione metabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptide biosynthetic process;peptide metabolic process;primary metabolic process;protein metabolic process;proteolysis;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;xenobiotic metabolic process "binding;carboxypeptidase activity;catalytic activity;cation binding;dipeptidase activity;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;tripeptidase activity" cell part;cytoplasmic part;cytosol;intracellular part 4.06E-131 15 20 20 51.8

P05198;H0YJS4;G3V4T5 Eukaryotic translation initiation factor 2 subunit 1EIF2S1 >sp|P05198|IF2A_HUMAN Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3;>tr|H0YJS4|H0YJS4_HUMAN Eukaryotic translation initiation factor 2 subunit 1 (Fragment) OS=Homo sapiens GN=EIF2S1 PE=4 SV=1;>tr|G3V4T5|G3V4T5_HUM 0.13 0.04 -0.01 0.00 0.10 -0.08 0.00 -0.19 0.501377752 0.082949227 activation of signaling protein activity involved in unfolded protein response;biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;macromolecule metabolic process;macromolecule modification;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;posttranscriptional regulation of gene expression;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;regulation of translation;regulation of translation in response to stress;regulation of translational initiation;regulation of translational initiation in response to stress;response to stimulus;response to stress;translational initiation "binding;nucleic acid binding;ribonucleoprotein binding;ribosome binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 2 complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;polysome;protein complex;ribonucleoprotein complex;RNA granule;stress granule Hepatitis C;Measles;Protein processing in endoplasmic reticulum;RNA transport 6.13E-294 3 20 20 55.6

P07954-2;P07954 "Fumarate hydratase, mitochondrial" FH ">sp|P07954-2|FUMH_HUMAN Isoform Cytoplasmic of Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH;>sp|P07954|FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3" -0.05 -0.03 -0.09 0.00 0.36 0.00 -0.03 -0.29 0.14216564 -0.053167687 acetyl-CoA catabolic process;acetyl-CoA metabolic process;anatomical structure homeostasis;biological regulation;carboxylic acid metabolic process;catabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;fumarate metabolic process;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;metabolic process;organic acid metabolic process;oxoacid metabolic process;regulation of biological quality;small molecule metabolic process;tissue homeostasis;tricarboxylic acid cycle carbon-oxygen lyase activity;catalytic activity;fumarate hydratase activity;hydro-lyase activity;lyase activity cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part;protein complex;tricarboxylic acid cycle enzyme complex Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle);Pathways in cancer;Renal cell carcinoma 4.33E-248 2 20 20 61

Q13451;B7Z7Z8;Q13451-2 Peptidyl-prolyl cis-trans isomerase FKBP5 FKBP5 >sp|Q13451|FKBP5_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens GN=FKBP5 PE=1 SV=2;>tr|B7Z7Z8|B7Z7Z8_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens GN=FKBP5 PE=2 SV=1 -0.02 -0.06 0.38 0.26 0.07 -0.67 -0.67 -1.37 1.075775423 0.801855677 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone-mediated protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process binding;catalytic activity;cis-trans isomerase activity;drug binding;FK506 binding;isomerase activity;macrolide binding;peptidyl-prolyl cis-trans isomerase activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle 7.25E-182 3 20 20 52.7

P63244;J3KPE3;D6RHH4;D6RAC2;H0YAF8;H0Y8W2;D6RFX4;D6R9Z1;D6R9L0;D6REE5;H0YAM7;D6RAU2;E9PD14;D6RFZ9;D6RBD0;H0Y8R5;D6RGK8;D6RF23;D6R909;D6RHJ5;H0Y9P0;D6RDI0 Guanine nucleotide-binding protein subunit beta-2-like 1 GNB2L1 >sp|P63244|GBLP_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3;>tr|J3KPE3|J3KPE3_HUMAN Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=4 SV=1;>tr|D6RHH4|D6RHH4_HUMAN 0.19 -0.04 0.03 0.01 -0.06 -0.32 0.17 -0.16 0.511536979 0.139546936 anatomical structure morphogenesis;biological regulation;cell cycle;cellular process;developmental process;embryonic morphogenesis;gastrulation;interaction with host;interspecies interaction between organisms;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of endocytosis;negative regulation of growth;negative regulation of intracellular protein kinase cascade;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phagocytosis;negative regulation of protein kinase B signaling cascade;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of translation;negative regulation of transport;negative regulation of Wnt receptor signaling pathway;positive regulation of apoptosis;positive regulation of biological process;positive regulation of catabolic process;positive regulation of catalytic activity;positive regulation of cell death;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular catabolic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of developmental process;positive regulation of gastrulation;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of locomotion;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;positive regulation of protein catabolic process;positive regulation of protein complex assembly;positive regulation of protein homooligomerization;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein oligomerization;positive regulation of protein phosphorylation;positive regulation of proteolysis;posttranscriptional regulation of gene expression;regulation of anatomical structure morphogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell division;regulation of cell growth;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of embryonic development;regulation of endocytosis;regulation of establishment of cell polarity;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of establishment or maintenance of cell polarity;regulation of gastrulation;regulation of gene expression;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of intracellular protein kinase cascade;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein catabolic process;regulation of protein complex assembly;regulation of protein homooligomerization;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein oligomerization;regulation of protein phosphorylation;regulation of proteolysis;regulation of purine nucleotide catabolic process;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of translation;regulation of transport;regulation of vesicle-mediated transport;regulation of Wnt receptor signaling pathway;reproductive process;rhythmic process;viral reproductive process;virus-host interaction apoptotic protease activator activity;binding;caspase activator activity;caspase regulator activity;channel inhibitor activity;channel regulator activity;enzyme activator activity;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;ion channel inhibitor activity;kinase binding;kinase inhibitor activity;kinase regulator activity;peptidase activator activity;peptidase regulator activity;protein binding;protein domain specific binding;protein kinase binding;protein kinase C binding;protein kinase inhibitor activity;protein kinase regulator activity;protein tyrosine kinase inhibitor activity;receptor binding;receptor tyrosine kinase binding;SH2 domain binding cell body;cell part;cell projection;cytoplasmic part;cytoskeleton;dendrite;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;midbody;neuron projection;neuronal cell body;non-membrane-bounded organelle;nucleus;organelle;organelle part;perikaryon;perinuclear region of cytoplasm;phagocytic cup;plasma membrane part;ribonucleoprotein complex;small ribosomal subunit Measles 5.87E-227 22 20 20 77.3

Q14789;Q14789-2;E7EU81;H0Y867 Golgin subfamily B member 1 GOLGB1>sp|Q14789|GOGB1_HUMAN Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1 PE=1 SV=2;>sp|Q14789-2|GOGB1_HUMAN Isoform 2 of Golgin subfamily B member 1 OS=Homo sapiens GN=GOLGB1;>tr|E7EU81|E7EU81_HUMAN Golgin subfamily B member 1 (Fragment) OS=Homo sapien -0.05 0.18 0.04 0.08 0.04 -0.21 -0.53 -0.10 0.865083973 0.262784804 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;Golgi organization;organelle organization cell part;cytoplasmic part;endoplasmic reticulum-Golgi intermediate compartment;Golgi apparatus;Golgi apparatus part;Golgi membrane;Golgi stack;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part 3.73E-133 4 20 20 10.3

Q8N1G4 Leucine-rich repeat-containing protein 47 LRRC47 >sp|Q8N1G4|LRC47_HUMAN Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1 0.09 -0.03 0.19 0.09 -0.17 -0.09 0.23 -0.24 0.570529448 0.150711969 "aminoacyl-tRNA ligase activity;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;phenylalanine-tRNA ligase activity;RNA binding" 4.83E-157 1 20 20 45.6

P48163;B4DZ70;F5H4W0 NADP-dependent malic enzyme;Malic enzyme ME1 >sp|P48163|MAOX_HUMAN NADP-dependent malic enzyme OS=Homo sapiens GN=ME1 PE=1 SV=1;>tr|B4DZ70|B4DZ70_HUMAN Malic enzyme OS=Homo sapiens GN=ME1 PE=2 SV=1;>tr|F5H4W0|F5H4W0_HUMAN Malic enzyme OS=Homo sapiens GN=ME1 PE=2 SV=1 0.06 -0.02 -0.14 -0.01 0.31 0.69 0.71 0.05 1.17748603 -0.467482711 biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;dicarboxylic acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;malate metabolic process;metabolic process;NADP biosynthetic process;NADP metabolic process;nicotinamide nucleotide biosynthetic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein tetramerization;pyridine nucleotide biosynthetic process;pyridine nucleotide metabolic process;pyridine-containing compound biosynthetic process;pyridine-containing compound metabolic process;response to carbohydrate stimulus;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to stimulus;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;electron carrier activity;ion binding;malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) activity;malate dehydrogenase (oxaloacetate-decarboxylating) activity;malate dehydrogenase activity;malic enzyme activity;manganese ion binding;metal ion binding;NAD binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;purine nucleotide binding;purine ribonucleotide binding;ribonucleotide binding;transition metal ion binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Carbon fixation in photosynthetic organisms;Pyruvate metabolism 1.96E-193 3 20 20 47.9

P28331-4;P28331-5;P28331;P28331-2;B4DJ81;P28331-3;C9JPQ5 "NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial" NDUFS1 ">sp|P28331-4|NDUS1_HUMAN Isoform 4 of NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1;>sp|P28331-5|NDUS1_HUMAN Isoform 5 of NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1;>sp|P2" -0.28 0.79 0.07 0.90 0.02 0.55 -1.39 0.44 0.354219715 0.46768042 "apoptosis;ATP metabolic process;ATP synthesis coupled electron transport;biological regulation;cell death;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;death;electron transport chain;generation of precursor metabolites and energy;heterocycle metabolic process;homeostatic process;ion homeostasis;metabolic process;mitochondrial electron transport, NADH to ubiquinone;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;programmed cell death;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;reactive oxygen species metabolic process;regulation of biological quality;regulation of membrane potential;regulation of mitochondrial membrane potential;respiratory electron transport chain;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;small molecule metabolic process" "2 iron, 2 sulfur cluster binding;4 iron, 4 sulfur cluster binding;binding;catalytic activity;cation binding;electron carrier activity;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;NADH dehydrogenase (quinone) activity;NADH dehydrogenase (ubiquinone) activity;NADH dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on NADH or NADPH;oxidoreductase activity, acting on NADH or NADPH, quinone or similar compound as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial intermembrane space;mitochondrial membrane part;mitochondrial part;mitochondrial respiratory chain complex I;mitochondrion;NADH dehydrogenase complex;organelle;organelle envelope lumen;organelle part;protein complex;respiratory chain complex I Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 1.32E-230 7 20 20 41.2

R4GNH3;P17980;E9PM69;E9PKD5;E9PMD8;E9PN50;E9PLG2;B4DH61 26S protease regulatory subunit 6A PSMC3 >tr|R4GNH3|R4GNH3_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=4 SV=1;>sp|P17980|PRS6A_HUMAN 26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3;>tr|E9PM69|E9PM69_HUMAN 26S protease regulatory subunit 6A OS=Homo sa -0.05 -0.02 0.00 0.02 0.02 -0.19 -0.13 -0.24 0.920057354 0.125385746 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;blastocyst development;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;developmental process;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;kinase activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;perinuclear region of cytoplasm;proteasome accessory complex;protein complex;ribonucleoprotein complex;RNA granule Proteasome 6.19E-278 8 20 20 62.6

P62424;Q5T8U3;Q5T8U2;O75688-3;O75688 60S ribosomal protein L7a RPL7A >sp|P62424|RL7A_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2;>tr|Q5T8U3|Q5T8U3_HUMAN 60S ribosomal protein L7a (Fragment) OS=Homo sapiens GN=RPL7A PE=2 SV=1;>tr|Q5T8U2|Q5T8U2_HUMAN 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE -0.39 0.09 0.13 0.03 0.00 -0.37 -0.58 -0.45 0.773380723 0.314014125 "biological regulation;biosynthetic process;catabolic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cotranslational protein targeting to membrane;cytokine-mediated signaling pathway;dephosphorylation;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;peptidyl-threonine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein dephosphorylation;protein metabolic process;protein modification process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of cellular process;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;ribonucleoprotein complex biogenesis;ribosome biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;signal transduction;SRP-dependent cotranslational protein targeting to membrane;translational elongation;translational initiation;translational termination;transport;viral transcription" "binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;magnesium ion binding;manganese ion binding;metal ion binding;nucleic acid binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein serine/threonine phosphatase activity;RNA binding;structural constituent of ribosome;structural molecule activity;transition metal ion binding" cell part;cytoplasmic part;cytosol;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;polysomal ribosome;ribonucleoprotein complex;ribosome MAPK signaling pathway;Ribosome 6.02E-186 5 20 20 51.9

P49591;Q5T5C7 "Serine--tRNA ligase, cytoplasmic" SARS ">sp|P49591|SYSC_HUMAN Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=3;>tr|Q5T5C7|Q5T5C7_HUMAN Serine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=2 SV=1" -0.10 -0.19 0.01 0.11 -0.01 -0.07 0.40 -0.19 0.197870804 -0.075824194 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;RNA processing;selenocysteinyl-tRNA(Sec) biosynthetic process;seryl-tRNA aminoacylation;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tRNA processing "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;serine-tRNA ligase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Aminoacyl-tRNA biosynthesis 7.49E-205 2 20 20 47.1

J3KNL6;O15027;O15027-2;O15027-4;O15027-3;O15027-5;Q8N9G1 Protein transport protein Sec16A SEC16A >tr|J3KNL6|J3KNL6_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=4 SV=1;>sp|O15027|SC16A_HUMAN Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=3;>sp|O15027-2|SC16A_HUMAN Isoform 2 of Protein transport protein Sec16A 0.10 -0.05 0.06 -0.20 0.10 -0.10 0.24 -0.05 0.271591425 -0.070990062 cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPII vesicle coating;endoplasmic reticulum organization;establishment of localization;establishment of protein localization;organelle organization;protein transport;transport;vesicle coating;vesicle organization cell part;cytoplasmic part;cytosol;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;intracellular organelle part;intracellular part;membrane;membrane part;organelle membrane;organelle part 5.35E-119 7 20 20 18.3

Q9BXP5-4;Q9BXP5-2;Q9BXP5-3;Q9BXP5;Q9BXP5-5;H7C3A1;H7C1K0;H7C159;H7C0U8;REV__Q8IWL3;REV__O43304;Q58EX7-2;Q58EX7 Serrate RNA effector molecule homolog SRRT >sp|Q9BXP5-4|SRRT_HUMAN Isoform 4 of Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT;>sp|Q9BXP5-2|SRRT_HUMAN Isoform 2 of Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT;>sp|Q9BXP5-3|SRRT_HUMAN Isoform 3 of Serrate RNA effector0.05 0.01 0.08 0.10 0.01 -0.32 -0.56 -0.57 1.258419228 0.423740621 "biological regulation;biosynthetic process;cell proliferation;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular process;negative regulation of developmental process;neuronal stem cell maintenance;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;primary miRNA processing;regulation of biological process;regulation of biosynthetic process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of Ras protein signal transduction;regulation of response to stimulus;regulation of Rho protein signal transduction;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of small GTPase mediated signal transduction;regulation of transcription, DNA-dependent;response to arsenic-containing substance;response to chemical stimulus;response to inorganic substance;response to stimulus;RNA biosynthetic process;RNA metabolic process;RNA processing;stem cell maintenance;transcription, DNA-dependent" binding;DNA binding;enzyme regulator activity;GTPase regulator activity;guanyl-nucleotide exchange factor activity;lipid binding;nucleic acid binding;nucleoside-triphosphatase regulator activity;phospholipid binding;Ras guanyl-nucleotide exchange factor activity;Rho guanyl-nucleotide exchange factor activity;small GTPase regulator activity cell part;cytoplasm;intracellular;intracellular organelle part;intracellular part;nuclear part;nucleoplasm;organelle part 5.78E-87 13 20 20 23.9

P49411;H3BNU3 "Elongation factor Tu, mitochondrial" TUFM ">sp|P49411|EFTU_HUMAN Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2" 0.16 -0.04 0.07 0.01 -0.03 -0.39 0.10 -0.42 0.735976361 0.234177953 catabolic process;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;intracellular;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nucleoid;organelle;organelle part Plant-pathogen interaction 7.97E-209 2 20 20 48

Q5SW79;Q5SW79-2;Q5SW79-3;H0Y2V6;E5RJT5;E5RFU8;E7EWM2;E7EMW0;E5RIH6;H0Y4T4;E5RGW7;H0YB66;E5RG47;Q96L14;H0YB92 Centrosomal protein of 170 kDa CEP170 >sp|Q5SW79|CE170_HUMAN Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170 PE=1 SV=1;>sp|Q5SW79-2|CE170_HUMAN Isoform 2 of Centrosomal protein of 170 kDa OS=Homo sapiens GN=CEP170;>sp|Q5SW79-3|CE170_HUMAN Isoform 3 of Centrosomal protein of 170 kDa OS -0.05 -0.32 -0.31 -0.05 2.02 1.20 0.03 0.07 0.893083546 -1.016028185 cell part;centriole;centrosome;cytoplasmic part;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule organizing center;microtubule organizing center part;non-membrane-bounded organelle;organelle;organelle part;protein complex;spindle 2.02E-60 15 21 20 17.1

Q9NSD9;F5H6Y1 Phenylalanine--tRNA ligase beta subunit FARSB >sp|Q9NSD9|SYFB_HUMAN Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3;>tr|F5H6Y1|F5H6Y1_HUMAN Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=2 SV=1 0.08 -0.01 0.03 -0.02 0.00 -0.10 0.27 -0.30 0.16386506 0.0541592 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;phenylalanyl-tRNA aminoacylation;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;magnesium ion binding;metal ion binding;nucleic acid binding;nucleotide binding;phenylalanine-tRNA ligase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Aminoacyl-tRNA biosynthesis 1.93E-136 2 21 20 37.2

P62191;B4DR63;G3V4X1 26S protease regulatory subunit 4 PSMC1 >sp|P62191|PRS4_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1;>tr|B4DR63|B4DR63_HUMAN 26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=2 SV=10.06 0.03 -0.03 0.07 0.13 -0.09 -0.08 -0.29 0.556776567 0.118397304 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome accessory complex;protein complex Proteasome 1.00E-297 3 21 20 56.8

Q9NZN4;B4DNU6 EH domain-containing protein 2 EHD2 >sp|Q9NZN4|EHD2_HUMAN EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=1 SV=2;>tr|B4DNU6|B4DNU6_HUMAN EH domain-containing protein 2 OS=Homo sapiens GN=EHD2 PE=2 SV=1 -0.11 -0.06 -0.37 -0.02 1.12 0.67 0.07 -0.17 0.79131462 -0.559990166 actin cytoskeleton organization;actin filament-based process;biological regulation;blood coagulation;catabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;coagulation;cortical actin cytoskeleton organization;cortical cytoskeleton organization;cytoskeleton organization;endocytic recycling;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;GTP catabolic process;GTP metabolic process;hemostasis;heterocycle catabolic process;heterocycle metabolic process;intracellular transport;membrane invagination;membrane organization;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organelle organization;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological quality;regulation of body fluid levels;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;endosomal part;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;recycling endosome membrane Endocytosis 2.51E-90 2 24 20 49

Q16555;Q16555-2;E5RFU4 Dihydropyrimidinase-related protein 2 DPYSL2 >sp|Q16555|DPYL2_HUMAN Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1;>sp|Q16555-2|DPYL2_HUMAN Isoform 2 of Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 -0.55 -0.14 -0.93 0.23 0.78 0.66 0.09 0.09 1.021466141 -0.748561487 anatomical structure development;axon guidance;biological regulation;catabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;establishment of localization;heterocycle catabolic process;heterocycle metabolic process;locomotion;metabolic process;nitrogen compound metabolic process;nucleobase catabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;olfactory bulb development;organelle organization;positive regulation of biological process;positive regulation of cellular process;positive regulation of glutamate secretion;positive regulation of secretion;positive regulation of transport;primary metabolic process;pyrimidine base catabolic process;pyrimidine base metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cellular localization;regulation of cellular process;regulation of developmental process;regulation of glutamate secretion;regulation of localization;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of secretion;regulation of signaling;regulation of transport;response to alkaloid;response to amine stimulus;response to amphetamine;response to chemical stimulus;response to cocaine;response to drug;response to endogenous stimulus;response to external stimulus;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to stimulus;response to tropane;signal transduction;small molecule metabolic process;spinal cord development;synaptic vesicle transport;taxis;transport;vesicle-mediated transport "catalytic activity;dihydropyrimidinase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides" axon;cell body;cell part;cell projection;cell projection part;cytoplasmic part;cytosol;dendrite;growth cone;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;neuron projection;neuronal cell body;organelle;protein complex;site of polarized growth Axon guidance 2.51E-253 3 25 20 62.2

Q14195-2;Q14195;H0YBT4;F5GWI3;D6RF19;H0YB87;Q14117 Dihydropyrimidinase-related protein 3 DPYSL3 >sp|Q14195-2|DPYL3_HUMAN Isoform LCRMP-4 of Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3;>sp|Q14195|DPYL3_HUMAN Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 -0.86 -0.34 -0.68 0.30 1.80 1.59 -0.69 -0.11 0.665226303 -1.043432361 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;amine metabolic process;anatomical structure development;axon guidance;beta-alanine metabolic process;biological regulation;carboxylic acid metabolic process;catabolic process;cell development;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;chemotaxis;cytoskeleton organization;developmental process;heterocycle catabolic process;heterocycle metabolic process;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;negative regulation of biological process;negative regulation of cell migration;negative regulation of cell motility;negative regulation of cell projection organization;negative regulation of cellular component movement;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of locomotion;negative regulation of neuron projection development;neuron development;nitrogen compound metabolic process;nucleobase catabolic process;nucleobase metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside catabolic process;nucleoside metabolic process;organelle organization;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of filopodium assembly;positive regulation of neuron projection development;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;pyrimidine base catabolic process;pyrimidine base metabolic process;pyrimidine nucleoside catabolic process;pyrimidine nucleoside metabolic process;pyrimidine-containing compound catabolic process;pyrimidine-containing compound metabolic process;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of filopodium assembly;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;response to axon injury;response to chemical stimulus;response to cytokine stimulus;response to external stimulus;response to organic substance;response to stimulus;response to stress;response to wounding;small molecule metabolic process;taxis;thymine catabolic process;thymine metabolic process;uracil catabolic process;uracil metabolic process "amine binding;amino acid binding;binding;carbohydrate binding;carboxylic acid binding;catalytic activity;cation binding;chondroitin sulfate binding;dihydropyrimidinase activity;glycosaminoglycan binding;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides;ion binding;metal ion binding;nucleobase binding;pattern binding;polysaccharide binding;protein binding;protein domain specific binding;pyrimidine base binding;SH3 domain binding;thymine binding;transition metal ion binding;uracil binding;zinc ion binding" cell body;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;extracellular region part;extracellular space;filamentous actin;growth cone;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;organelle part;protein complex;site of polarized growth beta-Alanine metabolism;Drug metabolism - other enzymes;Pantothenate and CoA biosynthesis;Pyrimidine metabolism 1.25E-129 7 25 20 53.2

O95782-2;O95782;M0R2D9;E9PPY8 AP-2 complex subunit alpha-1 AP2A1 >sp|O95782-2|AP2A1_HUMAN Isoform B of AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1;>sp|O95782|AP2A1_HUMAN AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3 -0.25 -0.10 -0.06 0.18 0.30 0.38 0.03 0.21 1.060733716 -0.288191065 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;chemotaxis;endocytosis;endosome transport;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi to endosome transport;Golgi vesicle transport;immune system process;intracellular protein transport;intracellular transport;locomotion;membrane invagination;membrane organization;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;nerve growth factor receptor signaling pathway;post-Golgi vesicle-mediated transport;protein transport;regulation of biological process;regulation of cell communication;regulation of cellular process;regulation of defense response;regulation of defense response to virus;regulation of defense response to virus by virus;regulation of epidermal growth factor receptor signaling pathway;regulation of immune effector process;regulation of immune system process;regulation of multi-organism process;regulation of response to biotic stimulus;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;signaling;synaptic transmission;taxis;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vesicle-mediated transport;viral reproduction protein transporter activity;substrate-specific transporter activity;transporter activity AP-2 adaptor complex;apical plasma membrane;AP-type membrane coat adaptor complex;basolateral plasma membrane;cell part;clathrin adaptor complex;clathrin coat;clathrin coat of trans-Golgi network vesicle;clathrin vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;plasma membrane part;protein complex;vesicle coat Endocrine and other factor-regulated calcium reabsorption;Endocytosis;Huntington's disease 8.38E-185 4 27 20 35.6

P47756-2;B1AK87;B1AK88;P47756;B1AK85;F6USW4;F6Q0E3 F-actin-capping protein subunit beta CAPZB ">sp|P47756-2|CAPZB_HUMAN Isoform 2 of F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB;>tr|B1AK87|B1AK87_HUMAN Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=2 SV=1;>tr|B1AK88|B1AK88_HUMAN Cappi" -0.11 0.07 -0.04 0.26 0.32 0.24 0.08 0.11 0.606726864 -0.140578002 actin cytoskeleton organization;actin filament capping;actin filament-based process;biological regulation;blood coagulation;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;coagulation;cytoskeleton organization;hemostasis;lamellipodium assembly;multicellular organismal process;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;organelle organization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure morphogenesis;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell morphogenesis;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization actin binding;binding;cytoskeletal protein binding;protein binding cell cortex part;cell part;cell projection;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;F-actin capping protein complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle part;protein complex;WASH complex 9.20E-152 7 21 21 72.1

O75534-2;O75534;O75534-3;G5E9Q2;E9PLT0;E9PLD4;E9PKN4;E9PNG3 Cold shock domain-containing protein E1 CSDE1 >sp|O75534-2|CSDE1_HUMAN Isoform Short of Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1;>sp|O75534|CSDE1_HUMAN Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2;>sp|O75534-3|CSDE1_HUMAN Isoform 3 of Cold shock do 0.18 0.04 -0.09 -0.01 0.11 -0.01 0.08 -0.26 0.177124647 0.048162009 "anatomical structure development;biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;developmental process involved in reproduction;gonad development;macromolecule catabolic process;macromolecule metabolic process;male gonad development;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, no-go decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;reproductive structure development;RNA catabolic process;RNA metabolic process" binding;DNA binding;nucleic acid binding;RNA binding cell part;CRD-mediated mRNA stability complex;cytoplasmic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex 2.51E-187 8 21 21 30.8

P32926 Desmoglein-3 DSG3 >sp|P32926|DSG3_HUMAN Desmoglein-3 OS=Homo sapiens GN=DSG3 PE=1 SV=2 -0.10 0.99 -0.68 0.41 -0.81 0.57 -0.48 0.15 0.24046063 0.297015173 biological adhesion;cell adhesion;cell-cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;homophilic cell adhesion binding;calcium ion binding;cation binding;ion binding;metal ion binding anchoring junction;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;desmosome;integral to membrane;intracellular part;intrinsic to membrane;membrane;membrane part;plasma membrane 5.31E-130 1 21 21 29.4

P26641;B4DTG2 Elongation factor 1-gamma EEF1G >sp|P26641|EF1G_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3;>tr|B4DTG2|B4DTG2_HUMAN Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=2 SV=1 0.07 0.02 -0.04 0.04 0.02 -0.09 -0.02 -0.23 0.738124046 0.102141377 multi-organism process;response to biotic stimulus;response to other organism;response to stimulus;response to virus "binding;nucleic acid binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;eukaryotic translation elongation factor 1 complex;intracellular part;macromolecular complex;protein complex 4.99E-196 2 21 21 42.1

G8JLD3;Q8IUD2;Q8IUD2-3;Q8IUD2-2;Q8IUD2-4;Q8IUD2-5;K7EPP6;K7EPD6;O15083;H7C4G9;K7EP25 ELKS/Rab6-interacting/CAST family member 1 ERC1 >tr|G8JLD3|G8JLD3_HUMAN ELKS/Rab6-interacting/CAST family member 1 OS=Homo sapiens GN=ERC1 PE=2 SV=1;>sp|Q8IUD2|RB6I2_HUMAN ELKS/Rab6-interacting/CAST family member 1 OS=Homo sapiens GN=ERC1 PE=1 SV=1;>sp|Q8IUD2-3|RB6I2_HUMAN Isoform 3 of ELKS/Rab6-interac -0.16 -0.19 0.22 0.02 -0.29 -0.10 0.15 -0.07 0.139754488 0.050511223 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;I-kappaB phosphorylation;intracellular transport;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal development;multicellular organismal process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;primary metabolic process;protein metabolic process;protein modification process;protein phosphorylation;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;retrograde transport, endosome to Golgi;transport;vesicle-mediated transport" binding;leucine zipper domain binding;LRR domain binding;protein binding;protein domain specific binding cell junction;cell part;cell projection part;cytoplasm;cytoplasmic part;cytoskeleton;cytosolic part;Golgi apparatus part;Golgi membrane;growth cone;IkappaB kinase complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;presynaptic membrane;protein complex;site of polarized growth;synapse part;synaptic membrane 1.77E-134 11 21 21 25.2

Q14566 DNA replication licensing factor MCM6 MCM6 >sp|Q14566|MCM6_HUMAN DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 0.14 -0.03 0.07 0.09 0.37 -0.51 -0.84 -0.98 0.780602591 0.558263304 biological regulation;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA unwinding involved in replication;DNA-dependent DNA replication initiation;G1/S transition of mitotic cell cycle;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;S phase;S phase of mitotic cell cycle "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;DNA helicase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;single-stranded DNA binding;structure-specific DNA binding" cell part;chromosomal part;intracellular organelle part;intracellular part;macromolecular complex;MCM complex;nuclear chromosome part;nuclear part;nucleoplasm;nucleoplasm part;organelle part;protein complex Cell cycle;Cell cycle - yeast;DNA replication;Meiosis - yeast 3.71E-107 1 21 21 30.7

P40926;E9PDB2;G3XAL0 "Malate dehydrogenase, mitochondrial;Malate dehydrogenase" MDH2 ">sp|P40926|MDHM_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3;>tr|E9PDB2|E9PDB2_HUMAN Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=2 SV=1;>tr|G3XAL0|G3XAL0_HUMAN Malate dehydrogenase OS=Homo sapiens GN=MDH2 P"-0.10 -0.10 -0.61 0.12 0.54 0.68 0.12 0.08 1.035206028 -0.526714996 acetyl-CoA catabolic process;acetyl-CoA metabolic process;alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;dicarboxylic acid metabolic process;gluconeogenesis;glucose metabolic process;heterocycle metabolic process;hexose biosynthetic process;hexose metabolic process;internal protein amino acid acetylation;macromolecule metabolic process;macromolecule modification;malate metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;NAD metabolic process;NADH metabolic process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxaloacetate metabolic process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule biosynthetic process;small molecule metabolic process;tricarboxylic acid cycle "catalytic activity;L-malate dehydrogenase activity;malate dehydrogenase (NADP+) activity;malate dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane Carbon fixation in photosynthetic organisms;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism;Pyruvate metabolism 0 3 21 21 68

O00567;H0Y653;H0YDU4;Q5JXT2 Nucleolar protein 56 NOP56 >sp|O00567|NOP56_HUMAN Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 -0.52 1.20 -0.02 1.14 -0.45 0.34 -1.56 0.41 0.511594752 0.76723296 cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing binding;nucleic acid binding;RNA binding;snoRNA binding box C/D snoRNP complex;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleolar part;organelle part;pre-snoRNP complex;ribonucleoprotein complex;small nucleolar ribonucleoprotein complex Ribosome biogenesis in eukaryotes 4.09E-138 4 21 21 50.5

E9PF10;O75694;O75694-2;D6RA13 Nuclear pore complex protein Nup155 NUP155 >tr|E9PF10|E9PF10_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=2 SV=1;>sp|O75694|NU155_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1;>sp|O75694-2|NU155_HUMAN Isoform 2 of Nuclear pore complex protei 0.12 0.32 0.16 0.37 0.05 0.02 -0.62 -0.31 1.139998179 0.457209769 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular protein transport;intracellular transport;membrane organization;metabolic process;monosaccharide transport;mRNA export from nucleus;mRNA transport;nuclear envelope organization;nuclear export;nuclear import;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;organic substance transport;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA export from nucleus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process structural constituent of nuclear pore;structural molecule activity;transporter activity cell part;envelope;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear envelope;nuclear membrane;nuclear part;nuclear pore;organelle envelope;organelle membrane;organelle part;pore complex;protein complex RNA transport 1.29E-235 4 21 21 23.2

Q8N1F7;H3BVG0;Q8N1F7-2;H3BM93;H3BRI8;H3BV11;H3BP95;H3BMX0;H3BNN5;H3BRD9;H3BVE2;H3BPA9;H3BNG7 Nuclear pore complex protein Nup93 NUP93 >sp|Q8N1F7|NUP93_HUMAN Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2;>tr|H3BVG0|H3BVG0_HUMAN Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=2 SV=1;>sp|Q8N1F7-2|NUP93_HUMAN Isoform 2 of Nuclear pore complex protein Nu 0.16 0.28 -0.08 0.24 -0.14 0.06 -0.25 0.05 0.854988902 0.219838383 biological regulation;carbohydrate metabolic process;carbohydrate transport;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide transport;mRNA transport;nuclear pore complex assembly;nuclear pore organization;nucleic acid transport;nucleobase-containing compound transport;nucleus organization;organelle organization;organic substance transport;pore complex assembly;primary metabolic process;protein complex assembly;protein complex subunit organization;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;viral reproductive process structural constituent of nuclear pore;structural molecule activity cell part;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear periphery;nuclear pore;organelle membrane;organelle part;pore complex;protein complex RNA transport 4.76E-148 14 21 21 33

P22234;E9PBS1;P22234-2;D6RF62;REV__Q8N6Z3;REV__Q9Y2W6-3;REV__Q5SZR4;REV__Q9Y2W6;REV__H7C0I1;REV__Q8NBF6-2;REV__B8ZZW5;REV__Q8NBF6 Multifunctional protein ADE2;Phosphoribosylaminoimidazole-succinocarboxamide synthase;Phosphoribosylaminoimidazole carboxylase PAICS >sp|P22234|PUR6_HUMAN Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3;>tr|E9PBS1|E9PBS1_HUMAN Phosphoribosylaminoimidazole carboxylase (Fragment) OS=Homo sapiens GN=PAICS PE=2 SV=1;>sp|P22234-2|PUR6_HUMAN Isoform 2 of Multifunctional protei 0.11 0.04 -0.11 0.01 -0.34 -0.80 -0.05 -0.64 1.142660479 0.46993775 biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;'de novo' IMP biosynthetic process;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;pigment biosynthetic process;pigment metabolic process;primary metabolic process;purine base biosynthetic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "5-(carboxyamino)imidazole ribonucleotide mutase activity;acid-amino acid ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbon-carbon lyase activity;carboxy-lyase activity;catalytic activity;intramolecular transferase activity;isomerase activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;lyase activity;nucleotide binding;phosphoribosylaminoimidazole carboxylase activity;phosphoribosylaminoimidazolesuccinocarboxamide synthase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part Purine metabolism 1.96E-256 12 21 21 51.3

B7Z254;Q15084;F8WA83;B5MCQ5;Q15084-2 Protein disulfide-isomerase A6 PDIA6 >tr|B7Z254|B7Z254_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=2 SV=1;>sp|Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1;>tr|F8WA83|F8WA83_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDI 0.12 -0.17 -0.27 -0.21 0.49 -0.12 0.47 -0.21 0.589618588 -0.287478343 activation of signaling protein activity involved in unfolded protein response;biological regulation;cell redox homeostasis;cellular homeostasis;cellular process;glycerol ether metabolic process;homeostatic process;metabolic process;organic ether metabolic process;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hydrolase activity;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of transferase activity;small molecule metabolic process "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle membrane;organelle part;pigment granule;plasma membrane;vesicle Protein processing in endoplasmic reticulum 0 5 21 21 51.5

P35998;B7Z5E2;C9JLS9 26S protease regulatory subunit 7 PSMC2 >sp|P35998|PRS7_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3;>tr|B7Z5E2|B7Z5E2_HUMAN 26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=2 SV=1 0.06 0.06 -0.08 0.00 0.09 -0.11 -0.13 -0.25 0.594124353 0.110146295 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;interaction with host;interspecies interaction between organisms;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;multi-organism process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;ubiquitin-dependent protein catabolic process;viral reproduction;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;proteasome accessory complex;protein complex;ribonucleoprotein complex;RNA granule Proteasome 1.94E-129 3 21 21 51.3

Q9H2M9;Q9H2M9-2;F8WDJ2;H7C4Y9 Rab3 GTPase-activating protein non-catalytic subunit RAB3GAP2 >sp|Q9H2M9|RBGPR_HUMAN Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1 0.12 -0.14 0.04 -0.13 -0.09 0.07 0.53 -0.03 0.393242211 -0.149626983 biological regulation;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;protein transport;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of GTP catabolic process;regulation of GTPase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;transport binding;enzyme activator activity;enzyme regulator activity;GTPase activator activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;protein dimerization activity;protein heterodimerization activity cell part;cytoplasm;intracellular part;membrane;plasma membrane 8.78E-168 4 21 21 17.9

Q9UQE7 Structural maintenance of chromosomes protein 3SMC3 >sp|Q9UQE7|SMC3_HUMAN Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 0.07 0.51 -0.06 0.30 -0.01 -0.30 -0.70 -0.46 1.240805206 0.575131404 anaphase;biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;cytokinesis;cytoskeleton organization;developmental process;DNA metabolic process;DNA repair;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;meiosis;metabolic process;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;mitotic spindle organization;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle process;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of DNA endoreduplication;negative regulation of DNA metabolic process;negative regulation of DNA replication;negative regulation of DNA-dependent DNA replication;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle process;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of DNA endoreduplication;regulation of DNA metabolic process;regulation of DNA replication;regulation of DNA-dependent DNA replication;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;response to DNA damage stimulus;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle;signal transduction;sister chromatid cohesion;spindle organization;stem cell maintenance "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;chromatin binding;dynein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" "basement membrane;cell part;chromatin;chromosomal part;chromosome, centromeric region;cohesin complex;cytoplasmic part;cytoskeletal part;cytosol;extracellular matrix part;extracellular region part;intracellular organelle part;intracellular part;lateral element;macromolecular complex;meiotic cohesin complex;nuclear chromosome part;nuclear cohesin complex;nuclear matrix;nuclear meiotic cohesin complex;nuclear part;nucleoplasm;organelle part;protein complex;spindle pole" Cell cycle;Cell cycle - yeast;Meiosis - yeast;Oocyte meiosis 1.52E-142 1 21 21 21.7

O76094;O76094-2;D6RDY6;R4GNC1 Signal recognition particle subunit SRP72 SRP72 >sp|O76094|SRP72_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72 PE=1 SV=3;>sp|O76094-2|SRP72_HUMAN Isoform 2 of Signal recognition particle subunit SRP72 OS=Homo sapiens GN=SRP72;>tr|D6RDY6|D6RDY6_HUMAN Signal recognition particle -0.28 0.06 0.12 -0.02 0.12 -0.11 -0.29 -0.14 0.241830689 0.077103534 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to drug;response to stimulus;SRP-dependent cotranslational protein targeting to membrane;translation;transport 7S RNA binding;binding;nucleic acid binding;ribonucleoprotein binding;RNA binding;signal recognition particle binding "cell part;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;ribonucleoprotein complex;signal recognition particle;signal recognition particle, endoplasmic reticulum targeting" Protein export 5.99E-205 4 21 21 39

O75874;C9J4N6;C9JLU6;C9JJE5 Isocitrate dehydrogenase [NADP] cytoplasmic IDH1 >sp|O75874|IDHC_HUMAN Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 0.10 -0.14 -0.15 -0.10 0.02 -0.08 0.48 -0.03 0.501674757 -0.171532087 2-oxoglutarate metabolic process;acetyl-CoA catabolic process;acetyl-CoA metabolic process;amine metabolic process;anatomical structure development;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular aldehyde metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;developmental process;developmental process involved in reproduction;dicarboxylic acid metabolic process;female gonad development;glutathione metabolic process;glyoxylate cycle;glyoxylate metabolic process;gonad development;heterocycle metabolic process;isocitrate metabolic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;NADP metabolic process;NADPH regeneration;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organ development;organic acid metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;peptide metabolic process;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;reproductive process;reproductive structure development;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to organic substance;response to oxidative stress;response to steroid hormone stimulus;response to stimulus;response to stress;small molecule metabolic process;sulfur compound metabolic process;tricarboxylic acid cycle "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;ion binding;isocitrate dehydrogenase (NADP+) activity;isocitrate dehydrogenase activity;magnesium ion binding;metal ion binding;NAD binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody part;mitochondrion;organelle;organelle lumen;organelle part;peroxisomal matrix;peroxisomal part;peroxisome Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle);Glutathione metabolism;Peroxisome 2.45E-192 4 22 21 56.5

K7ELL7;P14314-2;P14314;K7EPW7;K7EKX1;K7EJ70 Glucosidase 2 subunit beta PRKCSH >tr|K7ELL7|K7ELL7_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=4 SV=1;>sp|P14314-2|GLU2B_HUMAN Isoform 2 of Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH;>sp|P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE -0.06 -0.15 -0.15 -0.23 0.51 0.05 0.39 -0.07 1.085925123 -0.365208918 biological regulation;carbohydrate metabolic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;defense response;glycosylation;immune response;immune system process;innate immune response;intracellular protein kinase cascade;intracellular signal transduction;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of neuron projection development;N-glycan processing;oligosaccharide metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein glycosylation;protein heterooligomerization;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein oligomerization;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;response to stimulus;response to stress;signal transduction binding;calcium ion binding;cation binding;ion binding;metal ion binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Protein processing in endoplasmic reticulum 3.52E-124 6 22 21 43.9

P23526;P23526-2 Adenosylhomocysteinase AHCY >sp|P23526|SAHH_HUMAN Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4;>sp|P23526-2|SAHH_HUMAN Isoform 2 of Adenosylhomocysteinase OS=Homo sapiens GN=AHCY 0.06 -0.04 -0.48 0.01 -0.66 -0.26 0.43 -0.09 0.037042328 0.028607756 amine metabolic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;methylation;nitrogen compound metabolic process;one-carbon metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;small molecule metabolic process;sulfur amino acid metabolic process;sulfur compound metabolic process;xenobiotic metabolic process "adenosylhomocysteinase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ether bonds;trialkylsulfonium hydrolase activity" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;vesicle Cysteine and methionine metabolism 2.58E-174 2 23 21 50.5

P35222;B4DGU4;E7EMJ5;E9PDF9;E7EV28;P35222-2;C9IZ65Catenin beta-1 CTNNB1 >sp|P35222|CTNB1_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1;>tr|B4DGU4|B4DGU4_HUMAN Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=2 SV=1 0.25 0.21 -0.18 -0.11 -0.89 -0.23 -0.08 0.12 0.5343434 0.311083157 "adherens junction assembly;adherens junction organization;anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;anatomical structure morphogenesis;androgen receptor signaling pathway;anterior/posterior axis specification;apoptosis;appendage morphogenesis;axis specification;biological adhesion;biological regulation;biosynthetic process;bone resorption;branching involved in ureteric bud morphogenesis;branching morphogenesis of a tube;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling pathway involved in heart development;canonical Wnt receptor signaling pathway involved in negative regulation of apoptosis;canonical Wnt receptor signaling pathway involved in positive regulation of cardiac outflow tract cell proliferation;canonical Wnt receptor signaling pathway involved in positive regulation of epithelial to mesenchymal transition;canonical Wnt receptor signaling pathway involved in regulation of cell proliferation;cell activation;cell adhesion;cell communication;cell death;cell development;cell differentiation;cell fate commitment;cell fate commitment involved in formation of primary germ layers;cell fate determination;cell fate specification;cell junction assembly;cell junction organization;cell maturation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cell surface receptor linked signaling pathway involved in heart development;cell-cell adhesion;cell-cell junction organization;cell-cell signaling;cell-cell signaling involved in cell fate commitment;cell-matrix adhesion;cell-substrate adhesion;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein localization;cellular response to chemical stimulus;cellular response to growth factor stimulus;cellular response to indole-3-methanol;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;central nervous system vasculogenesis;chordate embryonic development;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;death;determination of bilateral symmetry;determination of dorsal/ventral asymmetry;developmental induction;developmental maturation;developmental process;developmental process involved in reproduction;digestive tract development;dorsal/ventral axis specification;ectoderm development;ectodermal placode formation;embryo development;embryo development ending in birth or egg hatching;embryonic appendage morphogenesis;embryonic axis specification;embryonic digit morphogenesis;embryonic epithelial tube formation;embryonic foregut morphogenesis;embryonic forelimb morphogenesis;embryonic heart tube development;embryonic hindlimb morphogenesis;embryonic limb morphogenesis;embryonic morphogenesis;embryonic pattern specification;endodermal cell fate commitment;endothelial tube morphogenesis;epidermal cell differentiation;epidermis development;epithelial cell differentiation;epithelial cell differentiation involved in prostate gland development;epithelial cell morphogenesis;epithelial to mesenchymal transition;epithelial tube branching involved in lung morphogenesis;epithelial tube formation;epithelial tube morphogenesis;epithelium development;establishment of localization;forebrain development;forelimb morphogenesis;fungiform papilla formation;gastrulation;gastrulation with mouth forming second;genitalia development;genitalia morphogenesis;germ cell development;glial cell fate determination;glial cell proliferation;hair cell differentiation;hair cycle process;hair follicle morphogenesis;hair follicle placode formation;hemopoietic or lymphoid organ development;hindbrain development;hindlimb morphogenesis;homeostatic process;immune system process;in utero embryonic development;intracellular receptor mediated signaling pathway;lens morphogenesis in camera-type eye;leukocyte activation;leukocyte differentiation;limb morphogenesis;liver development;localization;locomotion;lung cell differentiation;lung induction;lung-associated mesenchyme development;lymphocyte activation;lymphocyte differentiation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;male genitalia development;mesenchymal cell proliferation;mesenchymal cell proliferation involved in lung development;mesenchymal to epithelial transition;mesenchymal to epithelial transition involved in metanephros morphogenesis;mesenchyme development;metabolic process;midgut development;molting cycle;molting cycle process;morphogenesis of a branching epithelium;morphogenesis of a branching structure;morphogenesis of an endothelium;morphogenesis of an epithelium;multicellular organismal process;muscle cell differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;myoblast differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cardiac cell fate specification;negative regulation of cardioblast cell fate specification;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell fate commitment;negative regulation of cell fate specification;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of chondrocyte differentiation;negative regulation of developmental process;negative regulation of gene expression;negative regulation of glial cell differentiation;negative regulation of gliogenesis;negative regulation of heart induction by canonical Wnt receptor signaling pathway;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of myeloid cell differentiation;negative regulation of myeloid leukocyte differentiation;negative regulation of neurogenesis;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of oligodendrocyte differentiation;negative regulation of osteoclast differentiation;negative regulation of programmed cell death;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein sumoylation;negative regulation of RNA metabolic process;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nephron tubule formation;neural plate development;neuron migration;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;odontogenesis;odontogenesis of dentine-containing tooth;oocyte development;organ development;organ formation;organ induction;organ morphogenesis;organelle organization;osteoclast differentiation;oviduct development;pancreas development;pattern specification process;patterning of blood vessels;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of branching involved in lung morphogenesis;positive regulation of cell communication;positive regulation of cell death;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of determination of dorsal identity;positive regulation of developmental process;positive regulation of endothelial cell differentiation;positive regulation of epithelial cell differentiation;positive regulation of epithelial cell proliferation;positive regulation of epithelial cell proliferation involved in prostate gland development;positive regulation of fibroblast growth factor receptor signaling pathway;positive regulation of gene expression;positive regulation of glycoprotein biosynthetic process;positive regulation of heparan sulfate proteoglycan biosynthetic process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAPKKK cascade;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of multicellular organismal process;positive regulation of muscle cell differentiation;positive regulation of neural precursor cell proliferation;positive regulation of neuroblast proliferation;positive regulation of neurogenesis;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of osteoblast differentiation;positive regulation of programmed cell death;positive regulation of reproductive process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of sulfur metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;programmed cell death;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein localization;protein localization at cell surface;protein oligomerization;proximal/distal pattern formation;regionalization;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of branching involved in lung morphogenesis;regulation of calcium ion import;regulation of calcium ion transport;regulation of cardiac cell fate specification;regulation of cardioblast cell fate specification;regulation of cardioblast differentiation;regulation of cardioblast proliferation;regulation of cartilage development;regulation of cell activation;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell fate commitment;regulation of cell fate specification;regulation of cell proliferation;regulation of cell proliferation involved in heart morphogenesis;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of centriole-centriole cohesion;regulation of centromeric sister chromatid cohesion;regulation of chondrocyte differentiation;regulation of chromosome organization;regulation of chromosome segregation;regulation of cytoskeleton organization;regulation of determination of dorsal identity;regulation of developmental process;regulation of embryonic development;regulation of endothelial cell differentiation;regulation of epithelial cell differentiation;regulation of epithelial cell differentiation involved in kidney development;regulation of epithelial cell proliferation;regulation of epithelial cell proliferation involved in prostate gland development;regulation of fibroblast growth factor receptor signaling pathway;regulation of fibroblast proliferation;regulation of gene expression;regulation of glial cell differentiation;regulation of gliogenesis;regulation of glycoprotein biosynthetic process;regulation of heart induction;regulation of heart morphogenesis;regulation of heparan sulfate proteoglycan biosynthetic process;regulation of homeostatic process;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of ion homeostasis;regulation of ion transmembrane transport;regulation of ion transport;regulation of kidney development;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of localization;regulation of lymphocyte activation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAPKKK cascade;regulation of mesenchymal cell proliferation;regulation of metabolic process;regulation of metal ion transport;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of mononuclear cell proliferation;regulation of morphogenesis of a branching structure;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of myelination;regulation of myeloid cell differentiation;regulation of myeloid leukocyte differentiation;regulation of nephron tubule epithelial cell differentiation;regulation of nervous system development;regulation of neural precursor cell proliferation;regulation of neurogenesis;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of oligodendrocyte differentiation;regulation of organ formation;regulation of organ morphogenesis;regulation of organelle organization;regulation of ossification;regulation of osteoblast differentiation;regulation of osteoclast differentiation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein localization;regulation of protein localization at cell surface;regulation of protein metabolic process;regulation of protein modification process;regulation of protein sumoylation;regulation of reproductive process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of secondary heart field cardioblast proliferation;regulation of signal transduction;regulation of signaling;regulation of sister chromatid cohesion;regulation of smooth muscle cell proliferation;regulation of sulfur metabolic process;regulation of system process;regulation of T cell activation;regulation of T cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transmission of nerve impulse;regulation of transport;renal inner medulla development;renal outer medulla development;renal vesicle formation;reproductive process;reproductive structure development;response to cadmium ion;response to chemical stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to growth factor stimulus;response to hormone stimulus;response to indole-3-methanol;response to inorganic substance;response to metal ion;response to organic cyclic compound;response to organic substance;response to steroid hormone stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;Schwann cell proliferation;signal transduction;signaling;skin development;smooth muscle cell differentiation;specification of symmetry;steroid hormone receptor signaling pathway;synapse organization;synaptic vesicle transport;T cell activation;T cell differentiation;T cell differentiation in thymus;thymus development;tissue development;tissue homeostasis;tissue morphogenesis;tongue morphogenesis;trachea formation;transcription, DNA-dependent;transport;tube development;tube formation;tube morphogenesis;vasculogenesis;vesicle-mediated transport;Wnt receptor signaling pathway;Wnt receptor signaling pathway involved in heart development" androgen receptor binding;binding;chromatin binding;DNA binding;double-stranded DNA binding;enzyme binding;hormone receptor binding;kinase binding;molecular transducer activity;nuclear hormone receptor binding;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein binding transcription factor activity;protein kinase binding;receptor binding;regulatory region DNA binding;regulatory region nucleic acid binding;sequence-specific DNA binding transcription factor activity;signal transducer activity;steroid hormone receptor binding;structural molecule activity;structure-specific DNA binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;transcription regulatory region DNA binding adherens junction;anchoring junction;apical junction complex;apical part of cell;basolateral plasma membrane;beta-catenin destruction complex;beta-catenin-TCF7L2 complex;catenin complex;catenin-TCF7L2 complex;cell cortex;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;centrosome;contractile fiber part;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;dendritic shaft;desmosome;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;internal side of plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;lateral plasma membrane;macromolecular complex;membrane;membrane part;microtubule organizing center;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleoplasm part;organelle;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;protein-DNA complex;Scrib-APC-beta-catenin complex;spindle pole;synapse;transcription factor complex;Z disc;zonula adherens Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Basal cell carcinoma;Colorectal cancer;Endometrial cancer;Focal adhesion;Leukocyte transendothelial migration;Melanogenesis;Pathogenic Escherichia coli infection;Pathways in cancer;Prostate cancer;Thyroid cancer;Tight junction;Wnt signaling pathway 5.62E-287 7 23 21 41.6

P13796;Q5TBN3;B4DUA0;Q5TBN5 Plastin-2 LCP1 >sp|P13796|PLSL_HUMAN Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6 -2.64 -2.84 -0.66 -0.19 -1.82 -0.16 1.57 2.21 0.768742256 -2.032928981 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;anatomical structure morphogenesis;biological regulation;cell activation;cell activation involved in immune response;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;lymphocyte activation;lymphocyte activation involved in immune response;organ morphogenesis;organ regeneration;organelle organization;regeneration;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of protein localization;regulation of protein transport;regulation of transport;T cell activation;T cell activation involved in immune response actin binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding actin cytoskeleton;actin filament;cell junction;cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane;membrane part;non-membrane-bounded organelle;organelle;organelle part;phagocytic cup;plasma membrane;plasma membrane part;protein complex;ruffle;ruffle membrane 0 4 26 21 56.6

Q9H4M9;C9J2Z4;C9JC03;C9JDQ8;C9JIJ3;C9IZH1 EH domain-containing protein 1 EHD1 >sp|Q9H4M9|EHD1_HUMAN EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2;>tr|C9J2Z4|C9J2Z4_HUMAN EH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=EHD1 PE=2 SV=1;>tr|C9JC03|C9JC03_HUMAN EH domain-containing protein 1 (Fragment) OS= 0.26 0.10 -0.23 -0.11 0.17 0.14 0.31 -0.05 0.426966384 -0.137792134 biological regulation;blood coagulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;cholesterol homeostasis;coagulation;endocytic recycling;endocytosis;endosome transport;establishment of localization;establishment of localization in cell;establishment of protein localization;GTP catabolic process;GTP metabolic process;hemostasis;heterocycle catabolic process;heterocycle metabolic process;homeostatic process;intracellular protein transport;intracellular transport;lipid homeostasis;low-density lipoprotein particle clearance;macromolecular complex assembly;macromolecular complex subunit organization;membrane invagination;membrane organization;metabolic process;multicellular organismal process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;plasma lipoprotein particle clearance;positive regulation of biological process;positive regulation of cholesterol storage;positive regulation of lipid storage;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein oligomerization;protein transport;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cholesterol storage;regulation of lipid storage;regulation of localization;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;sterol homeostasis;transport;vesicle-mediated transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;catalytic activity;cation binding;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome;early endosome membrane;endocytic vesicle;endosomal part;endosome;endosome membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lipid particle;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;platelet dense tubular network membrane;recycling endosome membrane;vesicle Endocytosis 1.65E-261 6 30 21 62

P52272-2;P52272;M0R019;M0R2T0;M0R2I7;M0R0N3;M0QYQ7;M0R0Y6;M0QY96;M0QYL3 Heterogeneous nuclear ribonucleoprotein M HNRNPM >sp|P52272-2|HNRPM_HUMAN Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM;>sp|P52272|HNRPM_HUMAN Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 0.00 0.40 0.05 0.37 -0.05 -0.11 -0.96 -0.26 1.004791425 0.55020304 "alternative nuclear mRNA splicing, via spliceosome;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;nucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;integral to membrane;integral to plasma membrane;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;nuclear body;nuclear matrix;nuclear part;nucleoplasm part;organelle part;paraspeckles;plasma membrane part;ribonucleoprotein complex;spliceosomal complex Spliceosome 0 10 47 21 74.4

P54886-2;P54886 Delta-1-pyrroline-5-carboxylate synthase;Glutamate 5-kinase;Gamma-glutamyl phosphate reductase ALDH18A1 >sp|P54886-2|P5CS_HUMAN Isoform Short of Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1;>sp|P54886|P5CS_HUMAN Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 -0.04 0.07 -0.23 0.01 0.15 0.13 -0.33 0.10 0.170167334 -0.061021802 amine biosynthetic process;amine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;citrulline biosynthetic process;citrulline metabolic process;glutamate metabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;L-proline biosynthetic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;ornithine biosynthetic process;ornithine metabolic process;oxoacid metabolic process;primary metabolic process;proline biosynthetic process;proline metabolic process;small molecule biosynthetic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;amino acid kinase activity;ATP binding;binding;catalytic activity;glutamate 5-kinase activity;glutamate-5-semialdehyde dehydrogenase activity;kinase activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;phosphotransferase activity, carboxyl group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part Arginine and proline metabolism 4.12E-145 2 22 22 41.1

P49419-2;P49419;F8VS02;P49419-4;P49419-3;H0YHM6;F8VVF2;F8WDY6;F8WD33 Alpha-aminoadipic semialdehyde dehydrogenase ALDH7A1 >sp|P49419-2|AL7A1_HUMAN Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1;>sp|P49419|AL7A1_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5;>tr|F8VS02|F8VS02_HUMAN Alpha-aminoadipic -0.14 -0.13 0.11 0.10 -0.65 -0.66 0.04 -0.29 0.886303076 0.374863545 alcohol metabolic process;amine biosynthetic process;amine catabolic process;amine metabolic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;betaine biosynthetic process;betaine metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular aldehyde metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid biosynthetic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;choline metabolic process;ethanolamine-containing compound metabolic process;glycine betaine biosynthetic process;glycine betaine biosynthetic process from choline;glycine betaine metabolic process;lysine catabolic process;lysine metabolic process;metabolic process;multicellular organismal process;neurological system process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;system process "aldehyde dehydrogenase (NAD) activity;betaine-aldehyde dehydrogenase activity;catalytic activity;L-aminoadipate-semialdehyde dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nucleus;organelle;organelle lumen;organelle part "Arginine and proline metabolism;Ascorbate and aldarate metabolism;beta-Alanine metabolism;Fatty acid metabolism;Glycerolipid metabolism;Glycine, serine and threonine metabolism;Glycolysis / Gluconeogenesis;Histidine metabolism;Lysine biosynthesis;Lysine degradation;Propanoate metabolism;Pyruvate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 1.49E-254 9 22 22 53.2

E5RJ68;O00203;B7ZKR7;Q13367;B7ZKS0;H0YBD0;F5GWU4 AP-3 complex subunit beta-1 AP3B1 >tr|E5RJ68|E5RJ68_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=2 SV=1;>sp|O00203|AP3B1_HUMAN AP-3 complex subunit beta-1 OS=Homo sapiens GN=AP3B1 PE=1 SV=3 -0.05 -0.07 -0.05 -0.04 0.06 0.07 0.44 0.06 0.937147454 -0.20737878 "anterograde axon cargo transport;anterograde synaptic vesicle transport;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of lipid antigen via MHC class Ib;antigen processing and presentation via MHC class Ib;antigen processing and presentation, exogenous lipid antigen via MHC class Ib;axon cargo transport;biological regulation;blood coagulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular membrane organization;cellular process;coagulation;cytoskeleton-dependent intracellular transport;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization to organelle;establishment of protein localization to vacuole;Golgi vesicle transport;hemostasis;immune system process;intracellular protein transport;intracellular transport;lysosomal transport;melanosome organization;membrane invagination;membrane organization;microtubule-based movement;microtubule-based process;microtubule-based transport;multicellular organismal process;organelle organization;pigment granule organization;positive regulation of alpha-beta T cell activation;positive regulation of alpha-beta T cell differentiation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of NK T cell differentiation;positive regulation of T cell activation;positive regulation of T cell differentiation;post-Golgi vesicle-mediated transport;protein targeting;protein targeting to lysosome;protein targeting to vacuole;protein transport;regulation of alpha-beta T cell activation;regulation of alpha-beta T cell differentiation;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cell activation;regulation of cell differentiation;regulation of cellular process;regulation of developmental process;regulation of immune system process;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of NK T cell differentiation;regulation of T cell activation;regulation of T cell differentiation;synaptic vesicle transport;transport;vacuolar transport;vesicle organization;vesicle-mediated transport" transporter activity AP-3 adaptor complex;AP-type membrane coat adaptor complex;cell part;clathrin coated vesicle membrane;coated vesicle;coated vesicle membrane;COPI-coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;Golgi apparatus;Golgi apparatus part;Golgi-associated vesicle;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle membrane;organelle part;protein complex;vesicle;vesicle membrane Lysosome 1.23E-93 7 22 22 23.3

Q14444;Q14444-2;G3V153;E9PLA9;E9PP31 Caprin-1 CAPRIN1 >sp|Q14444|CAPR1_HUMAN Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2;>sp|Q14444-2|CAPR1_HUMAN Isoform 2 of Caprin-1 OS=Homo sapiens GN=CAPRIN1;>tr|G3V153|G3V153_HUMAN Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=2 SV=1;>tr|E9PLA9|E9PLA9_HUMAN Caprin-1 (Fragment) 0.09 0.09 -0.17 -0.12 -0.01 -0.29 -0.16 -0.25 0.670469364 0.146523397 biological regulation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of dendrite morphogenesis;positive regulation of dendritic spine development;positive regulation of dendritic spine morphogenesis;positive regulation of developmental process;positive regulation of neurogenesis;posttranscriptional regulation of gene expression;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biosynthetic process;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of dendritic spine development;regulation of dendritic spine morphogenesis;regulation of developmental process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation binding;nucleic acid binding;RNA binding cell part;cell projection;cytoplasm;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;dendrite;integral to membrane;integral to plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;neuron projection;non-membrane-bounded organelle;organelle;plasma membrane part;ribonucleoprotein complex;RNA granule;stress granule 1.95E-214 5 22 22 32.9

P33991;E5RG31;E5RFJ8;Q9UJA3-2;Q9UJA3-3;Q9UJA3;Q9UJA3-4 DNA replication licensing factor MCM4 MCM4 >sp|P33991|MCM4_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5 0.10 0.00 0.01 0.16 0.29 -0.46 -0.84 -1.01 0.841406216 0.57173115 biological regulation;biosynthetic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA recombination;DNA repair;DNA replication;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA unwinding involved in replication;DNA-dependent DNA replication initiation;double-strand break repair;double-strand break repair via homologous recombination;female gamete generation;G1/S transition of mitotic cell cycle;gamete generation;macromolecule biosynthetic process;macromolecule metabolic process;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;recombinational repair;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;DNA helicase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;single-stranded DNA binding;structure-specific DNA binding" cell part;chromosomal part;intracellular organelle part;intracellular part;macromolecular complex;MCM complex;nuclear chromosome part;nuclear part;nucleoplasm;nucleoplasm part;organelle part;protein complex Cell cycle;Cell cycle - yeast;DNA replication;Meiosis - yeast 1.09E-157 7 22 22 33.5

P33993;P33993-3;P33993-2;C9J8M6 DNA replication licensing factor MCM7 MCM7 >sp|P33993|MCM7_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4;>sp|P33993-3|MCM7_HUMAN Isoform 3 of DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 0.10 0.01 0.11 0.11 0.40 -0.54 -0.72 -0.73 0.759109778 0.480694565 biological regulation;cell cycle checkpoint;cell cycle phase;cell cycle process;cell proliferation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to epidermal growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA unwinding involved in replication;DNA-dependent DNA replication initiation;G1/S transition of mitotic cell cycle;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;response to chemical stimulus;response to DNA damage stimulus;response to drug;response to endogenous stimulus;response to epidermal growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;response to stress;S phase;S phase of mitotic cell cycle "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;DNA helicase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;single-stranded DNA binding;structure-specific DNA binding" cell part;chromatin;chromosomal part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;MCM complex;membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;protein complex Cell cycle;Cell cycle - yeast;DNA replication;Meiosis - yeast 1.54E-105 4 22 22 38.2

P26599;P26599-2;P26599-3;A6NLN1;K7ES59;K7EKJ7;K7EK45;K7ELW5;O95758-1;O95758-6;O95758-2;O95758;O95758-5;O95758-4;O95758-7;B4DI28;Q9UKA9-5;Q9UKA9-6;Q9UKA9;Q9UKA9-2;Q9UKA9-4;Q9UKA9-3;B4DSS8 Polypyrimidine tract-binding protein 1 PTBP1 >sp|P26599|PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1;>sp|P26599-2|PTBP1_HUMAN Isoform 2 of Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1;>sp|P26599-3|PTBP1_HUMAN Isoform 3 of Polypyrimidine trac -0.10 0.45 0.08 0.54 -0.09 -0.08 -0.91 -0.06 0.880466666 0.528548898 "anatomical structure morphogenesis;biological regulation;cell maturation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental maturation;developmental process;erythrocyte maturation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA splice site selection;negative regulation of biological process;negative regulation of cell differentiation;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of muscle cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of muscle cell differentiation;regulation of neural precursor cell proliferation;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;mRNA binding;nucleic acid binding;nucleotide binding;poly-pyrimidine tract binding;pre-mRNA binding;RNA binding;single-stranded RNA binding cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex 0 23 22 22 55.7

Q9H4A4;A6NKB8;C9JMZ3;H7C2T3 Aminopeptidase B RNPEP >sp|Q9H4A4|AMPB_HUMAN Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2;>tr|A6NKB8|A6NKB8_HUMAN Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=2 SV=10.11 -0.05 -0.09 -0.02 0.00 0.09 0.56 -0.01 0.492714419 -0.168966614 alkene biosynthetic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular alkene metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid biosynthetic process;fatty acid metabolic process;icosanoid biosynthetic process;icosanoid metabolic process;leukotriene biosynthetic process;leukotriene metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein metabolic process;proteolysis;small molecule biosynthetic process;small molecule metabolic process;unsaturated fatty acid biosynthetic process;unsaturated fatty acid metabolic process "aminopeptidase activity;binding;catalytic activity;cation binding;epoxide hydrolase activity;ether hydrolase activity;exopeptidase activity;hydrolase activity;hydrolase activity, acting on ether bonds;ion binding;metal ion binding;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding;zinc ion binding" cell part;extracellular region;extracellular region part;extracellular space;membrane;plasma membrane 7.73E-172 4 22 22 41.2

Q02878;F8W181;F8VZ45;F8VR69;F8VZA3;F8VWR1;F8VRY1 60S ribosomal protein L6 RPL6 >sp|Q02878|RL6_HUMAN 60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3;>tr|F8W181|F8W181_HUMAN 60S ribosomal protein L6 (Fragment) OS=Homo sapiens GN=RPL6 PE=2 SV=1 -0.08 0.02 0.01 -0.06 -0.03 -0.51 -0.40 -0.56 1.19504565 0.346706406 "biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" binding;DNA binding;nucleic acid binding;RNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;non-membrane-bounded organelle;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 3.65E-209 7 22 22 55.9

Q15393;Q15393-3;Q15393-2;J3QRB2;J3QL37 Splicing factor 3B subunit 3 SF3B3 >sp|Q15393|SF3B3_HUMAN Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4;>sp|Q15393-3|SF3B3_HUMAN Isoform 3 of Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 0.27 0.44 -0.13 0.11 0.40 0.49 -0.45 -0.18 0.152650248 0.107910769 "cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome 1.10E-117 5 22 22 23.8

O60271-4;O60271;O60271-2;O60271-5;O60271-3;O60271-9;E9PFH7;Q9UPT6;D6RHI8;Q9UPT6-2;H0YBE9;H0YBS5 C-Jun-amino-terminal kinase-interacting protein 4 SPAG9 >sp|O60271-4|JIP4_HUMAN Isoform 4 of C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9;>sp|O60271|JIP4_HUMAN C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 PE=1 SV=4;>sp|O60271-2|JIP4_HUMAN Isoform 2 of 0.44 -0.02 -0.16 -0.59 0.93 0.71 1.10 0.29 1.255501516 -0.838061649 "activation of JUN kinase activity;activation of MAPK activity;anatomical structure development;anatomical structure morphogenesis;axon guidance;biological regulation;cell differentiation;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chemotaxis;chordate embryonic development;developmental process;embryo development;embryo development ending in birth or egg hatching;endosome transport;establishment of localization;establishment of localization in cell;forebrain development;gamete generation;in utero embryonic development;intracellular transport;localization;locomotion;lung alveolus development;lung morphogenesis;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;macromolecule modification;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;muscle cell differentiation;negative regulation of binding;negative regulation of molecular function;negative regulation of protein binding;negative regulation of protein homodimerization activity;organ morphogenesis;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of developmental process;positive regulation of JUN kinase activity;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of MAP kinase activity;positive regulation of molecular function;positive regulation of muscle cell differentiation;positive regulation of neuron differentiation;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of transferase activity;post-embryonic development;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein localization;protein metabolic process;protein modification process;protein oligomerization;protein phosphorylation;regulation of binding;regulation of biological process;regulation of catalytic activity;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of developmental process;regulation of gene expression;regulation of intracellular protein kinase cascade;regulation of JNK cascade;regulation of JUN kinase activity;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein binding;regulation of protein homodimerization activity;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of stress-activated protein kinase signaling cascade;regulation of transferase activity;reproductive process;respiratory gaseous exchange;response to chemical stimulus;response to external stimulus;response to stimulus;retrograde transport, endosome to Golgi;spermatogenesis;striated muscle cell differentiation;taxis;transport;vesicle-mediated transport"	"binding;binding, bridging;cytoskeletal protein binding;enzyme binding;kinase binding;kinesin binding;MAP-kinase scaffold activity;protein binding;protein complex scaffold;protein kinase binding;signaling adaptor activity;structural molecule activity"	acrosomal vesicle;axolemma;axon part;cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;dendrite;endoplasmic reticulum;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;leading edge membrane;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;neuron projection;neuron projection membrane;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;smooth endoplasmic reticulum;stored secretory granule;vesicle	MAPK signaling pathway	4.11E-190	12	22	22	23.1

Q9UHB9;Q9UHB9-4;F5H5Y3;Q9UHB9-2;Q9UHB9-3;K7EN53;K7EQC2	Signal recognition particle subunit SRP68	SRP68	>sp|Q9UHB9|SRP68_HUMAN Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68 PE=1 SV=2;>sp|Q9UHB9-4|SRP68_HUMAN Isoform 4 of Signal recognition particle subunit SRP68 OS=Homo sapiens GN=SRP68;>tr|F5H5Y3|F5H5Y3_HUMAN Signal recognition particle	0.19	-0.06	0.18	-0.09	0.02	-0.27	0.06	-0.40	0.646906718	0.204134963	biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;response to chemical stimulus;response to drug;response to stimulus;SRP-dependent cotranslational protein targeting to membrane;translation;transport	7S RNA binding;binding;endoplasmic reticulum signal peptide binding;nucleic acid binding;peptide binding;ribonucleoprotein binding;RNA binding;signal recognition particle binding;signal sequence binding	"cell part;cytoplasm;cytoplasmic part;cytosol;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;ribonucleoprotein complex;ribosome;signal recognition particle;signal recognition particle, endoplasmic reticulum targeting"	Protein export	1.02E-127	7	22	22	45.5

P23381;P23381-2;G3V277;G3V3H8;G3V3Y5;G3V423;G3V5U1;G3V456;H0YJP3;G3V3P2;G3V227;G3V3X0;G3V2Y7;G3V5W1;G3V3S7;G3V2F2;G3V3R3;G3V4S4;G3V313;G3V339;G3V2C0;G3V4C7;G3V4N8;G3V5H5;P78534;G3V4A3;G3V4Q0;G3V4N0	"Tryptophan--tRNA ligase, cytoplasmic;T1-TrpRS;T2-TrpRS"	WARS	">sp|P23381|SYWC_HUMAN Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2;>sp|P23381-2|SYWC_HUMAN Isoform 2 of Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS"	0.05	-0.08	-0.16	-0.09	-0.01	-0.11	0.48	-0.07	0.404982882	-0.142392241	amine metabolic process;amino acid activation;anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tryptophanyl-tRNA aminoacylation	"adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;tryptophan-tRNA ligase activity"	cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part	Aminoacyl-tRNA biosynthesis;Tryptophan metabolism	0	28	22	22	54.8

P31947;P31947-2	14-3-3 protein sigma	SFN	>sp|P31947|1433S_HUMAN 14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1;>sp|P31947-2|1433S_HUMAN Isoform 2 of 14-3-3 protein sigma OS=Homo sapiens GN=SFN	-0.13	-0.09	-0.07	-0.04	-0.29	0.25	0.43	0.31	0.676391542	-0.255536457	"anatomical structure development;apoptotic mitochondrial changes;biological regulation;cell differentiation;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to stimulus;cellular response to stress;developmental process;DNA damage response, signal transduction resulting in induction of apoptosis;epidermal cell differentiation;epidermis development;epithelial cell differentiation;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;keratinocyte differentiation;keratinocyte proliferation;membrane organization;mitochondrion organization;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;organelle organization;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cell growth;positive regulation of cellular process;positive regulation of growth;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of programmed cell death;positive regulation of protein export from nucleus;positive regulation of protein transport;positive regulation of transport;regulation of apoptosis;regulation of biological process;regulation of catalytic activity;regulation of cell cycle;regulation of cell death;regulation of cell growth;regulation of cell proliferation;regulation of cellular component organization;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cyclin-dependent protein kinase activity;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of establishment of protein localization;regulation of growth;regulation of hydrolase activity;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nucleocytoplasmic transport;regulation of peptidase activity;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein export from nucleus;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of transferase activity;regulation of transport;release of cytochrome c from mitochondria;response to DNA damage stimulus;response to stimulus;response to stress;signal transduction;signal transduction in response to DNA damage;skin development;tissue development"	enzyme inhibitor activity;enzyme regulator activity;kinase inhibitor activity;kinase regulator activity;protein kinase C inhibitor activity;protein kinase inhibitor activity;protein kinase regulator activity;protein serine/threonine kinase inhibitor activity	cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;vesicle membrane Aldosterone-regulated sodium reabsorption;Cell cycle;p53 signaling pathway 0 2 28 22 78.6

P17844;J3KTA4;B4DLW8;J3QSF1;J3KRZ1;J3QRQ7;J3KRX8;J3QR02;J3QRN5;J3QLG9;J3QR62 Probable ATP-dependent RNA helicase DDX5 DDX5 >sp|P17844|DDX5_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1;>tr|J3KTA4|J3KTA4_HUMAN Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=3 SV=1;>tr|B4DLW8|B4DLW8_HUMAN Probable ATP-dependent RNA helicase0.12 0.53 -0.15 0.43 -0.14 -0.16 -0.88 -0.23 1.055165994 0.585458353 "biological regulation;biosynthetic process;cell growth;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;chordate embryonic development;circadian rhythm;developmental process;embryo development;embryo development ending in birth or egg hatching;growth;in utero embryonic development;induction of apoptosis;induction of apoptosis by intracellular signals;induction of programmed cell death;intracellular signal transduction;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA damage response, signal transduction by p53 class mediator;positive regulation of estrogen receptor signaling pathway;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of steroid hormone receptor signaling pathway;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of androgen receptor signaling pathway;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of developmental process;regulation of DNA damage response, signal transduction by p53 class mediator;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of ossification;regulation of osteoblast differentiation;regulation of primary metabolic process;regulation of programmed cell death;regulation of reproductive process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of RNA splicing;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of steroid hormone receptor signaling pathway;regulation of striated muscle cell differentiation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of viral genome replication;regulation of viral reproduction;response to stimulus;rhythmic process;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;signal transduction;signal transduction by p53 class mediator;signal transduction by p53 class mediator resulting in induction of apoptosis;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;androgen receptor binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;estrogen receptor binding;helicase activity;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;pre-mRNA binding;protein binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 4.34E-207 11 32 22 51.1

P14923 Junction plakoglobin JUP >sp|P14923|PLAK_HUMAN Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 -0.34 0.50 -0.01 0.50 -0.67 0.43 -0.37 -0.23 0.499881389 0.370272695 "adherens junction organization;anatomical structure development;anatomical structure morphogenesis;atrioventricular valve morphogenesis;biological adhesion;biological regulation;canonical Wnt receptor signaling pathway;canonical Wnt receptor signaling pathway involved in heart development;cell adhesion;cell development;cell junction assembly;cell junction organization;cell migration;cell morphogenesis;cell motility;cell surface receptor linked signaling pathway;cell surface receptor linked signaling pathway involved in heart development;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular process involved in reproduction;cellular response to chemical stimulus;cellular response to indole-3-methanol;cellular response to organic substance;cellular response to stimulus;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;desmosome assembly;detection of abiotic stimulus;detection of external stimulus;detection of mechanical stimulus;detection of stimulus;developmental process;developmental process involved in reproduction;ectoderm development;embryonic morphogenesis;endothelial cell-cell adhesion;epidermis development;epithelial cell-cell adhesion;gastrulation;germ cell development;heart valve morphogenesis;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;morphogenesis of an epithelium;morphogenesis of embryonic epithelium;negative regulation of biological process;negative regulation of cardiac cell fate specification;negative regulation of cardioblast cell fate specification;negative regulation of cell communication;negative regulation of cell differentiation;negative regulation of cell fate commitment;negative regulation of cell fate specification;negative regulation of cellular process;negative regulation of developmental process;negative regulation of heart induction by canonical Wnt receptor signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of Wnt receptor signaling pathway;negative regulation of Wnt receptor signaling pathway involved in heart development;nervous system development;oocyte development;organelle organization;positive regulation of biological process;positive regulation of canonical Wnt receptor signaling pathway;positive regulation of cell communication;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of molecular function;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of Wnt receptor signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of canonical Wnt receptor signaling pathway;regulation of cardiac cell fate specification;regulation of cardioblast cell fate specification;regulation of cardioblast differentiation;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell fate commitment;regulation of cell fate specification;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of establishment of protein localization;regulation of gene expression;regulation of heart induction;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein import into nucleus;regulation of protein localization;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;regulation of Wnt receptor signaling pathway;regulation of Wnt receptor signaling pathway involved in heart development;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to indole-3-methanol;response to mechanical stimulus;response to organic substance;response to stimulus;signal transduction;skin development;system development;tissue development;tissue morphogenesis;Wnt receptor signaling pathway;Wnt receptor signaling pathway involved in heart development" binding;enzyme binding;identical protein binding;kinase binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein homodimerization activity;protein kinase binding;structural constituent of cell wall;structural molecule activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity actin cytoskeleton;adherens junction;anchoring junction;apicolateral plasma membrane;basolateral plasma membrane;catenin complex;catenin-TCF7L2 complex;cell junction;cell part;cell-cell adherens junction;cell-cell junction;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;cytosolic part;desmosome;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;gamma-catenin-TCF7L2 complex;intermediate filament;internal side of plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;protein complex;protein-DNA complex;Z disc;zonula adherens Acute myeloid leukemia;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Pathways in cancer 0 1 38 22 60.3

P48444;B0YIW6;P48444-2;E9PK34 Coatomer subunit delta ARCN1 ">sp|P48444|COPD_HUMAN Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1;>tr|B0YIW6|B0YIW6_HUMAN Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=2 SV=1;>sp|P48444-2|COPD_HUMAN Isoform 2 of Coatomer subunit delta OS=Homo sapiens GN=ARCN1" 0.13 -0.03 -0.08 -0.04 0.42 0.05 0.13 -0.09 0.46053328 -0.132124348 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;organelle organization;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" AP-type membrane coat adaptor complex;cell part;clathrin adaptor complex;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;organelle part;protein complex;vesicle coat 3.33E-237 4 23 23 49.5

B7Z1R5;P38606;C9JA17;C9JVW8 V-type proton ATPase catalytic subunit A ATP6V1A >tr|B7Z1R5|B7Z1R5_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=2 SV=1;>sp|P38606|VATA_HUMAN V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2 -0.18 0.47 -0.29 0.48 -0.01 0.78 -0.03 0.33 0.188939733 -0.142000086 "ATP hydrolysis coupled proton transport;ATP metabolic process;biological regulation;cation homeostasis;cation transport;cell surface receptor linked signaling pathway;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;chemical homeostasis;energy coupled proton transport, against electrochemical gradient;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of protein localization;ferric iron transport;heterocycle metabolic process;homeostatic process;hydrogen transport;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;ion homeostasis;ion transmembrane transport;ion transport;iron ion homeostasis;iron ion transport;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation transport;multi-organism process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate metabolic process;nucleotide metabolic process;organelle organization;phagosome maturation;primary metabolic process;protein transport;proton transport;purine nucleoside triphosphate metabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide metabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cellular process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;ribonucleoside triphosphate metabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;transferrin transport;transition metal ion transport;transmembrane receptor protein tyrosine kinase signaling pathway;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;hydrogen ion transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "apical plasma membrane;cell part;cell projection;cytoplasmic part;cytosol;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;membrane-bounded organelle;microvillus;mitochondrion;organelle;plasma membrane part;protein complex;proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain;proton-transporting V-type ATPase, V1 domain" Collecting duct acid secretion;Epithelial cell signaling in Helicobacter pylori infection;Oxidative phosphorylation;Phagosome;Rheumatoid arthritis;Vibrio cholerae infection 4.09E-205 4 23 23 52.1

Q9NZB2;Q9NZB2-6;Q9NZB2-4;Q9NZB2-2;Q9NZB2-5;H7C0T0;Q5T035 Constitutive coactivator of PPAR-gamma-like protein 1 FAM120A >sp|Q9NZB2|F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2;>sp|Q9NZB2-6|F120A_HUMAN Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A;>sp|Q9NZB2-4|F120A_HUMA -0.10 -0.03 0.19 0.07 0.08 -0.09 -0.26 -0.25 0.678237046 0.163310472 binding;nucleic acid binding;RNA binding cell part;cytoplasm;intracellular part;membrane;plasma membrane 1.40E-162 7 23 23 30.3

P00367;B4DGN5;B3KV55;P49448 "Glutamate dehydrogenase 1, mitochondrial;Glutamate dehydrogenase;Glutamate dehydrogenase 2, mitochondrial" GLUD1;GLUD2 ">sp|P00367|DHE3_HUMAN Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2;>tr|B4DGN5|B4DGN5_HUMAN Glutamate dehydrogenase OS=Homo sapiens GN=GLUD1 PE=2 SV=1;>tr|B3KV55|B3KV55_HUMAN Glutamate dehydrogenase OS=Homo sapiens GN=GLUD1 PE" -0.15 -0.16 0.10 0.06 0.88 0.65 -0.02 -0.01 0.727335589 -0.408597254 amine biosynthetic process;amine catabolic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutamate biosynthetic process;glutamate catabolic process;glutamate metabolic process;glutamine family amino acid biosynthetic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular process;positive regulation of hormone secretion;positive regulation of insulin secretion;positive regulation of peptide hormone secretion;positive regulation of peptide secretion;positive regulation of secretion;positive regulation of transport;primary metabolic process;regulation of biological process;regulation of cell communication;regulation of cellular localization;regulation of cellular process;regulation of hormone secretion;regulation of insulin secretion;regulation of localization;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of secretion;regulation of signaling;regulation of transport;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;amine binding;amino acid binding;ATP binding;binding;carboxylic acid binding;catalytic activity;coenzyme binding;cofactor binding;glutamate dehydrogenase (NAD+) activity;glutamate dehydrogenase [NAD(P)+] activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;identical protein binding;leucine binding;NAD binding;NAD+ binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH2 group of donors;oxidoreductase activity, acting on the CH-NH2 group of donors, NAD or NADP as acceptor;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;D-Glutamine and D-glutamate metabolism;Nitrogen metabolism;Proximal tubule bicarbonate reclamation" 1.02E-173 4 23 23 48.7

P49915;F8W720 GMP synthase [glutamine-hydrolyzing]GMPS >sp|P49915|GUAA_HUMAN GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1;>tr|F8W720|F8W720_HUMAN GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=2 SV=1 0.21 0.00 0.04 0.07 -0.07 -0.53 -0.28 -0.83 1.227527237 0.504257759 amine metabolic process;biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;glutamine family amino acid metabolic process;glutamine metabolic process;GMP biosynthetic process;GMP metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid metabolic process;oxoacid metabolic process;pigment biosynthetic process;pigment metabolic process;primary metabolic process;purine base biosynthetic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbon-nitrogen ligase activity, with glutamine as amido-N-donor;catalytic activity;GMP synthase (glutamine-hydrolyzing) activity;GMP synthase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part Drug metabolism - other enzymes;Purine metabolism 7.06E-108 2 23 23 49.2

P14735;P14735-2;Q5T5N3 Insulin-degrading enzyme IDE >sp|P14735|IDE_HUMAN Insulin-degrading enzyme OS=Homo sapiens GN=IDE PE=1 SV=4 0.16 0.10 0.10 -0.03 -0.21 -0.04 0.17 -0.22 0.675107436 0.157429849 beta-amyloid metabolic process;biological regulation;bradykinin catabolic process;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;determination of adult lifespan;enzyme linked receptor protein signaling pathway;glycoprotein metabolic process;homeostatic process;hormone catabolic process;hormone metabolic process;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;multicellular organismal process;multi-organism process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;peptide catabolic process;peptide metabolic process;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of protein complex assembly;positive regulation of protein oligomerization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein homooligomerization;protein homotetramerization;protein metabolic process;protein oligomerization;protein tetramerization;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of hormone levels;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein complex assembly;regulation of protein metabolic process;regulation of protein oligomerization;regulation of proteolysis;reproductive process;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;ubiquitin homeostasis;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;beta-amyloid binding;beta-endorphin binding;binding;catalytic activity;cation binding;endopeptidase activity;hormone binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;insulin binding;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;neurotransmitter binding;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;peptide binding;peptide hormone binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transition metal ion binding;zinc ion binding" cell part;cell surface;cytoplasmic part;cytosol;cytosolic part;cytosolic proteasome complex;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody part;mitochondrion;nucleus;organelle;organelle lumen;organelle part;peroxisomal matrix;peroxisomal part;peroxisome;plasma membrane;proteasome complex;protein complex Alzheimer's disease 4.66E-113 3 23 23 23.8

P48449;P48449-3;P48449-2;C9J315;H7C3A5 Lanosterol synthaseLSS >sp|P48449|ERG7_HUMAN Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1;>sp|P48449-3|ERG7_HUMAN Isoform 3 of Lanosterol synthase OS=Homo sapiens GN=LSS;>sp|P48449-2|ERG7_HUMAN Isoform 2 of Lanosterol synthase OS=Homo sapiens GN=LSS -0.17 -0.07 -0.26 -0.08 -0.02 0.08 0.53 0.18 1.112068205 -0.341022458 alcohol metabolic process;biosynthetic process;cholesterol biosynthetic process;cholesterol metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;primary metabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process catalytic activity;intramolecular transferase activity;isomerase activity;lanosterol synthase activity;oxidosqualene cyclase activity cell part;cytoplasmic part;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular organelle part;intracellular part;lipid particle;membrane;membrane part;organelle membrane;organelle part Steroid biosynthesis 5.34E-126 5 23 23 36.5

P06748;P06748-2;P06748-3;E5RI98;E5RGW4;Q9C0A0-2;F5H107;Q9C0A0;E9PDN6 Nucleophosmin NPM1 >sp|P06748|NPM_HUMAN Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2;>sp|P06748-2|NPM_HUMAN Isoform 2 of Nucleophosmin OS=Homo sapiens GN=NPM1;>sp|P06748-3|NPM_HUMAN Isoform 3 of Nucleophosmin OS=Homo sapiens GN=NPM1 -0.27 0.57 0.05 0.65 -0.45 -0.31 -1.30 -0.22 1.045728213 0.816230115 "aging;ATP-dependent chromatin remodeling;biological adhesion;biological regulation;cell adhesion;cell aging;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;CenH3-containing nucleosome assembly at centromere;centrosome cycle;centrosome organization;chromatin assembly or disassembly;chromatin modification;chromatin organization;chromatin remodeling;chromatin remodeling at centromere;chromosome organization;developmental process;DNA metabolic process;DNA repair;DNA replication-independent nucleosome assembly;DNA replication-independent nucleosome organization;establishment of localization;establishment of localization in cell;establishment of protein localization;histone exchange;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule organizing center organization;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of centrosome duplication;negative regulation of organelle organization;negative regulation of programmed cell death;nitrogen compound metabolic process;nuclear transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;nucleosome assembly;nucleosome organization;organelle assembly;organelle organization;positive regulation of molecular function;positive regulation of NF-kappaB transcription factor activity;positive regulation of sequence-specific DNA binding transcription factor activity;primary metabolic process;protein complex assembly;protein complex subunit organization;protein oligomerization;protein transport;protein-DNA complex assembly;protein-DNA complex subunit organization;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of centriole replication;regulation of centrosome cycle;regulation of centrosome duplication;regulation of cytoskeleton organization;regulation of deoxyribonuclease activity;regulation of endodeoxyribonuclease activity;regulation of endoribonuclease activity;regulation of gene expression;regulation of hydrolase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of ribonuclease activity;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;ribosome assembly;signal transduction;transport;viral reproduction;viral reproductive process;virus-host interaction" binding;histone binding;identical protein binding;NF-kappaB binding;nucleic acid binding;protein binding;protein binding transcription factor activity;protein dimerization activity;protein heterodimerization activity;protein homodimerization activity;ribonucleoprotein binding;ribosomal large subunit binding;ribosomal small subunit binding;RNA binding;Tat protein binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;unfolded protein binding cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane part;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spindle pole centrosome 0 9 23 23 69

O43847;O43847-2;B1AKJ5;G3V1R5;F5H7V1;H0Y5G9;F8VRQ3;G3V1Y9;G3V1Z2;Q8N4U5;REV__P21675;REV__P21675-2;REV__B1Q2X3;REV__P21675-3;REV__P21675-4 Nardilysin NRD1 >sp|O43847|NRDC_HUMAN Nardilysin OS=Homo sapiens GN=NRD1 PE=1 SV=2;>sp|O43847-2|NRDC_HUMAN Isoform 2 of Nardilysin OS=Homo sapiens GN=NRD1;>tr|B1AKJ5|B1AKJ5_HUMAN Nardilysin OS=Homo sapiens GN=NRD1 PE=2 SV=1;>tr|G3V1R5|G3V1R5_HUMAN Nardilysin OS=Homo sapie 0.21 0.08 -0.20 -0.12 0.31 0.12 0.52 -0.29 0.354403921 -0.173400722 biological regulation;cell migration;cell motility;cell proliferation;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular process;locomotion;macromolecule metabolic process;metabolic process;neuromuscular junction development;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of macromolecule metabolic process;positive regulation of membrane protein ectodomain proteolysis;positive regulation of metabolic process;positive regulation of protein catabolic process;positive regulation of protein metabolic process;positive regulation of proteolysis;primary metabolic process;protein metabolic process;proteolysis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of macromolecule metabolic process;regulation of membrane protein ectodomain proteolysis;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;regulation of proteolysis;synapse organization "binding;catalytic activity;cation binding;endopeptidase activity;epidermal growth factor binding;growth factor binding;hormone binding;hydrolase activity;ion binding;metal ion binding;metalloendopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;protein binding" cell part;cell surface;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle 6.65E-105 15 23 23 23.1

Q96HC4;Q96HC4-4;F5H7Y0;E9PBF5;D6RB78;H0Y8Y3;Q96HC4-3;F5H0X8;Q96HC4-2;D3YTJ1;H0YBI4;H0Y929;D6RAA1;D6RGG6;Q96HC4-5 PDZ and LIM domain protein 5 PDLIM5 >sp|Q96HC4|PDLI5_HUMAN PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5;>sp|Q96HC4-4|PDLI5_HUMAN Isoform 4 of PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5;>tr|F5H7Y0|F5H7Y0_HUMAN PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDL -0.04 -0.16 0.13 0.05 -0.32 -0.11 0.07 -0.08 0.431838483 0.10722784 biological regulation;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of dendritic spine development;regulation of dendritic spine morphogenesis;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of synapse assembly;regulation of synapse organization actin binding;actinin binding;binding;cation binding;cytoskeletal protein binding;enzyme binding;ion binding;kinase binding;metal ion binding;protein binding;protein kinase binding;protein kinase C binding;transition metal ion binding;zinc ion binding actin cytoskeleton;cell junction;cell part;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;postsynaptic density;postsynaptic membrane;synapse part;synaptic membrane;Z disc 4.14E-242 15 23 23 48.2

B4DQJ8;P52209;F5H7U0;K7EM49;K7EMN2;K7EPF6;K7ELN9 "6-phosphogluconate dehydrogenase, decarboxylating" PGD ">tr|B4DQJ8|B4DQJ8_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1;>sp|P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3;>tr|F5H7U0|F5H7U0_HUMAN 6-phosphogluconate d" 0.37 0.12 -0.33 -0.29 0.32 0.15 0.42 0.07 0.626747891 -0.273749664 "alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;aldonic acid metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme metabolic process;cofactor metabolic process;D-gluconate metabolic process;glucose catabolic process;glucose metabolic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;NADP metabolic process;NADPH regeneration;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;pentose biosynthetic process;pentose metabolic process;pentose-phosphate shunt;pentose-phosphate shunt, oxidative branch;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process" "binding;catalytic activity;coenzyme binding;cofactor binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;phosphogluconate dehydrogenase (decarboxylating) activity" cell part;cytoplasmic part;cytosol;intracellular part Glutathione metabolism;Pentose phosphate pathway 7.87E-199 7 23 23 56.6

P46777;Q5T7N0;R4GNJ2 60S ribosomal protein L5 RPL5 >sp|P46777|RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3 0.21 -0.05 -0.21 -0.53 0.34 -0.25 0.16 -0.43 0.150116142 -0.097062342 "biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component biogenesis;cellular component biogenesis at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein complex disassembly;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;intracellular protein transport;intracellular transport;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;ncRNA metabolic process;ncRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;protein complex disassembly;protein complex subunit organization;protein metabolic process;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;reproductive process;ribonucleoprotein complex biogenesis;ribosomal large subunit biogenesis;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;rRNA metabolic process;rRNA processing;SRP-dependent cotranslational protein targeting to membrane;translation;translational elongation;translational initiation;translational termination;transport;viral transcription" 5S rRNA binding;binding;nucleic acid binding;RNA binding;rRNA binding;structural constituent of ribosome;structural molecule activity cell part;cytoplasmic part;cytosolic large ribosomal subunit;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;large ribosomal subunit;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;ribonucleoprotein complex;ribosome Ribosome 2.39E-157 3 23 23 55.6

Q15459;E9PAW1;H7C1L2;F8WC79;F8WB66;Q8TB33;B4DP05;Q9NZ56 Splicing factor 3A subunit 1 SF3A1 >sp|Q15459|SF3A1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1;>tr|E9PAW1|E9PAW1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=2 SV=1 -0.15 0.46 0.02 0.49 0.02 -0.03 -1.13 -0.28 0.773362049 0.560727791 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;apoptosis;biological regulation;cell cycle cytokinesis;cell cycle phase;cell cycle process;cell death;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to hypoxia;cellular response to oxygen levels;cellular response to stimulus;cellular response to stress;chromosome movement towards spindle pole;cytokinesis;cytokinesis after meiosis;cytoskeleton organization;death;developmental process;establishment of chromosome localization;establishment of localization;establishment of localization in cell;establishment of meiotic spindle localization;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;female gamete generation;formin-nucleated actin cable assembly;gamete generation;intracellular signal transduction;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;meiotic chromosome movement towards spindle pole;meiotic metaphase I;metabolic process;metaphase;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;mRNA splice site selection;multicellular organismal development;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of catabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein catabolic process;negative regulation of protein metabolic process;nitrogen compound metabolic process;nuclear mRNA 3'-splice site recognition;nucleic acid metabolic process;nucleobase-containing compound metabolic process;oogenesis;organelle organization;polar body extrusion after meiotic divisions;primary metabolic process;programmed cell death;protein transport;regulation of biological process;regulation of catabolic process;regulation of cellular process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein metabolic process;reproductive process;response to chemical stimulus;response to DNA damage stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA metabolic process;RNA processing;signal transduction;transport;vesicle-mediated transport actin binding;binding;cytoskeletal protein binding;nucleic acid binding;protein binding;RNA binding actin cytoskeleton;catalytic step 2 spliceosome;cell cortex;cell part;cytoplasmic part;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;ribonucleoprotein complex;spliceosomal complex;U2-type spliceosomal complex;vesicle membrane Dorso-ventral axis formation;Spliceosome 2.27E-196 8 23 23 35.4

Q15477;F5H7B0;H7C5N0;B4E0B4;H7C4L3;F8WDE8 Helicase SKI2W SKIV2L >sp|Q15477|SKIV2_HUMAN Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=1 SV=3;>tr|F5H7B0|F5H7B0_HUMAN Helicase SKI2W OS=Homo sapiens GN=SKIV2L PE=2 SV=1 -0.09 0.03 -0.08 -0.13 0.01 0.06 0.47 0.02 0.765078887 -0.208166474 "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;Ski complex RNA degradation 6.58E-114 6 23 23 26.9

Q9Y6N5;H3BNX3;H3BMS6;H3BNP9;H3BV36;REV__Q8N2W9 "Sulfide:quinone oxidoreductase, mitochondrial" SQRDL ">sp|Q9Y6N5|SQRD_HUMAN Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1;>tr|H3BNX3|H3BNX3_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1" -0.44 -0.25 0.05 0.12 0.43 0.39 -0.33 0.19 0.572316906 -0.297191809 "amine catabolic process;amine metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;metabolic process;nitrogen compound metabolic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process;sulfide oxidation;sulfide oxidation, using sulfide:quinone oxidoreductase;sulfur amino acid catabolic process;sulfur amino acid metabolic process;sulfur compound catabolic process;sulfur compound metabolic process" "catalytic activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;oxidoreductase activity, acting on a sulfur group of donors, quinone or similar compound as acceptor;sulfide:quinone oxidoreductase activity" cell part;cytoplasmic part;intracellular organelle part;intracellular part;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 1.85E-191 6 23 23 52.9

Q9UQ35;Q9UQ35-2;I3L1I8;Q9UQ35-3;I3L182;I3L4D8;I3L4U6;I3L1C0;I3L3Q8 Serine/arginine repetitive matrix protein 2 SRRM2 >sp|Q9UQ35|SRRM2_HUMAN Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2 0.06 0.01 0.35 -0.11 0.27 -0.55 -0.72 -0.47 0.789516491 0.441292149 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;C2H2 zinc finger domain binding;nucleic acid binding;protein binding;protein domain specific binding;RNA binding Cajal body;catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex 7.88E-128 9 23 23 13.1

Q9Y2W1 Thyroid hormone receptor-associated protein 3 THRAP3 >sp|Q9Y2W1|TR150_HUMAN Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 -0.18 0.15 0.11 0.27 0.11 -0.15 -1.03 -0.60 0.809716992 0.50661784 "androgen receptor signaling pathway;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;intracellular receptor mediated signaling pathway;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of mRNA processing;positive regulation of nitrogen compound metabolic process;positive regulation of nuclear mRNA splicing, via spliceosome;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA splicing;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;regulation of alternative nuclear mRNA splicing, via spliceosome;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;regulation of RNA stability;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;RNA biosynthetic process;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA stabilization;signal transduction;steroid hormone receptor signaling pathway;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;hormone receptor binding;ligand-dependent nuclear receptor transcription coactivator activity;nuclear hormone receptor binding;nucleotide binding;phosphoprotein binding;protein binding;protein binding transcription factor activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;receptor binding;ribonucleotide binding;RNA polymerase II transcription cofactor activity;RNA polymerase II transcription factor binding transcription factor activity;thyroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding;transcription factor binding transcription factor activity;vitamin D receptor binding cell part;intracellular organelle part;intracellular part;macromolecular complex;mediator complex;nuclear part;nucleoplasm part;organelle part;protein complex 2.32E-125 1 23 23 27.9

Q07157-2;G5E9E7;Q07157;G3V1L9;H0YKB1;H0Y3R8;H0YLT6 Tight junction protein ZO-1 TJP1 ">sp|Q07157-2|ZO1_HUMAN Isoform Short of Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1;>tr|G5E9E7|G5E9E7_HUMAN Tight junction protein 1 (Zona occludens 1), isoform CRA_e OS=Homo sapiens GN=TJP1 PE=2 SV=1;>sp|Q07157|ZO1_HUMAN Tight junction protein ZO-" 0.38 -0.01 0.33 -0.23 0.29 -0.19 0.18 -0.45 0.282821798 0.16165694 anatomical structure formation involved in morphogenesis;biological regulation;blastocyst formation;carbohydrate homeostasis;cell junction assembly;cell junction organization;cell-cell junction assembly;cell-cell junction organization;cellular chemical homeostasis;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular glucose homeostasis;cellular homeostasis;cellular process;cellular response to carbohydrate stimulus;cellular response to chemical stimulus;cellular response to glucose stimulus;cellular response to hexose stimulus;cellular response to monosaccharide stimulus;cellular response to organic substance;cellular response to stimulus;chemical homeostasis;circulatory system process;developmental process;glucose homeostasis;hippo signaling cascade;homeostatic process;intracellular signal transduction;multicellular organismal process;negative regulation of vascular permeability;regulation of biological process;regulation of biological quality;regulation of cellular process;regulation of vascular permeability;response to abiotic stimulus;response to biotic stimulus;response to carbohydrate stimulus;response to chemical stimulus;response to drug;response to ethanol;response to glucose stimulus;response to hexose stimulus;response to lipopolysaccharide;response to magnetism;response to molecule of bacterial origin;response to monosaccharide stimulus;response to organic substance;response to stimulus;signal transduction;system process;vascular process in circulatory system adherens junction;anchoring junction;apical part of cell;apicolateral plasma membrane;basolateral plasma membrane;cell junction;cell part;cell-cell adherens junction;cell-cell contact zone;cell-cell junction;cytoplasm;cytoplasmic part;cytosol;gap junction;intercalated disc;intercellular canaliculus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane part;membrane-bounded organelle;nucleus;occluding junction;organelle;plasma membrane;plasma membrane part;tight junction Adherens junction;Epithelial cell signaling in Helicobacter pylori infection;Gap junction;Tight junction;Vibrio cholerae infection 2.41E-116 7 23 23 19.5

P11387;Q969P6-2;Q969P6;E5RIC7;E5RJ95;E5RFS0;E5RJ33;H0YBR3;H0YAR3;H0YC03;E5RGE7;E5RGR4;E5RFE3;E5RGR2 DNA topoisomerase 1 TOP1 >sp|P11387|TOP1_HUMAN DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 -0.28 0.32 0.20 0.35 0.23 -0.21 -1.38 -0.57 0.72611374 0.632001057 biosynthetic process;cell death;cell division;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromatin modification;chromatin organization;chromatin remodeling;chromosome organization;chromosome segregation;death;DNA conformation change;DNA metabolic process;DNA replication;DNA topological change;embryonic cleavage;interaction with host;interspecies interaction between organisms;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;programmed cell death;reproductive process;response to chemical stimulus;response to drug;response to stimulus;viral reproductive process;virus-host interaction "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;chromatin binding;DNA binding;DNA topoisomerase (ATP-hydrolyzing) activity;DNA topoisomerase activity;DNA topoisomerase type I activity;DNA-dependent ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;isomerase activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;chromosomal part;chromosome;cytoplasmic mRNA processing body;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoid;nucleolus;nucleoplasm;organelle;organelle part;perikaryon;protein complex;replication fork protection complex;ribonucleoprotein complex;RNA granule 4.93E-113 14 23 23 29.4

Q9H3U1-2;Q9H3U1;Q9H3U1-3 Protein unc-45 homolog A UNC45A >sp|Q9H3U1-2|UN45A_HUMAN Isoform 2 of Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A;>sp|Q9H3U1|UN45A_HUMAN Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1 0.14 0.05 0.12 0.11 -0.05 0.23 0.24 -0.12 0.118887125 0.031509542 anatomical structure development;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone-mediated protein folding;developmental process;macromolecule metabolic process;metabolic process;muscle organ development;muscle structure development;organ development;primary metabolic process;protein folding;protein metabolic process cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm 7.94E-259 3 23 23 28.2

Q96QK1;I3L4S0;I3L4P4;J3KRW4;J3KSJ3;H7C101;REV__H3BVB3;Q12887;REV__Q32MH5;REV__Q32MH5-3 Vacuolar protein sorting-associated protein 35 VPS35 >sp|Q96QK1|VPS35_HUMAN Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 -0.02 0.03 -0.08 -0.02 -0.13 0.22 0.33 0.13 0.673943918 -0.156269559 "aerobic respiration;biosynthetic process;cell death;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular respiration;cofactor biosynthetic process;cofactor metabolic process;cytochrome complex assembly;death;electron transport chain;endosome transport;energy derivation by oxidation of organic compounds;establishment of localization;establishment of localization in cell;establishment of protein localization;generation of precursor metabolites and energy;heme a biosynthetic process;heme a metabolic process;heme biosynthetic process;heme metabolic process;heme O biosynthetic process;heme o metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;intracellular transport;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;mitochondrial electron transport, cytochrome c to oxygen;mitochondrial fission;mitochondrion organization;nitrogen compound metabolic process;organelle fission;organelle organization;oxidation-reduction process;pigment biosynthetic process;pigment metabolic process;porphyrin-containing compound biosynthetic process;porphyrin-containing compound metabolic process;protein complex assembly;protein complex subunit organization;protein transport;respiratory chain complex IV assembly;respiratory electron transport chain;retrograde transport, endosome to Golgi;tetrapyrrole biosynthetic process;tetrapyrrole metabolic process;transport;vesicle-mediated transport" "catalytic activity;farnesyltranstransferase activity;prenyltransferase activity;protoheme IX farnesyltransferase activity;transferase activity;transferase activity, transferring alkyl or aryl (other than methyl) groups" cell part;cytoplasmic part;cytosol;endosome;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane;mitochondrial part;mitochondrion;organelle;organelle membrane;organelle part Oxidative phosphorylation;Porphyrin and chlorophyll metabolism 5.24E-209 10 23 23 31.5

P00338;P00338-3;P00338-4;P00338-5;P00338-2;F5GXY2;F5GYU2;F5GXH2;F5H5J4;F5H6W8;F5GZQ4;F5H8H6;F5GXC7;F5GWW2;F5GXU1;Q9BYZ2 L-lactate dehydrogenase A chain LDHA >sp|P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2;>sp|P00338-3|LDHA_HUMAN Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA;>sp|P00338-4|LDHA_HUMAN Isoform 4 of L-lactate dehydrogenase A chain OS=Hom 0.02 -0.16 0.01 -0.06 0.18 0.28 0.40 -0.02 1.10273182 -0.257286249 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cell communication;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to stimulus;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;response to external stimulus;response to extracellular stimulus;response to stimulus;small molecule catabolic process;small molecule metabolic process "catalytic activity;lactate dehydrogenase activity;L-lactate dehydrogenase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Cysteine and methionine metabolism;Glycolysis / Gluconeogenesis;Propanoate metabolism;Pyruvate metabolism 0 16 25 23 66

P22626;P22626-2;REV__Q96MU7-2;REV__Q96MU7;REV__J3QR07 Heterogeneous nuclear ribonucleoproteins A2/B1 HNRNPA2B1 >sp|P22626|ROA2_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2;>sp|P22626-2|ROA2_HUMAN Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 -0.20 0.84 0.08 0.92 -0.02 0.20 -1.40 0.05 0.645771727 0.704460519 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of RNA localization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mRNA processing;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear mRNA splicing, via spliceosome;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of RNA splicing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA processing;regulation of nitrogen compound metabolic process;regulation of nuclear mRNA splicing, via spliceosome;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA splicing;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA transport;transport" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;sequence-specific DNA binding;single-stranded DNA binding;single-stranded telomeric DNA binding;structure-specific DNA binding;telomeric DNA binding catalytic step 2 spliceosome;cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex 0 5 26 23 68

P62258;P62258-2;B4DJF2;I3L3T1;K7EM20;K7EIT4;I3L0W5 14-3-3 protein epsilon YWHAE >sp|P62258|1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1;>sp|P62258-2|1433E_HUMAN Isoform SV of 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE;>tr|B4DJF2|B4DJF2_HUMAN 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=2 SV=1;>tr|I3 -0.10 0.00 -0.06 0.06 0.25 0.10 0.03 -0.03 0.670318808 -0.111268378 anatomical structure development;biological regulation;cell cycle process;cell migration;cell motility;cell surface receptor linked signaling pathway;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;cellular response to stimulus;cerebral cortex development;developmental process;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;G2/M transition of mitotic cell cycle;hippo signaling cascade;hippocampus development;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotion;membrane organization;multi-organism process;negative regulation of biological process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of dephosphorylation;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of protein dephosphorylation;negative regulation of protein metabolic process;negative regulation of protein modification process;nerve growth factor receptor signaling pathway;neuron migration;protein targeting;protein transport;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of dephosphorylation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of protein dephosphorylation;regulation of protein metabolic process;regulation of protein modification process;reproductive process;response to stimulus;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;transport;viral reproductive process;virus-host interaction axon part;cell part;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinesin complex;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule associated complex;mitochondrion;organelle;organelle membrane;organelle part;pigment granule;protein complex;vesicle;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis 0 7 26 23 73.7

Q15233;Q15233-2;H7C367;C9JYS8;C9IZL7;C9J4X2;C9JJ13 Non-POU domain-containing octamer-binding protein NONO >sp|Q15233|NONO_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4;>sp|Q15233-2|NONO_HUMAN Isoform 2 of Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO;>tr|H7C367|H7C367_HUMAN Non-POU domain- -0.30 0.53 0.08 0.66 0.13 0.11 -1.37 -0.07 0.542054977 0.543837449 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA recombination;DNA repair;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear body;nuclear matrix;nuclear part;nuclear speck;nucleolus;nucleoplasm part;organelle;organelle part;paraspeckles 0 7 27 23 52.2

P20700;E9PBF6 Lamin-B1 LMNB1 >sp|P20700|LMNB1_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2;>tr|E9PBF6|E9PBF6_HUMAN Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=2 SV=1 -0.52 0.45 0.22 0.92 0.14 -0.17 -1.47 -0.81 0.77325058 0.840947587 cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process structural molecule activity cell part;cytoskeletal part;envelope;intermediate filament;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane;nuclear envelope;nuclear inner membrane;nuclear membrane;nuclear part;nucleoplasm;organelle envelope;organelle inner membrane;organelle membrane;organelle part;protein complex 3.73E-226 2 28 23 52.9

P06744;P06744-2;K7EP41;K7ELR7;K7ERC6;K7ENR8;K7ERK8;K7EIL4;K7ESF4;Q8N196 Glucose-6-phosphate isomerase GPI >sp|P06744|G6PI_HUMAN Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4;>sp|P06744-2|G6PI_HUMAN Isoform 2 of Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI 0.20 -0.07 -0.07 -0.03 0.12 -0.12 0.31 -0.25 0.015484867 -0.006705799 "alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;aldehyde biosynthetic process;aldehyde catabolic process;anatomical structure development;anatomical structure formation involved in morphogenesis;angiogenesis;behavior;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell development;cellular aldehyde metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cognition;developmental process;developmental process involved in reproduction;generation of precursor metabolites and energy;germ cell development;gluconeogenesis;glucose 6-phosphate metabolic process;glucose catabolic process;glucose metabolic process;glycolysis;hemostasis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;humoral immune response;immune response;immune system process;learning or memory;lens development in camera-type eye;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;methylglyoxal biosynthetic process;methylglyoxal metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of caspase activity;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of neuron apoptosis;negative regulation of peptidase activity;negative regulation of programmed cell death;neurological system process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of catalytic activity;regulation of cell death;regulation of cell proliferation;regulation of cellular process;regulation of cysteine-type endopeptidase activity;regulation of cysteine-type endopeptidase activity involved in apoptotic process;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of peptidase activity;regulation of programmed cell death;reproductive process;response to stimulus;RNA biosynthetic process;RNA metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;spermatid development;system process;transcription, DNA-dependent" "binding;carbohydrate binding;catalytic activity;DNA binding;glucose-6-phosphate isomerase activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting aldoses and ketoses;intramolecular transferase activity;isomerase activity;monosaccharide binding;nucleic acid binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;sugar binding" cell part;cell projection;cytoplasm;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;neuron projection;nucleus;organelle;plasma membrane Amino sugar and nucleotide sugar metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway;Starch and sucrose metabolism 0 10 29 23 65.6

P30153;F5H3X9;B3KQV6;C9J9C1;E9PH38;E9PPI5;E9PHZ6;E9PNM7;M0QXG4;M0R0K6 Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform PPP2R1A >sp|P30153|2AAA_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4;>tr|F5H3X9|F5H3X9_HUMAN Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo s 0.08 0.06 -0.14 -0.01 0.15 0.12 0.21 -0.07 0.582050615 -0.107335029 "anaphase;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular lipid metabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;ceramide metabolic process;chromosome segregation;dephosphorylation;enzyme linked receptor protein signaling pathway;fibroblast growth factor receptor signaling pathway;G2/M transition of mitotic cell cycle;inactivation of MAPK activity;induction of apoptosis;induction of programmed cell death;intracellular signal transduction;lipid metabolic process;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;membrane lipid metabolic process;membrane organization;metabolic process;mitotic anaphase;mitotic nuclear envelope reassembly;mRNA catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell communication;negative regulation of cell growth;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of growth;negative regulation of intracellular protein kinase cascade;negative regulation of JAK-STAT cascade;negative regulation of kinase activity;negative regulation of macromolecule metabolic process;negative regulation of MAP kinase activity;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of peptidyl-tyrosine phosphorylation;negative regulation of phosphate metabolic process;negative regulation of phosphorus metabolic process;negative regulation of phosphorylation;negative regulation of protein kinase activity;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein phosphorylation;negative regulation of protein serine/threonine kinase activity;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transferase activity;negative regulation of tyrosine phosphorylation of STAT protein;negative regulation of tyrosine phosphorylation of Stat3 protein;nitrogen compound metabolic process;nuclear envelope organization;nuclear envelope reassembly;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleobase-containing compound metabolic process;peptidyl-serine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;protein complex assembly;protein complex subunit organization;protein dephosphorylation;protein metabolic process;protein modification process;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of gene expression;regulation of growth;regulation of intracellular protein kinase cascade;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat3 protein;regulation of Wnt receptor signaling pathway;response to chemical stimulus;response to endogenous stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to organic substance;response to stimulus;RNA catabolic process;RNA metabolic process;RNA processing;RNA splicing;second-messenger-mediated signaling;signal transduction;sphingoid metabolic process;sphingolipid metabolic process;transmembrane receptor protein tyrosine kinase signaling pathway" "antigen binding;binding;catalytic activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on ester bonds;phosphatase activity;phosphatase regulator activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;protein phosphatase regulator activity;protein phosphatase type 2A regulator activity;protein serine/threonine phosphatase activity" "cell part;chromosomal part;chromosome, centromeric region;cytoplasmic part;cytoskeleton;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule cytoskeleton;mitochondrion;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;protein phosphatase type 2A complex;protein serine/threonine phosphatase complex" Cell cycle - yeast;Chagas disease (American trypanosomiasis);Hepatitis C;Long-term depression;Meiosis - yeast;mRNA surveillance pathway;Oocyte meiosis;TGF-beta signaling pathway;Tight junction;Wnt signaling pathway 0 10 30 23 55.2

P63104;E7EX29;B0AZS6;E7ESK7;P63104-2;E7EX24;B7Z2E6;H0YB80;E9PD24;E7EVZ2;E5RIR4;E5RGE1;REV__B7ZLE7;REV__P53355;REV__P53355-3;REV__Q5T8F1 14-3-3 protein zeta/delta YWHAZ >sp|P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1;>tr|E7EX29|E7EX29_HUMAN 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1;>tr|B0AZS6|B0AZS6_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ P -0.10 -0.03 -0.13 -0.05 -0.09 0.19 0.24 0.27 1.118613273 -0.22809706 amine transport;biological regulation;cell activation;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;gene expression;histamine secretion;histamine secretion by mast cell;histamine secretion involved in inflammatory response;histamine transport;hormone secretion;hormone transport;intracellular protein transport;intracellular transport;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial transport;mRNA metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;nitrogen compound metabolic process;nitrogen compound transport;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic substance transport;platelet activation;primary metabolic process;protein import;protein targeting;protein targeting to mitochondrion;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;regulation of hormone levels;regulation of programmed cell death;RNA metabolic process;secretion;secretion by cell;signal release;transport "catalytic activity;kinase activity;transferase activity;transferase activity, transferring phosphorus-containing groups" cell leading edge;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;nuclear part;nucleoplasm;nucleus;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;pigment granule;postsynaptic density;protein complex;synapse part;vesicle;vesicle membrane Cell cycle;Neurotrophin signaling pathway;Oocyte meiosis 0 16 30 23 79.6

Q92841;H3BLZ8;Q92841-1;Q92841-3;Q92841-2;C9JMU5;G5E9L5 Probable ATP-dependent RNA helicase DDX17 DDX17 >sp|Q92841|DDX17_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2;>tr|H3BLZ8|H3BLZ8_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=2 SV=1;>sp|Q92841-1|DDX17_HUMAN Isoform 2 of Probable ATP-depe -0.07 0.32 -0.04 0.29 0.15 -0.14 -0.81 -0.36 0.770686152 0.410478765 "anatomical structure development;biological regulation;biosynthetic process;cardiovascular system development;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell communication;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of estrogen receptor signaling pathway;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of signal transduction;positive regulation of signaling;positive regulation of steroid hormone receptor signaling pathway;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;post-embryonic development;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell differentiation;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of estrogen receptor signaling pathway;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of muscle cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of skeletal muscle cell differentiation;regulation of steroid hormone receptor signaling pathway;regulation of striated muscle cell differentiation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;system development;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;estrogen receptor binding;helicase activity;hormone receptor binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nuclear hormone receptor binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part 1.31E-247 7 33 23 48.7

P05783;F8VZY9;CON__H-INV:HIT000015463;CON__Q92764;C4AM86;Q92764;CON__Q497I4 "Keratin, type I cytoskeletal 18" KRT18 ">sp|P05783|K1C18_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2;>tr|F8VZY9|F8VZY9_HUMAN Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=2 SV=1" -0.01 1.06 0.21 1.14 -2.33 -0.53 -0.89 0.79 0.814675186 1.341027726 anatomical structure morphogenesis;apoptosis;biological regulation;cell cycle;cell death;cell surface receptor linked signaling pathway;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to tumor necrosis factor;cytokine-mediated signaling pathway;death;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi to plasma membrane CFTR protein transport;Golgi to plasma membrane protein transport;Golgi to plasma membrane transport;Golgi vesicle transport;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;multi-organism process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;post-Golgi vesicle-mediated transport;programmed cell death;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;response to tumor necrosis factor;signal transduction;transport;tumor necrosis factor-mediated signaling pathway;vesicle-mediated transport;viral reproductive process;virus-host interaction structural molecule activity cell part;centriolar satellite;cytoplasm;cytoplasmic part;cytoskeletal part;intermediate filament;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;keratin filament;macromolecular complex;microtubule organizing center part;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;perinuclear region of cytoplasm;protein complex 0 7 34 23 69.1

P08107;P08107-2;E7EP94;Q5SP16;P48741 Heat shock 70 kDa protein 1A/1B HSPA1A >sp|P08107|HSP71_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5;>sp|P08107-2|HSP71_HUMAN Isoform 2 of Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A;>tr|E7EP94|E7EP94_HUMAN Heat shock 70 kDa protein 1A/1B OS=Homo sapie -0.20 0.05 -0.03 0.15 -0.73 -0.27 0.08 -0.09 0.551471281 0.248029777 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;gene expression;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA catabolic process;mRNA metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell growth;negative regulation of cell proliferation;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of growth;negative regulation of inclusion body assembly;negative regulation of programmed cell death;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of erythrocyte differentiation;positive regulation of myeloid cell differentiation;primary metabolic process;protein folding;protein metabolic process;protein refolding;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cell proliferation;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of erythrocyte differentiation;regulation of growth;regulation of homeostatic process;regulation of immune system process;regulation of inclusion body assembly;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of myeloid cell differentiation;regulation of programmed cell death;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;RNA catabolic process;RNA metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;protein binding involved in protein folding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding aggresome;cell part;cytoplasmic part;cytosol;endoplasmic reticulum;inclusion body;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle;organelle part;perinuclear region of cytoplasm;ribonucleoprotein complex Antigen processing and presentation;Endocytosis;MAPK signaling pathway;Measles;Protein processing in endoplasmic reticulum;Spliceosome;Toxoplasmosis 0 5 43 23 63.7

Q99798;A2A274 "Aconitate hydratase, mitochondrial" ACO2 ">sp|Q99798|ACON_HUMAN Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2;>tr|A2A274|A2A274_HUMAN Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=2 SV=1" -0.06 -0.06 -0.02 0.13 -0.47 -0.06 0.03 -0.10 0.523261787 0.148150772 acetyl-CoA catabolic process;acetyl-CoA metabolic process;carboxylic acid metabolic process;catabolic process;cell death;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;citrate metabolic process;coenzyme catabolic process;coenzyme metabolic process;cofactor catabolic process;cofactor metabolic process;death;isocitrate metabolic process;metabolic process;organic acid metabolic process;oxoacid metabolic process;small molecule metabolic process;tricarboxylic acid cycle;tricarboxylic acid metabolic process "3 iron, 4 sulfur cluster binding;4 iron, 4 sulfur cluster binding;aconitate hydratase activity;binding;carbon-oxygen lyase activity;catalytic activity;cation binding;citrate hydro-lyase (cis-aconitate-forming) activity;hydro-lyase activity;ion binding;iron ion binding;iron-sulfur cluster binding;isocitrate hydro-lyase (cis-aconitate-forming) activity;lyase activity;metal cluster binding;metal ion binding;transition metal ion binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;nucleus;organelle;organelle lumen;organelle part Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle);Glyoxylate and dicarboxylate metabolism 6.09E-298 2 24 24 39.5

P53618;E9PP73;E9PP63;E9PKQ1Coatomer subunit beta COPB1 >sp|P53618|COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3;>tr|E9PP73|E9PP73_HUMAN Coatomer subunit beta (Fragment) OS=Homo sapiens GN=COPB1 PE=2 SV=1 0.08 -0.02 -0.02 -0.07 0.38 0.19 0.19 0.02 1.070363556 -0.202663445 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;multi-organism process;organelle organization;protein transport;reproductive process;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport;viral reproductive process;virus-host interaction" structural molecule activity cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;endoplasmic reticulum-Golgi intermediate compartment;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane coat;membrane part;membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;vesicle coat 6.01E-211 4 24 24 32.1

Q9Y262;Q9Y262-2;B0QY89;B0QY90;C9JHP4;C9K0Q7;H7C3A0;H0Y7E6 Eukaryotic translation initiation factor 3 subunit L EIF3L >sp|Q9Y262|EIF3L_HUMAN Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1;>sp|Q9Y262-2|EIF3L_HUMAN Isoform 2 of Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L;>tr|B0QY89|B0QY89_HUMAN Eukar 0.24 -0.01 -0.17 -0.12 -0.02 -0.23 -0.01 -0.24 0.385063323 0.1072939 cellular process;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;eukaryotic translation initiation factor 3 complex;fibrillar center;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleolar part;nucleoplasm;organelle part;protein complex 0 8 24 24 48

P00505;E7ERW2 "Aspartate aminotransferase, mitochondrial;Aspartate aminotransferase" GOT2 ">sp|P00505|AATM_HUMAN Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3;>tr|E7ERW2|E7ERW2_HUMAN Aspartate aminotransferase OS=Homo sapiens GN=GOT2 PE=2 SV=1" 0.02 -0.23 0.08 -0.07 0.43 0.01 0.27 -0.20 0.471842291 -0.174550893 2-oxoglutarate metabolic process;4-hydroxyproline catabolic process;4-hydroxyproline metabolic process;alcohol biosynthetic process;alcohol metabolic process;amine biosynthetic process;amine catabolic process;amine metabolic process;aspartate biosynthetic process;aspartate catabolic process;aspartate family amino acid biosynthetic process;aspartate family amino acid catabolic process;aspartate family amino acid metabolic process;aspartate metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;carboxylic acid transport;catabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid catabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;dicarboxylic acid metabolic process;establishment of localization;fatty acid transport;fumarate metabolic process;gluconeogenesis;glucose metabolic process;glutamate catabolic process;glutamate catabolic process to 2-oxoglutarate;glutamate catabolic process to aspartate;glutamate metabolic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;heterocycle catabolic process;heterocycle metabolic process;hexose biosynthetic process;hexose metabolic process;lipid transport;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;monocarboxylic acid transport;monosaccharide biosynthetic process;monosaccharide metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;organic acid transport;organic substance transport;oxaloacetate metabolic process;oxoacid metabolic process;primary metabolic process;response to chemical stimulus;response to ethanol;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;transport "binding;catalytic activity;cofactor binding;kynurenine-oxoglutarate transaminase activity;L-aspartate:2-oxoglutarate aminotransferase activity;L-phenylalanine aminotransferase activity;L-phenylalanine:2-oxoglutarate aminotransferase activity;pyridoxal phosphate binding;transaminase activity;transferase activity;transferase activity, transferring nitrogenous groups;vitamin B6 binding;vitamin binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part;plasma membrane "Alanine, aspartate and glutamate metabolism;Arginine and proline metabolism;Cysteine and methionine metabolism;Fat digestion and absorption;Phenylalanine metabolism;Phenylalanine, tyrosine and tryptophan biosynthesis;Tyrosine metabolism" 3.03E-203 2 24 24 52.1

B9A067;Q16891-2;Q16891-4;Q16891;C9J406;Q16891-3;H7C463;D6RAW4 Mitochondrial inner membrane protein IMMT >tr|B9A067|B9A067_HUMAN Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT PE=2 SV=2;>sp|Q16891-2|IMMT_HUMAN Isoform 2 of Mitochondrial inner membrane protein OS=Homo sapiens GN=IMMT;>sp|Q16891-4|IMMT_HUMAN Isoform 4 of Mitochondrial inner membra -0.48 0.78 0.10 0.96 0.21 0.94 -1.15 0.64 0.110911079 0.177894507 biological regulation;calcium ion homeostasis;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;chemical homeostasis;divalent inorganic cation homeostasis;homeostatic process;ion homeostasis;metal ion homeostasis;mitochondrial calcium ion homeostasis;regulation of biological quality;response to abiotic stimulus;response to cold;response to stimulus;response to stress;response to temperature stimulus cell part;cytoplasmic part;integral to membrane;intracellular organelle part;intracellular part;intrinsic to membrane;membrane;membrane part;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part 7.99E-150 8 24 24 40.6

Q15021;F5GZJ1;E7EN77;F5GZK7;F5H431;REV__Q02790 Condensin complex subunit 1 NCAPD2 >sp|Q15021|CND1_HUMAN Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3;>tr|F5GZJ1|F5GZJ1_HUMAN Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=2 SV=1;>tr|E7EN77|E7EN77_HUMAN Condensin complex subunit 1 (Fragment) OS=Homo sapiens GN= 0.48 0.36 -0.04 -0.27 0.02 -0.73 -0.36 -0.78 0.991309074 0.5946003 cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome condensation;chromosome organization;DNA conformation change;DNA metabolic process;DNA packaging;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;metabolic process;mitotic chromosome condensation;mitotic prometaphase;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process binding;histone binding;protein binding cell part;chromosomal part;chromosome;condensed chromosome;condensin core heterodimer;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;pronucleus;protein complex Cell cycle - yeast 2.76E-135 6 24 24 24.1

P05120;H7C004;H7BYS2;E7EPJ9;E7ERB5;E9PDK7 Plasminogen activator inhibitor 2 SERPINB2;SERPINB10 >sp|P05120|PAI2_HUMAN Plasminogen activator inhibitor 2 OS=Homo sapiens GN=SERPINB2 PE=1

SV=2;>tr|H7C004|H7C004_HUMAN Serpin B10 (Fragment) OS=Homo sapiens GN=SERPINB10 PE=3 SV=1;>tr|H7BYS2|H7BYS2_HUMAN Serpin B10 (Fragment) OS=Homo sapiens GN=SERPINB10 PE 1.05 0.63 -0.25 -0.61 0.80 0.85 0.48 -0.27 0.215024105 -0.262882747 biological regulation;blood coagulation;coagulation;fibrinolysis;hemostasis;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood coagulation;negative regulation of cell death;negative regulation of cellular process;negative regulation of coagulation;negative regulation of multicellular organismal process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of blood coagulation;regulation of body fluid levels;regulation of cell death;regulation of cellular process;regulation of coagulation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein metabolic process;regulation of proteolysis;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of wound healing;response to stimulus;response to stress;response to wounding;wound healing endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasm;extracellular region;extracellular region part;extracellular space;intracellular part;membrane;plasma membrane Amoebiasis 0 6 24 24 48.7

P12429;D6RA82;D6RFG5;D6RCA8;D6RAZ8;D6RFJ9 Annexin A3;Annexin ANXA3 >sp|P12429|ANXA3_HUMAN Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3;>tr|D6RA82|D6RA82_HUMAN Annexin OS=Homo sapiens GN=ANXA3 PE=2 SV=1 0.46 0.18 0.02 -0.27 -0.75 -0.10 0.41 0.07 0.253706239 0.189885711 "biological regulation;cell activation;cell activation involved in immune response;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;defense response;defense response to bacterium;endocytosis;establishment of localization;establishment of localization in cell;exocytosis;immune effector process;immune system process;leukocyte activation;leukocyte activation involved in immune response;leukocyte degranulation;membrane invagination;membrane organization;multi-organism process;myeloid cell activation involved in immune response;myeloid leukocyte activation;neutrophil activation;neutrophil activation involved in immune response;neutrophil degranulation;phagocytosis;positive regulation of angiogenesis;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of developmental process;positive regulation of endothelial cell migration;positive regulation of locomotion;positive regulation of molecular function;positive regulation of sequence-specific DNA binding transcription factor activity;regulated secretory pathway;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of biological process;regulation of biosynthetic process;regulation of cell migration;regulation of cell motility;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of endothelial cell migration;regulation of gene expression;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of transcription, DNA-dependent;response to bacterium;response to biotic stimulus;response to other organism;response to stimulus;response to stress;secretion;secretion by cell;transport;vesicle-mediated transport" binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phospholipase A2 inhibitor activity;phospholipase inhibitor activity;phospholipid binding cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;endocytic vesicle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;organelle membrane;organelle part;phagocytic vesicle membrane;plasma membrane;specific granule;stored secretory granule;vesicle;vesicle membrane 0 6 25 25 58.8

P14868;Q68CR9;H7BZ35;C9J7S3;C9JLC1;H7C278;C9JQM9 "Aspartate--tRNA ligase, cytoplasmic" DARS;DKFZp781B11202 ">sp|P14868|SYDC_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2;>tr|Q68CR9|Q68CR9_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DKFZp781B11202 PE=2 SV=1" 0.10 -0.06 0.00 -0.07 0.04 -0.29 0.06 -0.42 0.47810311 0.145035725 amine metabolic process;amino acid activation;aspartyl-tRNA aminoacylation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacylase activity;aminoacyl-tRNA ligase activity;aspartate-tRNA ligase activity;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Aminoacyl-tRNA biosynthesis 4.49E-178 7 25 25 57.1

Q16531;F5GY55;B4DG00;F5H6C5;F5H238;F8WF81;F5GZ34;F5H775;F5H4N9;F5H581;F5H2L3;F5H0Y5;F5GWI0;F5GZY8;F5H7A0;F5GYG8;F5H198 DNA damage-binding protein 1 DDB1 >sp|Q16531|DDB1_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1;>tr|F5GY55|F5GY55_HUMAN DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=2 SV=1 0.25 0.13 -0.18 -0.26 0.13 0.07 -0.05 -0.42 0.102401403 0.050618855 "biological regulation;catabolic process;cell cycle checkpoint;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;DNA catabolic process;DNA excision;DNA metabolic process;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleotide-excision repair, DNA damage removal;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;reproductive process;response to stimulus;signal transduction;ubiquitin-dependent protein catabolic process;viral reproductive process;virus-host interaction;Wnt receptor signaling pathway" binding;damaged DNA binding;DNA binding;nucleic acid binding cell part;CUL4 RING ubiquitin ligase complex;Cul4A-RING ubiquitin ligase complex;Cul4B-RING ubiquitin ligase complex;cullin-RING ubiquitin ligase complex;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;ubiquitin ligase complex Nucleotide excision repair;Ubiquitin mediated proteolysis 2.95E-84 17 25 25 27.1

Q9NSE4;F6SBX2 "Isoleucine--tRNA ligase, mitochondrial" IARS2 ">sp|Q9NSE4|SYIM_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2;>tr|F6SBX2|F6SBX2_HUMAN Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=2 SV=1" -0.16 -0.08 0.12 0.06 -0.03 -0.04 0.10 -0.19 0.092733913 0.023278439 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;isoleucyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;isoleucine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;mitochondrion;organelle;organelle lumen;organelle part "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis" 6.20E-105 2 25 25 32.8

P28838-2;P28838;H0Y9Q1;H0Y983 Cytosol aminopeptidase LAP3 >sp|P28838-2|AMPL_HUMAN Isoform 2 of Cytosol aminopeptidase OS=Homo sapiens GN=LAP3;>sp|P28838|AMPL_HUMAN Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3 0.05 -0.05 -0.01 0.08 -0.51 -0.42 0.04 -0.28 1.058125684 0.312815061 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;ion binding;magnesium ion binding;manganese ion binding;metal ion binding;metalloexopeptidase activity;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding;zinc ion binding" cell part;cytoplasm;cytoplasmic part;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;mitochondrion;nucleus;organelle;organelle part;trans-Golgi network Arginine and proline metabolism;Glutathione metabolism 1.45E-269 4 25 25 61.9

K7EJE8;K7EKE6;Q8N8K8;P36776;F5GZ27;K7ER27;K7ER56;K7ERR6;K7EQF8 "Lon protease homolog, mitochondrial"LONP1 ">tr|K7EJE8|K7EJE8_HUMAN Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=3 SV=1;>tr|K7EKE6|K7EKE6_HUMAN Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=3 SV=1;>tr|Q8N8K8|Q8N8K8_HUMAN Lon protease homolog, mitochondrial OS=Hom" -0.21 -0.10 0.05 -0.05 0.10 -0.15 -0.65 -0.23 0.388854428 0.157657962 aging;catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;developmental process;DNA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule catabolic process;macromolecule metabolic process;metabolic process;misfolded or incompletely synthesized protein catabolic process;mitochondrial DNA metabolic process;mitochondrion organization;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;oxidation-dependent protein catabolic process;primary metabolic process;protein catabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein metabolic process;protein oligomerization;proteolysis;proteolysis involved in cellular protein catabolic process;response to aluminum ion;response to chemical stimulus;response to endogenous stimulus;response to hormone stimulus;response to hypoxia;response to inorganic substance;response to metal ion;response to organic substance;response to oxidative stress;response to oxygen levels;response to stimulus;response to stress "adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent peptidase activity;binding;catalytic activity;DNA binding;endopeptidase activity;G-quadruplex DNA binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;mitochondrial heavy strand promoter anti-sense binding;mitochondrial light strand promoter anti-sense binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;peptidase activity;peptidase activity, acting on L-amino acid peptides;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA binding;sequence-specific DNA binding;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity;single-stranded DNA binding;single-stranded RNA binding;structure-specific DNA binding;transcription regulatory region DNA binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle lumen;organelle part 1.41E-118 9 25 25 42.8

P25205;B4DWW4;J3KQ69;Q7Z6P5 DNA replication licensing factor MCM3 MCM3 >sp|P25205|MCM3_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3;>tr|B4DWW4|B4DWW4_HUMAN DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=2 SV=1;>tr|J3KQ69|J3KQ69_HUMAN DNA replication licensing factor MCM3 OS=H 0.15 0.01 -0.04 0.14 0.47 -0.47 -0.81 -1.23 0.672915176 0.574145259 biological regulation;biosynthetic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA replication;DNA strand elongation;DNA strand elongation involved in DNA replication;DNA-dependent DNA replication initiation;G1/S transition of mitotic cell cycle;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular process;S phase;S phase of mitotic cell cycle "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;DNA binding;DNA helicase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" alpha DNA polymerase:primase complex;cell part;centrosome;chromosomal part;cytoplasmic part;cytoskeletal part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;MCM complex;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear chromosome part;nuclear part;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle part;perinuclear region of cytoplasm;protein complex Cell cycle;Cell cycle - yeast;DNA replication;Meiosis - yeast 6.88E-200 4 25 25 34.8

O14974;O14974-4;O14974-3;O14974-5;O14974-2;F8VZN8;H0YHI8;H0YIM2;H0YIS3;H0YIS4;F8VW28;H0YHL8;H0YIL7 Protein phosphatase 1 regulatory subunit 12A PPP1R12A >sp|O14974|MYPT1_HUMAN Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1;>sp|O14974-4|MYPT1_HUMAN Isoform 4 of Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A;>sp|O14974-3|MYPT1_HUMAN Isoform 3 of P 0.01 0.07 0.29 0.07 0.23 0.18 0.13 -0.06 0.040844594 -0.010736145 "biological regulation;cell cycle phase;cell cycle process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;centrosome organization;dephosphorylation;G2/M transition of mitotic cell cycle;macromolecule metabolic process;macromolecule modification;metabolic process;microtubule organizing center organization;mitosis;nuclear division;organelle fission;organelle organization;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell adhesion;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of dephosphorylation;regulation of gene expression;regulation of hydrolase activity;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of myosin-light-chain-phosphatase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transport" 14-3-3 protein binding;binding;enzyme inhibitor activity;enzyme regulator activity;molecular transducer activity;phosphatase regulator activity;protein binding;signal transducer activity cell part;centrosome;chromosomal part;contractile fiber;cytoplasmic part;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;protein complex;protein serine/threonine phosphatase complex;PTW/PP1 phosphatase complex Focal adhesion;Long-term potentiation;Regulation of actin cytoskeleton;Vascular smooth muscle contraction 1.14E-258 13 25 25 26.9

O43242;B4DT72;H0YGV8 26S proteasome non-ATPase regulatory subunit 3PSMD3 >sp|O43242|PSMD3_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2;>tr|B4DT72|B4DT72_HUMAN 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=2 SV=1 0.13 0.00 -0.23 -0.14 0.14 0.03 0.04 -0.12 0.353472086 -0.08368273 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" enzyme regulator activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome accessory complex;proteasome complex;protein complex Proteasome 1.01E-243 3 25 25 49.1

P10586-2;P10586;H0Y6Z7;H0Y4H1;H0Y7Z9;F2Z3B8;H0Y380;A2A437;P23468-3;F5GWY7;F5GWT7;P23468-5;P23468-4;F5GWR7;P23468-6;G3XAD5;G3XAE2;P23468;P23468-2;Q13332-7;Q13332-5;Q13332-6;Q13332-3;G8JL96;Q13332-4;Q13332-2;Q13332;E9PDC5 Receptor-type tyrosine-protein phosphatase F PTPRF >sp|P10586-2|PTPRF_HUMAN Isoform 2 of Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF;>sp|P10586|PTPRF_HUMAN Receptor-type tyrosine-protein phosphatase F OS=Homo sapiens GN=PTPRF PE=1 SV=2;>tr|H0Y6Z7|H0Y6Z7_HUMAN Receptor-type tyrosin -0.28 -0.14 0.28 0.12 -1.50 -1.11 -0.07 -0.60 1.029095629 0.814374579 anatomical structure development;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cerebellum development;cerebral cortex development;corpus callosum development;dephosphorylation;developmental process;enzyme linked receptor protein signaling pathway;heterophilic cell-cell adhesion;hippocampus development;macromolecule metabolic process;macromolecule modification;membrane organization;metabolic process;neuron differentiation;peptidyl-tyrosine dephosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;positive regulation of biological process;positive regulation of cell development;positive regulation of cell differentiation;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of dendrite morphogenesis;positive regulation of developmental process;positive regulation of neurogenesis;presynaptic membrane assembly;presynaptic membrane organization;primary metabolic process;protein dephosphorylation;protein metabolic process;protein modification process;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of dendrite development;regulation of dendrite morphogenesis;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;response to stimulus;signal transduction;spinal cord development;synapse assembly;synapse organization;transmembrane receptor protein tyrosine phosphatase signaling pathway "binding;carbohydrate binding;catalytic activity;cell adhesion molecule binding;glycosaminoglycan binding;heparin binding;hydrolase activity;hydrolase activity, acting on ester bonds;molecular transducer activity;pattern binding;phosphatase activity;phosphoprotein phosphatase activity;phosphoric ester hydrolase activity;polysaccharide binding;protein binding;protein tyrosine phosphatase activity;receptor activity;receptor binding;signal transducer activity;signaling receptor activity;transmembrane receptor protein phosphatase activity;transmembrane receptor protein tyrosine phosphatase activity;transmembrane signaling receptor activity" cell part;integral to membrane;integral to plasma membrane;intrinsic to membrane;intrinsic to plasma membrane;membrane part;plasma membrane part Adherens junction;Cell adhesion molecules (CAMs);Insulin signaling pathway 3.30E-140 28 25 25 21.2

Q27J81-2;Q27J81;H7BXE4;Q27J81-3 Inverted formin-2 INF2 >sp|Q27J81-2|INF2_HUMAN Isoform 2 of Inverted formin-2 OS=Homo sapiens GN=INF2;>sp|Q27J81|INF2_HUMAN Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2 -0.11 0.14 0.04 0.29 -0.45 -0.07 -0.25 0.01 0.901950157 0.280697003 actin cytoskeleton organization;actin filament-based process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization cell part;cytoplasmic part;endoplasmic reticulum;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm 2.73E-213 4 26 25 28.8

Q8N163;Q8N163-2;H0YB24;G3V119;E5RFJ3;E5RHJ4;E5RGU7;H0YC69;H0YC58;E5RHH8 DBIRD complex subunit KIAA1967 KIAA1967 >sp|Q8N163|K1967_HUMAN DBIRD complex subunit KIAA1967 OS=Homo sapiens GN=KIAA1967 PE=1 SV=2;>sp|Q8N163-2|K1967_HUMAN Isoform 2 of DBIRD complex subunit KIAA1967 OS=Homo sapiens GN=KIAA1967;>tr|H0YB24|H0YB24_HUMAN DBIRD complex subunit KIAA1967 (Fragment) O -0.28 0.61 0.15 0.70 -0.10 0.09 -1.27 -0.19 0.745868536 0.663364612 "apoptosis;biological regulation;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;primary metabolic process;programmed cell death;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription elongation, DNA-dependent;regulation of transcription, DNA-dependent;RNA metabolic process;RNA processing;RNA splicing" basal RNA polymerase II transcription machinery binding;basal transcription machinery binding;binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;protein binding;RNA polymerase binding;RNA polymerase core enzyme binding;RNA polymerase II core binding cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nucleus;organelle;organelle lumen;organelle part 1.14E-185 10 26 25 39.4

P35241;P35241-5;P35241-4;P35241-2;H0YE16;P35241-3;E9PNV3;E9PQ82;E9PKN5 Radixin RDX >sp|P35241|RADI_HUMAN Radixin OS=Homo sapiens GN=RDX PE=1 SV=1;>sp|P35241-5|RADI_HUMAN Isoform 5 of Radixin OS=Homo sapiens GN=RDX;>sp|P35241-4|RADI_HUMAN Isoform 4 of Radixin OS=Homo sapiens GN=RDX 0.07 -0.02 0.02 -0.03 0.25 0.25 0.26 -0.11 0.70779926 -0.154136273 actin filament capping;apical protein localization;asymmetric protein localization;biological regulation;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;localization;macromolecule localization;microvillus assembly;microvillus organization;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;protein localization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization apical part of cell;cell division site part;cell part;cell projection;cleavage furrow;cytoplasm;cytoskeleton;extrinsic to membrane;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;membrane;membrane part;microvillus;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;ruffle;stereocilium Regulation of actin cytoskeleton 0 9 45 25 55.7

F5GWX5;Q14839;Q14839-2;Q8TDI0;Q5TG85;K7EMY3;Q12873-2;Q12873;Q12873-3;F2Z2R5;F5H6N4;I3L229;H7C3H7;H7C0J3 Chromodomain-helicase-DNA-binding protein 4 CHD4 >tr|F5GWX5|F5GWX5_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=2 SV=1;>sp|Q14839|CHD4_HUMAN Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2;>sp|Q14839-2|CHD4_HUMAN Isoform 2 of Chromodomain-heli 0.08 0.34 -0.05 0.21 0.05 -0.47 -0.95 -0.59 1.181676243 0.634027503 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;centrosome organization;chromatin modification;chromatin organization;chromosome organization;cytoskeleton organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;spindle organization;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;binding;catalytic activity;cation binding;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transition metal ion binding;zinc ion binding" cell part;centrosome;chromatin remodeling complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;histone deacetylase complex;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;nucleus;NuRD complex;organelle;organelle part;protein complex;transcriptional repressor complex 2.31E-102 14 26 26 20.6

Q16643;A8MV58;Q16643-2;D6R9W4;F8W9Z3;D6RFI1;D6R9Q9;D6RCR4 Drebrin DBN1 >sp|Q16643|DREB_HUMAN Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4;>tr|A8MV58|A8MV58_HUMAN Drebrin OS=Homo sapiens GN=DBN1 PE=2 SV=1;>sp|Q16643-2|DREB_HUMAN Isoform 2 of Drebrin OS=Homo sapiens GN=DBN1;>tr|D6R9W4|D6R9W4_HUMAN Drebrin (Fragment) OS=Homo sapien -0.52 0.65 -0.17 0.99 1.11 1.85 -0.12 1.39 0.634958519 -0.820198832 actin cytoskeleton organization;actin filament organization;actin filament-based process;biological regulation;cell communication;cell communication by chemical coupling;cell communication by electrical coupling;cell differentiation;cell proliferation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;developmental process;generation of neurons;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;neural precursor cell proliferation;neurogenesis;organelle organization;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of dendrite development;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neurological system process;regulation of neuron differentiation;regulation of neuron projection development;regulation of neuronal synaptic plasticity;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transmission of nerve impulse actin binding;binding;cytoskeletal protein binding;profilin binding;protein binding actin cytoskeleton;actomyosin;cell junction;cell part;cell projection;cell-cell junction;cytoplasm;cytoskeletal part;cytoskeleton;dendrite;gap junction;intracellular;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;neuron projection;non-membrane-bounded organelle;organelle;organelle part;plasma membrane 4.27E-130 8 26 26 49.3

Q92499 ATP-dependent RNA helicase DDX1 DDX1 >sp|Q92499|DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 0.05 0.08 0.02 0.03 0.13 0.08 -0.02 -0.10 0.130826298 0.019348766 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;developmental process;DNA conformation change;DNA duplex unwinding;DNA geometric change;DNA metabolic process;DNA repair;double-strand break repair;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;multicellular organismal development;multicellular organismal process;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;response to biotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to dsRNA;response to exogenous dsRNA;response to organic substance;response to other organism;response to stimulus;response to stress;response to virus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA biosynthetic process;RNA metabolic process;spliceosome assembly;transcription, DNA-dependent" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;binding;catalytic activity;chromatin binding;DNA binding;DNA/RNA helicase activity;double-stranded RNA binding;exonuclease activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;hydrolase activity, acting on ester bonds;mRNA binding;nuclease activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;poly(A) RNA binding;poly-purine tract binding;protein binding transcription factor activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;single-stranded RNA binding;transcription cofactor activity;transcription factor binding transcription factor activity" cell part;cleavage body;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear body;nuclear part;nucleoplasm part;organelle;organelle part;protein complex;ribonucleoprotein complex;RNA granule;stress granule;tRNA-splicing ligase complex 2.50E-259 1 26 26 39.2

P43304;P43304-2;F8W6E4;F5GYK7 "Glycerol-3-phosphate dehydrogenase, mitochondrial" GPD2 ">sp|P43304|GPDM_HUMAN Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2 PE=1 SV=3;>sp|P43304-2|GPDM_HUMAN Isoform 2 of Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2;>tr|F8W6E4|F8W6E4_HUMAN Glycerol-3-phos" 0.23 0.26 0.14 0.00 0.05 0.00 -0.99 -0.50 0.877384603 0.514087573 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;alditol catabolic process;alditol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;gluconeogenesis;glucose metabolic process;glycerol catabolic process;glycerol metabolic process;glycerol-3-phosphate metabolic process;hexose biosynthetic process;hexose metabolic process;lipid metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;organophosphate metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;polyol catabolic process;polyol metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "binding;calcium ion binding;catalytic activity;cation binding;glycerol-3-phosphate dehydrogenase activity;ion binding;metal ion binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor;sn-glycerol-3-phosphate:ubiquinone oxidoreductase activity;sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity" cell part;cytoplasmic part;glycerol-3-phosphate dehydrogenase complex;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle membrane;organelle part;protein complex Glycerophospholipid metabolism 4.27E-135 4 26 26 48.7

P51659;E7EWE5;P51659-3;P51659-2;E7ER27;G5E9S2;E7ET17;E7EPL9 Peroxisomal multifunctional enzyme type 2;(3R)-hydroxyacyl-CoA dehydrogenase;Enoyl-CoA hydratase 2 HSD17B4 >sp|P51659|DHB4_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3;>tr|E7EWE5|E7EWE5_HUMAN Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=2 SV=1;>sp|P51659-3|DHB4_HUMAN Isoform 3 of Peroxisomal mul 0.24 -0.03 -0.55 -0.35 0.69 0.54 0.48 0.12 1.220399942 -0.627359413 anatomical structure development;androgen metabolic process;bile acid biosynthetic process;bile acid metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cell development;cellular biosynthetic process;cellular catabolic process;cellular developmental process;cellular hormone metabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;developmental process;developmental process involved in reproduction;estrogen metabolic process;fatty acid beta-oxidation;fatty acid beta-oxidation using acyl-CoA oxidase;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;hormone metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid catabolic process;organic acid metabolic process;oxidation-reduction process;oxoacid metabolic process;primary metabolic process;regulation of biological quality;regulation of hormone levels;reproductive process;Sertoli cell development;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;very long-chain fatty acid metabolic process "3alpha,7alpha,12alpha-trihydroxy-5beta-cholest-24-enoyl-CoA hydratase activity;3-hydroxyacyl-CoA dehydrogenase activity;binding;carbon-oxygen lyase activity;catalytic activity;hydro-lyase activity;identical protein binding;isomerase activity;lipid binding;long-chain-enoyl-CoA hydratase activity;lyase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;protein binding;protein dimerization activity;protein homodimerization activity;steroid binding;sterol binding" cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;membrane-enclosed lumen;microbody;microbody lumen;microbody membrane;microbody part;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;peroxisomal matrix;peroxisomal membrane;peroxisomal part;peroxisome Peroxisome;Primary bile acid biosynthesis 9.28E-194 8 26 26 43.5

O15067;F5GWT9;H0YGH1;J3QSG0;J3QSH6;J3KTQ5;J3KTL4;J3KT98 Phosphoribosylformylglycinamidine synthase PFAS >sp|O15067|PUR4_HUMAN Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4;>tr|F5GWT9|F5GWT9_HUMAN Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=2 SV=1 0.34 -0.08 0.15 -0.01 0.34 -0.21 0.14 -0.74 0.340465737 0.217032336 amine metabolic process;biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;'de novo' IMP biosynthetic process;glutamine family amino acid metabolic process;glutamine metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;response to chemical stimulus;response to drug;response to stimulus;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbon-nitrogen ligase activity, with glutamine as amido-N-donor;catalytic activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleotide binding;phosphoribosylformylglycinamidine synthase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic part;cytosol;intracellular part Purine metabolism 4.83E-229 8 26 26 28.6

E9PD53;Q9NTJ3;Q9NTJ3-2;C9JR83;C9JVD8;C9J578;C9J9E4;C9JWF0;C9IYK2;C9JJ64 Structural maintenance of chromosomes protein;Structural maintenance of chromosomes protein 4 SMC4 >tr|E9PD53|E9PD53_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens GN=SMC4 PE=2 SV=1;>sp|Q9NTJ3|SMC4_HUMAN Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2;>sp|Q9NTJ3-2|SMC4_HUMAN Isoform 2 of Structural 0.43 0.14 -0.07 -0.25 -0.17 -0.82 -0.32 -0.65 1.111600085 0.551727692 cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome condensation;chromosome organization;chromosome organization involved in meiosis;chromosome segregation;DNA conformation change;DNA metabolic process;DNA packaging;DNA recombination;DNA repair;kinetochore organization;M phase;M phase of mitotic cell cycle;macromolecular complex subunit organization;macromolecule metabolic process;meiotic chromosome condensation;meiotic chromosome segregation;metabolic process;mitotic chromosome condensation;mitotic prometaphase;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;response to DNA damage stimulus;response to stimulus;response to stress;sister chromatid cohesion adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;chromosomal part;chromosome;condensin complex;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex Cell cycle - yeast 6.24E-106 10 26 26 25.7

P17655;P17655-2;A3QK37;REV__P49638 Calpain-2 catalytic subunit CAPN2 >sp|P17655|CAN2_HUMAN Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6;>sp|P17655-2|CAN2_HUMAN Isoform 2 of Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 0.19 -0.12 -0.07 -0.01 0.27 0.02 0.33 -0.11 0.438219808 -0.132346633 anatomical structure development;anatomical structure formation involved in morphogenesis;blastocyst development;cellular process;developmental process;macromolecule metabolic process;metabolic process;myoblast fusion;primary metabolic process;protein autoprocessing;protein maturation;protein metabolic process;protein processing;proteolysis;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;syncytium formation;syncytium formation by plasma membrane fusion "binding;calcium ion binding;calcium-dependent cysteine-type endopeptidase activity;catalytic activity;cation binding;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;chromatin;chromosomal part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane Alzheimer's disease;Apoptosis;Focal adhesion;Protein processing in endoplasmic reticulum 1.59E-194 4 27 26 51.6

O43776;B4DN60;K7EIU7;B4DG16;K7EQ35;K7EJ19;K7EPK2;K7EMQ6;REV__H7C110;REV__Q13315 "Asparagine--tRNA ligase, cytoplasmic" NARS ">sp|O43776|SYNC_HUMAN Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1;>tr|B4DN60|B4DN60_HUMAN Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=2 SV=1"0.09 -0.06 0.07 -0.08 -0.04 -0.22 0.36 -0.28 0.113020952 0.048371262 amine metabolic process;amino acid activation;asparaginyl-tRNA aminoacylation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;asparagine-tRNA ligase activity;ATP binding;binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle Aminoacyl-tRNA biosynthesis 9.52E-303 10 27 26 46.7

Q02790;F5H1U3;H0YFG2;F5H120;REV__P07333 "Peptidyl-prolyl cis-trans isomerase FKBP4;Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed" FKBP4 >sp|Q02790|FKBP4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 0.15 0.04 0.11 0.03 -0.50 -0.69 0.04 -0.43 1.244898181 0.477527106 anatomical structure development;androgen receptor signaling pathway;biological regulation;cation transport;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;cellular response to stimulus;chaperone-mediated protein folding;copper ion transport;developmental process;developmental process involved in reproduction;embryo implantation;establishment of localization;gland development;intracellular receptor mediated signaling pathway;ion transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;macromolecule modification;male sex differentiation;metabolic process;metal ion transport;negative regulation of biological process;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of microtubule polymerization;negative regulation of microtubule polymerization or depolymerization;negative regulation of neuron projection development;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein polymerization;organ development;peptidyl-amino acid modification;peptidyl-proline modification;primary metabolic process;prostate gland development;protein complex assembly;protein complex localization;protein complex subunit organization;protein folding;protein localization;protein metabolic process;protein modification process;protein peptidyl-prolyl isomerization;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of developmental process;regulation of microtubule cytoskeleton organization;regulation of microtubule polymerization;regulation of microtubule polymerization or depolymerization;regulation of microtubule-based process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of organelle organization;regulation of protein complex assembly;regulation of protein polymerization;reproductive process;reproductive structure development;response to stimulus;sex differentiation;signal transduction;steroid hormone receptor complex assembly;steroid hormone receptor signaling pathway;transition metal ion transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;binding, bridging;catalytic activity;cis-trans isomerase activity;drug binding;FK506 binding;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;isomerase activity;macrolide binding;nucleotide binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" axon part;axonal growth cone;cell body;cell part;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;growth cone;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule;mitochondrion;neuronal cell body;nucleus;organelle;organelle part;perinuclear region of cytoplasm;protein complex;site of polarized growth 1.33E-294 5 27 27 63.2

Q1KMD3;H3BQZ7 Heterogeneous nuclear ribonucleoprotein U-like protein 2 HNRNPUL2;hCG_2044799 >sp|Q1KMD3|HNRL2_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1;>tr|H3BQZ7|H3BQZ7_HUMAN HCG2044799 OS=Homo sapiens GN=hCG_2044799 PE=4 SV=1 -0.37 1.01 0.13 1.13 0.05 0.54 -1.37 0.38 0.41746058 0.576768611 binding;nucleic acid binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.37E-170 2 27 27 40

P36871;P36871-2;P36871-3 Phosphoglucomutase-1 PGM1 >sp|P36871|PGM1_HUMAN Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3;>sp|P36871-2|PGM1_HUMAN Isoform 2 of Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1;>sp|P36871-3|PGM1_HUMAN Isoform 3 of Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 -0.23 -0.23 -0.33 0.15 -0.86 -0.23 0.52 -0.05 0.006743176 -0.006372242 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide biosynthetic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;galactose catabolic process;galactose metabolic process;generation of precursor metabolites and energy;glucan biosynthetic process;glucan catabolic process;glucan metabolic process;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycogen biosynthetic process;glycogen catabolic process;glycogen metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;oxidation-reduction process;polysaccharide biosynthetic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process "binding;catalytic activity;cation binding;intramolecular transferase activity;intramolecular transferase activity, phosphotransferases;ion binding;isomerase activity;magnesium ion binding;metal ion binding;phosphoglucomutase activity" actin cytoskeleton;cell part;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle Amino sugar and nucleotide sugar metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway;Purine metabolism;Starch and sucrose metabolism;Streptomycin biosynthesis 7.24E-269 3 27 27 60.5

Q01970;Q01970-2 "1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3" PLCB3 ">sp|Q01970|PLCB3_HUMAN 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 PE=1 SV=2;>sp|Q01970-2|PLCB3_HUMAN Isoform 2 of 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3" 0.11 -0.10 0.26 0.05 -0.35 -0.36 0.23 -0.35 0.751007524 0.287102899 biological regulation;catabolic process;cell communication;cell-cell signaling;cellular process;cellular response to stimulus;inositol phosphate metabolic process;intracellular signal transduction;lipid catabolic process;lipid metabolic process;metabolic process;organophosphate metabolic process;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of blood pressure;regulation of cellular process;regulation of systemic arterial blood pressure;response to stimulus;signal transduction;signaling;synaptic transmission "binding;calcium ion binding;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;lipase activity;metal ion binding;molecular transducer activity;phosphatidylinositol phospholipase C activity;phospholipase activity;phospholipase C activity;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;signal transducer activity" cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;membrane;protein complex African trypanosomiasis;Alzheimer's disease;Amoebiasis;Calcium signaling pathway;Chagas disease (American trypanosomiasis);Chemokine signaling pathway;Endocrine and other factor-regulated calcium reabsorption;Gap junction;Gastric acid secretion;GnRH signaling pathway;Huntington's disease;Inositol phosphate metabolism;Long-term depression;Long-term potentiation;Melanogenesis;Pancreatic secretion;Phosphatidylinositol signaling system;Phototransduction - fly;Salivary secretion;Vascular smooth muscle contraction;Wnt signaling pathway 2.28E-248 2 27 27 33.4

O14980;C9JKM9;C9J673;C9IZS4;C9JQ02;C9JV99;F8WF71;C9JF49;C9IYM2;H7BZC5 Exportin-1 XPO1 >sp|O14980|XPO1_HUMAN Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1 0.07 -0.06 0.01 0.00 -0.10 -0.29 -0.08 -0.31 1.261084306 0.198979745 "anaphase;biological regulation;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular response to stimulus;enzyme linked receptor protein signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;gene expression;intracellular protein transport;intracellular transport;localization;M phase;M phase of mitotic cell cycle;macromolecule localization;macromolecule metabolic process;metabolic process;mitotic anaphase;mitotic prometaphase;mRNA metabolic process;mRNA transport;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;nitrogen compound metabolic process;nuclear export;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;primary metabolic process;protein export from nucleus;protein localization;protein localization to nucleus;protein localization to organelle;protein targeting;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of catabolic process;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of centrosome cycle;regulation of centrosome duplication;regulation of cytoskeleton organization;regulation of establishment of protein localization;regulation of gene expression;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of microtubule cytoskeleton organization;regulation of microtubule-based process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of organelle organization;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein export from nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transport;reproductive process;response to chemical stimulus;response to drug;response to stimulus;RNA metabolic process;RNA transport;signal transduction;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway;transport;viral infectious cycle;viral reproductive process" binding;nucleic acid binding;protein transporter activity;RNA binding;substrate-specific transporter activity;transporter activity annulate lamellae;Cajal body;cell part;chromosomal part;cytoplasmic part;cytosol;envelope;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nuclear body;nuclear envelope;nuclear part;nuclear pore;nucleolus;nucleoplasm;nucleoplasm part;nucleus;organelle;organelle envelope;organelle part;pore complex;protein complex;ribonucleoprotein complex Ribosome biogenesis in eukaryotes;RNA transport 0 10 27 27 32

O95573;H7BYZ7;H7C260;F5H062;F5GWH2;C9JC11 Long-chain-fatty-acid--CoA ligase 3 ACSL3 >sp|O95573|ACSL3_HUMAN Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3 -0.05 -0.08 -0.39 -0.20 0.65 0.59 0.04 0.12 1.245965221 -0.531954597 anatomical structure development;biological regulation;biosynthetic process;brain development;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;developmental process;fatty acid biosynthetic process;fatty acid metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monocarboxylic acid metabolic process;multicellular organismal process;organ development;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;plasma lipoprotein particle assembly;plasma lipoprotein particle organization;positive regulation of biological process;positive regulation of cellular process;positive regulation of Golgi to plasma membrane protein transport;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of protein transport;positive regulation of secretion;positive regulation of transport;primary metabolic process;protein-lipid complex assembly;protein-lipid complex subunit organization;regulation of biological process;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of Golgi to plasma membrane protein transport;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of protein localization;regulation of protein transport;regulation of secretion;regulation of transport;regulation of vesicle-mediated transport;response to chemical stimulus;response to external stimulus;response to extracellular stimulus;response to nutrient;response to nutrient levels;response to organic cyclic compound;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule metabolic process;very-low-density lipoprotein particle assembly "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;fatty acid ligase activity;ligase activity;ligase activity, forming carbon-sulfur bonds;long-chain fatty acid-CoA ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding"cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lipid particle;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane;perinuclear region of cytoplasm;peroxisomal membrane;peroxisomal part Adipocytokine signaling pathway;Fatty acid metabolism;Peroxisome;PPAR signaling pathway7.26E-223 6 30 27 49.4

P40227;B4DPJ8;P40227-2 T-complex protein 1 subunit zeta CCT6A >sp|P40227|TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3;>tr|B4DPJ8|B4DPJ8_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=2 SV=1;>sp|P40227-2|TCPZ_HUMAN Isoform 2 of T-complex protein 1 subunit zeta OS=H 0.16 0.03 0.00 -0.05 0.00 -0.33 -0.01 -0.41 0.835118211 0.223614543 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic processadenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular organelle part;intracellular part;macromolecular complex;microtubule;organelle part;protein complex 0 3 31 27 55.7

P27797;K7EJB9;K7EL50;K7EM77 Calreticulin CALR >sp|P27797|CALR_HUMAN Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1;>tr|K7EJB9|K7EJB9_HUMAN Calreticulin (Fragment) OS=Homo sapiens GN=CALR PE=3 SV=1 -0.09 -0.05 -0.75 -0.26 0.44 0.03 0.39 0.00 1.072668214 -0.503144891 "actin cytoskeleton organization;actin filament-based process;activation of signaling protein activity involved in unfolded protein response;aging;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;carbohydrate metabolic process;cardiac cell differentiation;cardiac muscle cell differentiation;cell aging;cell cycle arrest;cell cycle process;cell differentiation;cellular carbohydrate metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to inorganic substance;cellular response to lithium ion;cellular response to metal ion;cellular response to stimulus;cellular response to stress;cellular senescence;cortical actin cytoskeleton organization;cortical cytoskeleton organization;corticosteroid receptor signaling pathway;cytoskeleton organization;developmental process;establishment of localization;establishment of localization in cell;establishment of protein localization;gamete generation;glucocorticoid receptor signaling pathway;glycosylation;immune system process;intracellular protein transport;intracellular receptor mediated signaling pathway;intracellular transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule glycosylation;macromolecule localization;macromolecule metabolic process;macromolecule modification;maintenance of location;male gamete generation;metabolic process;multicellular organismal process;multicellular organismal reproductive process;muscle cell differentiation;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell cycle;negative regulation of cell differentiation;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of developmental process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of retinoic acid receptor signaling pathway;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of steroid hormone receptor signaling pathway;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;nuclear export;nuclear transport;nucleocytoplasmic transport;organelle organization;peptide antigen assembly with MHC class I protein complex;peptide antigen assembly with MHC protein complex;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell cycle;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of chemotaxis;positive regulation of dendritic cell chemotaxis;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of endocytosis;positive regulation of gene expression;positive regulation of hydrolase activity;positive regulation of immune system process;positive regulation of kinase activity;positive regulation of leukocyte chemotaxis;positive regulation of leukocyte migration;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitrogen compound metabolic process;positive regulation of nuclease activity;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phagocytosis;positive regulation of protein kinase activity;positive regulation of response to external stimulus;positive regulation of response to stimulus;positive regulation of transferase activity;positive regulation of transport;posttranscriptional regulation of gene expression;post-translational protein modification;primary metabolic process;protein complex assembly;protein complex subunit organization;protein export from nucleus;protein folding;protein glycosylation;protein localization;protein localization to nucleus;protein localization to organelle;protein maturation;protein maturation by protein folding;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein stabilization;protein targeting;protein transport;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catalytic activity;regulation of cell communication;regulation of cell cycle;regulation of cell cycle process;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chemotaxis;regulation of dendritic cell chemotaxis;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA replication;regulation of endocytosis;regulation of gene expression;regulation of hydrolase activity;regulation of immune system process;regulation of kinase activity;regulation of leukocyte chemotaxis;regulation of leukocyte migration;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of meiosis;regulation of meiotic cell cycle;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of phagocytosis;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein stability;regulation of response to external stimulus;regulation of response to stimulus;regulation of retinoic acid receptor signaling pathway;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of steroid hormone receptor signaling pathway;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of transport;regulation of vesicle-mediated transport;reproductive process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to hormone stimulus;response to inorganic substance;response to lithium ion;response to metal ion;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;sequestering of calcium ion;sequestering of metal ion;signal transduction;spermatogenesis;steroid hormone receptor signaling pathway;striated muscle cell differentiation;transport"androgen receptor binding;binding;calcium ion binding;carbohydrate binding;cation binding;chaperone binding;complement binding;complement component C1q binding;DNA binding;hormone binding;hormone receptor binding;ion binding;iron ion binding;metal ion binding;mRNA binding;nuclear hormone receptor binding;nucleic acid binding;opsonin binding;peptide binding;protein binding;protein binding involved in protein folding;receptor binding;RNA binding;steroid hormone receptor binding;transition metal ion binding;unfolded protein binding;zinc ion binding acrosomal vesicle;cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;external side of plasma membrane;extracellular matrix;extracellular region part;extracellular space;Golgi apparatus;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;MHC class I peptide loading complex;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;plasma membrane part;polysome;protein complex;proteinaceous extracellular matrix;ribonucleoprotein complex;sarcoplasmic reticulum lumen;stored secretory granule;vesicle Antigen processing and presentation;Chagas disease (American trypanosomiasis);Phagosome;Protein processing in endoplasmic reticulum 0 4 28 28 71.9

P48147 Prolyl endopeptidase PREP >sp|P48147|PPCE_HUMAN Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2 0.11 -0.18 0.05 -0.08 -0.03 0.06 0.64 0.11 0.560136472 -0.218693323 macromolecule metabolic process;metabolic process;primary metabolic process;protein metabolic process;proteolysis "catalytic activity;endopeptidase activity;exopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type exopeptidase activity;serine-type peptidase activity" cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.08E-270 1 28 28 47.7

Q92945;M0R0I5;M0QYH3;M0QXW7;M0R0C6;M0R3J3;M0QYG1;M0R251;M0R263 Far upstream element-binding protein 2 KHSRP >sp|Q92945|FUBP2_HUMAN Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 -0.02 0.07 0.15 0.16 0.41 -0.14 -0.74 -0.44 0.538767553 0.319243547 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;establishment of localization;establishment of RNA localization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA transport;transcription, DNA-dependent;transport" binding;DNA binding;nucleic acid binding;RNA binding cell part;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part;ribonucleoprotein complex;RNA granule;stress granule 4.97E-248 9 30 28 52.3

P06576;F8VPV9;H0YH81;F8W079;F8W0P7;H0YI37;F8VQY0 "ATP synthase subunit beta, mitochondrial;ATP synthase subunit beta" ATP5B ">sp|P06576|ATPB_HUMAN ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3;>tr|F8VPV9|F8VPV9_HUMAN ATP synthase subunit beta OS=Homo sapiens GN=ATP5B PE=2 SV=1;>tr|H0YH81|H0YH81_HUMAN ATP synthase subunit beta (Fragment) OS=Homo sapi" -0.34 0.13 0.00 0.29 0.06 0.04 -1.14 -0.33 0.489679162 0.365915024 "anatomical structure formation involved in morphogenesis;angiogenesis;ATP biosynthetic process;ATP hydrolysis coupled proton transport;ATP metabolic process;ATP synthesis coupled proton transport;biological regulation;biosynthetic process;cation homeostasis;cation transport;cellular biosynthetic process;cellular cation homeostasis;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular monovalent inorganic cation homeostasis;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;chemical homeostasis;developmental process;electron transport chain;energy coupled proton transport, against electrochemical gradient;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;homeostatic process;hydrogen transport;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;lipid metabolic process;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cell adhesion involved in substrate-bound cell migration;negative regulation of cellular process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of biological quality;regulation of cell adhesion;regulation of cellular pH;regulation of cellular process;regulation of intracellular pH;regulation of pH;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport""active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;cell surface binding;eukaryotic cell surface binding;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;MHC class I protein binding;MHC protein binding;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cell surface;cytoplasmic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrial membrane part;mitochondrial nucleoid;mitochondrial part;mitochondrial proton-transporting ATP synthase, catalytic core;mitochondrion;non-membrane-bounded organelle;nucleoid;organelle;organelle part;plasma membrane;protein complex;proton-transporting ATP synthase complex, catalytic core F(1);proton-transporting ATP synthase, catalytic core;proton-transporting two-sector ATPase complex, catalytic domain"Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 0 7 29 29 76.6

Q8TD16;Q8TD16-2;A8MVZ6;Q96G01-4;Q96G01-3;Q96G01 Protein bicaudal D homolog 2 BICD2 >sp|Q8TD16|BICD2_HUMAN Protein bicaudal D homolog 2 OS=Homo sapiens GN=BICD2 PE=1 SV=1;>sp|Q8TD16-2|BICD2_HUMAN Isoform 2 of Protein bicaudal D homolog 2 OS=Homo sapiens GN=BICD2 0.00 -0.02 0.07 0.03 -0.15 0.44 0.38 0.09 0.525608426 -0.174230555 anatomical structure morphogenesis;biological regulation;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;establishment of localization;establishment of localization in cell;interaction with host;interspecies interaction between organisms;intracellular mRNA localization;intracellular transport;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;metabolic process;microtubule anchoring;microtubule anchoring at microtubule organizing center;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;microtubule-based transport;minus-end-directed organelle transport along microtubule;multi-organism process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;organelle transport along microtubule;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of receptor-mediated endocytosis;positive regulation of transport;primary metabolic process;protein localization;protein localization to organelle;regulation of biological process;regulation of biological quality;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of localization;regulation of receptor-mediated endocytosis;regulation of transport;regulation of vesicle-mediated transport;reproductive process;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;RNA localization;RNA metabolic process;RNA processing;stress granule assembly;transport;viral reproduction;viral reproductive process;virus-host interaction "binding;binding, bridging;cytoskeletal adaptor activity;cytoskeletal protein binding;dynactin binding;dynein binding;enzyme binding;G-protein-coupled receptor binding;GTPase binding;protein binding;protein binding, bridging;proteinase activated receptor binding;Rab GTPase binding;Ras GTPase binding;receptor binding;small GTPase binding;structural constituent of cytoskeleton;structural molecule activity" cell part;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;cytosol;extracellular region part;Golgi apparatus;Golgi apparatus part;host cell cytoplasm part;host cell part;host cell viral assembly compartment;host intracellular membrane-bounded organelle;host intracellular organelle;host intracellular part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;non-membrane-bounded organelle;organelle;organelle part;other organism part;perinuclear region of cytoplasm;plasma membrane;trans-Golgi network;vesicle 9.51E-252 6 29 29 41.6

Q8WX93-3;Q8WX93;Q8WX93-4;Q8WX93-8;Q8WX93-5;Q8WX93-2;Q8WX93-9;Q8WX93-7;H0YA05;F8WA26;D6R9F5;F8WC13;H0Y952;Q8WX93-6;Q86TC9-2;Q86TC9;F5GWA6 Palladin PALLD >sp|Q8WX93-3|PALLD_HUMAN Isoform 3 of Palladin OS=Homo sapiens GN=PALLD;>sp|Q8WX93|PALLD_HUMAN Palladin OS=Homo sapiens GN=PALLD PE=1 SV=3;>sp|Q8WX93-4|PALLD_HUMAN Isoform 4 of Palladin OS=Homo sapiens GN=PALLD;>sp|Q8WX93-8|PALLD_HUMAN Isoform 8 of Palladi -0.32 -0.24 -0.02 0.08 -0.92 -0.16 0.27 0.42 0.02943878 -0.028066576 actin cytoskeleton organization;actin filament-based process;actomyosin structure organization;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;organelle organization;sarcomere organization actinin binding;alpha-actinin binding;binding;cytoskeletal protein binding;muscle alpha-actinin binding;protein binding actin filament;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasmic part;cytoskeletal part;cytoskeleton;focal adhesion;I band;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lamellipodium;macromolecular complex;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;ruffle;Z disc 1.14E-260 17 29 29 39.5

Q8WUF5;K7EN03;K7EPP1 RelA-associated inhibitor PPP1R13L >sp|Q8WUF5|IASPP_HUMAN RelA-associated inhibitor OS=Homo sapiens GN=PPP1R13L PE=1 SV=4 0.05 0.27 0.30 0.16 -1.24 -0.36 -0.14 0.05 0.910053674 0.615701028 "anatomical structure development;anatomical structure morphogenesis;apoptosis;biological regulation;biosynthetic process;camera-type eye development;cardiac chamber morphogenesis;cardiac muscle contraction;cardiac muscle tissue development;cardiac right ventricle morphogenesis;cardiac ventricle morphogenesis;cell death;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;developmental process;embryonic camera-type eye development;embryonic organ development;eye development;growth;hair cycle;homeostatic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;molting cycle;multicellular organism growth;multicellular organismal homeostasis;multicellular organismal process;muscle contraction;muscle system process;muscle tissue development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;post-embryonic development;primary metabolic process;programmed cell death;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;sensory organ development;striated muscle contraction;striated muscle tissue development;system process;tissue development;transcription, DNA-dependent;ventricular cardiac muscle tissue development" binding;protein binding;protein binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding;transcription factor binding transcription factor activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.34E-230 3 29 29 45.5

O95347;O95347-2;Q5T821 Structural maintenance of chromosomes protein 2SMC2 >sp|O95347|SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2;>sp|O95347-2|SMC2_HUMAN Isoform 2 of Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 0.31 0.11 -0.02 -0.05 -0.16 -0.99 -0.24 -0.84 1.191681901 0.642215112 cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome condensation;chromosome organization;chromosome organization involved in meiosis;chromosome segregation;DNA conformation change;DNA metabolic process;DNA packaging;DNA recombination;DNA repair;kinetochore organization;M phase;M phase of mitotic cell cycle;macromolecular complex subunit organization;macromolecule metabolic process;meiotic chromosome condensation;meiotic chromosome segregation;metabolic process;mitotic chromosome condensation;mitotic prometaphase;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;response to DNA damage stimulus;response to stimulus;response to stress;sister chromatid cohesion adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;chromosomal part;chromosome;condensin complex;cytoplasmic part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear chromosome;nuclear part;organelle;organelle part;protein complex Cell cycle - yeast 1.28E-168 3 29 29 31.2

Q9Y5B9;G3V5A4;G3V401;G3V2X0 FACT complex subunit SPT16 SUPT16H >sp|Q9Y5B9|SP16H_HUMAN FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 0.50 0.12 0.09 -0.31 0.40 -0.26 -0.11 -0.78 0.397433676 0.285821818 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromatin organization;chromosome organization;DNA metabolic process;DNA repair;DNA replication;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;nucleosome disassembly;nucleosome organization;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of reproductive process;positive regulation of RNA metabolic process;positive regulation of transcription elongation, DNA-dependent;positive regulation of viral reproduction;positive regulation of viral transcription;primary metabolic process;protein-DNA complex disassembly;protein-DNA complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of reproductive process;regulation of RNA metabolic process;regulation of transcription elongation, DNA-dependent;regulation of transcription, DNA-dependent;regulation of viral reproduction;regulation of viral transcription;reproductive process;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;transcription elongation from RNA polymerase II promoter;transcription elongation, DNA-dependent;viral reproductive process" cell part;chromosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;non-membrane-bounded organelle;nuclear part;nucleoplasm;organelle;organelle part 5.16E-150 4 29 29 30.1

P50991;B7Z9L0;P50991-2;B7Z2F4 T-complex protein 1 subunit delta CCT4 >sp|P50991|TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4;>tr|B7Z9L0|B7Z9L0_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=2 SV=1;>sp|P50991-2|TCPD_HUMAN Isoform 2 of T-complex protein 1 subunit delta OS= 0.27 0.01 -0.06 -0.02 -0.08 -0.34 0.01 -0.40 0.854342703 0.247615054 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic processadenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;centrosome;chaperonin-containing T-complex;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;cytosolic part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane-bounded organelle;membrane-bounded vesicle;microtubule;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;pigment granule;protein complex;vesicle 0 4 30 29 63.5

F5H6E2;O00159-3;O00159;O00159-2;I3L204;I3L501;I3L4D4;I3L3Y6;I3L168;I3L3F5 Unconventional myosin-Ic MYO1C >tr|F5H6E2|F5H6E2_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=2 SV=1;>sp|O00159-3|MYO1C_HUMAN Isoform 3 of Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C;>sp|O00159|MYO1C_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4;> -0.25 0.49 0.10 0.69 0.07 0.42 -0.30 0.37 0.160666898 0.116626579 biological regulation;cellular component organization;cellular component organization or biogenesis;cellular membrane organization;cellular process;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;immune response;immune system process;innate immune response;intracellular protein transport;intracellular transport;membrane organization;mRNA transport;nucleic acid transport;nucleobase-containing compound transport;positive regulation of biological process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of protein targeting to membrane;positive regulation of protein transport;positive regulation of transport;protein targeting;protein targeting to membrane;protein transport;regulation of biological process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of protein localization;regulation of protein targeting to membrane;regulation of protein transport;regulation of tight junction assembly;regulation of transport;response to stimulus;response to stress;RNA transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;motor activity;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" basal plasma membrane;brush border;cell part;cell projection;cell projection membrane;cell projection part;cytoplasmic part;cytoskeletal part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;filamentous actin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;microvillus;microvillus membrane;myosin complex;myosin I complex;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleolus;nucleoplasm;nucleus;organelle;organelle part;plasma membrane part;pore complex;protein complex;stereocilium;stereocilium membrane;unconventional myosin complex;vesicle 1.55E-258 10 30 29 33.1

Q14134;Q14134-2;B7Z8U9;E9PRL4;E9PJ25;H0YCT2;E9PIQ2;H0YD78;E9PI31;E9PPX1;E9PLI4;E9PJ94;H0YCK2;E9PM74;E9PJD4 Tripartite motif-containing protein 29 TRIM29 >sp|Q14134|TRI29_HUMAN Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2;>sp|Q14134-2|TRI29_HUMAN Isoform Beta of Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 -0.36 1.04 0.27 1.17 -1.58 0.03 -0.86 0.24 0.834578585 1.074127221 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription from RNA polymerase II promoter;transcription, DNA-dependent" binding;cation binding;ion binding;metal ion binding;nucleic acid binding transcription factor activity;sequence-specific DNA binding transcription factor activity;transition metal ion binding;zinc ion binding cell part;cytoplasm;intracellular part 4.00E-280 15 34 29 56.3

P78344;D3DQV9;P78344-2;H0Y3P2;H0YCH5;H0YD77;H0YEC5;E9PKF8;H0YE22;H0YD99;H0YEN8;H0YDC0;H0YCF8 Eukaryotic translation initiation factor 4 gamma 2EIF4G2 >sp|P78344|IF4G2_HUMAN Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1;>tr|D3DQV9|D3DQV9_HUMAN Eukaryotic translation initiation factor 4 gamma 2 (Fragment) OS=Homo sapiens GN=EIF4G2 PE=2 SV=1;>sp|P78344-2|IF4G2_HUMAN 0.11 -0.04 0.15 -0.06 0.07 -0.04 0.13 0.03 0.051545497 -0.009659316 biological regulation;cell cycle arrest;cell cycle process;cell death;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;death;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cellular process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;RNA metabolic process;signal transduction "binding;DNA binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex RNA transport;Viral myocarditis 6.69E-193 13 30 30 39.7

Q14974;B7ZAV6;F5H4R7;J3KTM9;J3QR48;J3QKQ5;J3KS06;J3QRG4 Importin subunit beta-1 KPNB1 >sp|Q14974|IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2;>tr|B7ZAV6|B7ZAV6_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=2 SV=1;>tr|F5H4R7|F5H4R7_HUMAN Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=2 SV=1;>tr|J3KTM -0.05 0.02 -0.05 0.03 0.05 0.12 0.09 -0.06 0.540114421 -0.05784368 "biological regulation;catabolic process;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;DNA catabolic process;DNA catabolic process, endonucleolytic;DNA fragmentation involved in apoptotic nuclear change;DNA metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;macromolecule catabolic process;macromolecule metabolic process;metabolic process;nitrogen compound metabolic process;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleic acid metabolic process;nucleic acid phosphodiester bond hydrolysis;nucleobase-containing compound metabolic process;nucleocytoplasmic transport;primary metabolic process;protein import;protein import into nucleus;protein import into nucleus, translocation;protein targeting;protein transport;regulation of biological process;regulation of cellular process;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;ribosomal protein import into nucleus;signal transduction;small molecule metabolic process;transport;viral infectious cycle;viral reproductive process" binding;cation binding;ion binding;metal ion binding;nuclear localization sequence binding;peptide binding;protein transporter activity;signal sequence binding;substrate-specific transporter activity;transition metal ion binding;transporter activity;zinc ion binding cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear membrane;nuclear part;nuclear pore;nucleoplasm;organelle membrane;organelle part;pore complex;protein complex RNA transport 0 8 30 30 37.1

O00515;E9PDI4;H0Y901 Ladinin-1 LAD1 >sp|O00515|LAD1_HUMAN Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2;>tr|E9PDI4|E9PDI4_HUMAN Ladinin-1 OS=Homo sapiens GN=LAD1 PE=2 SV=1 -0.35 0.53 0.08 0.42 -0.37 0.70 -0.45 0.32 0.124206694 0.118532617 structural molecule activity actin cytoskeleton;basement membrane;cell part;cytoskeleton;extracellular matrix part;extracellular region part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 6.45E-174 3 30 30 58.6

Q86V48-2;Q86V48-3;Q86V48;E5RFK8;E5RHU7 Leucine zipper protein 1 LUZP1 >sp|Q86V48-2|LUZP1_HUMAN Isoform 2 of Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1;>sp|Q86V48-3|LUZP1_HUMAN Isoform 3 of Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1;>sp|Q86V48|LUZP1_HUMAN Leucine zipper protein 1 OS=Homo sapiens GN=LUZP1 PE=1 SV -0.10 0.09 0.05 0.12 -0.49 -0.11 -0.07 0.17 0.470232103 0.164737211 anatomical structure development;anatomical structure morphogenesis;artery development;blood vessel development;cardiac septum development;developmental process;embryonic morphogenesis;morphogenesis of an epithelial fold;morphogenesis of an epithelium;neural fold bending;tissue morphogenesis;ventricular septum development cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 2.67E-182 5 30 30 39.1

P54136;P54136-2;F5H3T8;E5RJM9;E5RH09 "Arginine--tRNA ligase, cytoplasmic" RARS ">sp|P54136|SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2;>sp|P54136-2|SYRC_HUMAN Isoform Monomeric of Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS;>tr|F5H3T8|F5H3T8_HUMAN Arginine--tRNA ligase, cytoplasmic OS" -0.02 -0.06 0.00 0.01 -0.07

-0.08 0.20 -0.20 0.082332667 0.020347593 amine metabolic process;amino acid activation;arginyl-tRNA aminoacylation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;aminoacyl-tRNA ligase activity;arginine binding;arginine-tRNA ligase activity;ATP binding;binding;carboxylic acid binding;catalytic activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding" aminoacyl-tRNA synthetase multienzyme complex;cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;mitochondrion;nucleus;organelle;protein complex Aminoacyl-tRNA biosynthesis 6.15E-273 5 30 30 47.7

A0AVT1;A0AVT1-2;H0Y8S8;A0AVT1-3;A0AVT1-4;H0Y9U5 Ubiquitin-like modifier-activating enzyme 6 UBA6 >sp|A0AVT1|UBA6_HUMAN Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1;>sp|A0AVT1-2|UBA6_HUMAN Isoform 2 of Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 0.15 -0.11 -0.05 -0.12 -0.27 -0.12 0.40 0.02 0.087628981 -0.039507193 catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;FAT10 activating enzyme activity;ligase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;small protein activating enzyme activity cell part;cytoplasm;intracellular part Ubiquitin mediated proteolysis 1.34E-138 6 30 30 32.2

Q15029-2;K7EJ81;Q15029;K7EP67;K7EJ74;K7EIV5;K7EIT3 116 kDa U5 small nuclear ribonucleoprotein component EFTUD2 >sp|Q15029-2|U5S1_HUMAN Isoform 2 of 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2;>tr|K7EJ81|K7EJ81_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=4 SV=1;>sp|Q15029|U5S1_HUMAN 116 k -0.07 0.36 0.04 0.36 -0.17 -0.07 -0.77 -0.17 1.015192038 0.467164422 "catabolic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;small molecule metabolic process" "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" Cajal body;catalytic step 2 spliceosome;cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex Spliceosome 4.99E-222 7 31 30 44.2

Q9H2G2;Q9H2G2-2 STE20-like serine/threonine-protein kinase SLK >sp|Q9H2G2|SLK_HUMAN STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1;>sp|Q9H2G2-2|SLK_HUMAN Isoform 2 of STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK 0.14 0.03 0.18 -0.14 -0.02 -0.21 0.35 -0.45 0.293560405 0.1364714 apoptosis;cell death;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;death;macromolecule metabolic process;macromolecule modification;metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;programmed cell death;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;identical protein binding;kinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein dimerization activity;protein homodimerization activity;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasm;intracellular part;membrane;plasma membrane Oocyte meiosis 1.02E-145 2 32 30 32.6

Q9Y678;H0Y8X7;D6RG17;H0Y8G2 Coatomer subunit gamma-1 COPG1 >sp|Q9Y678|COPG1_HUMAN Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1 0.18 0.02 -0.14 -0.09 0.54 0.36 0.24 0.08 1.089198061 -0.310605329 "cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;cytoskeleton-dependent intracellular transport;establishment of Golgi localization;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;microtubule-based movement;microtubule-based process;microtubule-based transport;organelle organization;organelle transport along microtubule;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport" structural molecule activity cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;membrane-bounded organelle;nucleus;organelle;organelle part;protein complex;vesicle coat 0 4 33 30 44.4

P04075;J3KPS3;H3BQN4;P04075-2;H3BPS8;H3BUH7;H3BR04;H3BMQ8;H3BU78;H3BR68;Q5T7D5;P05062 Fructose-bisphosphate aldolase A;Fructose-bisphosphate aldolase ALDOA >sp|P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2;>tr|J3KPS3|J3KPS3_HUMAN Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=3 SV=1;>tr|H3BQN4|H3BQN4_HUMAN Fructose-bisphosphate aldolase OS=Homo sapiens GN=A 0.21 -0.13 -0.09 -0.04 -0.09 -0.21 0.43 -0.13 0.02596979 -0.013063113 "actin cytoskeleton organization;actin filament organization;actin filament-based process;alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;anatomical structure homeostasis;ATP biosynthetic process;ATP metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell activation;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;coenzyme metabolic process;cofactor metabolic process;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;fructose 1,6-bisphosphate metabolic process;fructose catabolic process;fructose metabolic process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;heterocycle biosynthetic process;heterocycle metabolic process;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;homeostatic process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multicellular organismal process;muscle cell homeostasis;muscle contraction;muscle system process;NAD metabolic process;NADH metabolic process;NADH oxidation;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organelle organization;oxidation-reduction process;oxidoreduction coenzyme metabolic process;platelet activation;platelet degranulation;positive regulation of ATPase activity;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of molecular function;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein oligomerization;protein tetramerization;proton-transporting two-sector ATPase complex assembly;proton-transporting V-type ATPase complex assembly;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;regulation of anatomical structure morphogenesis;regulation of ATPase activity;regulation of biological process;regulation of biological quality;regulation of catabolic process;regulation of catalytic activity;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular catabolic process;regulation of cellular component organization;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of purine nucleotide catabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;secretion by cell;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;striated muscle contraction;system process;transport;vacuolar proton-transporting V-type ATPase complex assembly;vesicle-mediated transport" actin binding;aldehyde-lyase activity;ATPase binding;binding;carbohydrate binding;carbon-carbon lyase activity;catalytic activity;cytoskeletal protein binding;enzyme binding;fructose binding;fructose-bisphosphate aldolase activity;identical protein binding;lyase activity;monosaccharide binding;protein binding;sugar binding;tubulin binding actin cytoskeleton;cell part;centriolar satellite;contractile fiber part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;I band;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;microtubule organizing center part;non-membrane-bounded organelle;organelle;organelle lumen;organelle part;platelet alpha granule lumen;secretory granule lumen;vesicle;vesicle lumen Carbon fixation in photosynthetic organisms;Fructose and mannose metabolism;Glycolysis / Gluconeogenesis;Pentose phosphate pathway 0 12 35 30 92.6

Q9BXJ9;Q9BXJ9-4;Q6N069-5;Q6N069-4;REV__F5H7V1;REV__G3V1R5;REV__O43847;REV__O43847-2;REV__B1AKJ5 "N-alpha-acetyltransferase 15, NatA auxiliary subunit" NAA15 ">sp|Q9BXJ9|NAA15_HUMAN N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1" 0.15 -0.09 0.10 -0.01 -0.19 -0.32 0.16 -0.42 0.717143175 0.227752643 "anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;biosynthetic process;cell differentiation;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;developmental process;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;N-terminal protein amino acid acetylation;N-terminal protein amino acid modification;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;transcription, DNA-dependent" "acetyltransferase activity;catalytic activity;N-acetyltransferase activity;N-acyltransferase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasm;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm part;organelle part;protein complex;transcription factor complex 8.81E-154 9 35 30 42.8

P00533;E9PFD7;Q504U8;P00533-4;P00533-3;P00533-2;C9JYS6;J3KTI5;P04626-3;P04626-2;H3BLT0;B4DTR1;J3QLU9;P04626-4;P04626;Q15303-4;Q15303-3;Q15303-2;Q15303 Epidermal growth factor receptor EGFR >sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2;>tr|E9PFD7|E9PFD7_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=2 SV=2;>tr|Q504U8|Q504U8_HUMAN EGFR protein OS=Homo sapiens GN=EGFR PE=2 SV=1;>sp|P 0.04 0.00 0.07 0.00 -1.41 -0.73 0.10 -0.26 0.787960839 0.600398261 "activation of phospholipase A2 activity;activation of phospholipase A2 activity by calcium-mediated signaling;activation of phospholipase C activity;ameboidal cell migration;anatomical structure development;anatomical structure morphogenesis;apoptosis;axon ensheathment;axon guidance;biological adhesion;biological regulation;biosynthetic process;body fluid secretion;calcium-mediated signaling;cardiac muscle tissue regeneration;cell adhesion;cell death;cell differentiation;cell fate commitment;cell migration;cell morphogenesis;cell motility;cell proliferation;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular biosynthetic process;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to fibroblast growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;central nervous system morphogenesis;cerebral cortex cell migration;chemotaxis;death;defense response;developmental growth;developmental process;digestive tract morphogenesis;embryonic organ development;embryonic pattern specification;embryonic placenta development;ensheathment of neurons;enzyme linked receptor protein signaling pathway;epidermal growth factor receptor signaling pathway;epidermis development;epithelial cell differentiation;establishment of localization;fibroblast growth factor receptor signaling pathway;forebrain cell migration;gland development;gland morphogenesis;growth;hair cycle process;hair follicle development;heart development;immune response;immune system process;innate immune response;inositol lipid-mediated signaling;intracellular signal transduction;lactation;localization;localization within membrane;locomotion;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;macromolecule modification;mammary gland alveolus development;mammary gland development;mammary gland epithelial cell differentiation;metabolic process;molting cycle;molting cycle process;morphogenesis of an epithelial fold;morphogenesis of an epithelium;motor axon guidance;multicellular organismal process;multicellular organismal reproductive process;myelination;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cell activation;negative regulation of cell communication;negative regulation of cell death;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of epidermal growth factor receptor signaling pathway;negative regulation of immature T cell proliferation;negative regulation of immature T cell proliferation in thymus;negative regulation of immune system process;negative regulation of leukocyte activation;negative regulation of leukocyte proliferation;negative regulation of lymphocyte activation;negative regulation of lymphocyte proliferation;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mononuclear cell proliferation;negative regulation of programmed cell death;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;negative regulation of T cell activation;negative regulation of T cell proliferation;nerve growth factor receptor signaling pathway;neural crest cell migration;neuromuscular junction development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;olfactory bulb interneuron differentiation;organ development;ossification;pattern specification process;peptidyl-amino acid modification;peptidyl-tyrosine modification;peptidyl-tyrosine phosphorylation;peripheral nervous system development;phosphate-containing compound metabolic process;phosphatidylinositol 3-kinase cascade;phosphatidylinositol-mediated signaling;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cardiac muscle cell proliferation;positive regulation of catalytic activity;positive regulation of catenin import into nucleus;positive regulation of cell adhesion;positive regulation of cell communication;positive regulation of cell cycle;positive regulation of cell growth;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of cyclin-dependent protein kinase activity;positive regulation of cyclin-dependent protein kinase activity involved in G1/S;positive regulation of developmental process;positive regulation of DNA metabolic process;positive regulation of DNA repair;positive regulation of DNA replication;positive regulation of epithelial cell proliferation;positive regulation of ERK1 and ERK2 cascade;positive regulation of fibroblast proliferation;positive regulation of gene expression;positive regulation of growth;positive regulation of GTPase activity;positive regulation of hydrolase activity;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of JAK-STAT cascade;positive regulation of kinase activity;positive regulation of lipase activity;positive regulation of lipid kinase activity;positive regulation of lipid metabolic process;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of MAP kinase activity;positive regulation of MAPKKK cascade;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal process;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of nucleocytoplasmic transport;positive regulation of peptidyl-tyrosine phosphorylation;positive regulation of phosphate metabolic process;positive regulation of phosphatidylinositol 3-kinase activity;positive regulation of phospholipase A2 activity;positive regulation of phospholipase activity;positive regulation of phospholipase C activity;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of protein import into nucleus;positive regulation of protein kinase activity;positive regulation of protein kinase B signaling cascade;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein phosphorylation;positive regulation of protein serine/threonine kinase activity;positive regulation of protein transport;positive regulation of Ras GTPase activity;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of Rho GTPase activity;positive regulation of RNA metabolic process;positive regulation of signal

transduction;positive regulation of signaling;positive regulation of STAT protein import into nucleus;positive regulation of transcription from RNA polymerase I promoter;positive regulation of transcription from RNA polymerase III promoter;positive regulation of transcription, DNA-dependent;positive regulation of transferase activity;positive regulation of translation;positive regulation of transmembrane transport;positive regulation of transport;positive regulation of tyrosine phosphorylation of STAT protein;positive regulation of tyrosine phosphorylation of Stat5 protein;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein autophosphorylation;protein insertion into membrane;protein localization;protein metabolic process;protein modification process;protein phosphorylation;regeneration;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cardiac muscle cell proliferation;regulation of cardiac muscle tissue development;regulation of cardiac muscle tissue growth;regulation of catabolic process;regulation of catalytic activity;regulation of catenin import into nucleus;regulation of cell activation;regulation of cell adhesion;regulation of cell communication;regulation of cell cycle;regulation of cell death;regulation of cell differentiation;regulation of cell growth;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of cyclin-dependent protein kinase activity;regulation of cyclin-dependent protein kinase activity involved in G1/S;regulation of developmental growth;regulation of developmental process;regulation of DNA metabolic process;regulation of DNA repair;regulation of DNA replication;regulation of epidermal growth factor receptor signaling pathway;regulation of epithelial cell proliferation;regulation of ERK1 and ERK2 cascade;regulation of establishment of protein localization;regulation of fibroblast proliferation;regulation of gene expression;regulation of growth;regulation of GTP catabolic process;regulation of GTPase activity;regulation of heart growth;regulation of hydrolase activity;regulation of immature T cell proliferation;regulation of immature T cell proliferation in thymus;regulation of immune system process;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of JAK-STAT cascade;regulation of kinase activity;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lipase activity;regulation of lipid kinase activity;regulation of lipid metabolic process;regulation of localization;regulation of locomotion;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of lymphocyte proliferation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of MAP kinase activity;regulation of MAPKKK cascade;regulation of metabolic process;regulation of microtubule-based process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of monooxygenase activity;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide catabolic process;regulation of nucleotide metabolic process;regulation of organ growth;regulation of oxidoreductase activity;regulation of peptidyl-tyrosine phosphorylation;regulation of phosphate metabolic process;regulation of phosphatidylinositol 3-kinase activity;regulation of phospholipase A2 activity;regulation of phospholipase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein kinase activity;regulation of protein kinase B signaling cascade;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of purine nucleotide catabolic process;regulation of Ras GTPase activity;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of Rho GTPase activity;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of STAT protein import into nucleus;regulation of striated muscle tissue development;regulation of T cell activation;regulation of T cell differentiation;regulation of T cell differentiation in thymus;regulation of T cell proliferation;regulation of transcription from RNA polymerase I promoter;regulation of transcription from RNA polymerase III promoter;regulation of transcription, DNA-dependent;regulation of transferase activity;regulation of translation;regulation of transmembrane transport;regulation of transport;regulation of tyrosine phosphorylation of STAT protein;regulation of tyrosine phosphorylation of Stat5 protein;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to fibroblast growth factor stimulus;response to growth factor stimulus;response to light stimulus;response to organic substance;response to radiation;response to stimulus;response to stress;response to UV;response to UV-A;response to wounding;RNA biosynthetic process;RNA metabolic process;salivary gland morphogenesis;second-messenger-mediated signaling;secretion;signal transduction;signal transduction via phosphorylation event;synapse organization;system development;taxis;telencephalon cell migration;tissue development;tissue morphogenesis;tissue regeneration;transcription, DNA-dependent;transmembrane receptor protein tyrosine kinase signaling pathway;transport;wound healing" "actin binding;actin filament binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cytoskeletal protein binding;DNA binding;double-stranded DNA binding;enzyme binding;epidermal growth factor-activated receptor activity;ErbB-3 class receptor binding;kinase activity;MAP kinase kinase kinase activity;molecular transducer activity;nucleic acid binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein dimerization activity;protein heterodimerization activity;protein kinase activity;protein serine/threonine kinase activity;protein tyrosine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;receptor binding;receptor signaling protein activity;receptor signaling protein serine/threonine kinase activity;receptor signaling protein tyrosine kinase activity;regulatory region DNA binding;regulatory region nucleic acid binding;ribonucleotide binding;RNA polymerase binding;RNA polymerase core enzyme binding;RNA polymerase I core binding;signal transducer activity;signaling receptor activity;structure-specific DNA binding;transcription regulatory region DNA binding;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane receptor protein kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane signaling receptor activity" apical plasma membrane;basolateral plasma membrane;cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endocytic vesicle;endoplasmic reticulum membrane;endoplasmic reticulum part;endosomal part;endosome;endosome membrane;extracellular region;extracellular region part;extracellular space;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;nuclear membrane;nuclear part;nucleoplasm;nucleus;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;receptor complex;Shc-EGFR complex;vesicle Adherens junction;Bladder cancer;Calcium signaling pathway;Cytokine-cytokine receptor interaction;Dorso-ventral axis formation;Endocytosis;Endometrial cancer;Epithelial cell signaling in Helicobacter pylori infection;ErbB signaling pathway;Focal adhesion;Gap junction;Glioma;GnRH signaling pathway;Hepatitis C;MAPK signaling pathway;MAPK signaling pathway - fly;Melanoma;Non-small cell lung cancer;Pancreatic cancer;Pathways in cancer;Prostate cancer;Regulation of actin cytoskeleton 4.96E-273 19 31 31 32.6
P55884;P55884-2;C9JZG1;C9JQN7 Eukaryotic translation initiation factor 3 subunit B EIF3B >sp|P55884|EIF3B_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3;>sp|P55884-2|EIF3B_HUMAN Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B 0.07 0.02 -0.09 -0.04 -0.01 -0.09 0.08 -0.23 0.266748014 0.050708778 biological regulation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation "binding;nucleic acid binding;nucleotide binding;protein binding;protein complex scaffold;RNA binding;structural molecule activity;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport 2.89E-262 4 31 31 47.9
Q99613;H3BRV0;B5ME19;H3BPE4;H3BPE3;H3BTY8 Eukaryotic translation initiation factor 3 subunit C EIF3C;EIF3CL >sp|Q99613|EIF3C_HUMAN Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1;>tr|H3BRV0|H3BRV0_HUMAN Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=2 SV=1;>sp|B5ME19|EIFCL_HUMAN Eukaryotic 0.18 0.06 -0.01 -0.03 -0.08 -0.24 -0.08 -0.41 1.143212915 0.252269263 cellular process;translational initiation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular part;macromolecular complex;protein complex RNA transport 0 6 31 31 36
P11413;P11413-2;P11413-3;E7EUI8;E9PD92;E7EM57 Glucose-6-phosphate 1-dehydrogenase G6PD >sp|P11413|G6PD_HUMAN Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4;>sp|P11413-2|G6PD_HUMAN Isoform Long of Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD;>sp|P11413-3|G6PD_HUMAN Isoform 3 of Glucose-6-phosphate 1-dehyd 0.34 -0.15 -0.29 -0.23 0.90 0.24 0.66 -0.18 0.753053003 -0.489266746 "alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;amine metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cell maturation;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular developmental process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to oxidative stress;cellular response to stimulus;cellular response to stress;cholesterol biosynthetic process;cholesterol metabolic process;coenzyme metabolic process;cofactor metabolic process;cytokine production;developmental maturation;developmental process;D-ribose biosynthetic process;D-ribose metabolic process;erythrocyte maturation;glucose 6-phosphate metabolic process;glucose catabolic process;glucose metabolic process;glutathione metabolic process;heterocycle metabolic process;hexose catabolic process;hexose metabolic process;lipid biosynthetic process;lipid metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multicellular organismal process;NADP metabolic process;NADPH regeneration;negative regulation of biological process;negative regulation of cellular metabolic

process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein glutathionylation;negative regulation of protein metabolic process;negative regulation of protein modification process;nicotinamide nucleotide metabolic process;nitrogen compound metabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide metabolic process;organic acid metabolic process;oxidation-reduction process;oxidoreduction coenzyme metabolic process;oxoacid metabolic process;pentose biosynthetic process;pentose metabolic process;pentose-phosphate shunt;pentose-phosphate shunt, oxidative branch;peptide metabolic process;primary metabolic process;pyridine nucleotide metabolic process;pyridine-containing compound metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein glutathionylation;regulation of protein metabolic process;regulation of protein modification process;response to chemical stimulus;response to ethanol;response to external stimulus;response to extracellular stimulus;response to food;response to nutrient levels;response to organic cyclic compound;response to organic substance;response to oxidative stress;response to stimulus;response to stress;ribose phosphate biosynthetic process;ribose phosphate metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;steroid biosynthetic process;steroid metabolic process;sterol biosynthetic process;sterol metabolic process;sulfur compound metabolic process" "binding;carbohydrate binding;catalytic activity;coenzyme binding;cofactor binding;glucose binding;glucose-6-phosphate dehydrogenase activity;monosaccharide binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;sugar binding" cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;internal side of plasma membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane part;membrane-bounded organelle;microtubule organizing center;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane part Glutathione metabolism;Pentose phosphate pathway 6.35E-265 6 31 31 65.8

P09874;Q5VX84;Q5VX85 Poly [ADP-ribose] polymerase 1 PARP1 >sp|P09874|PARP1_HUMAN Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 0.06 -0.02 -0.14 0.04 0.29 -0.37 -0.60 -0.60 0.596674515 0.303678001 "anatomical structure homeostasis;base-excision repair;biological regulation;biosynthetic process;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chromosome organization;detection of stimulus;DNA damage response, detection of DNA damage;DNA metabolic process;DNA repair;double-strand break repair;enzyme linked receptor protein signaling pathway;homeostatic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;protein ADP-ribosylation;protein autoprocessing;protein maturation;protein metabolic process;protein modification process;protein poly-ADP-ribosylation;protein processing;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of growth rate;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to chemical stimulus;response to DNA damage stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;signal transduction;telomere maintenance;telomere organization;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent;transforming growth factor beta receptor signaling pathway;transmembrane receptor protein serine/threonine kinase signaling pathway" "binding;catalytic activity;cation binding;coenzyme binding;cofactor binding;DNA binding;ion binding;metal ion binding;NAD binding;NAD+ ADP-ribosyltransferase activity;nucleic acid binding;nucleotide binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring pentosyl groups;transition metal ion binding;zinc ion binding" cell part;envelope;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear envelope;nuclear part;nucleolus;nucleoplasm part;organelle;organelle envelope;organelle part;protein complex;transcription factor complex Base excision repair 3.41E-163 3 31 31 38.1

Q13263;Q13263-2;M0R0K9;M0R3C0;M0R2I3 Transcription intermediary factor 1-beta TRIM28 >sp|Q13263|TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5;>sp|Q13263-2|TIF1B_HUMAN Isoform 2 of Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 -0.08 0.17 0.07 0.19 0.08 -0.36 -0.92 -0.50 1.011195532 0.512903171 "anatomical structure morphogenesis;biological regulation;biosynthetic process;cell morphogenesis;cell morphogenesis involved in differentiation;cellular biosynthetic process;cellular component assembly;cellular component morphogenesis;cellular component organization;cellular component organization or biogenesis;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;convergent extension;convergent extension involved in axis elongation;developmental process;DNA metabolic process;DNA repair;embryonic morphogenesis;embryonic placenta morphogenesis;epithelial to mesenchymal transition;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;macromolecule modification;metabolic process;morphogenesis of an epithelium;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA repair;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of response to DNA damage stimulus;positive regulation of response to stimulus;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;protein autophosphorylation;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein oligomerization;protein phosphorylation;protein sumoylation;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA repair;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;tissue morphogenesis;transcription initiation from RNA polymerase II promoter;transcription initiation, DNA-dependent" "acid-amino acid ligase activity;binding;catalytic activity;cation binding;DNA binding;enzyme binding;ion binding;kinase activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;phosphotransferase activity, alcohol group as acceptor;protein binding;protein binding transcription factor activity;protein kinase activity;sequence-specific DNA binding;sequence-specific DNA binding transcription factor activity;small conjugating protein ligase activity;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transition metal ion binding;ubiquitin protein ligase binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;chromatin;chromosomal part;euchromatin;heterochromatin;intracellular;intracellular organelle part;intracellular part;nuclear chromatin;nuclear chromosome part;nuclear euchromatin;nuclear heterochromatin;nuclear part;nucleoplasm;organelle part 0 5 31 31 46

O95757;E7ES43;E9PDE8;D6RJ96 Heat shock 70 kDa protein 4L HSPA4L >sp|O95757|HS74L_HUMAN Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3;>tr|E7ES43|E7ES43_HUMAN Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=2 SV=2;>tr|E9PDE8|E9PDE8_HUMAN Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L 0.00 -0.01 0.47 0.15 -1.05 -0.36

-0.08 -0.49 1.168656148 0.648311089 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Protein processing in endoplasmic reticulum 0 4 37 31 53.9

P27824;B4DGP8;B4E2T8;D6RGY2;H0Y9Q7;D6RFL1;D6RAU8;D6RB85;D6RDP7;H0Y9H1;D6RAQ8;D6RHJ3;D6RD16;O14967 Calnexin CANX >sp|P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2;>tr|B4DGP8|B4DGP8_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1;>tr|B4E2T8|B4E2T8_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1 -0.21 0.03 -0.24 -0.08 0.47 0.18 -0.07 0.01 0.870370841 -0.272111577 aging;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;binding of sperm to zona pellucida;carbohydrate metabolic process;cell recognition;cell-cell recognition;cellular carbohydrate metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;clathrin-mediated endocytosis;developmental process;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;fertilization;glycosylation;immune system process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;membrane invagination;membrane organization;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein secretion;protein transport;receptor-mediated endocytosis;reproductive process;secretion;secretion by cell;single fertilization;sperm-egg recognition;synaptic vesicle endocytosis;synaptic vesicle transport;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;ion binding;metal ion binding;protein binding;unfolded protein binding axon;cell body;cell part;cell projection;cell projection cytoplasm;cell projection part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;dendrite cytoplasm;dendritic spine;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;envelope;integral to endoplasmic reticulum membrane;integral to lumenal side of endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;neuron projection;neuron spine;neuronal cell body;non-membrane-bounded organelle;nuclear envelope;nuclear part;organelle;organelle envelope;organelle lumen;organelle membrane;organelle part;pigment granule;ribonucleoprotein complex;ribosome;vesicle Antigen processing and presentation;Phagosome;Protein processing in endoplasmic reticulum 1.50E-184 14 32 32 41.9

P07384;E9PL37;E9PRM1;E9PLX0;E9PJJ3;E9PLC9;E9PMC6;E9PJA6;E9PSA6;E9PLQ6;E9PQB3;E9PIA9 Calpain-1 catalytic subunit CAPN1 >sp|P07384|CAN1_HUMAN Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1 -0.07 -0.21 0.01 0.06 -0.06 0.32 0.66 0.25 0.926606074 -0.346412337 biological regulation;catabolic process;cellular catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;positive regulation of biological process;positive regulation of cell proliferation;positive regulation of cellular process;primary metabolic process;protein metabolic process;proteolysis;receptor catabolic process;receptor metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process "binding;calcium ion binding;calcium-dependent cysteine-type endopeptidase activity;catalytic activity;cation binding;cysteine-type endopeptidase activity;cysteine-type peptidase activity;endopeptidase activity;hydrolase activity;ion binding;metal ion binding;peptidase activity;peptidase activity, acting on L-amino acid peptides" cell part;cytoplasm;intracellular;intracellular part;membrane;plasma membrane Alzheimer's disease;Apoptosis;Protein processing in endoplasmic reticulum 1.42E-241 12 32 32 46.2

B4DZI8;P35606;H0Y938;H0YAC7;D6R997;D6RBZ7;D6RCL6;D6RBG7;D6RBT6 Coatomer subunit beta COPB2 ">tr|B4DZI8|B4DZI8_HUMAN Coatomer protein complex, subunit beta 2 (Beta prime), isoform CRA_b OS=Homo sapiens GN=COPB2 PE=2 SV=1;>sp|P35606|COPB2_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB2 PE=1 SV=2" 0.28 0.01 -0.30 -0.45 0.61 0.41 0.46 0.18 1.193146659 -0.53073349 "cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;COPI coating of Golgi vesicle;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;organelle organization;protein transport;retrograde vesicle-mediated transport, Golgi to ER;transport;vesicle coating;vesicle organization;vesicle-mediated transport"structural molecule activity actin cytoskeleton;cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytoskeleton;cytosol;Golgi apparatus;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;organelle;organelle part;protein complex;vesicle coat 8.45E-266 9 32 32 44.8

Q5VYK3;J3KN16;R4GMY1;Q5VYK5;F6XAQ5;R4GMY3 Proteasome-associated protein ECM29 homolog ECM29;KIAA0368>sp|Q5VYK3|ECM29_HUMAN Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2;>tr|J3KN16|J3KN16_HUMAN Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=KIAA0368 PE=4 SV=1;>tr|R4GMY1|R4GMY1_HUMAN Proteasome-associated pr 0.28 0.04 0.07 -0.06 0.17 -0.25 0.25 -0.22 0.239488708 0.091822359 catabolic process;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;ER-associated protein catabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;ubiquitin-dependent protein catabolic process cell part;centrosome;coated vesicle;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;early endosome;endocytic vesicle;endoplasmic reticulum;endoplasmic reticulum-Golgi intermediate compartment;endosome;ER to Golgi transport vesicle;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;multivesicular body;non-membrane-bounded organelle;nucleus;organelle;organelle part;proteasome complex;protein complex;transport vesicle;vesicle 3.45E-170 6 32 32 24.2

Q6PKG0;Q6PKG0-3;E5RH50;H0YBW1;H0YC33;H0YC73;E5RHK4;H0YAN4;H0YBM7;Q659C4-5;Q659C4-9;Q659C4-2;Q659C4;H0YBR8;H0YAX9;Q659C4-7;Q659C4-6;D6RJB0 La-related protein 1 LARP1 >sp|Q6PKG0|LARP1_HUMAN La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2;>sp|Q6PKG0-3|LARP1_HUMAN Isoform 2 of La-related protein 1 OS=Homo sapiens GN=LARP1;>tr|E5RH50|E5RH50_HUMAN La-related protein 1 (Fragment) OS=Homo sapiens GN=LARP1 PE=2 SV=1 -0.03 0.06 -0.01 0.03 0.00 -0.21 -0.05 -0.44 0.798237506 0.189298831 biological regulation;positive regulation of autophagy;positive regulation of biological process;positive regulation of catabolic process;positive regulation of cell communication;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of macroautophagy;positive regulation of metabolic process;positive regulation of response to external stimulus;positive regulation of response to extracellular stimulus;positive regulation of response to nutrient levels;positive regulation of response to stimulus;regulation of autophagy;regulation of biological process;regulation of catabolic process;regulation of cell communication;regulation of cellular catabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular response to stress;regulation of macroautophagy;regulation of metabolic process;regulation of response to external stimulus;regulation of response to extracellular stimulus;regulation of response to nutrient levels;regulation of response to stimulus;regulation of response to stress binding;nucleic acid binding;RNA binding 4.43E-172 18 32 32 43

P09960;P09960-4;P09960-2;P09960-3;B4DEH5 Leukotriene A-4 hydrolase LTA4H >sp|P09960|LKHA4_HUMAN Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2;>sp|P09960-4|LKHA4_HUMAN Isoform 4 of Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H;>sp|P09960-2|LKHA4_HUMAN Isoform 2 of Leukotriene A-4 hydrolase OS=Homo sapiens GN= 0.16 0.03 0.05 -0.05 -0.47 0.00 0.55 0.04 0.027101722 0.017485291 alkene biosynthetic process;arachidonic acid metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;catabolic process;cellular alkene metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;defense response;fatty acid biosynthetic process;fatty acid metabolic process;icosanoid biosynthetic process;icosanoid metabolic process;inflammatory response;leukotriene biosynthetic process;leukotriene metabolic process;lipid biosynthetic process;lipid metabolic process;macromolecule metabolic process;metabolic process;monocarboxylic acid metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;peptide catabolic process;peptide metabolic process;primary metabolic process;protein metabolic process;proteolysis;response to stimulus;response to stress;response to wounding;small molecule biosynthetic process;small molecule metabolic process;unsaturated fatty acid biosynthetic process;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process "aminopeptidase activity;binding;catalytic activity;cation binding;epoxide hydrolase activity;ether hydrolase activity;exopeptidase activity;hydrolase activity;hydrolase activity, acting on ether bonds;ion binding;leukotriene-A4 hydrolase activity;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Arachidonic acid metabolism 0 5 32 32 54.2

Q9UM54-6;E7EW20;Q9UM54-5;Q9UM54-2;Q9UM54-4;Q9UM54-1;Q9UM54;Q5JVM0 Unconventional myosin-VI MYO6 >sp|Q9UM54-6|MYO6_HUMAN Isoform 6 of Unconventional myosin-VI OS=Homo sapiens GN=MYO6;>tr|E7EW20|E7EW20_HUMAN Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=2 SV=1;>sp|Q9UM54-5|MYO6_HUMAN Isoform 5 of Unconventional myosin-VI OS=Homo sapiens GN=MYO6;> 0.21 0.29 0.15 0.27 -0.05 0.63 0.51 0.29 0.290423693 -0.11277273 "actin filament-based movement;actin filament-based process;anatomical structure development;anatomical structure morphogenesis;auditory receptor cell differentiation;behavior;biological regulation;cell communication;cell differentiation;cell projection organization;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to abiotic stimulus;cellular response to electrical stimulus;cellular response to stimulus;cellular response to stress;dendrite development;developmental process;DNA damage response, signal transduction by p53 class mediator;embryonic morphogenesis;endocytosis;establishment of localization;establishment of localization in cell;establishment of protein localization;glutamate secretion;inner ear morphogenesis;inner ear receptor cell differentiation;intracellular protein transport;intracellular signal transduction;intracellular transport;locomotory behavior;mechanoreceptor differentiation;membrane invagination;membrane organization;multicellular organismal process;neurological system process;neuron differentiation;neuron projection development;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;protein targeting;protein transport;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of secretion;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of system process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of transmission of nerve impulse;regulation of transport;response to abiotic stimulus;response to DNA damage stimulus;response to electrical stimulus;response to stimulus;response to stress;secretion;secretion by cell;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;signal release;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signaling;synapse assembly;synapse organization;synaptic transmission;system process;transport;vesicle-mediated transport" "actin binding;actin filament binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;binding;calmodulin binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microfilament motor activity;minus-end directed microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" "axon;cell body;cell cortex;cell part;cell projection;cell projection membrane;cell projection part;clathrin coated vesicle membrane;coated pit;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytoskeletal part;cytosol;DNA-directed RNA polymerase II, holoenzyme;filamentous actin;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;lysosomal membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;myosin complex;neuron projection;neuronal cell body;nuclear membrane;nuclear part;nucleoplasm part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane;plasma membrane part;protein complex;ruffle;ruffle membrane;unconventional myosin complex;vacuolar membrane;vacuolar part;vesicle;vesicle membrane" 3.13E-230 8 32 32 29

Q13835-2;Q13835 Plakophilin-1 PKP1 >sp|Q13835-2|PKP1_HUMAN Isoform 1 of Plakophilin-1 OS=Homo sapiens GN=PKP1;>sp|Q13835|PKP1_HUMAN Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2 -0.73 0.44 0.40 0.86 -0.86 0.30 -0.19 -0.70 0.591830909 0.603897404 biological adhesion;cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;developmental process;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;multicellular organismal development;multicellular organismal process;organelle organization binding;intermediate filament binding;lamin binding;molecular transducer activity;protein binding;protein complex binding;signal transducer activity;structural constituent of epidermis;structural molecule activity anchoring junction;cell junction;cell part;cell-cell junction;cytoskeletal part;desmosome;intermediate filament;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex 0 2 32 32 52.5

P36952;P36952-2;C9JLM5 Serpin B5 SERPINB5 >sp|P36952|SPB5_HUMAN Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2;>sp|P36952-2|SPB5_HUMAN Isoform 2 of Serpin B5 OS=Homo sapiens GN=SERPINB5 -0.24 -0.16 0.15 0.16 -0.76 -0.12 0.65 0.07 0.017513782 0.016649123 anatomical structure morphogenesis;biological regulation;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;developmental process involved in reproduction;extracellular matrix organization;extracellular structure organization;gland morphogenesis;morphogenesis of an epithelium;organ morphogenesis;prostate gland morphogenesis;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of epithelial cell proliferation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of proteolysis;reproductive process;tissue morphogenesis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity cell part;cytoplasm;extracellular region part;extracellular space;intracellular part p53 signaling pathway 0 3 32 32 74.1

P54577 "Tyrosine--tRNA ligase, cytoplasmic" YARS ">sp|P54577|SYYC_HUMAN Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4" 0.04 -0.15 0.02 -0.09 -0.12 -0.45 0.30 -0.43 0.282060658 0.130821039 amine metabolic process;amino acid activation;apoptosis;carboxylic acid metabolic process;cell death;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;death;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;programmed cell death;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tyrosyl-tRNA aminoacylation "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;chemokine receptor binding;CXCR chemokine receptor binding;cytokine receptor binding;G-protein-coupled receptor binding;interleukin-8 receptor binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;molecular transducer activity;nucleic acid binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;RNA binding;signal transducer activity;tRNA binding;tyrosine-tRNA ligase activity" cell part;cytoplasmic part;cytosol;extracellular region part;extracellular space;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Aminoacyl-tRNA biosynthesis 8.79E-172 1 32 32 63.6

Q03252;J9JID7 Lamin-B2 LMNB2 ">sp|Q03252|LMNB2_HUMAN Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=3;>tr|J9JID7|J9JID7_HUMAN Lamin B2, isoform CRA_a OS=Homo sapiens GN=LMNB2 PE=3 SV=1" -0.30 0.52 0.27 0.83 0.12 0.17 -1.36 -0.22 0.648633246 0.653998941 structural molecule activity cell part;cytoskeletal part;intermediate filament;intracellular organelle part;intracellular part;lamin filament;macromolecular complex;membrane;nuclear inner membrane;nuclear lamina;nuclear membrane;nuclear part;organelle inner membrane;organelle membrane;organelle part;protein complex 1.81E-202 2 37 32 55.5

P13797;B7Z6M1;B4DGB4;F8W8D8;B4DI60;H7C4N2;F2Z2Z9 Plastin-3 PLS3 >sp|P13797|PLST_HUMAN Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4;>tr|B7Z6M1|B7Z6M1_HUMAN Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1;>tr|B4DGB4|B4DGB4_HUMAN Plastin-3 OS=Homo sapiens GN=PLS3 PE=2 SV=1;>tr|F8W8D8|F8W8D8_HUMAN Plastin-3 OS=Homo sapiens GN=P -0.08 -0.14 -0.06 -0.08 -0.18 0.19 0.62 0.16 0.746032254 -0.287145132 binding;calcium ion binding;cation binding;ion binding;metal ion binding cell part;cytoplasm;intracellular part 0 7 39 32 69.8

Q99832;Q99832-3;F5GZK5;Q99832-4;B7Z1C9;Q99832-2;F8WAM2;F8WBP8 T-complex protein 1 subunit eta CCT7 >sp|Q99832|TCPH_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2;>sp|Q99832-3|TCPH_HUMAN Isoform 3 of T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7;>tr|F5GZK5|F5GZK5_HUMAN T-complex protein 1 subunit eta OS=Homo sapiens GN= 0.19 0.02

-0.08 -0.03 -0.01 -0.35 -0.06 -0.49 0.8372327 0.251883722 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;mitochondrion;organelle;organelle part;protein complex 0 8 33 33 66.1

Q96TA1-2;Q96TA1 Niban-like protein 1 FAM129B >sp|Q96TA1-2|NIBL1_HUMAN Isoform 2 of Niban-like protein 1 OS=Homo sapiens GN=FAM129B;>sp|Q96TA1|NIBL1_HUMAN Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 0.19 0.01 0.16 -0.01 0.61 0.33 0.08 -0.21 0.2418031 -0.114744008 biological regulation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of programmed cell death binding;lipid binding;phospholipid binding adherens junction;anchoring junction;cell junction;cell part;cytoplasmic part;cytosol;intracellular part 2.02E-286 2 33 33 56.3

P43243;A8MXP9;D6REM6;D6R991;B3KM87;P43243-2;H0Y8T4;D6RBK5;D6R8Z5;D6RBI2;D6RE02;D6RIA2;D6RB45;D6R9F3;D6RAM9;D6RAY2;D6RBS2;D6RCM3;D6REK4 Matrin-3 MATR3 >sp|P43243|MATR3_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2;>tr|A8MXP9|A8MXP9_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1;>tr|D6REM6|D6REM6_HUMAN Matrin-3 OS=Homo sapiens GN=MATR3 PE=2 SV=1;>tr|D6R991|D6R991_HUMAN Matrin-3 (Fragment) OS=Homo s -0.08 0.90 -0.08 0.93 0.05 0.50 -1.21 0.29 0.442319723 0.513262956 binding;cation binding;ion binding;metal ion binding;nucleic acid binding;nucleotide binding;RNA binding;structural molecule activity;transition metal ion binding;zinc ion binding cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane-bounded organelle;nuclear inner membrane;nuclear matrix;nuclear membrane;nuclear part;nucleus;organelle;organelle inner membrane;organelle membrane;organelle part 0 19 33 33 40.5

O43795-2;E9PDF6;O43795;E7EPB4;E7EQD9;H7C2Y7;C9JYW1;C9JUP5;C9K0I9;Q9UBC5;G3V342;F5GWY8;F5H2J1;Q8WXR4-6;Q8WXR4-3;Q8WXR4-5;Q8WXR4-2;Q8WXR4-4;Q8WXR4;Q8WXR4-7 Unconventional myosin-Ib MYO1B >sp|O43795-2|MYO1B_HUMAN Isoform 2 of Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B;>tr|E9PDF6|E9PDF6_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=2 SV=1;>sp|O43795|MYO1B_HUMAN Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3 -0.10 0.17 -0.31 0.09 -0.02 0.36 0.46 0.54 0.968398083 -0.376065228 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based movement;actin filament-based process;biological regulation;cell projection assembly;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cytoskeleton organization;localization;macromolecule metabolic process;macromolecule modification;metabolic process;microvillus assembly;microvillus organization;multicellular organismal process;neurological system process;organelle localization;organelle organization;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;peptidyl-threonine modification;peptidyl-threonine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of biological process;positive regulation of cell projection organization;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of filopodium assembly;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;regulation of biological process;regulation of cell projection assembly;regulation of cell projection organization;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular process;regulation of filopodium assembly;response to stimulus;sensory perception;sensory perception of light stimulus;sensory perception of mechanical stimulus;sensory perception of sound;system process;vesicle localization;visual perception "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;kinase activity;lipid binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;phosphatidylinositol binding;phosphatidylinositol-3,4,5-trisphosphate binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipid binding;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" apical plasma membrane;basal plasma membrane;basolateral plasma membrane;brush border;cell cortex part;cell part;cell projection;cell projection part;cilium;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;filamentous actin;filopodium;filopodium tip;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;macromolecular complex;membrane;membrane part;microvillus;myosin complex;non-membrane-bounded organelle;nonmotile primary cilium;organelle;organelle part;photoreceptor inner segment;photoreceptor outer segment;plasma membrane;plasma membrane part;primary cilium;protein complex;stereocilium bundle tip Phototransduction - fly 0 20 33 33 33.6

P17987;E7EQR6;F5H282;E7ERF2;F5GZ03;F5H136;F5GZI8;F5H676;F5H7Y1;F5GYL4;F5H726 T-complex protein 1 subunit alpha TCP1 >sp|P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1;>tr|E7EQR6|E7EQR6_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=2 SV=1;>tr|F5H282|F5H282_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens 0.26 0.03 -0.07 -0.05 0.04 -0.31 0.01 -0.41 0.665436617 0.21347392 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process;tubulin complex assembly adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell junction;cell part;centrosome;chaperonin-containing T-complex;chromatin;chromosomal part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;Golgi apparatus;heterochromatin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;microtubule;microtubule organizing center;microtubule organizing center part;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear heterochromatin;nuclear part;nucleus;organelle;organelle part;pericentriolar material;plasma membrane;protein complex 0 11 33 33 69.2

O00410;O00410-3;B4E0R6;H0Y8C6;O00410-2;E7ETV3;E7EQT5;C9JZD8;E7EWK4;E7EX05;E7EV12;C9JMV5;H0Y3V4;C9JQT6;E7ESA1;E7ESZ1;E7ETV8;C9J875;C9JZ53;C9JXE0;C9J5I6 Importin-5 IPO5 >sp|O00410|IPO5_HUMAN Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4;>sp|O00410-3|IPO5_HUMAN Isoform 3 of Importin-5 OS=Homo sapiens GN=IPO5;>tr|B4E0R6|B4E0R6_HUMAN Importin-5 OS=Homo sapiens GN=IPO5 PE=2 SV=1;>tr|H0Y8C6|H0Y8C6_HUMAN Importin-5 (Fragment) OS 0.05 -0.01 -0.08 -0.05 0.21 0.04 0.07 -0.19 0.246145083 -0.056295552 establishment of localization;establishment of localization in cell;establishment of protein localization;interaction with host;interspecies interaction between organisms;intracellular protein transport;intracellular transport;multi-organism process;NLS-bearing substrate import into nucleus;nuclear import;nuclear transport;nucleocytoplasmic transport;protein import;protein import into nucleus;protein targeting;protein transport;reproductive process;ribosomal protein import into nucleus;transport;viral reproductive process;virus-host interaction binding;enzyme binding;enzyme inhibitor activity;enzyme regulator activity;GTPase binding;GTPase inhibitor activity;GTPase regulator activity;nucleoside-triphosphatase regulator activity;protein binding;protein transporter activity;Ran GTPase binding;Ras GTPase binding;small GTPase binding;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;non-membrane-bounded organelle;nuclear part;nuclear pore;nucleolus;organelle;organelle part;pore complex;protein complex 0 21 36 33 41.4

P16615;P16615-5;P16615-2;P16615-3;P16615-4;H7C5W9;O14983-2;O14983;B3KY17;Q93084-4;Q93084-2;Q93084-3;Q93084-7;Q93084;Q93084-6;Q93084-5;J3QSY6;F8VSH0;H3BVB2;H3BTW4 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 ATP2A2 >sp|P16615|AT2A2_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1;>sp|P16615-5|AT2A2_HUMAN Isoform 5 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2;>sp|P16615-2|AT2A2_HUMAN Isof -0.05 0.29 -0.48 -0.04 0.34 0.50 -0.24 0.29 0.53758084 -0.291611467 anatomical structure development;apoptosis;apoptosis in response to endoplasmic reticulum stress;apoptotic mitochondrial changes;biological adhesion;biological regulation;blood coagulation;calcium ion homeostasis;calcium ion import;calcium ion transmembrane transport;calcium ion transport;cation homeostasis;cation transport;cell adhesion;cell death;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;cellular response to stimulus;chemical homeostasis;coagulation;death;developmental process;divalent inorganic cation homeostasis;divalent inorganic cation transport;divalent metal ion transport;elevation of endoplasmic reticulum calcium ion concentration;elevation of mitochondrial calcium ion concentration;endoplasmic reticulum calcium ion homeostasis;epidermis development;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;hemostasis;homeostatic process;intracellular transport;ion homeostasis;ion transmembrane transport;ion transport;maintenance of location;maintenance of location in cell;maintenance of mitochondrion location;maintenance of organelle location;metal ion homeostasis;metal ion transport;mitochondrial calcium ion homeostasis;mitochondrion organization;multicellular organismal process;muscle system process;negative regulation of biological process;negative regulation of cardiac muscle contraction;negative regulation of heart contraction;negative regulation of multicellular organismal process;negative regulation of muscle contraction;negative regulation of striated muscle contraction;organelle organization;positive regulation of biological process;positive regulation of fast-twitch skeletal muscle fiber contraction;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of striated muscle contraction;programmed cell death;reduction of endoplasmic reticulum calcium ion concentration;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cardiac muscle contraction;regulation of cellular process;regulation of fast-twitch skeletal muscle fiber contraction;regulation of heart contraction;regulation of heart rate;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of skeletal muscle contraction;regulation of striated muscle contraction;regulation of system process;regulation of the force of heart contraction;regulation of twitch skeletal muscle contraction;relaxation of cardiac muscle;relaxation of muscle;relaxation of skeletal muscle;response to stimulus;sarcoplasmic reticulum calcium ion transport;signal transduction;system process;tissue development;transmembrane transport;transport "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;calcium ion binding;calcium ion transmembrane transporter activity;calcium-transporting ATPase activity;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;divalent inorganic cation transmembrane transporter activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;metal ion binding;metal ion transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" calcium channel complex;cation channel complex;cell part;contractile fiber part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;H zone;I band;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;ion channel complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;nuclear membrane;nuclear part;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;platelet dense tubular network membrane;protein complex;sarcoplasmic reticulum;sarcoplasmic reticulum membrane Alzheimer's disease;Calcium signaling pathway;Pancreatic secretion 1.07E-302 20 34 34 37.4

Q14980-2;Q14980;Q14980-4;Q14980-3;H0YFY6;Q9BTE9;F5H6Y5;F5H4J1;K4DIE0;F5H2F3;F5H3L6;F5H0Z7;F5H763;F5H1L0;F5GZW1 Nuclear mitotic apparatus protein 1 NUMA1 >sp|Q14980-2|NUMA1_HUMAN Isoform 2 of Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1;>sp|Q14980|NUMA1_HUMAN Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2;>sp|Q14980-4|NUMA1_HUMAN Isoform Numa-s of Nuclear mitotic appa 0.18 1.19 0.17 0.94 -0.16 -0.21 -1.27 -0.11 1.151207974 1.053830834 anaphase;cell cycle phase;cell cycle process;cell differentiation;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;developmental process;epithelial cell differentiation;establishment of localization;establishment of localization in cell;establishment of mitotic spindle localization;establishment of mitotic spindle orientation;establishment of organelle localization;establishment of spindle localization;establishment of spindle orientation;G2/M transition of mitotic cell cycle;lung cell differentiation;lung epithelial cell differentiation;microtubule cytoskeleton organization;microtubule-based process;mitotic anaphase;nucleus organization;organelle organization structural molecule activity apical part of cell;cell part;chromosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;non-membrane-bounded organelle;nuclear matrix;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;spindle microtubule;spindle pole 1.88E-237 15 34 34 23

Q01813;Q01813-2;B1APP8;B1APP6;H0Y757;Q5VSR5;H0Y3Y3;Q5VSR6 6-phosphofructokinase type C PFKP >sp|Q01813|K6PP_HUMAN 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2;>sp|Q01813-2|K6PP_HUMAN Isoform 2 of 6-phosphofructokinase type C OS=Homo sapiens GN=PFKP 0.22 -0.09 -0.24 -0.21 0.36 0.17 0.35 0.08 1.074819448 -0.321161913 alcohol catabolic process;alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;fructose 6-phosphate metabolic process;fructose metabolic process;generation of precursor metabolites and energy;glucose catabolic process;glucose metabolic process;glycolysis;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;primary metabolic process;small molecule catabolic process;small molecule metabolic process "6-phosphofructokinase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate kinase activity;catalytic activity;cation binding;ion binding;kinase activity;metal ion binding;nucleotide binding;phosphofructokinase activity;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" 6-phosphofructokinase complex;cell part;cytoplasmic part;cytosolic part;intracellular part;macromolecular complex;protein complex Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Methane metabolism;Pentose phosphate pathway 0 8 40 34 50.3

P55060-3;P55060;P55060-4;B4DUC5;P55060-2 Exportin-2 CSE1L >sp|P55060-3|XPO2_HUMAN Isoform 3 of Exportin-2 OS=Homo sapiens GN=CSE1L;>sp|P55060|XPO2_HUMAN Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3;>sp|P55060-4|XPO2_HUMAN Isoform 4 of Exportin-2 OS=Homo sapiens GN=CSE1L;>tr|B4DUC5|B4DUC5_HUMAN Exportin-2 OS=Homo 0.18 0.03 -0.02 -0.05 -0.15 -0.40 -0.05 -0.49 1.114748792 0.307248113 apoptosis;cell death;cell proliferation;cellular process;death;establishment of localization;establishment of localization in cell;establishment of protein localization;intracellular protein transport;intracellular transport;programmed cell death;protein transport;transport binding;importin-alpha export receptor activity;nuclear export signal receptor activity;protein binding;protein transporter activity;substrate-specific transporter activity;transporter activity cell part;cytoplasm;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane part;membrane-bounded organelle;nuclear part;nuclear pore;nucleus;organelle;organelle part;pore complex;protein complex 0 5 35 35 44.3

P41250;H7C443 Glycine--tRNA ligase GARS >sp|P41250|SYG_HUMAN Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 0.02 -0.11 0.04 -0.09 0.40 0.26 0.46 -0.02 1.158450877 -0.314563355 amine metabolic process;amino acid activation;biosynthetic process;bis(5'-nucleosidyl) oligophosphate biosynthetic process;bis(5'-nucleosidyl) oligophosphate metabolic process;carboxylic acid metabolic process;cell death;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;death;diadenosine polyphosphate biosynthetic process;diadenosine polyphosphate metabolic process;diadenosine tetraphosphate biosynthetic process;diadenosine tetraphosphate metabolic process;glycyl-tRNA aminoacylation;heterocycle biosynthetic process;heterocycle metabolic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;purine nucleoside biosynthetic process;purine nucleoside metabolic process;purine ribonucleoside biosynthetic process;purine ribonucleoside metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside biosynthetic process;ribonucleoside metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;glycine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;protein binding;protein dimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle;organelle lumen;organelle part;stored secretory granule;vesicle Aminoacyl-tRNA biosynthesis 0 2 35 35 56.3

Q12965;H0YNQ8;O00160;H0YN00;H0YLE5;H0YLJ4;M0QXU2 Unconventional myosin-Ie MYO1E >sp|Q12965|MYO1E_HUMAN Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2 0.06 0.08 0.09 0.11 -0.49 -0.04 0.40 0.03 0.226228539 0.109711419 actin filament-based movement;actin filament-based process;anatomical structure development;biological regulation;cell activation;cell activation involved in immune response;cell development;cell differentiation;cell surface receptor linked signaling pathway;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cellular response to stimulus;chordate embryonic development;defense response;defense response to bacterium;defense response to Gram-positive bacterium;developmental process;embryo development;embryo development ending in birth or egg hatching;endocytosis;enzyme linked receptor protein signaling pathway;epithelial cell development;establishment of localization;establishment of localization in cell;exocytosis;extracellular matrix organization;extracellular structure organization;glomerular basement membrane development;glomerular epithelial cell development;glomerular filtration;glomerular visceral epithelial cell development;hemopoiesis;hemopoietic or lymphoid organ development;immune effector process;immune system process;in utero embryonic development;leukocyte activation;leukocyte activation involved in immune response;leukocyte degranulation;membrane invagination;membrane organization;multicellular organismal process;multi-organism process;myeloid cell activation involved in immune response;myeloid leukocyte activation;negative regulation of biological process;negative regulation of cell adhesion;negative regulation of cellular process;neutrophil activation;neutrophil activation involved in immune response;neutrophil degranulation;organ development;platelet-derived growth factor receptor signaling pathway;positive regulation of biological process;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cellular component movement;positive regulation of cellular process;positive regulation of locomotion;post-embryonic hemopoiesis;post-embryonic organ development;regulated secretory pathway;regulation of actin cytoskeleton organization;regulation of actin filament-based process;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of cytoskeleton organization;regulation of defense response;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of localization;regulation of locomotion;regulation of organelle organization;regulation of response to stimulus;regulation of response to stress;renal system process;response to bacterium;response to biotic stimulus;response to other organism;response to stimulus;response to stress;secretion;secretion by cell;signal transduction;system process;transmembrane receptor protein tyrosine kinase signaling pathway;transport;vasculogenesis;vesicle-mediated transport "actin binding;actin filament binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;calmodulin binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;lipid binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;phosphatidylinositol binding;phospholipid binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" adherens junction;anchoring junction;cell cortex part;cell junction;cell part;cell-cell junction;clathrin-coated vesicle;coated vesicle;cortical actin cytoskeleton;cortical cytoskeleton;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytoskeleton;filamentous actin;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;myosin complex;non-membrane-bounded organelle;organelle;organelle part;protein complex;unconventional myosin complex;vesicle 5.74E-282 7 35 35 34.8

P11498;B4DN00;E9PRE7;E9PS68 "Pyruvate carboxylase, mitochondrial" PC ">sp|P11498|PYC_HUMAN Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2" -0.18 -0.17 0.21 0.09 -0.83 -0.22 0.06 0.17 0.315442565 0.193603933 alcohol biosynthetic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular ketone metabolic process;cellular metabolic process;cellular process;dicarboxylic acid metabolic process;gluconeogenesis;glucose metabolic process;hexose biosynthetic process;hexose metabolic process;lipid metabolic process;metabolic process;monocarboxylic acid metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;organic acid metabolic process;oxaloacetate metabolic process;oxoacid metabolic process;primary metabolic process;pyruvate metabolic process;small molecule biosynthetic process;small molecule metabolic process"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;biotin binding;biotin carboxylase activity;carboxylic acid binding;catalytic activity;cation binding;DNA binding;ion binding;ligase activity;ligase activity, forming carbon-carbon bonds;ligase activity, forming carbon-nitrogen bonds;metal ion binding;monocarboxylic acid binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyruvate carboxylase activity;ribonucleotide binding;vitamin binding" cell part;cytoplasmic part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;mitochondrial inner membrane;mitochondrial matrix;mitochondrial membrane;mitochondrial part;organelle inner membrane;organelle lumen;organelle membrane;organelle part Citrate cycle (TCA cycle);Pyruvate metabolism 1.77E-291 4 35 35 42.1

Q9Y446;E9PKC4;E9PRW6;E9PK71;E9PJR7;E9PQ15;H0YEY5 Plakophilin-3 PKP3 >sp|Q9Y446|PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1 -0.15 0.49 0.35 0.71 -0.96 0.22 -0.16 0.12 0.722829595 0.545437381 biological adhesion;cell adhesion;cellular process anchoring junction;cell junction;cell part;cell-cell junction;desmosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 1.15E-279 7 35 35 53.2

Q6P2Q9;I3L0J9;I3L3Z8 Pre-mRNA-processing-splicing factor 8 PRPF8 >sp|Q6P2Q9|PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 0.17 0.37 0.00 0.26 0.00 -0.33 -0.91 -0.44 1.247074539 0.619961017 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;nucleic acid binding;RNA binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;small nuclear ribonucleoprotein complex;spliceosomal complex;U5 snRNP Spliceosome 2.93E-232 3 35 35 21.2

P47897;B4DWJ2;C9J165;H7C0R3;B7Z840;C9JSG9;F2Z2V6 Glutamine--tRNA ligase QARS >sp|P47897|SYQ_HUMAN Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1;>tr|B4DWJ2|B4DWJ2_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=QARS PE=2 SV=1 0.03 -0.02 -0.10 -0.02 0.02 -0.02 0.11 -0.11 0.200644678 -0.028402442 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;glutaminyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;glutamine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;mitochondrial matrix;mitochondrial part;organelle lumen;organelle part Aminoacyl-tRNA biosynthesis 3.93E-248 7 35 35 51.9

P04843;B7Z4L4;F8WF32 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 RPN1 >sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1;>tr|B7Z4L4|B7Z4L4_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=2 S-0.20 0.08 -0.25 -0.02 0.73 0.52 -0.38 0.02 0.502816144 -0.315536145 biosynthetic process;carbohydrate metabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cotranslational protein targeting to membrane;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in endoplasmic reticulum;establishment of protein localization to organelle;glycosylation;intracellular protein transport;intracellular transport;macromolecule biosynthetic process;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;post-translational protein modification;primary metabolic process;protein glycosylation;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein targeting;protein targeting to ER;protein targeting to membrane;protein transport;SRP-dependent cotranslational protein targeting to membrane;translation;transport "catalytic activity;dolichyl-diphosphooligosaccharide-protein glycotransferase activity;oligosaccharyl transferase activity;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;oligosaccharyltransferase complex;organelle;organelle membrane;organelle part;pigment granule;protein complex;rough endoplasmic reticulum;vesicle N-Glycan biosynthesis;Protein processing in endoplasmic reticulum;Various types of N-glycan biosynthesis 1.13E-250 3 35 35 62.4

P49792;A6NKT7;J3KNE0;Q7Z3J3;J3KNY6;J3KQ37;O14715;P0DJD0;J3QTV4;P0DJD1;F8VYC4;Q99666;Q99666-2;F8W705;F8WBP7;H7BZ48 E3 SUMO-protein ligase RanBP2;Putative peptidyl-prolyl cis-trans isomerase RANBP2 >sp|P49792|RBP2_HUMAN E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 0.12 0.24 0.04 0.14 0.04 -0.30 -0.82 -0.29 1.096891208 0.47815844 "anaphase;biological regulation;carbohydrate metabolic process;carbohydrate transport;cell cycle phase;cell cycle process;cell surface receptor linked signaling pathway;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to organic substance;cellular response to stimulus;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in Golgi;establishment of protein localization to organelle;establishment of RNA localization;glucose transport;Golgi vesicle transport;hexose transport;intracellular protein transport;intracellular transport;intra-Golgi vesicle-mediated transport;M phase;M phase of mitotic cell cycle;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;mitotic prometaphase;monosaccharide transport;mRNA transport;nuclear import;nuclear transport;nucleic acid transport;nucleobase-containing compound transport;nucleocytoplasmic transport;organic substance transport;peptidyl-amino acid modification;peptidyl-proline modification;primary metabolic process;protein folding;protein import;protein import into nucleus;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein peptidyl-prolyl isomerization;protein sumoylation;protein targeting;protein targeting to Golgi;protein transport;regulation of biological process;regulation of cellular process;regulation of glucose transport;regulation of localization;regulation of transport;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to organic substance;response to stimulus;retrograde transport, vesicle recycling within Golgi;RNA transport;signal transduction;small molecule metabolic process;transmembrane transport;transport;vesicle-mediated transport;viral reproductive process" binding;catalytic activity;cation binding;cis-trans isomerase activity;enzyme binding;GTPase binding;ion binding;isomerase activity;ligase activity;metal ion binding;peptidyl-prolyl cis-trans isomerase activity;protein binding;Ran GTPase binding;Ras GTPase binding;small GTPase binding;transition metal ion binding;zinc ion binding cell part;cytoplasm;cytoplasmic part;cytosol;inclusion body;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;nuclear inclusion body;nuclear membrane;nuclear part;nuclear pore;organelle membrane;organelle part;pore complex;protein complex RNA transport 5.86E-227 16 36 35 16.5

Q9NR30;Q9NR30-2;P48995-2;P48995;REV__Q86X10-4;REV__Q86X10-2;REV__A2A2F0;REV__O15399;REV__Q86X10-3;REV__A2A2E9;REV__Q86X10 Nucleolar RNA helicase 2 DDX21 >sp|Q9NR30|DDX21_HUMAN Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5;>sp|Q9NR30-2|DDX21_HUMAN Isoform 2 of Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 -0.19 0.97 -0.13 0.78 -0.63 -0.17 -1.21 0.08 0.868603522 0.84287183 axon guidance;biological regulation;body fluid secretion;calcium ion homeostasis;cation homeostasis;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metal ion homeostasis;cellular process;chemical homeostasis;chemotaxis;cytosolic calcium ion homeostasis;digestive system process;divalent inorganic cation homeostasis;establishment of localization;homeostatic process;ion homeostasis;locomotion;metal ion homeostasis;multicellular organismal process;multi-organism process;positive regulation of biological process;positive regulation of calcium ion transport;positive regulation of calcium ion transport into cytosol;positive regulation of cellular process;positive regulation of homeostatic process;positive regulation of ion transport;positive regulation of release of sequestered calcium ion into cytosol;positive regulation of transport;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cellular process;regulation of homeostatic process;regulation of ion homeostasis;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of release of sequestered calcium ion into cytosol;regulation of transport;response to biotic stimulus;response to calcium ion;response to chemical stimulus;response to dsRNA;response to exogenous dsRNA;response to external stimulus;response to inorganic substance;response to metal ion;response to organic substance;response to other organism;response to stimulus;response to virus;saliva secretion;secretion;system process;taxis;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;alcohol binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;calcium channel activity;catalytic activity;cation channel activity;cation transmembrane transporter activity;channel activity;double-stranded RNA binding;gated channel activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inositol 1,4,5 trisphosphate binding;ion channel activity;ion transmembrane transporter activity;ligand-gated channel activity;ligand-gated ion channel activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;passive transmembrane transporter activity;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;store-operated calcium channel activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" basolateral plasma membrane;cell part;contractile fiber part;costamere;cytoplasmic part;integral to membrane;integral to plasma membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane part;membrane raft;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane part;protein complex;sarcomere Calcium signaling pathway;Pancreatic secretion 4.54E-276 11 38 35 53.5

P23246;P23246-2;H0Y9K7;H0Y9U2 "Splicing factor, proline- and glutamine-rich" SFPQ ">sp|P23246|SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2;>sp|P23246-2|SFPQ_HUMAN Isoform Short of Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ" -0.16 0.61 0.10 0.59 0.00 0.12 -1.23 -0.16 0.709835764 0.602960848 "alternative nuclear mRNA splicing, via spliceosome;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;DNA metabolic process;DNA recombination;DNA repair;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to DNA damage stimulus;response to stimulus;response to stress;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;transcription, DNA-dependent" binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding cell part;cytoplasm;intracellular organelle part;intracellular part;nuclear body;nuclear matrix;nuclear part;nucleoplasm part;organelle part;paraspeckles 0 4 38 35 51.8

Q99460;Q99460-2;C9J9M4;H7BZR6;H7C378;F8WCE3 26S proteasome non-ATPase regulatory subunit 1 PSMD1 >sp|Q99460|PSMD1_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2;>sp|Q99460-2|PSMD1_HUMAN Isoform 2 of 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 0.07 0.01 -0.12 -0.05 0.20 0.18 0.01 -0.01 0.74983666 -0.120740093 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" enzyme regulator activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome regulatory particle;protein complexProteasome 1.70E-274 6 36 36 47.1

G5EA52;P30101 Protein disulfide-isomerase A3 PDIA3 ">tr|G5EA52|G5EA52_HUMAN Protein disulfide isomerase family A, member 3, isoform CRA_b OS=Homo sapiens GN=PDIA3 PE=2 SV=1;>sp|P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4" -0.02 -0.15 -0.40 -0.22 0.31 -0.16 0.58 -0.03 0.870436841 -0.374654131 "antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;biological regulation;carbohydrate metabolic process;cell redox homeostasis;cellular carbohydrate metabolic process;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;establishment of localization;establishment of localization in cell;establishment of protein localization;glycerol ether metabolic process;glycosylation;homeostatic process;immune system process;intracellular protein transport;intracellular transport;macromolecule glycosylation;macromolecule metabolic process;macromolecule modification;maintenance of location;maintenance of location in cell;maintenance of protein localization in endoplasmic reticulum;maintenance of protein localization to organelle;maintenance of protein location;maintenance of protein location in cell;metabolic process;nuclear import;nuclear transport;nucleocytoplasmic transport;organic ether metabolic process;peptidyl-amino acid modification;peptidyl-asparagine modification;positive regulation of apoptosis;positive regulation of biological process;positive regulation of cell death;positive regulation of cellular process;positive regulation of programmed cell death;post-translational protein modification;primary metabolic process;protein glycosylation;protein import;protein import into nucleus;protein metabolic process;protein modification process;protein N-linked glycosylation;protein N-linked glycosylation via asparagine;protein retention in ER lumen;protein targeting;protein transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell death;regulation of cellular process;regulation of programmed cell death;response to stimulus;signal transduction;small molecule metabolic process;transport" "catalytic activity;cysteine-type endopeptidase activity;cysteine-type peptidase activity;disulfide oxidoreductase activity;electron carrier activity;endopeptidase activity;hydrolase activity;hydrolase activity, acting on ester bonds;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;lipase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;peptidase activity;peptidase activity, acting on L-amino acid peptides;phospholipase activity;phospholipase C activity;phosphoric diester hydrolase activity;phosphoric ester hydrolase activity;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;vesicle Antigen processing and presentation;Protein processing in endoplasmic reticulum 0 2 43 36 75.1

E7EVA0;P27816;P27816-6;P27816-2;B9ZVR1;E9PGM5;P27816-4;B5MEG9;H0Y2V1;F8W9U4;H7C456;B4DSQ1;P27816-7 Microtubule-associated protein;Microtubule-associated protein 4MAP4 >tr|E7EVA0|E7EVA0_HUMAN Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=2 SV=1;>sp|P27816|MAP4_HUMAN Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3;>sp|P27816-6|MAP4_HUMAN Isoform 6 of Microtubule-associated protein 4 OS=Homo -0.65 -0.17 -0.01 0.04 0.34 0.63 0.15 0.30 1.222735967 -0.552108943 cell cycle process;cell division;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of spindle localization;establishment of spindle orientation;microtubule cytoskeleton organization;microtubule sliding;microtubule-based movement;microtubule-based process;mitotic spindle organization;organelle organization;spindle organization structural molecule activity cell part;cytoplasm;cytoskeletal part;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;microtubule associated complex;microtubule cytoskeleton;mitotic spindle;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;spindle 0 13 73 36 34.6

P58107 Epiplakin EPPK1 >sp|P58107|EPIPL_HUMAN Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 -0.55 -0.47 0.61 0.31 -0.31 0.01 0.24 -0.75 0.18402441 0.178065807 structural molecule activity cell part;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 0 1 154 36 73.7

P04406;P04406-2;E7EUT5;O14556 Glyceraldehyde-3-phosphate dehydrogenase GAPDH >sp|P04406|G3P_HUMAN Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3;>sp|P04406-2|G3P_HUMAN Isoform 2 of Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH;>tr|E7EUT5|E7EUT5_HUMAN Glyceraldehyde-3-phosphate dehydr 0.22 -0.11 -0.07 0.01 -0.19 -0.26 0.19 -0.17 0.403237422 0.122617532 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;anatomical structure development;apoptosis;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cell death;cell development;cell motility;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;death;developmental process;developmental process involved in reproduction;generation of precursor metabolites and energy;germ cell development;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;locomotion;macromolecule metabolic process;macromolecule modification;metabolic process;microtubule cytoskeleton organization;microtubule-based process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;neuron apoptosis;neuron death;organelle organization;peptidyl-amino acid modification;peptidyl-cysteine modification;peptidyl-cysteine S-nitrosylation;peptidyl-cysteine S-trans-nitrosylation;positive regulation of biological process;positive regulation of carbohydrate metabolic process;positive regulation of catabolic process;positive regulation of cellular carbohydrate metabolic process;positive regulation of cellular catabolic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of glucose metabolic process;positive regulation of glycolysis;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;programmed cell death;protein metabolic process;protein modification process;protein nitrosylation;protein stabilization;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of carbohydrate catabolic process;regulation of carbohydrate metabolic process;regulation of catabolic process;regulation of cellular biosynthetic process;regulation of cellular carbohydrate catabolic process;regulation of cellular carbohydrate metabolic process;regulation of cellular catabolic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of generation of precursor metabolites and energy;regulation of glucose metabolic process;regulation of glycolysis;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of protein stability;regulation of translation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;sperm motility;spermatid development "binding;catalytic activity;coenzyme binding;cofactor binding;cytoskeletal protein binding;glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity;microtubule binding;NAD binding;NADP binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the aldehyde or oxo group of donors;oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor;peptidyl-cysteine S-nitrosylase activity;protein binding;transferase activity;transferase activity, transferring nitrogenous groups;tubulin binding" cell part;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lipid particle;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;microtubule cytoskeleton;non-membrane-bounded organelle;nucleus;organelle;perinuclear region of cytoplasm;plasma membrane;ribonucleoprotein complex;vesicle Alzheimer's disease;Glycolysis / Gluconeogenesis 0 4 37 37 83.9

P23229-4;P23229-2;P23229-5;P23229-3;P23229-9;P23229-6;P23229;P23229-7;H7BZ97;C9JXX7 Integrin alpha-6;Integrin alpha-6 heavy chain;Integrin alpha-6 light chain ITGA6 >sp|P23229-4|ITA6_HUMAN Isoform Alpha-6X2A of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;>sp|P23229-2|ITA6_HUMAN Isoform Alpha-6X1A of Integrin alpha-6 OS=Homo sapiens GN=ITGA6;>sp|P23229-5|ITA6_HUMAN Isoform Alpha-6X2B of Integrin alpha-6 OS=Homo sapiens G -0.14 0.32 -0.12 0.52 -1.63 -0.06 -0.71 -0.01 0.781299538 0.75066961 "anatomical structure morphogenesis;biological adhesion;biological regulation;blood coagulation;brown fat cell differentiation;cell adhesion;cell adhesion mediated by integrin;cell communication;cell differentiation;cell junction assembly;cell junction organization;cell migration;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to stimulus;coagulation;developmental process;extracellular matrix organization;extracellular structure organization;fat cell differentiation;filopodium assembly;hemidesmosome assembly;hemostasis;immune system process;integrin-mediated signaling pathway;leukocyte migration;locomotion;microspike assembly;multicellular organismal process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;odontogenesis;odontogenesis of dentine-containing tooth;organ morphogenesis;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell adhesion;positive regulation of cell death;positive regulation of cell-cell adhesion;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of phosphate metabolic process;positive regulation of phosphorus metabolic process;positive regulation of phosphorylation;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of body fluid levels;regulation of cell adhesion;regulation of cell death;regulation of cell-cell adhesion;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to external stimulus;response to extracellular stimulus;response to stimulus;signal transduction" binding;cation binding;ion binding;metal ion binding basal plasma membrane;basement membrane;cell junction;cell part;cell-substrate junction;external side of plasma membrane;extracellular matrix part;extracellular region part;hemidesmosome;integrin complex;macromolecular complex;membrane;membrane part;plasma membrane;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Cell adhesion molecules (CAMs);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hematopoietic cell lineage;Hypertrophic cardiomyopathy (HCM);Pathways in cancer;Regulation of actin cytoskeleton;Small cell lung cancer;Toxoplasmosis 8.85E-270 10 37 37 41.6

P25705;P25705-2;K7ENP3;K7EK77;K7ENJ4;K7ERX7;K7EJP1;K7EQH4;K7ESA0;REV__C9JJM9;REV__C9JD81;REV__C9J3W7;REV__C9JBN7;REV__C9JEW7;REV__F8WDL9;REV__C9J7X7;REV__C9J718;REV__C9JF32;REV__C9JRT6;REV__F8WDB6;REV__Q8TBF8;Q32P41;REV__O00522-3;REV__O00522 "ATP synthase subunit alpha, mitochondrial;ATP synthase subunit alpha" ATP5A1 ">sp|P25705|ATPA_HUMAN ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1;>sp|P25705-2|ATPA_HUMAN Isoform 2 of ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1;>tr|K7ENP3|K7ENP3_HUMAN ATP synthase subunit alpha" -0.28 0.12 0.10 0.24 0.21 0.09 -1.12 -0.35 0.433573179 0.338898953 "ATP biosynthetic process;ATP hydrolysis coupled proton transport;ATP metabolic process;ATP synthesis coupled proton transport;biological regulation;biosynthetic process;cation transport;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;developmental process;electron transport chain;embryo development;energy coupled proton transport, against electrochemical gradient;energy coupled proton transport, down electrochemical gradient;establishment of localization;establishment of localization in cell;generation of precursor metabolites and energy;heterocycle biosynthetic process;heterocycle metabolic process;hydrogen transport;intracellular transport;ion transmembrane transport;ion transport;lipid metabolic process;metabolic process;mitochondrial ATP synthesis coupled proton transport;mitochondrial transport;monovalent inorganic cation transport;negative regulation of biological process;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell proliferation;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;oxidation-reduction process;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regulation of biological process;regulation of cell proliferation;regulation of cellular process;regulation of endothelial cell proliferation;regulation of epithelial cell proliferation;respiratory electron transport chain;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;transmembrane transport;transport" "active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation transmembrane transporter activity;cation-transporting ATPase activity;cell surface binding;eukaryotic cell surface binding;hydrogen ion transmembrane transporter activity;hydrogen ion transporting ATP synthase activity, rotational mechanism;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;inorganic cation transmembrane transporter activity;ion transmembrane transporter activity;MHC class I protein binding;MHC protein binding;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;proton-transporting ATPase activity, rotational mechanism;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleotide binding;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" "cell part;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-enclosed lumen;mitochondrial matrix;mitochondrial membrane part;mitochondrial part;mitochondrial proton-transporting ATP synthase complex;nucleus;organelle;organelle lumen;organelle part;plasma membrane;protein complex;proton-transporting ATP synthase complex;proton-transporting ATP synthase complex, catalytic core F(1);proton-transporting two-sector ATPase complex;proton-transporting two-sector ATPase complex, catalytic domain" Alzheimer's disease;Huntington's disease;Oxidative phosphorylation;Parkinson's disease 0 24 38 37 66

P48643;E7ENZ3;B7ZAR1;E9PCA1;B4DYD8;D6RIZ7;H0Y914 T-complex protein 1 subunit epsilon CCT5 >sp|P48643|TCPE_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1;>tr|E7ENZ3|E7ENZ3_HUMAN T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1;>tr|B7ZAR1|B7ZAR1_HUMAN T-complex protein 1 subunit epsilon OS=Homo sa 0.16 0.00 -0.07 -0.02 -0.01 -0.38 -0.04 -0.50 0.811331584 0.249295052 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;multi-organism process;primary metabolic process;protein folding;protein metabolic process;response to biotic stimulus;response to other organism;response to stimulus;response to virusadenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;centrosome;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex 0 7 38 37 77.8

P11142;E9PKE3;E9PNE6;P11142-2;A8K7Q2;E9PN89;E9PLF4;E9PS65;E9PQQ4;E9PQK7;E9PK54;E9PPY6;E9PN25;E9PM13;E9PI65 Heat shock cognate 71 kDa protein HSPA8 >sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1;>tr|E9PKE3|E9PKE3_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=2 SV=1;>tr|E9PNE6|E9PNE6_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapie 0.12 0.08 -0.17 0.05 -0.44 -0.21 0.04 -0.20 0.807616759 0.22394615 "biological regulation;biosynthetic process;cellular biosynthetic process;cellular component organization;cellular component organization or biogenesis;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;chaperone mediated protein folding requiring cofactor;chaperone-mediated protein folding;'de novo' posttranslational protein folding;'de novo' protein folding;establishment of localization;establishment of localization in cell;gene expression;Golgi vesicle transport;interaction with host;interspecies interaction between organisms;intracellular transport;macromolecule biosynthetic process;macromolecule metabolic process;membrane organization;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;neurotransmitter secretion;neurotransmitter transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;post-Golgi vesicle-mediated transport;primary metabolic process;protein folding;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell cycle;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of neurotransmitter levels;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to chemical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;RNA biosynthetic process;RNA metabolic process;RNA processing;RNA splicing;secretion;secretion by cell;signal release;transcription, DNA-dependent;transport;vesicle-mediated transport;viral reproductive process;virus-host interaction" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" cell part;cell surface;clathrin coated vesicle membrane;clathrin sculpted gamma-aminobutyric acid transport vesicle membrane;coated vesicle membrane;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle membrane;cytoplasmic vesicle part;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle membrane;organelle part;pigment granule;plasma membrane;protein complex;Prp19 complex;ribonucleoprotein complex;spliceosomal complex;vesicle;vesicle membrane Antigen processing and presentation;Endocytosis;MAPK signaling pathway;Measles;Protein processing in endoplasmic reticulum;Spliceosome;Toxoplasmosis 0 15 56 37 74

Q16658;J3KNT0;C9JFC0;H7BYX5;C9JPH9 Fascin FSCN1 >sp|Q16658|FSCN1_HUMAN Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3;>tr|J3KNT0|J3KNT0_HUMAN Fascin OS=Homo sapiens GN=FSCN1 PE=3 SV=1 0.24 -0.08 -0.09 -0.05 -0.27 -0.43 0.48 -0.25 0.203600764 0.11839774 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;cell migration;cell motility;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;locomotion;organelle organization actin binding;actin filament binding;binding;cytoskeletal protein binding;drug binding;protein binding actin filament bundle;actomyosin;cell junction;cell part;cell projection;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;invadopodium;non-membrane-bounded organelle;organelle;organelle part;stress fiber 0 5 38 38 74.2

P42224;P42224-2;J3KPM9;E7EPD2;D2KFR9;E7ENM1;E9PH66;H7BZB5;H7BZ88 Signal transducer and activator of transcription 1-alpha/betaSTAT1 >sp|P42224|STAT1_HUMAN Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2;>sp|P42224-2|STAT1_HUMAN Isoform Beta of Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1;>tr|J3KP 0.18 0.07 -0.02 0.00 -0.91 -0.56 0.06 -0.26 0.951549703 0.473800204 "anatomical structure development;biological regulation;biosynthetic process;blood circulation;cell differentiation;cell differentiation involved in kidney development;cell differentiation involved in metanephros development;cell proliferation;cell proliferation involved in kidney development;cell proliferation involved in metanephros development;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to biotic stimulus;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-beta;cellular response to interferon-gamma;cellular response to lipopolysaccharide;cellular response to molecule of bacterial origin;cellular response to organic substance;cellular response to stimulus;cellular response to tumor necrosis factor;cellular response to type I interferon;circulatory system process;cytokine-mediated signaling pathway;defense response;defense response to virus;developmental process;immune effector process;immune system process;induction of apoptosis;induction of programmed cell death;interaction with host;interferon-gamma-mediated signaling pathway;interspecies interaction between organisms;intracellular protein kinase cascade;intracellular signal transduction;JAK-STAT cascade;JAK-STAT cascade involved in growth hormone signaling pathway;kidney mesenchymal cell proliferation;lipopolysaccharide-mediated signaling pathway;macromolecule biosynthetic process;macromolecule metabolic process;mesenchymal cell differentiation;mesenchymal cell differentiation involved in kidney development;mesenchymal cell differentiation involved in renal system development;mesenchymal cell proliferation;metabolic process;metanephric mesenchymal cell differentiation;metanephric mesenchymal cell proliferation involved in metanephros development;multicellular organismal process;multi-organism process;negative regulation of angiogenesis;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell communication;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell morphogenesis involved in differentiation;negative regulation of cell proliferation;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of developmental process;negative regulation of endothelial cell proliferation;negative regulation of epithelial cell differentiation;negative regulation of epithelial cell differentiation involved in kidney development;negative regulation of epithelial cell proliferation;negative regulation of gene expression;negative regulation of I-kappaB kinase/NF-kappaB cascade;negative regulation of intracellular protein kinase cascade;negative regulation of kidney development;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis;negative regulation of metabolic process;negative regulation of metanephric nephron tubule epithelial cell differentiation;negative regulation of multicellular organismal process;negative regulation of nephron tubule epithelial cell differentiation;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of response to stimulus;negative regulation of RNA metabolic process;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cell proliferation;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of mesenchymal cell proliferation;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of smooth muscle cell proliferation;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of biological process;regulation of biosynthetic process;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of developmental process;regulation of endothelial cell proliferation;regulation of epithelial cell differentiation;regulation of epithelial cell differentiation involved in kidney development;regulation of epithelial cell proliferation;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-gamma-mediated signaling pathway;regulation of intracellular protein kinase cascade;regulation of kidney development;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of mesenchymal cell proliferation;regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis;regulation of metabolic process;regulation of metanephric nephron tubule epithelial cell differentiation;regulation of metanephros development;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nephron tubule epithelial cell differentiation;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of organ morphogenesis;regulation of primary metabolic process;regulation of programmed cell death;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of RNA metabolic process;regulation of signal transduction;regulation of signaling;regulation of smooth muscle cell proliferation;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of type I interferon-mediated signaling pathway;renal tubule development;reproductive process;response to biotic stimulus;response to cAMP;response to chemical stimulus;response to cytokine stimulus;response to dsRNA;response to exogenous dsRNA;response to interferon-beta;response to interferon-gamma;response to lipopolysaccharide;response to molecule of bacterial origin;response to organic substance;response to other organism;response to stimulus;response to stress;response to tumor necrosis factor;response to type I interferon;response to virus;RNA biosynthetic process;RNA metabolic process;signal transduction;system process;transcription, DNA-dependent;tube development;tumor necrosis factor-mediated signaling pathway;type I interferon-mediated signaling pathway;viral reproductive process;virus-host interaction" binding;calcium ion binding;cation binding;core promoter binding;core promoter proximal region DNA binding;core promoter proximal region sequence-specific DNA binding;core promoter sequence-specific DNA binding;DNA binding;double-stranded DNA binding;identical protein binding;ion binding;metal ion binding;molecular transducer activity;nucleic acid binding;nucleic acid binding transcription factor activity;protein binding;protein dimerization activity;protein homodimerization activity;regulatory region DNA binding;regulatory region nucleic acid binding;RNA polymerase II core promoter proximal region sequence-specific DNA binding;RNA polymerase II core promoter sequence-specific DNA binding;RNA polymerase II core promoter sequence-specific DNA binding transcription factor activity;RNA polymerase II regulatory region DNA binding;RNA polymerase II regulatory region sequence-specific DNA binding;sequence-specific DNA binding;sequence-specific DNA binding RNA polymerase II transcription factor activity;sequence-specific DNA binding transcription factor activity;signal transducer activity;structure-specific DNA binding;transcription regulatory region DNA binding;transcription regulatory region sequence-specific DNA binding axon;cell part;cell projection;chromatin;chromosomal part;cytoplasm;cytoplasmic part;cytosol;dendrite;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane-bounded organelle;neuron projection;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear part;nucleolus;nucleoplasm;nucleus;organelle;organelle part Chemokine signaling pathway;Hepatitis C;Jak-STAT signaling pathway;ko05152;Leishmaniasis;Measles;Osteoclast differentiation;Pancreatic cancer;Pathways in cancer;Toll-like receptor signaling pathway;Toxoplasmosis 0 9 38 38 49.6

P26639;P26639-2;G3XAN9;E7ERI3;D6R9F8;D6RCA5;D6RDJ6;A2RTX5-2;A2RTX5;D6RBR8;B7ZLP8;D6RJ97;D6RHV7;D6RCS6;H0YK98 "Threonine--tRNA ligase, cytoplasmic" TARS ">sp|P26639|SYTC_HUMAN Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3;>sp|P26639-2|SYTC_HUMAN Isoform 2 of Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS;>tr|G3XAN9|G3XAN9_HUMAN Threonine--tRNA ligase, cytoplasmic OS=Homo" 0.06 -0.13 0.05 -0.04 -0.15 -0.17 0.52 0.09 0.192065374 -0.086594359 amine metabolic process;amino acid activation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;RNA metabolic process;small molecule metabolic process;threonyl-tRNA aminoacylation;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;identical protein binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;threonine-tRNA ligase activity" actin cytoskeleton;cell part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle Aminoacyl-tRNA biosynthesis 7.24E-283 15 39 38 57.4

P49368;P49368-2;B4DUR8;E9PRC8;Q5SZX6;E9PM09;E9PQ35;Q5SZX9;Q5SZW8 T-complex protein 1 subunit gamma CCT3 >sp|P49368|TCPG_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4;>sp|P49368-2|TCPG_HUMAN Isoform 2 of T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3;>tr|B4DUR8|B4DUR8_HUMAN T-complex protein 1 subunit gamma OS=Homo sapie 0.20 -0.01 -0.04 -0.04 -0.03 -0.32 0.05 -0.44 0.695512084 0.211979296 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular organelle part;intracellular part;macromolecular complex;membrane;microtubule;organelle part;plasma membrane;protein complex 0 9 40 38 69.5

Q92598-2;Q92598;Q92598-3;B4DYH1;B4DY72;R4GN69;Q5TBM3;O95754-2;O95754;Q8TDX9 Heat shock protein 105 kDa HSPH1 >sp|Q92598-2|HS105_HUMAN Isoform Beta of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1;>sp|Q92598|HS105_HUMAN Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1;>sp|Q92598-3|HS105_HUMAN Isoform 3 of Heat shock protein 105 kDa OS=Homo sapie 0.24 0.18 -0.14 -0.04 -0.39 -0.28 0.10 -0.29 0.837125985 0.273289598 axis specification;axon guidance;biological adhesion;biological regulation;cell adhesion;cell communication;cell-cell adhesion;cell-cell signaling;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chaperone mediated protein folding requiring cofactor;chaperone-mediated protein folding;chemotaxis;'de novo' posttranslational protein folding;'de novo' protein folding;detection of abiotic stimulus;detection of endogenous stimulus;detection of external stimulus;detection of mechanical stimulus;detection of nodal flow;detection of stimulus;developmental process;left/right axis specification;locomotion;macromolecule metabolic process;metabolic process;negative regulation of axon extension;negative regulation of axonogenesis;negative regulation of biological process;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell growth;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of developmental growth;negative regulation of developmental process;negative regulation of growth;negative regulation of neurogenesis;pattern specification process;positive regulation of alpha-beta T cell activation;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell activation;positive regulation of cellular process;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of lymphocyte activation;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of MHC class I biosynthetic process;positive regulation of NK T cell activation;positive regulation of T cell activation;primary metabolic process;protein folding;protein metabolic process;regulation of alpha-beta T cell activation;regulation of anatomical structure morphogenesis;regulation of axon extension;regulation of axonogenesis;regulation of biological process;regulation of biosynthetic process;regulation of cell activation;regulation of cell development;regulation of cell differentiation;regulation of cell growth;regulation of cell morphogenesis;regulation of cell morphogenesis involved in differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental growth;regulation of developmental process;regulation of extent of cell growth;regulation of growth;regulation of immune system process;regulation of leukocyte activation;regulation of lymphocyte activation;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of MHC class I biosynthetic process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;regulation of NK T cell activation;regulation of T cell activation;response to abiotic stimulus;response to chemical stimulus;response to endogenous stimulus;response to external stimulus;response to mechanical stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;retinal ganglion cell axon guidance;signaling;taxis adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium channel activity;cation channel activity;cation transmembrane transporter activity;channel activity;ion channel activity;ion transmembrane transporter activity;nucleotide binding;passive transmembrane transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;ribonucleotide binding;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity cell part;cell projection;cilium;cytoplasm;cytoplasmic part;cytoskeletal part;endoplasmic reticulum;extracellular region;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;nucleus;organelle;organelle part;plasma membrane part;postsynaptic membrane;protein complex;synapse part;synaptic membrane Axon guidance;Protein processing in endoplasmic reticulum 0 10 43 38 53.7

P04083;Q5T3N1;Q5T3N0 Annexin A1 ANXA1 >sp|P04083|ANXA1_HUMAN Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2 0.31 0.14 0.02 -0.14 0.26 0.52 0.54 -0.18 0.432472374 -0.202133999 acid secretion;alpha-beta T cell activation;alpha-beta T cell differentiation;anatomical structure development;arachidonic acid secretion;biological regulation;carboxylic acid transport;cell activation;cell cycle;cell differentiation;cell surface receptor linked signaling pathway;cellular component movement;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to corticosteroid stimulus;cellular response to endogenous stimulus;cellular response to glucocorticoid stimulus;cellular response to hormone stimulus;cellular response to hydrogen peroxide;cellular response to organic substance;cellular response to oxidative stress;cellular response to reactive oxygen species;cellular response to steroid hormone stimulus;cellular response to stimulus;cellular response to stress;defense response;developmental process;endocrine pancreas development;epidermal cell differentiation;epithelial cell differentiation;establishment of localization;establishment of localization in cell;estrous cycle phase;fatty acid transport;gliogenesis;hepatocyte differentiation;homeostasis of number of cells;homeostatic process;hormone secretion;hormone transport;icosanoid secretion;icosanoid transport;immune system process;inflammatory response;insulin secretion;keratinocyte differentiation;leukocyte activation;leukocyte differentiation;lipid transport;long-chain fatty acid transport;lymphocyte activation;lymphocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;monocarboxylic acid transport;myeloid cell homeostasis;negative regulation of acute inflammatory response;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of defense response;negative regulation of inflammatory response;negative regulation of programmed cell death;negative regulation of protein secretion;negative regulation of protein transport;negative regulation of response to external stimulus;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of transport;neurogenesis;neutrophil homeostasis;organic acid transport;organic substance transport;ovulation cycle process;peptide cross-linking;peptide hormone secretion;peptide secretion;peptide transport;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of fatty acid biosynthetic process;positive regulation of fatty acid metabolic process;positive regulation of lipid biosynthetic process;positive regulation of lipid metabolic process;positive regulation of metabolic process;positive regulation of myeloid cell apoptosis;positive regulation of neutrophil apoptosis;positive regulation of organelle organization;positive regulation of programmed cell death;positive regulation of prostaglandin biosynthetic process;positive regulation of transport;positive regulation of vesicle fusion;primary metabolic process;protein metabolic process;protein modification process;regulation of acute inflammatory response;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cell proliferation;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular ketone metabolic process;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of defense response;regulation of establishment of protein localization;regulation of fatty acid biosynthetic process;regulation of fatty acid metabolic process;regulation of homeostatic process;regulation of hormone levels;regulation of immune system process;regulation of inflammatory response;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of metabolic process;regulation of myeloid cell apoptosis;regulation of neutrophil apoptosis;regulation of organelle organization;regulation of primary metabolic process;regulation of programmed cell death;regulation of prostaglandin biosynthetic process;regulation of protein localization;regulation of protein secretion;regulation of protein transport;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of secretion;regulation of transport;regulation of vesicle fusion;regulation of vesicle-mediated transport;response to abiotic stimulus;response to chemical stimulus;response to corticosteroid stimulus;response to cytokine stimulus;response to drug;response to endogenous stimulus;response to estradiol stimulus;response to estrogen stimulus;response to glucocorticoid stimulus;response to hormone stimulus;response to hydrogen peroxide;response to inorganic substance;response to interleukin-1;response to ionizing radiation;response to organic substance;response to oxidative stress;response to peptide hormone stimulus;response to radiation;response to reactive oxygen species;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;response to X-ray;rhythmic process;secretion;secretion by cell;signal release;signal transduction;T cell activation;T cell differentiation;transport "binding;binding, bridging;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phospholipase A2 inhibitor activity;phospholipase inhibitor activity;phospholipid binding;protein binding;protein binding, bridging;receptor binding;structural molecule activity" basolateral plasma membrane;cell part;cell projection;cilium;cornified envelope;cytoplasm;cytoplasmic part;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular space;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrial membrane;mitochondrial part;non-membrane-bounded organelle;nucleus;organelle;organelle membrane;organelle part;plasma membrane;plasma membrane part;protein complex;sarcolemma;vesicle 0 3 39 39 84.7

P05023-4;P05023;P05023-3;P05023-2;M0R116;P13637;P13637-2;P13637-3;B1AKY9;P50993;Q5TC01;H0Y7C1;Q5TC02;Q13733;P54707;P54707-2;E9PRA5;P20648;M0QXF2;Q5TC05;REV__Q15772-1;REV__Q15772 Sodium/potassium-transporting ATPase subunit alpha-1 ATP1A1 >sp|P05023-4|AT1A1_HUMAN Isoform 4 of Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1;>sp|P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1;>sp|P05023-3|AT1A1_HUMAN Is -0.19 -0.06 -0.07 -0.05 -0.11 -0.12 -0.01 -0.36 0.259984582 0.054982252 "adult behavior;adult locomotory behavior;associative learning;ATP biosynthetic process;ATP hydrolysis coupled proton transport;ATP metabolic process;behavior;biological regulation;biosynthetic process;calcium ion homeostasis;cation homeostasis;cation transport;cell motility;cell surface receptor linked signaling pathway;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component movement;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular metabolic process;cellular metal ion homeostasis;cellular monovalent inorganic cation homeostasis;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular potassium ion transport;cellular process;cellular response to abiotic stimulus;cellular response to external stimulus;cellular response to mechanical stimulus;cellular response to stimulus;chemical homeostasis;cognition;cytosolic calcium ion homeostasis;divalent inorganic cation homeostasis;energy coupled proton transport, against electrochemical gradient;establishment of localization;fertilization;gamete generation;glutamate signaling pathway;heterocycle biosynthetic process;heterocycle metabolic process;homeostatic process;hydrogen transport;ion homeostasis;ion transmembrane transport;ion transport;ionotropic glutamate receptor signaling pathway;learning;learning or memory;locomotion;locomotory behavior;male gamete generation;membrane hyperpolarization;memory;metabolic process;metal ion homeostasis;metal ion transport;monovalent inorganic cation homeostasis;monovalent inorganic cation transport;multicellular organismal process;multicellular organismal reproductive process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of glucocorticoid biosynthetic process;negative regulation of glucocorticoid metabolic process;negative regulation of heart contraction;negative regulation of hormone biosynthetic process;negative regulation of hormone metabolic process;negative regulation of lipid biosynthetic process;negative regulation of lipid metabolic process;negative regulation of metabolic process;negative regulation of multicellular organismal process;negative regulation of muscle contraction;negative regulation of steroid biosynthetic process;negative regulation of steroid hormone biosynthetic process;negative regulation of steroid metabolic process;negative regulation of striated muscle contraction;neurological system process;neurotransmitter transport;neurotransmitter uptake;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;pH reduction;positive regulation of biological process;positive regulation of heart contraction;positive regulation of multicellular organismal process;positive regulation of muscle contraction;positive regulation of striated muscle contraction;potassium ion homeostasis;potassium ion import;potassium ion transmembrane transport;potassium ion transport;primary metabolic process;proton transport;purine nucleoside triphosphate biosynthetic process;purine nucleoside triphosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate biosynthetic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;reduction of cytosolic calcium ion concentration;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular pH;regulation of cellular process;regulation of glucocorticoid biosynthetic process;regulation of glucocorticoid metabolic process;regulation of heart contraction;regulation of hormone biosynthetic process;regulation of hormone metabolic process;regulation of ion transport;regulation of lipid biosynthetic process;regulation of lipid metabolic process;regulation of localization;regulation of membrane potential;regulation of metabolic process;regulation of metal ion transport;regulation of multicellular organismal process;regulation of muscle contraction;regulation of muscle system process;regulation of neurotransmitter levels;regulation of pH;regulation of primary metabolic process;regulation of proton transport;regulation of respiratory gaseous exchange;regulation of respiratory gaseous exchange by neurological system process;regulation of respiratory system process;regulation of smooth muscle contraction;regulation of sodium ion transport;regulation of steroid biosynthetic process;regulation of steroid hormone biosynthetic process;regulation of steroid metabolic process;regulation of striated muscle contraction;regulation of system process;regulation of the force of heart contraction;regulation of transport;regulation of vasoconstriction;reproductive process;response to abiotic stimulus;response to alkaloid;response to chemical stimulus;response to drug;response to external stimulus;response to light stimulus;response to mechanical stimulus;response to nicotine;response to organic cyclic compound;response to organic substance;response to radiation;response to stimulus;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process;sperm motility;spermatogenesis;system process;transmembrane transport;transport;visual behavior;visual learning" "4-nitrophenylphosphatase activity;active transmembrane transporter activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;alkali metal ion binding;ATP binding;ATPase activity;ATPase activity, coupled;ATPase activity, coupled to movement of substances;ATPase activity, coupled to transmembrane movement of ions;ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism;ATPase activity, coupled to transmembrane movement of substances;binding;catalytic activity;cation binding;cation transmembrane transporter activity;cation-transporting ATPase activity;chaperone binding;hydrogen ion transmembrane transporter activity;hydrogen:potassium-exchanging ATPase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;hydrolase activity, acting on ester bonds;inorganic cation transmembrane transporter activity;ion binding;ion transmembrane transporter activity;magnesium ion binding;metal ion binding;metal ion transmembrane transporter activity;monovalent inorganic cation transmembrane transporter activity;nucleoside-triphosphatase activity;nucleotide binding;phosphatase activity;phosphoric ester hydrolase activity;potassium ion binding;potassium ion transmembrane transporter activity;potassium-transporting ATPase activity;P-P-bond-hydrolysis-driven transmembrane transporter activity;primary active transmembrane transporter activity;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;sodium ion binding;sodium ion transmembrane transporter activity;sodium:potassium-exchanging ATPase activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transmembrane transporter activity;transporter activity" axon;basolateral plasma membrane;caveola;cell part;cell projection;cell projection part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;dendritic spine;endoplasmic reticulum;endosome;Golgi apparatus;hydrogen:potassium-exchanging ATPase complex;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;macromolecular complex;melanosome;membrane part;membrane raft;membrane-bounded organelle;membrane-bounded vesicle;myelin sheath;neuron projection;neuron spine;nucleus;organelle;pigment granule;plasma membrane part;protein complex;sodium:potassium-exchanging ATPase complex;synapse;T-tubule;vesicle Aldosterone-regulated sodium reabsorption;Bile secretion;Carbohydrate digestion and absorption;Cardiac muscle contraction;Collecting duct acid secretion;Endocrine and other factor-regulated calcium reabsorption;Gastric acid secretion;Mineral absorption;Oxidative phosphorylation;Pancreatic secretion;Protein digestion and absorption;Proximal tubule bicarbonate reclamation;Salivary secretion 0 22 39 39 40.7

Q14008-2;Q14008;Q14008-3;E9PQH5;H0YDX5;H0YCF6;H0YEK7Cytoskeleton-associated protein 5 CKAP5 >sp|Q14008-2|CKAP5_HUMAN Isoform 2 of Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5;>sp|Q14008|CKAP5_HUMAN Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3;>sp|Q14008-3|CKAP5_HUMAN Isoform 3 of Cytoskeleton-associated prote 0.19 0.07 -0.05 -0.13 0.17 -0.26 0.06 -0.50 0.354725306 0.148558556 anaphase;cell cycle phase;cell cycle process;cell division;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;centrosome organization;cytoskeleton organization;establishment of localization;establishment of RNA localization;establishment or maintenance of cell polarity;establishment or maintenance of cytoskeleton polarity;establishment or maintenance of microtubule cytoskeleton polarity;G2/M transition of mitotic cell cycle;M phase;M phase of mitotic cell cycle;microtubule cytoskeleton organization;microtubule organizing center organization;microtubule-based process;mitotic anaphase;mitotic prometaphase;nucleic acid transport;nucleobase-containing compound transport;organelle organization;RNA transport;spindle organization;transport cell part;centrosome;cytoplasmic part;cytoskeletal part;cytosol;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;spindle pole 7.11E-180 7 39 39 27.6

Q00839;Q00839-2;Q5RI18 Heterogeneous nuclear ribonucleoprotein U HNRNPU >sp|Q00839|HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6;>sp|Q00839-2|HNRPU_HUMAN Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU -0.25 0.85 0.05 0.90 -0.27 0.09 -1.34 -0.10 0.789748612 0.795400926 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;CRD-mediated mRNA stabilization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;DNA binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding catalytic step 2 spliceosome;cell part;cell surface;CRD-mediated mRNA stability complex;cytoplasmic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;protein complex;ribonucleoprotein complex;spliceosomal complex Spliceosome 0 3 39 39 40.7

Q7Z6Z7-3;Q7Z6Z7;Q7Z6Z7-2;H0Y5W0;H0Y659;Q5H962;H0Y7U1 E3 ubiquitin-protein ligase HUWE1 HUWE1 >sp|Q7Z6Z7-3|HUWE1_HUMAN Isoform 3 of E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1;>sp|Q7Z6Z7|HUWE1_HUMAN E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3;>sp|Q7Z6Z7-2|HUWE1_HUMAN Isoform 2 of E3 ubiquitin-protein ligase H 0.26 -0.13 0.03 -0.15 0.23 -0.32 0.39 -0.19 0.044573374 -0.025883612 base-excision repair;cell differentiation;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;chromatin modification;chromatin organization;chromosome organization;covalent chromatin modification;developmental process;DNA metabolic process;DNA repair;histone modification;histone ubiquitination;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein monoubiquitination;protein polyubiquitination;protein ubiquitination;protein ubiquitination involved in ubiquitin-dependent protein catabolic process;response to DNA damage stimulus;response to stimulus;response to stress "acid-amino acid ligase activity;binding;catalytic activity;DNA binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;nucleic acid binding;small conjugating protein ligase activity;ubiquitin-protein ligase activity" cell part;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle Ubiquitin mediated proteolysis 3.28E-278 7 39 39 15.1

P00558;B7Z7A9;E7ERH5;P07205 Phosphoglycerate kinase 1;Phosphoglycerate kinase PGK1 >sp|P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3;>tr|B7Z7A9|B7Z7A9_HUMAN Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1 -0.04 -0.08 -0.30 -0.03 -0.01 0.03 0.53 -0.02 0.703903976 -0.24167022 alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;primary metabolic process;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;kinase activity;nucleotide binding;phosphoglycerate kinase activity;phosphotransferase activity, carboxyl group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular part Carbon fixation in photosynthetic organisms;Glycolysis / Gluconeogenesis0 4 39 39 82.7

Q13435;E9PPJ0;E9PJ04;H0YCG1;E9PJT3;H0YEX5;E9PIL8 Splicing factor 3B subunit 2 SF3B2 >sp|Q13435|SF3B2_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2;>tr|E9PPJ0|E9PPJ0_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=2 SV=1 -0.18 0.51 0.06 0.44 0.19 0.08 -1.12 -0.49 0.670613251 0.539380582 "cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;reproductive process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;viral reproductive process;virus-host interaction" binding;nucleic acid binding catalytic step 2 spliceosome;cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm;nucleus;organelle;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome 9.77E-214 7 39 39 52.7

Q9UDY2;Q9UDY2-3;Q9UDY2-7;Q9UDY2-6;Q9UDY2-2;Q9UDY2-5;Q9UDY2-4;B1AN86;B1AN85 Tight junction protein ZO-2 TJP2 >sp|Q9UDY2|ZO2_HUMAN Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2;>sp|Q9UDY2-3|ZO2_HUMAN Isoform C1 of Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2;>sp|Q9UDY2-7|ZO2_HUMAN Isoform 7 of Tight junction protein ZO-2 OS=Homo sapiens GN=T 0.18 -0.01 0.22 -0.03 -0.35 -0.18 0.38 -0.10 0.372241139 0.154900241 biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;hippo signaling cascade;intracellular signal transduction;regulation of biological process;regulation of cellular process;response to stimulus;signal transduction "catalytic activity;guanylate kinase activity;kinase activity;nucleobase-containing compound kinase activity;nucleotide kinase activity;phosphotransferase activity, phosphate group as acceptor;transferase activity;transferase activity, transferring phosphorus-containing groups" adherens junction;anchoring junction;cell junction;cell part;cell-cell junction;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;membrane;nuclear part;nucleoplasm;occluding junction;organelle part;plasma membrane;tight junction Tight junction;Vibrio cholerae infection 5.07E-237 9 39 39 38.3

P29144;Q5VZU9 Tripeptidyl-peptidase 2 TPP2 >sp|P29144|TPP2_HUMAN Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4;>tr|Q5VZU9|Q5VZU9_HUMAN Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=2 SV=1 0.07 -0.11 -0.08 -0.08 0.06 -0.15 0.33 -0.13 0.254715109 -0.078668506 antigen processing and presentation;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;immune system process;macromolecule metabolic process;macromolecule modification;metabolic process;primary metabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis "aminopeptidase activity;catalytic activity;endopeptidase activity;exopeptidase activity;hydrolase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;serine hydrolase activity;serine-type endopeptidase activity;serine-type peptidase activity;tripeptidyl-peptidase activity" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 4.61E-287 2 39 39 40.5

P02787;J3KN47;H7C5E8;C9JVG0;F8WCI6;C9JB55;F8WEK9;CON__Q2HJF0;F8WC57 SerotransferrinTF >sp|P02787|TRFE_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3;>tr|J3KN47|J3KN47_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=4 SV=1 -3.14 3.03 -4.54 2.57 -4.81 -0.67 -2.65 2.19 0.143041198 0.965374798 biological regulation;cation homeostasis;cation transport;cell activation;cellular cation homeostasis;cellular chemical homeostasis;cellular homeostasis;cellular ion homeostasis;cellular iron ion homeostasis;cellular metal ion homeostasis;cellular process;chemical homeostasis;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;ferric iron transport;homeostatic process;ion homeostasis;ion transport;iron ion homeostasis;iron ion transport;metal ion homeostasis;metal ion transport;platelet activation;platelet degranulation;protein transport;regulation of biological quality;secretion;secretion by cell;transferrin transport;transition metal ion transport;transmembrane transport;transport;vesicle-mediated transport binding;cation binding;ferric iron binding;ion binding;iron ion binding;metal ion binding;transition metal ion binding apical plasma membrane;basal plasma membrane;cell part;coated pit;cytoplasmic membrane-bounded vesicle;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle;cytoplasmic vesicle part;early endosome;endocytic vesicle;endosomal part;endosome;endosome membrane;extracellular region;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;late endosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;mitochondrion;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane part;recycling endosome;secretory granule lumen;vesicle;vesicle lumen Mineral absorption 0 9 41 39 62.9

Q13085;Q13085-4;Q13085-3;Q13085-2;Q59FY4;K4DID9;O00763-2;F8W8T8;O00763;K7EK64;K7EII5;D3YTK0;K7EJ22;F6QQI9;H0YGH5;A8MYL5;K7EPF1;E9PEW7;K7EMF7 Acetyl-CoA carboxylase 1;Biotin carboxylase ACACA >sp|Q13085|ACACA_HUMAN Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2;>sp|Q13085-4|ACACA_HUMAN Isoform 4 of Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA;>sp|Q13085-3|ACACA_HUMAN Isoform 3 of Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACA 0.31 -0.02 -0.06 -0.23 -0.26 -0.45 0.53 -0.34 0.195566711 0.130422926 acetyl-CoA metabolic process;acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;amine transport;amino acid transmembrane transport;amino acid transport;anatomical structure homeostasis;betaine transport;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;carnitine shuttle;carnitine transport;cation transport;cellular biosynthetic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;chemical homeostasis;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;establishment of localization;establishment of localization in cell;fatty acid biosynthetic process;fatty acid metabolic process;fatty acid transport;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;generation of precursor metabolites and energy;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;homeostatic process;intracellular lipid transport;intracellular transport;ion transport;lipid biosynthetic process;lipid homeostasis;lipid metabolic process;lipid transport;long-chain fatty acid transport;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;mitochondrial transport;monocarboxylic acid metabolic process;monocarboxylic acid transport;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;multicellular organismal protein metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;nitrogen compound transport;organic acid biosynthetic process;organic acid metabolic process;organic acid transport;organic cation transport;organic ether metabolic process;organic substance transport;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein homooligomerization;protein homotetramerization;protein metabolic process;protein oligomerization;protein tetramerization;quaternary ammonium group transport;regulation of biological process;regulation of biological quality;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;small molecule biosynthetic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;tissue homeostasis;transmembrane transport;transport;triglyceride biosynthetic process;triglyceride metabolic process "acetyl-CoA carboxylase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;biotin carboxylase activity;catalytic activity;cation binding;CoA carboxylase activity;ion binding;ligase activity;ligase activity, forming carbon-carbon bonds;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;endomembrane system;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;organelle Fatty acid biosynthesis;Insulin signaling pathway;Propanoate metabolism;Pyruvate metabolism 1.02E-218 19 40 40 22.3

P22102;B4DJ93;P22102-2;F8WD69;C9JBJ1;C9JTV6;H7C489;C9JZG2;C9JKQ7;H7C366;H7C5I9 Trifunctional purine biosynthetic protein adenosine-3;Phosphoribosylamine--glycine ligase;Phosphoribosylformylglycinamidine cyclo-ligase;Phosphoribosylglycinamide formyltransferase GART >sp|P22102|PUR2_HUMAN Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1;>tr|B4DJ93|B4DJ93_HUMAN Phosphoribosylformylglycinamidine cyclo-ligase OS=Homo sapiens GN=GART PE=2 SV=1 0.17 -0.09 0.06 -0.01 -0.55 -0.71 0.17 -0.35 0.843298117 0.393991009 biosynthetic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;'de novo' IMP biosynthetic process;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;metabolic process;methylation;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;one-carbon metabolic process;pigment biosynthetic process;pigment metabolic process;primary metabolic process;purine base biosynthetic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;cyclo-ligase activity;hydroxymethyl-, formyl- and related transferase activity;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;methyltransferase activity;nucleotide binding;phosphoribosylamine-glycine ligase activity;phosphoribosylformylglycinamidine cyclo-ligase activity;phosphoribosylglycinamide formyltransferase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part One carbon pool by folate;Purine metabolism 3.95E-260 11 40 40 56

Q12906-7;Q12906;Q12906-4;Q12906-6;Q12906-5;Q12906-2;Q12906-3;K7EKJ9;K7EQR9;K7ER69;K7EKY0;K7ERM6;K7ENK6;K7EM82;K7EJ09;Q96SI9-2;Q96SI9;K7EPG3;K7ELV3;K7EQ75 Interleukin enhancer-binding factor 3 ILF3 >sp|Q12906-7|ILF3_HUMAN Isoform 7 of Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3;>sp|Q12906|ILF3_HUMAN Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3;>sp|Q12906-4|ILF3_HUMAN Isoform 4 of Interleukin enhancer-bindi -0.32 0.61 0.12 0.56 -0.01 0.08 -1.18 -0.03 0.602136327 0.526372406 "anatomical structure development;behavior;biological regulation;biosynthetic process;cell cycle phase;cell cycle process;cell development;cellular biosynthetic process;cellular component movement;cellular developmental process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;developmental process;developmental process involved in reproduction;germ cell development;M phase;macromolecule biosynthetic process;macromolecule metabolic process;mechanosensory behavior;metabolic process;multicellular organismal development;multicellular organismal process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;reproductive process;response to abiotic stimulus;response to external stimulus;response to mechanical stimulus;response to stimulus;RNA biosynthetic process;RNA metabolic process;spermatid development;transcription, DNA-dependent" binding;DNA binding;double-stranded RNA binding;nucleic acid binding;RNA binding;single-stranded RNA binding cell part;cytoplasm;cytoplasmic part;cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule cytoskeleton;mitochondrion;non-membrane-bounded organelle;nuclear part;nucleolus;nucleus;organelle;organelle part;ribonucleoprotein complex 8.97E-215 20 40 40 59.1

Q04637-5;Q04637-4;Q04637-3;Q04637;Q04637-9;E7EX73;E9PGM1;E7EUU4;Q04637-8;Q04637-6;Q04637-7;C9JF13;C9J6B6;C9K073;C9J2Z7;H7C044;H7C0V6;F8WCF2;C9JHW9;C9JWH7;C9J556;REV__Q8NEG2-2;C9JSU8;C9JWW9;REV__Q8NEG2;REV__F5H7J8;REV__C9JQZ6;REV__J3KQX6 Eukaryotic translation initiation factor 4 gamma 1EIF4G1 >sp|Q04637-5|IF4G1_HUMAN Isoform D of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1;>sp|Q04637-4|IF4G1_HUMAN Isoform C of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1;>sp|Q04637-3|IF4G1_HUMAN I0.23 0.01 0.02 -0.25 0.07 -0.36 0.25 -0.50 0.257076948 0.134604354 "biological regulation;catabolic process;cell death;cell surface receptor linked signaling pathway;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cytokine-mediated signaling pathway;death;enzyme linked receptor protein signaling pathway;insulin receptor signaling pathway;interaction with host;interspecies interaction between organisms;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;multi-organism process;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;reproductive process;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;signal transduction;transmembrane receptor protein tyrosine kinase signaling pathway;viral reproductive process;virus-host interaction" "binding;DNA binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 4F complex;intracellular part;macromolecular complex;protein complex RNA transport;Viral myocarditis 0 28 46 40 36.2

P35221;P35221-2;F8W845;G3XAM7;Q8N1C0;E5RIB1;E5RIC3;E5RG03;E5RGY6;E5RJ41;E5RJL0;E5RIE0;E5RHV7;E5RGD2;E5RFM3;E5RJP7;E5RGY7;P26232-4;P26232-6;E5RFM5;E5RFG3;E5RFK9;H0YBB8;E5RGU3;E5RHJ5;E5RJZ2;E5RGG4;E5RJ43;E5RGS1;E5RIT8;B9A010;A6NKP0;Q9UI47 Catenin alpha-1 CTNNA1>sp|P35221|CTNA1_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1;>sp|P35221-2|CTNA1_HUMAN Isoform 2 of Catenin alpha-1 OS=Homo sapiens GN=CTNNA1;>tr|F8W845|F8W845_HUMAN Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=2 SV=1;>tr|G3XAM7|G3XAM7_HUMAN C -0.05 0.11 0.10 0.12 -0.94 -0.36 -0.21 0.02 0.906981589 0.444419614 adherens junction organization;aging;anatomical structure development;anatomical structure morphogenesis;apical junction assembly;axon regeneration;axonogenesis;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell part morphogenesis;cell projection morphogenesis;cell projection organization;cell-cell adhesion;cell-cell junction assembly;cell-cell junction organization;cellular component assembly;cellular component assembly at cellular level;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to chemical stimulus;cellular response to indole-3-methanol;cellular response to organic substance;cellular response to stimulus;cellular response to stress;developmental process;developmental process involved in reproduction;establishment or maintenance of cell polarity;gap junction assembly;gonad development;macromolecular complex assembly;macromolecular complex subunit organization;male gonad development;muscle cell differentiation;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cell development;negative regulation of cell differentiation;negative regulation of cell proliferation;negative regulation of cellular process;negative regulation of developmental process;negative regulation of neural precursor cell proliferation;negative regulation of neuroblast proliferation;negative regulation of neurogenesis;negative regulation of programmed cell death;neuron projection morphogenesis;neuron projection regeneration;odontogenesis;odontogenesis of dentine-containing tooth;organ development;organ morphogenesis;ovarian follicle development;ovulation cycle process;positive regulation of biological process;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of muscle cell differentiation;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of smoothened signaling pathway;protein complex assembly;protein complex subunit organization;protein heterooligomerization;protein oligomerization;regeneration;regulation of apoptosis;regulation of biological process;regulation of cell communication;regulation of cell death;regulation of cell development;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle cell differentiation;regulation of nervous system development;regulation of neural precursor cell proliferation;regulation of neurogenesis;regulation of programmed cell death;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;regulation of smoothened signaling pathway;reproductive process;reproductive structure development;response to axon injury;response to chemical stimulus;response to endogenous stimulus;response to estrogen stimulus;response to hormone stimulus;response to indole-3-methanol;response to organic substance;response to steroid hormone stimulus;response to stimulus;response to stress;response to wounding;rhythmic process binding;cadherin binding;cell adhesion molecule binding;protein binding;structural molecule activity acrosomal vesicle;actin cytoskeleton;adherens junction;anchoring junction;catenin complex;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell contact zone;cell-cell junction;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeleton;cytosol;extrinsic to membrane;extrinsic to plasma membrane;fascia adherens;intercalated disc;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;lamellipodium;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;non-membrane-bounded organelle;organelle;plasma membrane;plasma membrane part;protein complex;stored secretory granule;vesicle;zonula adherens Adherens junction;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Bacterial invasion of epithelial cells;Endometrial cancer;Leukocyte transendothelial migration;Pathways in cancer;Tight junction 0 33 48 40 70.4

P35580;P35580-2;F8W6L6;P35580-3;P35580-4;E7ERA5 Myosin-10 MYH10 >sp|P35580|MYH10_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3;>sp|P35580-2|MYH10_HUMAN Isoform 2 of Myosin-10 OS=Homo sapiens GN=MYH10;>tr|F8W6L6|F8W6L6_HUMAN Myosin-10 OS=Homo sapiens GN=MYH10 PE=2 SV=1;>sp|P35580-3|MYH10_HUMAN Isoform 3 of Myosin-1 -0.09 0.92 0.03 0.82 -0.13 0.31 -0.62 0.35 0.529299095 0.438632044 "actin cytoskeleton organization;actin filament-based movement;actin filament-based process;actomyosin structure organization;adult heart development;anatomical structure development;anatomical structure formation involved in morphogenesis;axon guidance;biological regulation;cardiac cell development;cardiac muscle cell development;cardiac myofibril assembly;cell cycle cytokinesis;cell cycle process;cell development;cell migration;cell motility;cell projection assembly;cell projection organization;cell proliferation;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane organization;cellular process;cerebellar Purkinje cell layer development;chemotaxis;chordate embryonic development;cytokinesis;cytokinesis after mitosis;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;establishment of localization;establishment of localization in cell;establishment of nucleus localization;establishment of organelle localization;exocytosis;fourth ventricle development;heart development;in utero embryonic development;lateral ventricle development;locomotion;membrane organization;multicellular organismal process;muscle cell development;myofibril assembly;neurological system process;neuromuscular process;neuromuscular process controlling balance;neuron migration;nuclear migration;organ development;organelle organization;plasma membrane organization;plasma membrane repair;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to chemical stimulus;response to external stimulus;response to stimulus;retina development in camera-type eye;secretion;secretion by cell;substrate-dependent cell migration, cell extension;system process;taxis;third ventricle development;transport;ventricular cardiac muscle cell development;vesicle-mediated transport" "actin binding;actin filament binding;actin-dependent ATPase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin filament bundle;actomyosin;axon;cell body;cell cortex;cell division site part;cell part;cell projection;cell projection part;cleavage furrow;cytoplasmic part;cytoskeletal part;dendritic spine;growth cone;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;midbody;myosin complex;myosin II complex;neuromuscular junction;neuron projection;neuron spine;neuronal cell body;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;site of polarized growth;spindle;stress fiber;synapse Tight junction;Viral myocarditis 0 6 68 40 40

P29401;P29401-2;B4E022;E9PFF2;F8W888;F8WAX4;Q9H0I9 Transketolase TKT>sp|P29401|TKT_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3;>sp|P29401-2|TKT_HUMAN Isoform 2 of Transketolase OS=Homo sapiens GN=TKT;>tr|B4E022|B4E022_HUMAN Transketolase OS=Homo sapiens GN=TKT PE=2 SV=1 0.12 -0.15 -0.11 -0.08 -0.23 -0.19 0.35 -0.22 0.041632178 0.019158272 "alcohol biosynthetic process;alcohol metabolic process;aldehyde biosynthetic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate metabolic process;cellular aldehyde metabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate metabolic process;cellular metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glyceraldehyde-3-phosphate biosynthetic process;glyceraldehyde-3-phosphate metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;organophosphate metabolic process;oxidation-reduction process;pentose biosynthetic process;pentose metabolic process;pentose-phosphate shunt, non-oxidative branch;primary metabolic process;regulation of biological process;regulation of growth;small molecule biosynthetic process;small molecule metabolic process;xylulose biosynthetic process;xylulose metabolic process" "binding;catalytic activity;cation binding;cofactor binding;identical protein binding;ion binding;metal ion binding;protein binding;protein dimerization activity;protein homodimerization activity;transferase activity;transferase activity, transferring aldehyde or ketonic groups;transketolase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;microbody;nucleus;organelle;peroxisome Biosynthesis of ansamycins;Carbon fixation in photosynthetic organisms;Pentose phosphate pathway 0 7 41 41 63.2

P06733;P06733-2;K7EM90;E5RI09;E5RG95;K7EPM1;K7EKN2;K7ERS8 Alpha-enolase ENO1 >sp|P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2;>sp|P06733-2|ENOA_HUMAN

Isoform MBP-1 of Alpha-enolase OS=Homo sapiens GN=ENO1 0.10 -0.14 -0.13 -0.06 -0.18 -0.39 0.32 -0.20 0.119564498 0.054424537 "aging;alcohol biosynthetic process;alcohol catabolic process;alcohol metabolic process;anatomical structure development;anatomical structure morphogenesis;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental growth;developmental process;generation of precursor metabolites and energy;gluconeogenesis;glucose catabolic process;glucose metabolic process;glycolysis;growth;hexose biosynthetic process;hexose catabolic process;hexose metabolic process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide catabolic process;monosaccharide metabolic process;multi-organism process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell growth;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of growth;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;primary metabolic process;regeneration;regulation of biological process;regulation of biosynthetic process;regulation of cell growth;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of growth;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to biotic stimulus;response to chemical stimulus;response to drug;response to other organism;response to stimulus;response to virus;RNA biosynthetic process;RNA metabolic process;skeletal muscle tissue regeneration;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;tissue development;tissue regeneration;transcription, DNA-dependent"binding;carbon-oxygen lyase activity;catalytic activity;cation binding;DNA binding;hydro-lyase activity;ion binding;lyase activity;magnesium ion binding;metal ion binding;nucleic acid binding;nucleic acid binding transcription factor activity;phosphopyruvate hydratase activity;protein binding transcription factor activity;sequence-specific DNA binding transcription factor activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;contractile fiber part;cytoplasmic part;cytosol;cytosolic part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;M band;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;nucleus;organelle;organelle part;phosphopyruvate hydratase complex;plasma membrane;protein complex;vesicle Glycolysis / Gluconeogenesis;Methane metabolism;RNA degradation 0 8 47 41 85.3

P15311;E7EQR4;E9PNP4 Ezrin EZR >sp|P15311|EZRI_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4;>tr|E7EQR4|E7EQR4_HUMAN Ezrin OS=Homo sapiens GN=EZR PE=2 SV=2 0.20 0.02 0.09 -0.10 -0.38 0.12 0.48 0.05 0.023148188 -0.01324253 actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;axon guidance;biological adhesion;biological regulation;cell adhesion;cell differentiation;cell-cell adhesion;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;chemotaxis;cytoskeletal anchoring at plasma membrane;cytoskeleton organization;developmental process;epithelial cell differentiation;establishment or maintenance of apical/basal cell polarity;establishment or maintenance of bipolar cell polarity;establishment or maintenance of cell polarity;leukocyte cell-cell adhesion;locomotion;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane docking;membrane to membrane docking;organelle organization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;response to chemical stimulus;response to external stimulus;response to stimulus;taxis actin binding;actin filament binding;binding;cytoskeletal protein binding;protein binding actin filament;apical part of cell;apical plasma membrane;basolateral plasma membrane;cell cortex part;cell part;cell projection;cell projection membrane;cell projection part;cortical cytoskeleton;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extrinsic to membrane;filopodium;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;macromolecular complex;membrane;membrane part;microtubule basal body;microtubule organizing center;microvillus;microvillus membrane;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ruffle;ruffle membrane;uropod Gastric acid secretion;Leukocyte transendothelial migration;Pathogenic Escherichia coli infection;Regulation of actin cytoskeleton 0 3 58 41 71.2

P31939;E9PBU3;F5GWY2;H7C1S2;H7C084;C9JLK0;F8WEF0;H7BZU3 Bifunctional purine biosynthesis protein PURH;Phosphoribosylaminoimidazolecarboxamide formyltransferase;IMP cyclohydrolase ATIC >sp|P31939|PUR9_HUMAN Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3;>tr|E9PBU3|E9PBU3_HUMAN Phosphoribosylaminoimidazolecarboxamide formyltransferase OS=Homo sapiens GN=ATIC PE=2 SV=1;>tr|F5GWY2|F5GWY2_HUMAN Phosphoribosyl 0.21 0.00 -0.18 -0.08 -0.15 -0.23 0.48 -0.12 0.016621445 -0.009400406 anatomical structure development;anatomical structure morphogenesis;aromatic compound biosynthetic process;biosynthetic process;brainstem development;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cerebellum development;cerebral cortex development;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;'de novo' IMP biosynthetic process;developmental process;dihydrofolate metabolic process;folic acid-containing compound biosynthetic process;folic acid-containing compound metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;IMP biosynthetic process;IMP metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organ morphogenesis;organ regeneration;primary metabolic process;pteridine-containing compound biosynthetic process;pteridine-containing compound metabolic process;purine base metabolic process;purine nucleoside monophosphate biosynthetic process;purine nucleoside monophosphate metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine ribonucleoside monophosphate biosynthetic process;purine ribonucleoside monophosphate metabolic process;purine ribonucleotide biosynthetic process;purine ribonucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;regeneration;response to chemical stimulus;response to inorganic substance;response to stimulus;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;small molecule metabolic process;tetrahydrofolate biosynthetic process;tetrahydrofolate metabolic process "catalytic activity;cyclohydrolase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;hydroxymethyl-, formyl- and related transferase activity;IMP cyclohydrolase activity;phosphoribosylaminoimidazolecarboxamide formyltransferase activity;transferase activity;transferase activity, transferring one-carbon groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle One carbon pool by folate;Purine metabolism 0 8 42 42 82.1

P78371;P78371-2;F5GWF6;F8VQ14;REV__D6RIG4;REV__Q9HCL0-2;REV__Q9HCL0 T-complex protein 1 subunit beta CCT2 >sp|P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4;>sp|P78371-2|TCPB_HUMAN Isoform 2 of T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2;>tr|F5GWF6|F5GWF6_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens 0.22 0.05 -0.06 -0.06 -0.07 -0.31 -0.01 -0.39 0.888751076 0.234760345 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chaperone-mediated protein complex assembly;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein metabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;unfolded protein binding cell part;chaperonin-containing T-complex;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;cytosolic part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;microtubule;nucleus;organelle;organelle part;protein complex 0 7 42 42 81.5

P50990;B4DEM7;B4DQH4;H7C4C8;H7C2U0 T-complex protein 1 subunit theta CCT8 >sp|P50990|TCPQ_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4;>tr|B4DEM7|B4DEM7_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=2 SV=1;>tr|B4DQH4|B4DQH4_HUMAN T-complex protein 1 subunit theta OS=Homo sapiens 0.23 0.05 -0.04 -0.02 -0.06 -0.41 -0.04 -0.46 1.003121769 0.29684402 cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;'de novo' posttranslational protein folding;'de novo' protein folding;macromolecule metabolic process;metabolic process;primary metabolic process;protein folding;protein metabolic process"adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" aggresome;cell part;centrosome;cytoplasm;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;inclusion body;intermediate filament cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule;microtubule organizing center;non-membrane-bounded organelle;organelle;organelle part;protein complex 0 5 42 42 69.2

P40939;H0YFD6;B4DYP2;G3V379 "Trifunctional enzyme subunit alpha, mitochondrial;Long-chain enoyl-CoA hydratase;Long chain 3-hydroxyacyl-CoA dehydrogenase" HADHA ">sp|P40939|ECHA_HUMAN Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2" -0.42 -0.17 0.07 0.16 0.18 0.30 -0.26 0.10 0.389261344 -0.1704296 biosynthetic process;carboxylic acid catabolic process;carboxylic acid metabolic process;cardiolipin acyl-chain remodeling;cardiolipin metabolic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular metabolic process;cellular process;fatty acid beta-oxidation;fatty acid catabolic process;fatty acid metabolic process;fatty acid oxidation;glycerolipid biosynthetic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid modification;lipid oxidation;metabolic process;monocarboxylic acid catabolic process;monocarboxylic acid metabolic process;organic acid catabolic process;organic acid metabolic process;organophosphate metabolic process;oxidation-reduction process;oxoacid metabolic process;phosphatidylglycerol metabolic process;phospholipid biosynthetic process;phospholipid metabolic process;primary metabolic process;response to chemical stimulus;response to drug;response to endogenous stimulus;response to hormone stimulus;response to insulin stimulus;response to organic substance;response to peptide hormone stimulus;response to stimulus;small molecule catabolic process;small molecule metabolic process "3-hydroxyacyl-CoA dehydrogenase activity;acetyl-CoA C-acetyltransferase activity;acetyl-CoA C-acyltransferase activity;acetyltransferase activity;binding;C-acetyltransferase activity;C-acyltransferase activity;carbon-oxygen lyase activity;carboxylic acid binding;catalytic activity;coenzyme binding;cofactor binding;enoyl-CoA hydratase activity;fatty acid binding;fatty-acyl-CoA binding;hydro-lyase activity;lipid binding;long-chain-3-hydroxyacyl-CoA dehydrogenase activity;long-chain-enoyl-CoA hydratase activity;lyase activity;monocarboxylic acid binding;NAD binding;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups" cell part;cytoplasmic part;fatty acid beta-oxidation multienzyme complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;mitochondrial inner membrane;mitochondrial membrane;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nuclear part;nucleoid;nucleolus;organelle;organelle inner membrane;organelle membrane;organelle part;protein complex "Aminobenzoate degradation;Benzoate degradation;beta-Alanine metabolism;Biosynthesis of unsaturated fatty acids;Butanoate metabolism;Caprolactam degradation;Fatty acid elongation in mitochondria;Fatty acid metabolism;Lysine degradation;Propanoate metabolism;Tryptophan metabolism;Valine, leucine and isoleucine degradation" 0 4 42 42 62.8

Q07065;H3BUW6;H3BN64;Q96K21-4;H3BRM1;Q96K21-3;H3BRF9;Q96K21-2;Q96K21;REV__P25054-2;REV__P25054 Cytoskeleton-associated protein 4 CKAP4 >sp|Q07065|CKAP4_HUMAN Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 -0.69 0.02 -0.13 0.17 1.01 1.19 -0.53 0.75 0.753538099 -0.760525441 binding;cation binding;ion binding;metal ion binding;transition metal ion binding;zinc ion binding cell part;cytoplasmic part;cytoskeleton;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;lipid particle;membrane;membrane part;non-membrane-bounded organelle;organelle;organelle membrane;organelle part;perinuclear region of cytoplasm;plasma membrane Protein processing in endoplasmic reticulum 0 11 44 42 76.1

P19367;P19367-4;P19367-2;P19367-3;E7ENR4;B1AR63;B1AR62;B1AR61;Q2TB90;Q2TB90-3;Q2TB90-2 Hexokinase-1 HK1 >sp|P19367|HXK1_HUMAN Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3;>sp|P19367-4|HXK1_HUMAN Isoform 4 of Hexokinase-1 OS=Homo sapiens GN=HK1;>sp|P19367-2|HXK1_HUMAN Isoform 2 of Hexokinase-1 OS=Homo sapiens GN=HK1;>sp|P19367-3|HXK1_HUMAN Isoform 3 of Hexok -0.17 0.24 0.06 0.24 0.47 0.77 -0.53 0.24 0.184933773 -0.146542118 alcohol catabolic process;alcohol metabolic process;biological regulation;carbohydrate catabolic process;carbohydrate homeostasis;carbohydrate metabolic process;carbohydrate transport;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular chemical homeostasis;cellular glucose homeostasis;cellular homeostasis;cellular metabolic process;cellular process;chemical homeostasis;establishment of localization;generation of precursor metabolites and energy;glucose catabolic process;glucose homeostasis;glucose metabolic process;glucose transport;glycolysis;hexose catabolic process;hexose metabolic process;hexose transport;homeostatic process;metabolic process;monosaccharide catabolic process;monosaccharide metabolic process;monosaccharide transport;organic substance transport;primary metabolic process;regulation of biological quality;small molecule catabolic process;small molecule metabolic process;transmembrane transport;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;carbohydrate kinase activity;catalytic activity;fructokinase activity;glucokinase activity;hexokinase activity;kinase activity;mannokinase activity;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring phosphorus-containing groups" cell part;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;membrane;membrane part;membrane raft;membrane-bounded organelle;mitochondrial membrane;mitochondrial outer membrane;mitochondrial part;mitochondrion;nucleus;organelle;organelle membrane;organelle outer membrane;organelle part;outer membrane Amino sugar and nucleotide sugar metabolism;Butirosin and neomycin biosynthesis;Carbohydrate digestion and absorption;Fructose and mannose metabolism;Galactose metabolism;Glycolysis / Gluconeogenesis;Insulin signaling pathway;Starch and sucrose metabolism;Streptomycin biosynthesis;Type II diabetes mellitus 0 11 46 42 44.3

E9PEZ3;O60610;H9KV28;O60610-2;B9ZVX0;E9PHQ0;O60610-3;E7ET75;E7ERW8;E7EMV0;B4E2I7;E5RJ79 Protein diaphanous homolog 1 DIAPH1 >tr|E9PEZ3|E9PEZ3_HUMAN Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=2 SV=1;>sp|O60610|DIAP1_HUMAN Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2;>tr|H9KV28|H9KV28_HUMAN Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 0.03 -0.13 0.12 -0.04 -0.28 -0.26 0.35 -0.29 0.268899168 0.114928194 actin cytoskeleton organization;actin filament organization;actin filament polymerization;actin filament-based process;actin polymerization or depolymerization;biological regulation;cell projection organization;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule localization;cellular process;cellular protein complex assembly;cellular protein localization;cellular response to amine stimulus;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to histamine;cellular response to organic nitrogen;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;localization;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule localization;multicellular organismal process;neurological system process;neuron projection development;organelle organization;protein complex assembly;protein complex subunit organization;protein localization;protein localization to microtubule;protein localization to organelle;protein polymerization;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of calcium ion transport;regulation of calcium ion transport into cytosol;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of homeostatic process;regulation of ion homeostasis;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of microtubule-based process;regulation of release of sequestered calcium ion into cytosol;regulation of transport;response to amine stimulus;response to chemical stimulus;response to endogenous stimulus;response to histamine;response to organic nitrogen;response to organic substance;response to stimulus;sensory perception;sensory perception of mechanical stimulus;sensory perception of sound;system process binding;protein binding;receptor binding cell part;cell projection;cell projection membrane;cell projection part;cytoplasm;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;leading edge membrane;membrane part;mitotic spindle;neuron projection;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;ruffle membrane;spindle Focal adhesion;Regulation of actin cytoskeleton;Shigellosis0 12 43 43 35.1

Q6ZRV2;J3KPS2 Protein FAM83H FAM83H >sp|Q6ZRV2|FA83H_HUMAN Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3;>tr|J3KPS2|J3KPS2_HUMAN Protein FAM83H (Fragment) OS=Homo sapiens GN=FAM83H PE=4 SV=1 -0.16 1.20 0.29 1.16 -1.78 -0.15 -1.17 0.07 1.066729459 1.381963152 anatomical structure development;biomineral tissue development;developmental process;tissue development 0 2 43 43 51.2

Q92900-2;Q92900;H0Y455;F8VR31;P51530-3;P51530-4;P51530;J3KPX5 Regulator of nonsense transcripts 1 UPF1 >sp|Q92900-2|RENT1_HUMAN Isoform 2 of Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1;>sp|Q92900|RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2 0.10 -0.08 0.16 0.04 -0.08 -0.18 0.01 -0.44 0.898711038 0.230321613 "anatomical structure homeostasis;base-excision repair;biological regulation;biosynthetic process;catabolic process;cell cycle;cell cycle checkpoint;cell cycle phase;cell cycle process;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;cellular response to stress;chromosome organization;DNA catabolic process;DNA catabolic process, exonucleolytic;DNA double-strand break processing;DNA integrity checkpoint;DNA metabolic process;DNA recombination;DNA repair;DNA replication;DNA replication checkpoint;DNA replication, Okazaki fragment processing;DNA replication, removal of RNA primer;DNA-dependent DNA replication;dosage compensation;dosage compensation, by inactivation of X chromosome;establishment of localization;establishment of localization in cell;establishment of RNA localization;gene expression;histone mRNA catabolic process;histone mRNA metabolic

process;homeostatic process;intracellular transport;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mitochondrial DNA metabolic process;mitochondrial DNA repair;mitochondrial DNA replication;mitotic recombination;mRNA catabolic process;mRNA export from nucleus;mRNA metabolic process;mRNA transport;negative regulation of biological process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cellular process;negative regulation of G2/M transition of mitotic cell cycle;negative regulation of mitotic cell cycle;nitrogen compound metabolic process;nuclear export;nuclear transport;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;organelle organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of DNA metabolic process;positive regulation of DNA replication;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of DNA metabolic process;regulation of DNA replication;regulation of G2/M transition of mitotic cell cycle;regulation of gene expression;regulation of gene expression, epigenetic;regulation of interphase of mitotic cell cycle;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitotic cell cycle;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein complex disassembly;regulation of protein metabolic process;regulation of translation;regulation of translational termination;response to DNA damage stimulus;response to stimulus;response to stress;RNA catabolic process;RNA export from nucleus;RNA metabolic process;RNA transport;S phase;S phase of mitotic cell cycle;telomere maintenance;telomere maintenance via recombination;telomere maintenance via semi-conservative replication;telomere maintenance via telomere lengthening;telomere organization;transport" "4 iron, 4 sulfur cluster binding;5'-3' DNA helicase activity;5'-flap endonuclease activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;cation binding;chromatin binding;deoxyribonuclease activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;endodeoxyribonuclease activity;endodeoxyribonuclease activity, producing 5'-phosphomonoesters;endonuclease activity;endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphomonoesters;flap endonuclease activity;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;hydrolase activity, acting on ester bonds;ion binding;iron-sulfur cluster binding;metal cluster binding;metal ion binding;nuclease activity;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity;single-stranded DNA-dependent ATPase activity;site-specific endodeoxyribonuclease activity, specific for altered base;transition metal ion binding;zinc ion binding" cell part;chromatin;chromosomal part;cytoplasmic mRNA processing body;cytoplasmic part;cytosol;exon-exon junction complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;mitochondrial nucleoid;mitochondrial part;non-membrane-bounded organelle;nuclear part;nucleoid;nucleoplasm;organelle;organelle part;protein complex;ribonucleoprotein complex;RNA granule DNA replication;mRNA surveillance pathway;RNA transport
3.91E-257 8 43 43 47.9

P07900;P07900-2;Q86U12;G3V2J8;Q14568;Q58FG0;Q58FG1;Q9NQH7-3;Q9NQH7-5;REV__H3BMH3 Heat shock protein HSP 90-alpha HSP90AA1 >sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5;>sp|P07900-2|HS90A_HUMAN Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1;>tr|Q86U12|Q86U12_HUMAN Full-length cDNA clone CS0CAP007YF18 of T 0.24 0.07 -0.16 -0.04 -0.08 -0.38 0.00 -0.46 0.785892683 0.256011214 axon guidance;biological regulation;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;chaperone-mediated protein complex assembly;chemotaxis;defense response;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;G2/M transition of mitotic cell cycle;immune response;immune system process;innate immune response;intracellular protein transport;intracellular transport;locomotion;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;membrane organization;metabolic process;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;nitric oxide metabolic process;nitrogen compound metabolic process;organelle organization;outer mitochondrial membrane organization;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;primary metabolic process;protein complex assembly;protein complex subunit organization;protein folding;protein import;protein import into mitochondrial outer membrane;protein metabolic process;protein refolding;protein targeting;protein targeting to membrane;protein targeting to mitochondrion;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;regulation of molecular function;regulation of monooxygenase activity;regulation of nitric oxide biosynthetic process;regulation of nitric-oxide synthase activity;regulation of nitrogen compound metabolic process;regulation of oxidoreductase activity;response to chemical stimulus;response to external stimulus;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;taxis;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;catalytic activity;enzyme regulator activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;nitric-oxide synthase regulator activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein dimerization activity;protein domain specific binding;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;TPR domain binding" cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;organelle;pigment granule;plasma membrane;vesicle Antigen processing and presentation;NOD-like receptor signaling pathway;Pathways in cancer;Plant-pathogen interaction;Progesterone-mediated oocyte maturation;Prostate cancer;Protein processing in endoplasmic reticulum 0 10 69 43
63.4

Q13753;Q13753-2 Laminin subunit gamma-2 LAMC2 >sp|Q13753|LAMC2_HUMAN Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 PE=1 SV=2;>sp|Q13753-2|LAMC2_HUMAN Isoform Short of Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 0.16 0.28 -0.08 -0.03 -1.48 -0.26 -0.07 0.61 0.346862706 0.385387585 anatomical structure development;biological adhesion;cell adhesion;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;tissue development binding;carbohydrate binding;glycosaminoglycan binding;heparin binding;pattern binding;polysaccharide binding extracellular matrix part;extracellular region;extracellular region part;laminin complex;laminin-5 complex;macromolecular complex;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 0 2 44 44 36.5

Q13200;E7EW34;E9PCS3;H7C1H2;C9JPC0;H7C2Q3;F8WBS8 26S proteasome non-ATPase regulatory subunit 2PSMD2 >sp|Q13200|PSMD2_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3;>tr|E7EW34|E7EW34_HUMAN 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=2 SV=1;>tr|E9PCS3|E9PCS3_HUMAN 26S proteasome non-AT
0.13 0.05 -0.16 -0.07 0.15 0.11 0.05 -0.06 0.379031103 -0.074351183 "anaphase;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class I;antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class I;apoptosis;biological regulation;catabolic process;cell cycle phase;cell cycle process;cell death;cellular catabolic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;death;DNA damage response, signal transduction by p53 class mediator;DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest;G1/S transition of mitotic cell cycle;gene expression;immune system process;intracellular signal transduction;M phase;M phase of mitotic cell cycle;macromolecule catabolic process;macromolecule metabolic process;macromolecule modification;metabolic process;mitotic anaphase;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;mRNA metabolic process;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of ligase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein metabolic process;negative regulation of protein modification process;negative regulation of protein ubiquitination;negative regulation of ubiquitin-

protein ligase activity;negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of cell cycle arrest;positive regulation of cell cycle process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of ligase activity;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of ubiquitin-protein ligase activity;positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;primary metabolic process;programmed cell death;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein polyubiquitination;protein ubiquitination;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of catabolic process;regulation of catalytic activity;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cell death;regulation of cellular amine metabolic process;regulation of cellular amino acid metabolic process;regulation of cellular ketone metabolic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of ligase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein catabolic process;regulation of protein metabolic process;regulation of protein modification process;regulation of protein ubiquitination;regulation of ubiquitin-protein ligase activity;regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle;response to DNA damage stimulus;response to stimulus;response to stress;RNA metabolic process;S phase;S phase of mitotic cell cycle;signal transduction;signal transduction by p53 class mediator;signal transduction in response to DNA damage;signal transduction involved in cell cycle checkpoint;signal transduction involved in DNA damage checkpoint;signal transduction involved in DNA integrity checkpoint;signal transduction involved in G1/S transition checkpoint;signal transduction involved in mitotic cell cycle checkpoint;signal transduction involved in mitotic cell cycle G1/S checkpoint;signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint;small molecule metabolic process;ubiquitin-dependent protein catabolic process;viral reproduction" enzyme regulator activity cell part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;nuclear part;nucleoplasm;organelle part;proteasome complex;proteasome regulatory particle;protein complex Proteasome 0 7 44 44 56.1

Q86VP6;Q86VP6-2;Q86VP6-3;H0YH27;O75155-2;O75155;F5H6I6;F8WBB8 Cullin-associated NEDD8-dissociated protein 1 CAND1 >sp|Q86VP6|CAND1_HUMAN Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2;>sp|Q86VP6-2|CAND1_HUMAN Isoform 2 of Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 0.05 -0.01 -0.13 -0.02 -0.11 0.03 0.31 -0.29 0.038267322 -0.015352532 "biological regulation;biosynthetic process;cell differentiation;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;cellular protein metabolic process;developmental process;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;macromolecule modification;metabolic process;negative regulation of catalytic activity;negative regulation of molecular function;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular component organization;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of RNA polymerase II transcriptional preinitiation complex assembly;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;protein complex assembly;protein complex subunit organization;protein metabolic process;protein modification by small protein conjugation;protein modification by small protein conjugation or removal;protein modification process;protein ubiquitination;regulation of biological process;regulation of biosynthetic process;regulation of catalytic activity;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of protein complex assembly;regulation of RNA metabolic process;regulation of RNA polymerase II transcriptional preinitiation complex assembly;regulation of transcription from RNA polymerase II promoter;regulation of transcription initiation from RNA polymerase II promoter;regulation of transcription initiation, DNA-dependent;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;SCF complex assembly;transcription, DNA-dependent" cell part;cullin-RING ubiquitin ligase complex;cytoplasm;intracellular;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex;ubiquitin ligase complex 0 8 45 44 40.1

P33176;E9PET8;Q12840;J3KNA1;O60282-2;C9JWB9 Kinesin-1 heavy chain KIF5B >sp|P33176|KINH_HUMAN Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1 0.03 0.17 0.01 0.07 0.11 0.42 0.14 0.04 0.490837734 -0.107570812 antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;axon guidance;biological regulation;blood coagulation;cell communication;cell death;cell-cell signaling;cellular chemical homeostasis;cellular component disassembly;cellular component disassembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecular complex disassembly;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chemical homeostasis;chemotaxis;coagulation;cytoplasm organization;cytoskeleton-dependent intracellular transport;death;establishment of localization;establishment of localization in cell;hemostasis;homeostatic process;immune system process;intracellular transport;ion homeostasis;localization;locomotion;macromolecular complex disassembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;motor axon guidance;multicellular organismal process;organelle localization;organelle transport along microtubule;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of establishment of protein localization in plasma membrane;positive regulation of ion transport;positive regulation of potassium ion transport;positive regulation of transport;primary metabolic process;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular localization;regulation of cellular process;regulation of establishment of protein localization;regulation of establishment of protein localization in plasma membrane;regulation of ion transport;regulation of localization;regulation of membrane potential;regulation of metal ion transport;regulation of potassium ion transport;regulation of protein localization;regulation of transport;response to chemical stimulus;response to external stimulus;response to stimulus;ribonucleoprotein complex disassembly;ribonucleoprotein complex subunit organization;signaling;stress granule disassembly;synaptic transmission;taxis;transport;vesicle localization;vesicle transport along microtubule "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;microtubule binding;microtubule motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;tubulin binding" cell part;cell projection;cell projection part;ciliary rootlet;cilium part;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;intracellular organelle part;intracellular part;kinesin complex;macromolecular complex;membrane;microtubule;microtubule associated complex;neuron projection;organelle;organelle part;perinuclear region of cytoplasm;protein complex;vesicle 0 6 57 44 64

A8K2U0;H0YGG5;F5H2Z2;H0YH14;F5GXP1;F5GYG7 Alpha-2-macroglobulin-like protein 1 A2ML1 >sp|A8K2U0|A2ML1_HUMAN Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens GN=A2ML1 PE=1 SV=3;>tr|H0YGG5|H0YGG5_HUMAN Alpha-2-macroglobulin-like protein 1 (Fragment) OS=Homo sapiens GN=A2ML1 PE=2 SV=1;>tr|F5H2Z2|F5H2Z2_HUMAN Alpha-2-macroglobulin-like pro 0.34 0.53 0.02 -0.13 1.02 1.77 0.78 0.07 0.813668172 -0.721213242 biological regulation;negative regulation of catalytic activity;negative regulation of endopeptidase activity;negative regulation of hydrolase activity;negative regulation of molecular function;negative regulation of peptidase activity;regulation of biological process;regulation of catalytic activity;regulation of endopeptidase activity;regulation of hydrolase activity;regulation of metabolic process;regulation of molecular function;regulation of peptidase activity endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity extracellular region;extracellular region part;extracellular space 0 6 45 45 39.3

Q13751;Q5THA1;REV__Q9BVR6;REV__H3BPU4;REV__Q9UGJ1-2;REV__Q9UGJ1;F5H149;Q9P1Z9;Q9P1Z9-2 Laminin subunit beta-3 LAMB3 >sp|Q13751|LAMB3_HUMAN Laminin subunit beta-3 OS=Homo sapiens GN=LAMB3 PE=1 SV=1 0.03 0.16 0.29 0.23 -1.46 -0.11 -0.09 0.63 0.402251701 0.433329136 anatomical structure development;biological adhesion;brown fat cell differentiation;cell adhesion;cell differentiation;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;fat cell differentiation;hemidesmosome assembly;tissue development structural molecule activity cell part;extracellular matrix part;extracellular region;extracellular region part;integral to membrane;intrinsic to membrane;laminin complex;laminin-5 complex;macromolecular complex;membrane part;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 0 9 45 45 51.9

P08238;Q58FF7;Q5T9W8;Q58FF8;Q58FF6 Heat shock protein HSP 90-beta HSP90AB1 >sp|P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 0.18 0.00 -0.08 -0.04 -0.33 -0.44 0.12 -0.30 0.791000707 0.252062231 "anatomical structure development;axon guidance;biological regulation;cellular component organization;cellular component organization or biogenesis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic cyclic compound;cellular response to organic substance;cellular response to stimulus;chemotaxis;defense response;developmental process;immune response;immune system process;innate immune response;intracellular receptor mediated signaling pathway;locomotion;macromolecule metabolic process;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catabolic process;negative regulation of cell death;negative regulation of cellular catabolic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of proteasomal ubiquitin-dependent protein catabolic process;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of proteolysis;nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway;organ development;placenta development;positive regulation of binding;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of catalytic activity;positive regulation of cell size;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of kinase activity;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of nitric oxide biosynthetic process;positive regulation of nitrogen compound metabolic process;positive regulation of protein binding;positive regulation of protein import into nucleus, translocation;positive regulation of protein kinase activity;positive regulation of protein serine/threonine kinase activity;positive regulation of protein transport;positive regulation of transferase activity;positive regulation of transport;primary metabolic process;protein folding;protein metabolic process;regulation of anatomical structure size;regulation of apoptosis;regulation of binding;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell death;regulation of cell size;regulation of cellular biosynthetic process;regulation of cellular catabolic process;regulation of cellular component size;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cytokine-mediated signaling pathway;regulation of defense response;regulation of establishment of protein localization;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of interferon-gamma-mediated signaling pathway;regulation of intracellular protein transport;regulation of intracellular transport;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of neuron apoptosis;regulation of nitric oxide biosynthetic process;regulation of nitrogen compound metabolic process;regulation of nucleocytoplasmic transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of proteasomal protein catabolic process;regulation of proteasomal ubiquitin-dependent protein catabolic process;regulation of protein binding;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein import into nucleus, translocation;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein serine/threonine kinase activity;regulation of protein transport;regulation of proteolysis;regulation of response to cytokine stimulus;regulation of response to interferon-gamma;regulation of response to stimulus;regulation of response to stress;regulation of signal transduction;regulation of signaling;regulation of transferase activity;regulation of transmembrane transport;regulation of transport;regulation of type I interferon-mediated signaling pathway;response to abiotic stimulus;response to chemical stimulus;response to external stimulus;response to organic cyclic compound;response to organic substance;response to osmotic stress;response to salt stress;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;signal transduction;taxis" adenyl deoxyribonucleotide binding;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;CTP binding;dATP binding;deoxyribonucleotide binding;enzyme regulator activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;nitric-oxide synthase regulator activity;nucleotide binding;protein binding;protein domain specific binding;purine deoxyribonucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrimidine nucleotide binding;pyrimidine ribonucleotide binding;ribonucleotide binding;TPR domain binding;UTP binding apical plasma membrane;basolateral plasma membrane;brush border membrane;cell part;cell projection membrane;cell projection part;cell surface;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;inclusion body;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;pigment granule;plasma membrane part;vesicle Antigen processing and presentation;NOD-like receptor signaling pathway;Pathways in cancer;Plant-pathogen interaction;Progesterone-mediated oocyte maturation;Prostate cancer;Protein processing in endoplasmic reticulum 0 5 73 45 73.5

P06737-2;P06737;E9PK47;E9PMM6 "Glycogen phosphorylase, liver form;Phosphorylase" PYGL ">sp|P06737-2|PYGL_HUMAN Isoform 2 of Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL;>sp|P06737|PYGL_HUMAN Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4;>tr|E9PK47|E9PK47_HUMAN Phosphorylase OS=Homo sapiens GN=PYGL PE=2 SV" -0.40 -0.31 0.11 0.10 -1.01 -0.32 0.53 0.17 0.03139 0.034134798 5-phosphoribose 1-diphosphate biosynthetic process;5-phosphoribose 1-diphosphate metabolic process;alcohol biosynthetic process;alcohol metabolic process;biological regulation;biosynthetic process;carbohydrate biosynthetic process;carbohydrate catabolic process;carbohydrate homeostasis;carbohydrate metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate biosynthetic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;chemical homeostasis;D-ribose biosynthetic process;D-ribose metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan catabolic process;glucan metabolic process;glucose homeostasis;glucose metabolic process;glycogen catabolic process;glycogen metabolic process;heterocycle metabolic process;hexose metabolic process;homeostatic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide biosynthetic process;monosaccharide metabolic process;oxidation-reduction process;pentose biosynthetic process;pentose metabolic process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;regulation of biological quality;ribose phosphate biosynthetic process;ribose phosphate metabolic process;small molecule biosynthetic process;small molecule metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;AMP binding;ATP binding;bile acid binding;binding;carbohydrate binding;carboxylic acid binding;catalytic activity;cofactor binding;drug binding;glucose binding;glycogen phosphorylase activity;identical protein binding;lipid binding;monocarboxylic acid binding;monosaccharide binding;nucleobase binding;nucleotide binding;phosphorylase activity;protein binding;protein dimerization activity;protein homodimerization activity;purine base binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyridoxal phosphate binding;ribonucleotide binding;steroid binding;sugar binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;vitamin B6 binding;vitamin binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part;membrane;plasma membrane Insulin signaling pathway;Starch and sucrose metabolism 0 4 57 46 66.3

P49588;H3BPK7 "Alanine--tRNA ligase, cytoplasmic" AARS ">sp|P49588|SYAC_HUMAN Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2" 0.06 0.01 -0.06 -0.09 -0.10 -0.41 0.25 -0.41 0.368301328 0.14799757 alanyl-tRNA aminoacylation;amine metabolic process;amino acid activation;anatomical structure development;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cellular response to topologically incorrect protein;cellular response to unfolded protein;cerebellar Purkinje cell layer development;developmental process;endoplasmic reticulum unfolded protein response;epidermis development;ER-nucleus signaling pathway;hair cycle process;hair follicle development;macromolecule metabolic process;macromolecule modification;metabolic process;molting cycle;molting cycle process;multicellular organismal process;ncRNA metabolic process;ncRNA processing;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;neurological system process;neuromuscular process;neuromuscular process controlling balance;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;protein folding;protein metabolic process;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular process;regulation of neuron apoptosis;regulation of programmed cell death;response to acid;response to amine stimulus;response to amino acid stimulus;response to chemical stimulus;response to endogenous stimulus;response to endoplasmic reticulum stress;response to organic nitrogen;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;RNA metabolic process;RNA modification;RNA processing;signal transduction;skin development;small molecule metabolic process;system process;tissue development;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;tRNA modification;tRNA processing "adenyl nucleotide binding;adenyl ribonucleotide binding;alanine-tRNA ligase activity;amine binding;amino acid binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic acid binding;carboxylic ester hydrolase activity;catalytic activity;cation binding;hydrolase activity;hydrolase activity, acting on ester bonds;ion binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;metal ion binding;nucleic acid binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;tRNA binding"cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part Aminoacyl-tRNA biosynthesis 0 2

48 48 57.1

P15144;H0YKT6;H0YMC1;H0YLZ8 Aminopeptidase N ANPEP >sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 -1.96 -1.46 -0.43 0.08 3.34 3.21 -0.41 0.71 1.075113852 -2.654431045 anatomical structure formation involved in morphogenesis;angiogenesis;angiotensin maturation;biological regulation;cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;hormone metabolic process;interaction with host;interspecies interaction between organisms;macromolecule metabolic process;metabolic process;multi-organism process;peptide hormone processing;primary metabolic process;protein maturation;protein metabolic process;protein processing;proteolysis;regulation of biological quality;regulation of hormone levels;reproductive process;viral reproductive process;virus-host interaction "aminopeptidase activity;binding;catalytic activity;cation binding;exopeptidase activity;hydrolase activity;ion binding;metal ion binding;metallopeptidase activity;peptidase activity;peptidase activity, acting on L-amino acid peptides;receptor activity;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;endoplasmic reticulum-Golgi intermediate compartment;external side of plasma membrane;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane part;membrane-bounded organelle;organelle;plasma membrane part Glutathione metabolism;Hematopoietic cell lineage;Renin-angiotensin system 4.87E-294 4 48 48 43

Q8WUM4;Q8WUM4-2;C9IZF9;F8WEQ7;F8WBR8;F8WDK9 Programmed cell death 6-interacting protein PDCD6IP >sp|Q8WUM4|PDC6I_HUMAN Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1;>sp|Q8WUM4-2|PDC6I_HUMAN Isoform 2 of Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP 0.14 -0.16 0.07 -0.34 0.22 0.30 0.59 0.03 0.953021616 -0.358312978 apoptosis;cell cycle;cell death;cell division;cellular process;death;establishment of localization;establishment of protein localization;interaction with host;interspecies interaction between organisms;multi-organism process;programmed cell death;protein transport;reproductive process;transport;viral reproductive process;virus-host interaction cell part;cytoplasm;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytoskeletal part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;microtubule organizing center;organelle;organelle part;pigment granule;vesicle Endocytosis 0 6 48 48 55.3

Q9C0C2;Q9C0C2-2;E9PKK0;E9PKE7 182 kDa tankyrase-1-binding protein TNKS1BP1 >sp|Q9C0C2|TB182_HUMAN 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 PE=1 SV=4;>sp|Q9C0C2-2|TB182_HUMAN Isoform 2 of 182 kDa tankyrase-1-binding protein OS=Homo sapiens GN=TNKS1BP1 -0.09 -0.20 0.31 0.04 -0.14 -0.11 0.35 -0.21 0.089711585 0.043267854 anatomical structure homeostasis;biological regulation;biosynthetic process;catabolic process;cellular biosynthetic process;cellular catabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule biosynthetic process;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;chromosome organization;DNA metabolic process;DNA replication;homeostatic process;macromolecule biosynthetic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;mRNA 3'-end processing;mRNA catabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear-transcribed mRNA catabolic process;nuclear-transcribed mRNA poly(A) tail shortening;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle organization;primary metabolic process;regulation of biological quality;RNA 3'-end processing;RNA catabolic process;RNA metabolic process;RNA processing;RNA-dependent DNA replication;telomere maintenance;telomere maintenance via telomerase;telomere maintenance via telomere lengthening;telomere organization ankyrin binding;binding;cytoskeletal protein binding;enzyme binding;protein binding CCR4-NOT complex;cell part;chromatin;chromosomal part;cytoplasmic part;cytoskeleton;cytosol;heterochromatin;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear chromatin;nuclear chromosome part;nuclear heterochromatin;nuclear part;nuclear telomeric heterochromatin;nucleoplasm part;organelle;organelle part;protein complex;telomeric heterochromatin;transcription factor complex 0 4 48 48 41.9

P41252;J3KR24;Q5TCC4;Q5TCD1;Q5TCC5;Q5TCC6;Q5TCD2;Q5TCC9;H0Y9S8;H0Y9Y6 "Isoleucine--tRNA ligase, cytoplasmic" IARS ">sp|P41252|SYIC_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2;>tr|J3KR24|J3KR24_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=4 SV=1" 0.01 -0.12 0.13 -0.02 0.06 -0.13 0.23 -0.36 0.137460171 0.05185611 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;isoleucyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;isoleucine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis" 0 10 49 48 42.2

F5H698;B4DER1;Q9P2J5;B4DJ10 "Leucine--tRNA ligase, cytoplasmic" LARS ">tr|F5H698|F5H698_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1;>tr|B4DER1|B4DER1_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=2 SV=1;>sp|Q9P2J5|SYLC_HUMAN Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens" 0.00 -0.05 0.13 -0.10 0.16 -0.06 0.21 -0.27 0.047577702 -0.017336842 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;leucyl-tRNA aminoacylation;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;leucine-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular part "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis" 0 4 49 49 46.5

O75533;O75533-2;B4DGZ4;H7C341;F8WC19 Splicing factor 3B subunit 1 SF3B1 >sp|O75533|SF3B1_HUMAN Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 -0.15 0.53 0.06 0.51 -0.02 0.06 -1.05 -0.30 0.791676513 0.56230467 "anterior/posterior pattern specification;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;developmental process;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;pattern specification process;primary metabolic process;regionalization;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile" binding;chromatin binding catalytic step 2 spliceosome;cell part;intracellular organelle part;intracellular part;macromolecular complex;nuclear body;nuclear part;nuclear speck;nucleoplasm;nucleoplasm part;organelle part;ribonucleoprotein complex;spliceosomal complex;U12-type spliceosomal complex Spliceosome 0 5 49 49 51.3

P31948;G3XAD8;F5H0T1;F5H783;F5GXD8;H0YGI8;REV__F8W6J8 Stress-induced-phosphoprotein 1 STIP1 >sp|P31948|STIP1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1;>tr|G3XAD8|G3XAD8_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=2 SV=1;>tr|F5H0T1|F5H0T1_HUMAN Stress-induced-phosphoprotein 1 OS=Homo sapiens GN= 0.06 0.02 -0.06 -0.07 0.18 -0.06 0.24 -0.32 0.062680739 -0.023929463 axon guidance;chemotaxis;locomotion;response to chemical stimulus;response to external stimulus;response to stimulus;response to stress;taxis cell part;cytoplasmic part;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane-bounded organelle;nucleus;organelle;protein complex Prion diseases 0 7 49 49 66.7

O60841;Q9H2L5-3;Q9H2L5;Q9H2L5-2;G8JLC1 Eukaryotic translation initiation factor 5B EIF5B >sp|O60841|IF2P_HUMAN Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4 -0.31 -0.07 0.21 0.02 0.00 -0.14 -0.01 -0.38 0.263203588 0.094673566 biological regulation;catabolic process;cell cycle;cellular catabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;GTP catabolic process;GTP metabolic process;heterocycle catabolic process;heterocycle metabolic process;metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational initiation;response to stimulus;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;signal transduction;small molecule metabolic process "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasmic part;cytosol;intracellular part RNA transport 6.29E-254 5 50 50 44.8

Q16787-1;B0YJ33;Q16787;Q16787-4;Q16787-3;K7EIP4;K7ERM0 Laminin subunit alpha-3 LAMA3 >sp|Q16787-1|LAMA3_HUMAN Isoform 1 of Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3;>tr|B0YJ33|B0YJ33_HUMAN Laminin alpha-3 chain variant 2 OS=Homo sapiens GN=LAMA3 PE=2 SV=1;>sp|Q16787|LAMA3_HUMAN Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3 PE=1 S 0.29 0.39 -0.39 -0.13 -1.31 -0.19 -0.24 0.64 0.28364426 0.318998974 anatomical structure development;biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;developmental process;epidermis development;extracellular matrix organization;extracellular structure organization;hemidesmosome assembly;regulation of biological process;regulation of cell adhesion;regulation of cell migration;regulation of cell motility;regulation of cellular component movement;regulation of cellular process;regulation of developmental process;regulation of embryonic development;regulation of localization;regulation of locomotion;regulation of multicellular organismal development;regulation of multicellular organismal process;tissue development structural molecule activity basement membrane;extracellular matrix part;extracellular region part;laminin complex;laminin-1 complex;laminin-5 complex;macromolecular complex;protein complex Amoebiasis;ECM-receptor interaction;Focal adhesion;Pathways in cancer;Small cell lung cancer;Toxoplasmosis 0 7 50 50 40.3

Q5T4S7-3;Q5T4S7-4;Q5T4S7;Q5T4S7-2;Q5T4S7-5;B4DYV5;B4DPF6;Q5TBN9;Q5T4S7-6 E3 ubiquitin-protein ligase UBR4 UBR4 >sp|Q5T4S7-3|UBR4_HUMAN Isoform 3 of E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4;>sp|Q5T4S7-4|UBR4_HUMAN Isoform 4 of E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4;>sp|Q5T4S7|UBR4_HUMAN E3 ubiquitin-protein ligase UBR4 OS=Homo sapie 0.12 0.02 0.20 0.02 -0.20 -0.34 0.20 -0.05 0.655339925 0.188963346 interaction with host;interspecies interaction between organisms;multi-organism process;reproductive process;viral reproductive process;virus-host interaction "acid-amino acid ligase activity;binding;catalytic activity;cation binding;ion binding;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;small conjugating protein ligase activity;transition metal ion binding;ubiquitin-protein ligase activity;zinc ion binding" cell part;cytoplasm;cytoskeleton;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;intrinsic to membrane;membrane part;membrane-bounded organelle;non-membrane-bounded organelle;nucleus;organelle 4.19E-259 9 50 50 12.9

P26640;B0V043;Q5SP20;B4DZ61;H0Y426;B0V044;A2ABF4 Valine--tRNA ligase VARS >sp|P26640|SYVC_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4;>tr|B0V043|B0V043_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=2 SV=1 -0.08 0.07 -0.14 0.04 -0.02 -0.09 0.07 -0.32 0.252015782 0.063736786 amine metabolic process;amino acid activation;biological regulation;biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;ncRNA metabolic process;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;regulation of translational elongation;regulation of translational fidelity;RNA metabolic process;small molecule metabolic process;translational elongation;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;valyl-tRNA aminoacylation "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA editing activity;aminoacyl-tRNA ligase activity;ATP binding;binding;carboxylic ester hydrolase activity;catalytic activity;hydrolase activity;hydrolase activity, acting on ester bonds;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;valine-tRNA ligase activity" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle "Aminoacyl-tRNA biosynthesis;Valine, leucine and isoleucine biosynthesis" 0 7 51 51 44.5

Q03001-3 >sp|Q03001-3|DYST_HUMAN Isoform 3 of Dystonin OS=Homo sapiens GN=DST -0.21 -0.24 0.04 0.21 -2.14 -1.26 0.37 -0.48 0.642150169 0.829247505 0 1 88 52 39.7

P07355;P07355-2;H0YN42;H0YM50;H0YMD0;H0YMU9;A6NMY6;H0YN28;H0YL33;H0YNP5;H0YKS4;H0YMM1;H0YNA0;H0YKZ7;H0YLV6;H0YMT9;H0YKX9;H0YN52;H0YKL9;H0YMW4;H0YKV8;H0YMD9;H0YLE2;H0YNB8;H0YKN4;REV__C9JND6;REV__C9J363;REV__C9J6F3;REV__C9J5C3;REV__Q9BUL8 Annexin A2;Annexin;Putative annexin A2-like proteinANXA2;ANXA2P2 >sp|P07355|ANXA2_HUMAN Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2;>sp|P07355-2|ANXA2_HUMAN Isoform 2 of Annexin A2 OS=Homo sapiens GN=ANXA2;>tr|H0YN42|H0YN42_HUMAN Annexin (Fragment) OS=Homo sapiens GN=ANXA2 PE=2 SV=1;>tr|H0YM50|H0YM50_HUMAN Annexin (Fr 0.25 0.01 -0.22 -0.17 -0.22 0.09 0.46 0.32 0.436742297 -0.195116755 anatomical structure development;anatomical structure formation involved in morphogenesis;angiogenesis;biological regulation;body fluid secretion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to acid;cellular response to chemical stimulus;cellular response to stimulus;collagen fibril organization;developmental process;establishment of localization;extracellular matrix organization;extracellular structure organization;fibrinolysis;multicellular organismal process;negative regulation of biological process;negative regulation of blood coagulation;negative regulation of coagulation;negative regulation of multicellular organismal process;positive regulation of binding;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of molecular function;positive regulation of organelle organization;positive regulation of transport;positive regulation of vesicle fusion;regulation of binding;regulation of biological process;regulation of biological quality;regulation of blood coagulation;regulation of body fluid levels;regulation of cellular component organization;regulation of cellular process;regulation of coagulation;regulation of localization;regulation of molecular function;regulation of multicellular organismal process;regulation of organelle organization;regulation of response to external stimulus;regulation of response to stimulus;regulation of response to stress;regulation of transport;regulation of vesicle fusion;regulation of vesicle-mediated transport;regulation of wound healing;response to acid;response to chemical stimulus;response to stimulus;secretion;skeletal system development;system development;transport "binding;calcium ion binding;calcium-dependent phospholipid binding;cation binding;enzyme inhibitor activity;enzyme regulator activity;ion binding;lipase inhibitor activity;lipid binding;metal ion binding;phosphatidylinositol binding;phosphatidylinositol-4,5-bisphosphate binding;phospholipase inhibitor activity;phospholipid binding" basement membrane;cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;early endosome;endosome;extracellular matrix part;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;extrinsic to membrane;extrinsic to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;lipid particle;macromolecular complex;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;midbody;myelin sheath adaxonal region;organelle;perinuclear region of cytoplasm;pigment granule;plasma membrane;plasma membrane part;protein complex;sarcolemma;Schmidt-Lanterman incisure;vesicle 0 30 53 53 92.9

F8VPD4;P27708;H7C2E4;H7BZB3;H7C3Z5 CAD protein;Glutamine-dependent carbamoyl-phosphate synthase;Aspartate carbamoyltransferase;Dihydroorotase CAD >tr|F8VPD4|F8VPD4_HUMAN DNA fragmentation factor subunit beta OS=Homo sapiens GN=CAD PE=2 SV=1;>sp|P27708|PYR1_HUMAN CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3 0.24 -0.08 -0.06 -0.18 -0.26 -0.89 0.24 -0.63 0.59347307 0.367454527 amine catabolic process;amine metabolic process;anatomical structure morphogenesis;biological regulation;biosynthetic process;body fluid secretion;carbamoyl phosphate biosynthetic process;carbamoyl phosphate metabolic process;carboxylic acid catabolic process;carboxylic acid metabolic process;catabolic process;cellular amine metabolic process;cellular amino acid catabolic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular catabolic process;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to drug;cellular response to endogenous stimulus;cellular response to epidermal growth factor stimulus;cellular response to growth factor stimulus;cellular response to organic substance;cellular response to stimulus;'de novo' pyrimidine base biosynthetic process;'de novo' UMP biosynthetic process;developmental process;drug metabolic process;embryo development;establishment of localization;female pregnancy;glutamine catabolic process;glutamine family amino acid catabolic process;glutamine family amino acid metabolic process;glutamine metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;lactation;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;multicellular organismal reproductive process;multi-organism process;nitrogen compound metabolic process;nucleobase biosynthetic process;nucleobase metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside biosynthetic process;nucleoside metabolic process;nucleoside monophosphate biosynthetic process;nucleoside monophosphate metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate biosynthetic process;nucleoside triphosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;organ morphogenesis;organ regeneration;organic acid catabolic process;organic acid metabolic process;oxoacid metabolic process;peptidyl-amino acid modification;peptidyl-threonine modification;peptidyl-threonine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;primary metabolic process;protein autophosphorylation;protein metabolic process;protein modification process;protein phosphorylation;pyrimidine base biosynthetic process;pyrimidine base metabolic process;pyrimidine nucleoside biosynthetic process;pyrimidine nucleoside metabolic process;pyrimidine nucleoside monophosphate biosynthetic process;pyrimidine nucleoside monophosphate metabolic process;pyrimidine nucleoside triphosphate biosynthetic process;pyrimidine nucleoside triphosphate metabolic process;pyrimidine nucleotide biosynthetic process;pyrimidine nucleotide metabolic process;pyrimidine ribonucleoside metabolic process;pyrimidine ribonucleoside monophosphate biosynthetic process;pyrimidine ribonucleoside monophosphate metabolic process;pyrimidine ribonucleoside triphosphate biosynthetic process;pyrimidine ribonucleoside triphosphate metabolic process;pyrimidine ribonucleotide biosynthetic process;pyrimidine ribonucleotide metabolic process;pyrimidine-containing compound biosynthetic process;pyrimidine-containing compound metabolic process;regeneration;regulation of biological quality;regulation of body fluid levels;reproductive process;response to alkaloid;response to amine stimulus;response to caffeine;response to chemical stimulus;response to corticosteroid stimulus;response to cortisol stimulus;response to drug;response to endogenous stimulus;response to epidermal growth factor stimulus;response to glucocorticoid stimulus;response to growth factor stimulus;response to hormone stimulus;response to organic cyclic compound;response to organic nitrogen;response to organic substance;response to purine-containing compound;response to steroid hormone stimulus;response to stimulus;response to testosterone stimulus;ribonucleoside metabolic process;ribonucleoside monophosphate biosynthetic process;ribonucleoside monophosphate metabolic process;ribonucleoside triphosphate biosynthetic process;ribonucleoside triphosphate metabolic process;ribonucleotide biosynthetic process;ribonucleotide metabolic process;secretion;small molecule catabolic process;small molecule metabolic process;transport;UMP biosynthetic process;UMP metabolic process;UTP biosynthetic process;UTP metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;amine binding;amino acid binding;aspartate binding;aspartate carbamoyltransferase activity;ATP binding;binding;carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity;carbon-nitrogen ligase activity, with glutamine as amido-N-donor;carboxyl- or carbamoyltransferase activity;carboxylic acid binding;catalytic activity;cation binding;dihydroorotase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides;identical protein binding;ion binding;kinase activity;ligase activity;ligase activity, forming carbon-nitrogen bonds;metal ion binding;nucleotide binding;phosphotransferase activity, alcohol group as acceptor;protein binding;protein kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;transferase activity;transferase activity, transferring one-carbon groups;transferase activity, transferring phosphorus-containing groups" axon part;cell body;cell part;cell projection part;cytoplasmic part;cytosol;intracellular organelle part;intracellular part;macromolecular complex;neuronal cell body;nuclear matrix;nuclear part;organelle part;protein complex;synapse part;terminal button "Alanine, aspartate and glutamate metabolism;Pyrimidine metabolism" 0 5 53 53 35.9

P16144-4;P16144-2;P16144-3;P16144;P16144-5;J3QS11;J3QQL2;J3QRK0;J3KSH9 Integrin beta-4 ITGB4 >sp|P16144-4|ITB4_HUMAN Isoform Beta-4D of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp|P16144-2|ITB4_HUMAN Isoform Beta-4A of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp|P16144-3|ITB4_HUMAN Isoform Beta-4B of Integrin beta-4 OS=Homo sapiens GN=ITGB4;>sp| 0.24 0.48 -0.24 0.13 -2.07 -0.91 -0.52 0.00 0.944494784 1.028295291 biological adhesion;biological regulation;cell adhesion;cell junction assembly;cell junction organization;cell motility;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cell-matrix adhesion;cell-substrate adhesion;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cellular response to stimulus;developmental process;extracellular matrix organization;extracellular structure organization;filopodium assembly;hemidesmosome assembly;integrin-mediated signaling pathway;locomotion;microspike assembly;multicellular organismal development;multicellular organismal process;regulation of biological process;regulation of cellular process;response to stimulus;response to stress;response to wounding;signal transduction receptor activity basal plasma membrane;basement membrane;cell junction;cell leading edge;cell part;cell surface;cell-substrate junction;extracellular matrix part;extracellular region part;hemidesmosome;integrin complex;macromolecular complex;membrane part;plasma membrane part;protein complex;receptor complex Arrhythmogenic right ventricular cardiomyopathy (ARVC);Dilated cardiomyopathy;ECM-receptor interaction;Focal adhesion;Hypertrophic cardiomyopathy (HCM);Regulation of actin cytoskeleton 0 9 53 53 39

Q08211;Q08211-2;REV__H0YA90;REV__Q7Z6J0-3 ATP-dependent RNA helicase A DHX9 >sp|Q08211|DHX9_HUMAN ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 0.17 0.26 -0.10 0.12 0.13 -0.14 -0.50 -0.49 0.904256395 0.358476289 "biological regulation;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to heat;cellular response to stimulus;cellular response to stress;circadian rhythm;CRD-mediated mRNA stabilization;macromolecule metabolic process;metabolic process;mRNA metabolic process;mRNA processing;mRNA stabilization;nitrogen compound metabolic process;nuclear mRNA splicing, via spliceosome;nucleic acid metabolic process;nucleobase-containing compound metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mRNA stability;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of RNA stability;response to abiotic stimulus;response to heat;response to stimulus;response to stress;response to temperature stimulus;rhythmic process;RNA metabolic process;RNA processing;RNA splicing;RNA splicing, via transesterification reactions;RNA splicing, via transesterification reactions with bulged adenosine as nucleophile;RNA stabilization" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;ATP-dependent DNA helicase activity;ATP-dependent helicase activity;ATP-dependent RNA helicase activity;binding;catalytic activity;DNA binding;DNA helicase activity;DNA-dependent ATPase activity;double-stranded RNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine NTP-dependent helicase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;RNA helicase activity;RNA-dependent ATPase activity" cell part;centrosome;CRD-mediated mRNA stability complex;cytoplasmic part;cytoskeletal part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;microtubule organizing center;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;protein complex;ribonucleoprotein complex 0 4 54 54 47.3

P07476;J3KPN6 Involucrin IVL >sp|P07476|INVO_HUMAN Involucrin OS=Homo sapiens GN=IVL PE=1 SV=2;>tr|J3KPN6|J3KPN6_HUMAN Involucrin OS=Homo sapiens GN=IVL PE=4 SV=1 -0.14 0.64 -0.33 -0.26 1.60 2.33 1.13 0.36 1.215370946 -1.375952698 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;isopeptide cross-linking;isopeptide cross-linking via N6-(L-isoglutamyl)-L-lysine;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;peptidyl-amino acid modification;peptidyl-glutamine modification;peptidyl-lysine modification;primary metabolic process;protein metabolic process;protein modification process;response to abiotic stimulus;response to light stimulus;response to radiation;response to stimulus;response to UV;response to UV-B "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity" cell part;cornified envelope;cytoplasm;cytoskeleton;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 0 2 55 55 80.9

E9PL22;Q9Y4L1;E9PJ21;B7Z909;J3KTF1;J3QL06;J3QQH7;J3QLE9;J3KT27;J3KSJ2;Q9BXT5 Hypoxia up-regulated protein 1 HYOU1 >tr|E9PL22|E9PL22_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=2 SV=1;>sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1;>tr|E9PJ21|E9PJ21_HUMAN Hypoxia up-regulated protein 1 (Fragment) OS=Homo sap -0.02 -0.16 -0.36 -0.32 0.10 -0.20 0.74 0.10 0.799265451 -0.399072119 activation of signaling protein activity involved in unfolded protein response;anatomical structure development;anatomical structure homeostasis;biological regulation;cell cycle phase;cell cycle process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular localization;cellular macromolecule localization;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein localization;cellular protein metabolic process;chromosome organization;chromosome organization involved in meiosis;developmental process;developmental process involved in reproduction;fertilization;gamete generation;genitalia development;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;localization;macromolecule localization;macromolecule metabolic process;male gamete generation;male genitalia development;male meiosis;meiosis;metabolic process;multicellular organismal process;multicellular organismal reproductive process;organ development;organelle organization;positive regulation of catalytic activity;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of transferase activity;primary metabolic process;protein localization;protein localization to chromosome;protein localization to organelle;protein metabolic process;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of cellular response to stress;regulation of DNA metabolic process;regulation of DNA recombination;regulation of DNA repair;regulation of double-strand break repair;regulation of double-strand break repair via homologous recombination;regulation of hydrolase activity;regulation of kinase activity;regulation of localization;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nuclease activity;regulation of nucleobase-containing compound metabolic process;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of protein kinase activity;regulation of protein localization;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to DNA damage stimulus;regulation of response to stimulus;regulation of response to stress;regulation of transferase activity;reproductive process;spermatogenesis;synaptonemal complex assembly;synaptonemal complex organization;tissue homeostasis adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane-enclosed lumen;organelle lumen;organelle part Protein processing in endoplasmic reticulum 0 11 57 56 55.7

P12270;Q5SWX9 Nucleoprotein TPR TPR >sp|P12270|TPR_HUMAN Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 -0.08 0.86 0.13 0.78 0.02 0.10 -1.22 -0.22 0.838507546 0.75136119 "amine metabolic process;amino acid activation;biological regulation;carbohydrate metabolic process;carbohydrate transport;carboxylic acid metabolic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell division;cell surface receptor linked signaling pathway;cellular amine metabolic process;cellular amino acid metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular ketone metabolic process;cellular macromolecular complex subunit organization;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to heat;cellular response to interferon-alpha;cellular response to organic substance;cellular response to stimulus;cellular response to stress;cytokine-mediated signaling pathway;establishment of localization;establishment of localization in cell;establishment of protein localization;establishment of RNA localization;glucose transport;hexose transport;intracellular protein transport;intracellular transport;macromolecular complex subunit organization;macromolecule metabolic process;MAPK import into nucleus;metabolic process;mitosis;mitotic cell cycle checkpoint;mitotic cell cycle spindle assembly checkpoint;mitotic cell cycle spindle checkpoint;monosaccharide transport;mRNA export from nucleus;mRNA export from nucleus in response to heat stress;mRNA transport;ncRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of gene expression;negative regulation of intracellular transport;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitosis;negative regulation of mitotic metaphase/anaphase transition;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear division;negative regulation of nucleobase-containing compound metabolic process;negative regulation of nucleobase-containing compound transport;negative regulation of nucleocytoplasmic transport;negative regulation of organelle organization;negative regulation of protein metabolic process;negative regulation of RNA export from nucleus;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;negative regulation of translation;negative regulation of translational initiation;negative regulation of transport;nitrogen compound metabolic process;nuclear division;nuclear export;nuclear import;nuclear pore organization;nuclear transport;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;nucleocytoplasmic transport;nucleus organization;organelle fission;organelle organization;organic acid metabolic process;organic substance transport;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of chromatin assembly or disassembly;positive regulation of heterochromatin formation;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of mitotic cell cycle spindle assembly checkpoint;positive regulation of nucleocytoplasmic transport;positive regulation of organelle organization;positive regulation of protein export from nucleus;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of spindle checkpoint;positive regulation of transmembrane transport;positive regulation of transport;posttranscriptional regulation of gene expression;primary metabolic process;protein import;protein import into nucleus;protein targeting;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of chromatin assembly;regulation of chromatin assembly or disassembly;regulation of chromosome organization;regulation of chromosome segregation;regulation of establishment of protein localization;regulation of gene expression;regulation of glucose transport;regulation of heterochromatin formation;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic cell cycle spindle assembly checkpoint;regulation of mitotic metaphase/anaphase transition;regulation of mitotic sister chromatid segregation;regulation of mitotic sister chromatid separation;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of nucleobase-containing compound transport;regulation of nucleocytoplasmic transport;regulation of organelle organization;regulation of primary metabolic process;regulation of protein export from nucleus;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein transport;regulation of RNA export from nucleus;regulation of RNA metabolic process;regulation of sister chromatid segregation;regulation of spindle checkpoint;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;regulation of translation;regulation of translational initiation;regulation of transmembrane transport;regulation of transport;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to cytokine stimulus;response to endogenous stimulus;response to epidermal growth factor stimulus;response to growth factor stimulus;response to heat;response to interferon-alpha;response to organic substance;response to stimulus;response to stress;response to temperature stimulus;RNA export from nucleus;RNA import into nucleus;RNA metabolic process;RNA transport;seryl-tRNA aminoacylation;signal transduction;small molecule metabolic process;spindle assembly checkpoint;spindle checkpoint;transmembrane transport;transport;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process;viral reproductive process" "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;chromatin binding;cytoskeletal protein binding;dynein complex binding;enzyme binding;heat shock protein binding;identical protein binding;kinase binding;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;mitogen-activated protein kinase binding;mRNA binding;nucleic acid binding;nucleocytoplasmic transporter activity;nucleotide binding;protein binding;protein complex binding;protein dimerization activity;protein homodimerization activity;protein kinase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;serine-tRNA ligase activity;transporter activity;tubulin binding" cell part;chromosomal part;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;dynein complex;extrinsic to membrane;inclusion body;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;kinetochore;macromolecular complex;membrane;membrane part;microtubule associated complex;mitotic spindle;non-membrane-bounded organelle;nuclear inclusion body;nuclear membrane;nuclear part;nuclear periphery;nucleoplasm;organelle;organelle membrane;organelle part;protein complex;spindle MAPK signaling pathway - yeast;Pathways in cancer;RNA transport;Thyroid cancer 0 2 57 56 31.6

Q15075;P13232-3;P13232-2;P13232;E9PPB2;E9PIY2;A6NJ10;Q8TAV3;E9PJR5;Q05D60 Early endosome antigen 1 EEA1 >sp|Q15075|EEA1_HUMAN Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2 0.04 -0.02 0.18 0.00 0.00 0.08 -0.02 -0.15 0.456875541 0.072142615 anatomical structure homeostasis;anatomical structure morphogenesis;biological regulation;bone resorption;cell communication;cell fate commitment;cell-cell signaling;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular membrane fusion;cellular membrane organization;cellular metabolic process;cellular process;developmental process;early endosome to late endosome transport;endosome transport;establishment of localization;establishment of localization in cell;homeostasis of number of cells;homeostasis of number of cells within a tissue;homeostatic process;humoral immune response;immune response;immune system process;intracellular transport;membrane fusion;membrane organization;metabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of catalytic activity;negative regulation of cell death;negative regulation of cellular process;negative regulation of molecular function;negative regulation of programmed cell death;organ morphogenesis;organelle fusion;organelle organization;positive regulation of B cell activation;positive regulation of B cell proliferation;positive regulation of biological process;positive regulation of cell activation;positive regulation of cell differentiation;positive regulation of cell proliferation;positive regulation of cellular process;positive regulation of developmental process;positive regulation of growth;positive regulation of immune system process;positive regulation of leukocyte activation;positive regulation of leukocyte proliferation;positive regulation of lymphocyte activation;positive regulation of lymphocyte differentiation;positive regulation of lymphocyte proliferation;positive regulation of mononuclear cell proliferation;positive regulation of organ growth;positive regulation of T cell activation;positive regulation of T cell differentiation;regulation of apoptosis;regulation of B cell activation;regulation of B cell proliferation;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell activation;regulation of cell death;regulation of cell differentiation;regulation of cell proliferation;regulation of cellular process;regulation of developmental process;regulation of gene expression;regulation of growth;regulation of immune system process;regulation of leukocyte activation;regulation of leukocyte proliferation;regulation of lymphocyte activation;regulation of lymphocyte differentiation;regulation of lymphocyte proliferation;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of mononuclear cell proliferation;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of organ growth;regulation of programmed cell death;regulation of T cell activation;regulation of T cell differentiation;response to stimulus;signaling;small molecule metabolic process;synaptic vesicle to endosome fusion;T cell lineage commitment;tissue homeostasis;transport;vesicle fusion;vesicle organization;vesicle-mediated transport;xenobiotic metabolic process "1-phosphatidylinositol binding;binding;calmodulin binding;catalytic activity;cation binding;cytokine receptor binding;electron carrier activity;growth factor activity;growth factor receptor binding;GTP-dependent protein binding;heme binding;identical protein binding;interleukin-7 receptor binding;ion binding;iron ion binding;lipid binding;metal ion binding;monooxygenase activity;oxidoreductase activity;oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen;phosphatidylinositol binding;phospholipid binding;protein binding;protein dimerization activity;protein homodimerization activity;receptor binding;tetrapyrrole binding;transition metal ion binding;zinc ion binding" cell part;cytoplasmic part;cytosol;early endosome;early endosome membrane;endoplasmic reticulum membrane;endoplasmic reticulum part;endosomal part;endosome;endosome membrane;extracellular region;extracellular region part;extracellular space;extrinsic to membrane;extrinsic to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part;protein complex;recycling endosome;serine-pyruvate aminotransferase complex Cytokine-cytokine receptor interaction;Endocytosis;Hematopoietic cell lineage;Jak-STAT signaling pathway;ko05152;Phagosome 0 10 58 56 44.4

P12814;P12814-3;P12814-2;B7TY16;H9KV75;H7C5W8;G3V2W4;G3V2N5;H0YJW3;H0YJ11;Q08043;G3V5M4;G3V2X9;G3V380;G3V2E8;B7Z4P8 Alpha-actinin-1 ACTN1 >sp|P12814|ACTN1_HUMAN Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2;>sp|P12814-3|ACTN1_HUMAN Isoform 3 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1;>sp|P12814-2|ACTN1_HUMAN Isoform 2 of Alpha-actinin-1 OS=Homo sapiens GN=ACTN1;>tr|B7TY16|B7TY16_HUMAN -0.03 -0.06 0.01 -0.02 -0.31 -0.03 0.24 0.16 0.11479674 -0.03983312 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;biological regulation;cell activation;cell junction assembly;cell junction organization;cell-substrate junction assembly;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;exocytosis;focal adhesion assembly;multicellular organismal process;muscle contraction;muscle filament sliding;muscle system process;negative regulation of biological process;negative regulation of cellular component movement;negative regulation of cellular process;organelle organization;platelet activation;platelet degranulation;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component movement;regulation of cellular process;regulation of localization;regulation of programmed cell death;secretion;secretion by cell;system process;transport;vesicle-mediated transport binding;calcium ion binding;cation binding;identical protein binding;integrin binding;ion binding;ligand-dependent nuclear receptor transcription coactivator activity;metal ion binding;protein binding;protein binding transcription factor activity;protein complex binding;protein dimerization activity;protein homodimerization activity;receptor activator activity;receptor binding;receptor regulator activity;structural constituent of muscle;structural molecule activity;thyroid hormone receptor activator activity;thyroid hormone receptor coactivator activity;transcription coactivator activity;transcription cofactor activity;transcription factor binding transcription factor activity actin filament;adherens junction;anchoring junction;cell junction;cell part;cell projection;cell projection part;cell-cell adherens junction;cell-cell junction;cell-substrate adherens junction;cell-substrate junction;contractile fiber part;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeletal part;cytoskeleton;cytosol;dendritic spine;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;fascia adherens;focal adhesion;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;neuron projection;neuron spine;non-membrane-bounded organelle;nucleus;organelle;organelle lumen;organelle part;plasma membrane;platelet alpha granule lumen;protein complex;pseudopodium;ruffle;secretory granule lumen;vesicle;vesicle lumen;Z disc Adherens junction;Amoebiasis;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Systemic lupus erythematosus;Tight junction0 16 88 56 80.6

P13667;C9JMN9 Protein disulfide-isomerase A4 PDIA4 >sp|P13667|PDIA4_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2 0.08 -0.05 -0.31 -0.26 0.49 -0.09 0.34 -0.19 0.62022501 -0.27208219 biological regulation;cell redox homeostasis;cellular homeostasis;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;establishment of localization;establishment of localization in cell;establishment of protein localization;glycerol ether metabolic process;homeostatic process;macromolecule metabolic process;metabolic process;organic ether metabolic process;primary metabolic process;protein folding;protein metabolic process;protein secretion;protein transport;regulation of biological process;regulation of biological quality;regulation of cellular process;secretion;secretion by cell;small molecule metabolic process;transport "catalytic activity;disulfide oxidoreductase activity;electron carrier activity;intramolecular oxidoreductase activity;intramolecular oxidoreductase activity, interconverting keto- and enol-groups;intramolecular oxidoreductase activity, transposing S-S bonds;isomerase activity;oxidoreductase activity;oxidoreductase activity, acting on a sulfur group of donors;protein disulfide isomerase activity;protein disulfide oxidoreductase activity" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum lumen;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;organelle;organelle lumen;organelle part;pigment granule;vesicle Protein processing in endoplasmic reticulum;Vibrio cholerae infection 0 2 57 57 64.2

P11586;G3V2B8;F5H2F4;G3V3L6 "C-1-tetrahydrofolate synthase, cytoplasmic;Methylenetetrahydrofolate dehydrogenase;Methenyltetrahydrofolate cyclohydrolase;Formyltetrahydrofolate synthetase" MTHFD1 ">sp|P11586|C1TC_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3;>tr|G3V2B8|G3V2B8_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=2 SV=1;>tr|F5H2F4|F5H2F4_HUMAN C-1-tetrahydrofolate synthas" 0.08 -0.07 0.09 0.04 -0.19 -0.52 0.11 -0.58 0.870183685 0.331415829 amine biosynthetic process;amine metabolic process;aromatic compound biosynthetic process;aspartate family amino acid biosynthetic process;aspartate family amino acid metabolic process;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid biosynthetic process;cellular amino acid metabolic process;cellular aromatic compound metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound biosynthetic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;folic acid metabolic process;folic acid-containing compound biosynthetic process;folic acid-containing compound metabolic process;heterocycle biosynthetic process;heterocycle metabolic process;histidine biosynthetic process;histidine family amino acid biosynthetic process;histidine family amino acid metabolic process;histidine metabolic process;metabolic process;methionine biosynthetic process;methionine metabolic process;nitrogen compound metabolic process;nucleobase-containing compound biosynthetic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside phosphate metabolic process;nucleotide biosynthetic process;nucleotide metabolic process;one-carbon metabolic process;organic acid biosynthetic process;organic acid metabolic process;oxoacid metabolic process;primary metabolic process;pteridine-containing compound biosynthetic process;pteridine-containing compound metabolic process;purine nucleotide biosynthetic process;purine nucleotide metabolic process;purine-containing compound biosynthetic process;purine-containing compound metabolic process;small molecule biosynthetic process;small molecule metabolic process;sulfur amino acid biosynthetic process;sulfur amino acid metabolic process;sulfur compound biosynthetic process;sulfur compound metabolic process;tetrahydrofolate interconversion;tetrahydrofolate metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cyclohydrolase activity;formate-tetrahydrofolate ligase activity;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amidines;ligase activity;ligase activity, forming carbon-nitrogen bonds;methenyltetrahydrofolate cyclohydrolase activity;methylenetetrahydrofolate dehydrogenase (NADP+) activity;methylenetetrahydrofolate dehydrogenase [NAD(P)+] activity;nucleotide binding;oxidoreductase activity;oxidoreductase activity, acting on the CH-NH group of donors;oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding" cell part;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;mitochondrion;organelle One carbon pool by folate 0 4 58 57 63.7

Q86UP2;Q86UP2-2;Q86UP2-3;G3V4Y7;H0YJZ8;G3V5G2;B7Z6P3;G3V5P0;H0YJP2;H0YJV5 Kinectin KTN1 >sp|Q86UP2|KTN1_HUMAN Kinectin OS=Homo sapiens GN=KTN1 PE=1 SV=1;>sp|Q86UP2-2|KTN1_HUMAN Isoform 2 of Kinectin OS=Homo sapiens GN=KTN1;>sp|Q86UP2-3|KTN1_HUMAN Isoform 3 of Kinectin OS=Homo sapiens GN=KTN1-0.43 0.15 0.18 0.31 -0.22 0.11 -0.81 -0.03 0.462550314 0.290923867 cellular component movement;cellular process;microtubule-based movement;microtubule-based process cell part;cytoplasmic part;endoplasmic reticulum;endoplasmic reticulum membrane;endoplasmic reticulum part;integral to membrane;integral to plasma membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;intrinsic to plasma membrane;membrane;membrane part;membrane-bounded organelle;organelle;organelle membrane;organelle part;plasma membrane part 0 10 58 58 50.3

P53621;P53621-2;F8WCN8;REV__Q9P2M7;Q7Z570;A7E2D7;Q96L91-4;Q96L91-3;Q96L91-5;Q96L91-2;Q96L91 Coatomer subunit alpha;Xenin;Proxenin COPA >sp|P53621|COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2;>sp|P53621-2|COPA_HUMAN Isoform 2 of Coatomer subunit alpha OS=Homo sapiens GN=COPA 0.23 -0.07 -0.21 -0.29 0.56 0.34 0.56 0.01 1.100285271 -0.452455176 "biological regulation;body fluid secretion;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;chromatin modification;chromatin organization;chromosome organization;COPI coating of Golgi vesicle;covalent chromatin modification;digestive system process;establishment of localization;establishment of localization in cell;establishment of protein localization;Golgi transport vesicle coating;Golgi vesicle transport;histone acetylation;histone H2A acetylation;histone H4 acetylation;histone modification;internal peptidyl-lysine acetylation;internal protein amino acid acetylation;intracellular protein transport;intracellular transport;macromolecule metabolic process;macromolecule modification;metabolic process;multicellular organismal process;organelle organization;pancreatic juice secretion;peptidyl-amino acid modification;peptidyl-lysine acetylation;peptidyl-lysine modification;primary metabolic process;protein acetylation;protein acylation;protein metabolic process;protein modification process;protein transport;regulation of biological quality;regulation of body fluid levels;retrograde vesicle-mediated transport, Golgi to ER;secretion;system process;transport;vesicle coating;vesicle organization;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation binding;chromatin binding;DNA binding;helicase activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;structural molecule activity;transition metal ion binding;zinc ion binding" cell part;COPI vesicle coat;cytoplasmic part;cytoplasmic vesicle part;cytosol;extracellular region part;extracellular space;Golgi apparatus part;H4/H2A histone acetyltransferase complex;histone acetyltransferase complex;intracellular organelle part;intracellular part;macromolecular complex;membrane coat;membrane part;NuA4 histone acetyltransferase complex;nuclear body;nuclear part;nuclear speck;nucleoplasm part;organelle part;protein complex;vesicle coat Neuroactive ligand-receptor interaction 0 11 59 58 59.2

Q9P2E9;Q9P2E9-2;Q9P2E9-3;F8W7S5;A2A2S5;G3XAD3;Q8WXH0-6;Q8WXH0-5;Q13002-3;Q86YP9;Q13002-6;Q13002-7;Q8WXH0-4;Q13002-4;Q8WXH0-3;F8WEZ8;Q13002-2;H7BYG7;Q13002-5;E7EPZ0;P39086-2;Q13002;P39086;F8W7X3;E9PD61;F5H1W5;E7EPY9;E7ENK3;Q8N4C6-6;F8W6D3;Q8N4C6-11;H0YDJ4;H9KV85;E9PN67;Q8N4C6-4;C9J066;Q8N4C6-9;Q8N4C6-2;Q8N4C6;Q8N4C6-5;Q8N4C6-10;Q8N4C6-7;O60673-2;O60673;Q8WXH0-7;REV__F6QMI7 Ribosome-binding protein 1 RRBP1 >sp|Q9P2E9|RRBP1_HUMAN Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4;>sp|Q9P2E9-2|RRBP1_HUMAN Isoform 1 of Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1;>sp|Q9P2E9-3|RRBP1_HUMAN Isoform 2 of Ribosome-binding protein 1 OS=Homo sapiens -0.39 0.11 -0.03 0.01 0.82 0.44 -0.79 0.20 0.264490605 -0.245837003 "adult behavior;anatomical structure development;behavior;behavioral defense response;behavioral fear response;behavioral response to pain;biological regulation;biosynthetic process;calcium ion homeostasis;cation homeostasis;cell communication;cell surface receptor linked signaling pathway;cell-cell signaling;cellular biosynthetic process;cellular calcium ion homeostasis;cellular cation homeostasis;cellular chemical homeostasis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular localization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular nitrogen compound metabolic process;cellular process;cellular protein metabolic process;cellular response to stimulus;cellular response to stress;central nervous system development;centrosome localization;centrosome-templated microtubule nucleation;chemical homeostasis;cytoskeleton organization;defense response;developmental process;divalent inorganic cation homeostasis;DNA biosynthetic process;DNA metabolic process;DNA repair;DNA replication;DNA-dependent DNA replication;establishment of localization;establishment of localization in cell;establishment of protein localization;fear response;glutamate signaling pathway;homeostatic process;intracellular protein transport;intracellular transport;ion homeostasis;ionotropic glutamate receptor signaling pathway;localization;macromolecule biosynthetic process;macromolecule metabolic process;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane depolarization;membrane hyperpolarization;metabolic process;metal ion homeostasis;microtubule anchoring;microtubule anchoring at centrosome;microtubule anchoring at microtubule organizing center;microtubule cytoskeleton organization;microtubule nucleation;microtubule-based process;multicellular organismal process;multicellular organismal response to stress;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular process;negative regulation of multicellular organismal process;negative regulation of neurological system process;negative regulation of neuron apoptosis;negative regulation of programmed cell death;negative regulation of signaling;negative regulation of synaptic transmission;negative regulation of synaptic transmission, glutamatergic;negative regulation of transmission of nerve impulse;neuron-neuron synaptic transmission;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organelle localization;organelle organization;positive regulation of amine transport;positive regulation of amino acid transport;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of gamma-aminobutyric acid secretion;positive regulation of multicellular organismal process;positive regulation of neurological system process;positive regulation of organic acid transport;positive regulation of secretion;positive regulation of signaling;positive regulation of synaptic transmission;positive regulation of synaptic transmission, GABAergic;positive regulation of transmission of nerve impulse;positive regulation of transport;postreplication repair;primary metabolic process;protein metabolic process;protein transport;regulation of action potential;regulation of action potential in neuron;regulation of amine transport;regulation of amino acid transport;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell death;regulation of cellular process;regulation of excitatory postsynaptic membrane potential;regulation of gamma-aminobutyric acid secretion;regulation of inhibitory postsynaptic membrane potential;regulation of localization;regulation of long-term neuronal synaptic plasticity;regulation of membrane potential;regulation of multicellular organismal process;regulation of neurological system process;regulation of neuron apoptosis;regulation of neuronal synaptic plasticity;regulation of organic acid transport;regulation of postsynaptic membrane potential;regulation of programmed cell death;regulation of secretion;regulation of short-term neuronal synaptic plasticity;regulation of signaling;regulation of synaptic plasticity;regulation of synaptic transmission;regulation of synaptic transmission, GABAergic;regulation of synaptic transmission, glutamatergic;regulation of system process;regulation of transmission of nerve impulse;regulation of transport;response to DNA damage stimulus;response to pain;response to stimulus;response to stress;signal transduction;signaling;synaptic transmission;synaptic transmission, glutamatergic;system development;translation;translesion synthesis;transport" "4 iron, 4 sulfur cluster binding;binding;calcium ion binding;catalytic activity;cation binding;channel activity;DNA binding;DNA polymerase activity;DNA-directed DNA polymerase activity;excitatory extracellular ligand-gated ion channel activity;extracellular ligand-gated ion channel activity;extracellular-glutamate-gated ion channel activity;gated channel activity;glutamate receptor activity;GTP binding;guanyl nucleotide binding;guanyl ribonucleotide binding;ion binding;ion channel activity;ion transmembrane transporter activity;ionotropic glutamate receptor activity;iron-sulfur cluster binding;kainate selective glutamate receptor activity;ligand-gated channel activity;ligand-gated ion channel activity;metal cluster binding;metal ion binding;molecular transducer activity;nucleic acid binding;nucleotide binding;nucleotidyltransferase activity;passive transmembrane transporter activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor activity;ribonucleotide binding;signal transducer activity;signaling receptor activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane signaling receptor activity;transmembrane transporter activity;transporter activity" cell body;cell junction;cell part;cell projection;centriole;centrosome;chromosome;cytoplasmic part;cytoskeletal part;dendrite;DNA polymerase complex;endoplasmic reticulum;endoplasmic reticulum part;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;integral to plasma membrane;intracellular;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;intrinsic to plasma membrane;ionotropic glutamate receptor complex;kainate selective glutamate receptor complex;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microtubule;microtubule organizing center;microtubule organizing center part;neuron projection;neuronal cell body;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;postsynaptic membrane;presynaptic membrane;protein complex;receptor complex;ribonucleoprotein complex;ribosome;synapse part;synaptic membrane;zeta DNA polymerase complex Neuroactive ligand-receptor interaction;Protein processing in endoplasmic reticulum 0 46 59 58 46.2

P11021;O95399;Q5H8X8;O95399-2;REV__B4DLB6;REV__H3BUZ0;REV__Q9NXD2-2;REV__Q9NXD278 kDa glucose-regulated protein HSPA5 >sp|P11021|GRP78_HUMAN 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=20.07 0.00 -0.62 -0.41 0.25 -0.09 0.33 0.08 0.864185655 -0.382980264 "activation of signaling protein activity involved in unfolded protein response;anatomical structure arrangement;anatomical structure development;behavior;biological regulation;calcium ion homeostasis;catabolic process;cation homeostasis;cell activation;cell communication;cell-cell signaling;cellular calcium ion homeostasis;cellular catabolic process;cellular cation homeostasis;cellular chemical homeostasis;cellular divalent inorganic cation homeostasis;cellular homeostasis;cellular ion homeostasis;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular metal ion homeostasis;cellular process;cellular response to biotic stimulus;cellular response to external stimulus;cellular response to extracellular stimulus;cellular response to glucose starvation;cellular response to nutrient levels;cellular response to starvation;cellular response to stimulus;cellular response to stress;cerebellar Purkinje cell layer development;cerebellum structural organization;chemical homeostasis;circadian behavior;circadian rhythm;circadian sleep/wake cycle process;cytosolic calcium ion homeostasis;developmental process;divalent inorganic cation homeostasis;elevation of cytosolic calcium ion concentration;ER overload response;ER-associated protein catabolic process;ER-nucleus signaling pathway;establishment of localization;establishment of localization in cell;exocytosis;homeostatic process;ion homeostasis;macromolecule catabolic process;macromolecule metabolic process;metabolic process;metal ion homeostasis;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;multicellular organismal process;muscle contraction;muscle system process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of blood pressure;negative regulation of cell communication;negative regulation of cell death;negative regulation of cellular process;negative regulation of glomerular filtration;negative regulation of heart contraction;negative regulation of heart rate;negative regulation of hormone secretion;negative regulation of insulin secretion;negative regulation of multicellular organismal process;negative regulation of peptide hormone secretion;negative regulation of peptide secretion;negative regulation of programmed cell death;negative regulation of renal sodium excretion;negative regulation of response to stimulus;negative regulation of secretion;negative regulation of signal transduction;negative regulation of signaling;negative regulation of transforming growth factor beta receptor signaling pathway;negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;negative regulation of transport;negative regulation of urine volume;platelet activation;platelet degranulation;positive regulation of angiogenesis;positive regulation of behavior;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of blood pressure;positive regulation of catalytic activity;positive regulation of cell communication;positive regulation of cell differentiation;positive regulation of cell migration;positive regulation of cell motility;positive regulation of cell proliferation;positive regulation of cellular component movement;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of cellular protein metabolic process;positive regulation of circadian rhythm;positive regulation of circadian sleep/wake cycle, REM sleep;positive regulation of circadian sleep/wake cycle, sleep;positive regulation of circadian sleep/wake cycle, wakefulness;positive regulation of collagen biosynthetic process;positive regulation of collagen metabolic process;positive regulation of developmental process;positive regulation of fibroblast migration;positive regulation of fibroblast proliferation;positive regulation of heart contraction;positive regulation of heart rate;positive regulation of hydrolase activity;positive regulation of kinase activity;positive regulation of locomotion;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of molecular function;positive regulation of multicellular organismal metabolic process;positive regulation of multicellular organismal process;positive regulation of neurological system process;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of protein metabolic process;positive regulation of protein modification process;positive regulation of protein ubiquitination;positive regulation of response to stimulus;positive regulation of signaling;positive regulation of synaptic transmission;positive regulation of synaptic transmission, cholinergic;positive regulation of transferase activity;positive regulation of transmission of nerve impulse;positive regulation of vasodilation;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein metabolic process;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of anatomical structure morphogenesis;regulation of angiogenesis;regulation of apoptosis;regulation of behavior;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of blood pressure;regulation of body fluid levels;regulation of catalytic activity;regulation of cell communication;regulation of cell death;regulation of cell differentiation;regulation of cell migration;regulation of cell motility;regulation of cell proliferation;regulation of cellular component movement;regulation of cellular localization;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of circadian rhythm;regulation of circadian sleep/wake cycle;regulation of circadian sleep/wake cycle, REM sleep;regulation of circadian sleep/wake cycle, sleep;regulation of circadian sleep/wake cycle, wakefulness;regulation of collagen biosynthetic process;regulation of collagen metabolic process;regulation of developmental process;regulation of excretion;regulation of fibroblast migration;regulation of fibroblast proliferation;regulation of glomerular filtration;regulation of heart contraction;regulation of heart rate;regulation of homeostatic process;regulation of hormone secretion;regulation of hydrolase activity;regulation of insulin secretion;regulation of ion homeostasis;regulation of kinase activity;regulation of localization;regulation of locomotion;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of multicellular organismal development;regulation of multicellular organismal metabolic process;regulation of multicellular organismal process;regulation of neurological system process;regulation of nuclease activity;regulation of peptide hormone secretion;regulation of peptide secretion;regulation of peptide transport;regulation of phosphate metabolic process;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein folding in endoplasmic reticulum;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of protein ubiquitination;regulation of renal sodium excretion;regulation of response to stimulus;regulation of secretion;regulation of signal transduction;regulation of signaling;regulation of synaptic transmission;regulation of synaptic transmission, cholinergic;regulation of system process;regulation of transferase activity;regulation of transforming growth factor beta receptor signaling pathway;regulation of transmembrane receptor protein serine/threonine kinase signaling pathway;regulation of transmission of nerve impulse;regulation of transport;regulation of urine volume;regulation of vasodilation;renal system process;renal system process involved in regulation of blood volume;renal system process involved in regulation of systemic arterial blood pressure;response to biotic stimulus;response to chemical stimulus;response to drug;response to endogenous stimulus;response to endoplasmic reticulum stress;response to external stimulus;response to extracellular stimulus;response to hormone stimulus;response to hypoxia;response to nutrient levels;response to organic substance;response to oxygen levels;response to starvation;response to steroid hormone stimulus;response to stimulus;response to stress;response to testosterone stimulus;rhythmic behavior;rhythmic process;secretion;secretion by cell;signal transduction;signaling;synaptic transmission;system process;transport;ubiquitin-dependent protein catabolic process;vesicle-mediated transport" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;binding;binding, bridging;calcium ion binding;catalytic activity;cation binding;chaperone binding;hormone activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;misfolded protein binding;nucleoside-triphosphatase activity;nucleotide binding;protein binding;protein binding, bridging;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor binding;ribonucleoprotein binding;ribonucleotide binding;ribosome binding;unfolded protein binding" cell part;cell surface;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;endoplasmic reticulum chaperone complex;endoplasmic reticulum lumen;endoplasmic reticulum part;endoplasmic reticulum-Golgi intermediate compartment;extracellular region part;extracellular space;integral to endoplasmic reticulum membrane;integral to membrane;integral to organelle membrane;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;intrinsic to endoplasmic reticulum membrane;intrinsic to membrane;intrinsic to organelle membrane;macromolecular complex;melanosome;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;midbody;nucleus;organelle;organelle lumen;organelle part;pigment granule;protein complex;vesicle

Neuroactive ligand-receptor interaction;Prion diseases;Protein export;Protein processing in endoplasmic reticulum 0 8 60 58 65

P34932;REV__Q3KQV9;REV__P17024;P49454 Heat shock 70 kDa protein 4 HSPA4 >sp|P34932|HSP74_HUMAN Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 -0.02 -0.02 -0.04 -0.01 -0.02 0.01 0.29 -0.12 0.267231444 -0.062004224 "anaphase;anatomical structure development;biological regulation;biosynthetic process;cell cycle checkpoint;cell cycle phase;cell cycle process;cell differentiation;cell division;cell proliferation;cellular biosynthetic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular membrane organization;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular protein complex assembly;chaperone-mediated protein complex assembly;chromosome organization;developmental process;DNA metabolic process;DNA replication;establishment of chromosome localization;establishment of localization;establishment of localization in cell;establishment of organelle localization;establishment of protein localization;establishment of protein localization in mitochondrion;establishment of protein localization to organelle;G2 phase;G2 phase of mitotic cell cycle;intracellular protein transport;intracellular transport;kinetochore assembly;kinetochore organization;M phase;M phase of mitotic cell cycle;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule biosynthetic process;macromolecule metabolic process;membrane organization;metabolic process;metaphase plate congression;mitochondrial membrane organization;mitochondrial transport;mitochondrion organization;mitotic anaphase;mitotic cell cycle checkpoint;mitotic cell cycle spindle assembly checkpoint;mitotic cell cycle spindle checkpoint;mitotic prometaphase;muscle organ development;muscle structure development;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cell cycle;negative regulation of cell cycle process;negative regulation of cellular biosynthetic process;negative regulation of cellular component organization;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of mitosis;negative regulation of mitotic metaphase/anaphase transition;negative regulation of nitrogen compound metabolic process;negative regulation of nuclear division;negative regulation of nucleobase-containing compound metabolic process;negative regulation of organelle organization;negative regulation of RNA metabolic process;negative regulation of transcription, DNA-dependent;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle assembly;organelle organization;outer mitochondrial membrane organization;primary metabolic process;protein complex assembly;protein complex subunit organization;protein import;protein import into mitochondrial outer membrane;protein targeting;protein targeting to membrane;protein targeting to mitochondrion;protein transport;regulation of biological process;regulation of biosynthetic process;regulation of cell cycle;regulation of cell cycle arrest;regulation of cell cycle process;regulation of cellular biosynthetic process;regulation of cellular component organization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of developmental process;regulation of G2/M transition of mitotic cell cycle;regulation of gene expression;regulation of interphase of mitotic cell cycle;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of mitosis;regulation of mitotic cell cycle;regulation of mitotic metaphase/anaphase transition;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of muscle organ development;regulation of nitrogen compound metabolic process;regulation of nuclear division;regulation of nucleobase-containing compound metabolic process;regulation of organelle organization;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of striated muscle tissue development;regulation of transcription, DNA-dependent;response to chemical stimulus;response to drug;response to organic substance;response to stimulus;response to stress;response to topologically incorrect protein;response to unfolded protein;spindle assembly checkpoint;spindle checkpoint;transport" adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;chromatin binding;dynein binding;nucleotide binding;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding cell part;chromosomal part;condensed chromosome outer kinetochore;cytoplasm;cytoplasmic part;cytoskeletal part;cytosol;envelope;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;midbody;nuclear envelope;nuclear matrix;nuclear part;nucleus;organelle;organelle envelope;organelle part;perinuclear region of cytoplasm;pronucleus;protein complex;spindle pole Antigen processing and presentation 0 4 63 58 77.7

P11216;H0Y4Z6 "Glycogen phosphorylase, brain form" PYGB ">sp|P11216|PYGB_HUMAN Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5" 0.31 0.10 0.06 -0.10 -0.45 0.08 0.37 0.09 0.131354028 0.0700502 alcohol metabolic process;carbohydrate catabolic process;carbohydrate metabolic process;catabolic process;cellular carbohydrate catabolic process;cellular carbohydrate metabolic process;cellular glucan metabolic process;cellular macromolecule catabolic process;cellular metabolic process;cellular polysaccharide catabolic process;cellular polysaccharide metabolic process;cellular process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;generation of precursor metabolites and energy;glucan catabolic process;glucan metabolic process;glucose metabolic process;glycogen catabolic process;glycogen metabolic process;hexose metabolic process;macromolecule catabolic process;macromolecule metabolic process;metabolic process;monosaccharide metabolic process;oxidation-reduction process;polysaccharide catabolic process;polysaccharide metabolic process;primary metabolic process;small molecule metabolic process "binding;catalytic activity;cofactor binding;glycogen phosphorylase activity;phosphorylase activity;pyridoxal phosphate binding;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups;vitamin B6 binding;vitamin binding"cell part;cytoplasm;intracellular part Insulin signaling pathway;Starch and sucrose metabolism 0 2 70 59 69.3

O43707;D6PXK4;F5GXS2;H7C144;K7EJH8;K7EP19;D6RH00 Alpha-actinin-4 ACTN4 >sp|O43707|ACTN4_HUMAN Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2;>tr|D6PXK4|D6PXK4_HUMAN Alpha actinin 4 short isoform OS=Homo sapiens GN=ACTN4 PE=2 SV=1 -0.08 0.00 0.05 0.03 -0.13 0.07 0.16 0.01 0.12501328 -0.023816177 actin crosslink formation;actin cytoskeleton organization;actin filament bundle assembly;actin filament organization;actin filament-based process;biological regulation;cell activation;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cytoskeleton organization;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;negative regulation of biological process;negative regulation of cellular component movement;negative regulation of cellular process;organelle organization;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cellular component movement;positive regulation of cellular component organization;positive regulation of cellular process;positive regulation of endocytosis;positive regulation of ion transmembrane transporter activity;positive regulation of molecular function;positive regulation of pinocytosis;positive regulation of sodium ion transmembrane transporter activity;positive regulation of sodium:hydrogen antiporter activity;positive regulation of transport;positive regulation of transporter activity;protein transport;regulation of apoptosis;regulation of biological process;regulation of cell death;regulation of cellular component movement;regulation of cellular component organization;regulation of cellular process;regulation of endocytosis;regulation of ion transmembrane transport;regulation of ion transmembrane transporter activity;regulation of ion transport;regulation of localization;regulation of metal ion transport;regulation of molecular function;regulation of pinocytosis;regulation of programmed cell death;regulation of proton transport;regulation of sodium ion transmembrane transporter activity;regulation of sodium ion transport;regulation of sodium:hydrogen antiporter activity;regulation of transmembrane transport;regulation of transmembrane transporter activity;regulation of transport;regulation of transporter activity;regulation of vesicle-mediated transport;response to chemical stimulus;response to hypoxia;response to oxygen levels;response to stimulus;response to stress;secretion;secretion by cell;transport;vesicle-mediated transport actin binding;actin filament binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;identical protein binding;integrin binding;ion binding;metal ion binding;nucleoside binding;protein binding;protein complex binding;protein dimerization activity;protein homodimerization activity;receptor binding cell cortex part;cell part;cell projection;contractile fiber part;cortical cytoskeleton;cytoplasmic membrane-bounded vesicle lumen;cytoplasmic part;cytoplasmic vesicle part;cytoskeleton;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;non-membrane-bounded organelle;nucleus;organelle;organelle lumen;organelle part;perinuclear region of cytoplasm;platelet alpha granule lumen;protein complex;pseudopodium;ribonucleoprotein complex;secretory granule lumen;vesicle;vesicle lumen;Z disc Adherens junction;Amoebiasis;Arrhythmogenic right ventricular cardiomyopathy (ARVC);Focal adhesion;Leukocyte transendothelial migration;Regulation of actin cytoskeleton;Systemic lupus erythematosus;Tight junction 0 7 87 59 80.5

P08670;B0YJC4;B0YJC5;Q5JVS8;Q16352;P07197-2;K7EKH6;F8W835;P07196 Vimentin VIM>sp|P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4;>tr|B0YJC4|B0YJC4_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=2 SV=1 -1.58 -0.51 -0.40 0.81 2.32 2.72 -1.09 1.48 0.77153411 -1.778058738 actin filament-based movement;actin filament-based process;actin-mediated cell contraction;actin-myosin filament sliding;anatomical structure development;anterograde axon cargo transport;astrocyte development;astrocyte differentiation;axon cargo transport;axon transport of mitochondrion;Bergmann glial cell differentiation;biological regulation;cell communication;cell development;cell differentiation;cell-cell signaling;cellular component assembly;cellular component assembly at cellular level;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cytoskeleton organization;cytoskeleton-dependent intracellular transport;developmental process;establishment of localization;establishment of localization in cell;glial cell development;glial cell differentiation;interaction with host;intermediate filament bundle assembly;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;interspecies interaction between organisms;intracellular transport;lens fiber cell development;microtubule-based movement;microtubule-based process;microtubule-based transport;multi-organism process;muscle filament sliding;negative regulation of biological process;negative regulation of cell projection organization;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of neuron projection development;nervous system development;neurofilament bundle assembly;neurofilament cytoskeleton organization;organelle organization;regulation of biological process;regulation of cell development;regulation of cell differentiation;regulation of cell projection organization;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of multicellular organismal development;regulation of multicellular organismal process;regulation of nervous system development;regulation of neurogenesis;regulation of neuron differentiation;regulation of neuron projection development;reproductive process;retrograde axon cargo transport;signaling;synaptic transmission;system development;transport;viral reproductive process;virus-host interaction structural constituent of cytoskeleton;structural constituent of eye lens;structural molecule activity axon part;cell leading edge;cell part;cell projection;cell projection part;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;intermediate filament;intermediate filament cytoskeleton;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;membrane-bounded vesicle;microbody;neurofilament;non-membrane-bounded organelle;organelle;organelle part;peroxisome;protein complex;vesicle Amyotrophic lateral sclerosis (ALS) 0 9 71 60 92.5

P19338;H7BY16;C9JYW2;C9JLB1;C9J1H7;C9JWL1 NucleolinNCL >sp|P19338|NUCL_HUMAN Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3;>tr|H7BY16|H7BY16_HUMAN Nucleolin (Fragment) OS=Homo sapiens GN=NCL PE=2 SV=1 -0.53 0.10 0.28 0.13 -0.32 -0.71 -1.37 -0.80 1.176192539 0.794808593 anatomical structure formation involved in morphogenesis;angiogenesis;developmental process binding;DNA binding;nucleic acid binding;nucleotide binding;RNA binding;sequence-specific DNA binding;telomeric DNA binding cell cortex;cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm;organelle;organelle part;ribonucleoprotein complex Pathogenic Escherichia coli infection 0 6 61 61 47.7

Q92817;K7EKI0;A8MZ36;K7EQ87 Envoplakin EVPL >sp|Q92817|EVPL_HUMAN Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3;>tr|K7EKI0|K7EKI0_HUMAN Envoplakin OS=Homo sapiens GN=EVPL PE=4 SV=1 0.02 0.24 0.82 0.19 0.21 0.44 0.00 -1.22 0.464160563 0.460661188 cell differentiation;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;developmental process;epidermal cell differentiation;epithelial cell differentiation;keratinization;keratinocyte differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;peptide cross-linking;primary metabolic process;protein metabolic process;protein modification process "binding;binding, bridging;protein binding;protein binding, bridging;structural molecule activity" anchoring junction;cell junction;cell part;cell-cell junction;cornified envelope;cytoplasm;cytoskeleton;desmosome;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;non-membrane-bounded organelle;organelle 0 4 66 66 38.3

Q00341;Q00341-2;H0Y394;H7C0A4;C9JIZ1;C9J5E5;H7C2D1;C9JZI8;H7BZC3;C9JHZ8;C9JES8;C9JHS7;C9JT62;C9JK79;C9JQ82;C9JBS3;C9JEJ8;C9JKQ5;C9JHN6;C9JMQ6;H7C3D0;C9JHS9;C9J739;REV__Q0VF96-2;Q9NVE4;Q9BXX2 Vigilin HDLBP >sp|Q00341|VIGLN_HUMAN Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2;>sp|Q00341-2|VIGLN_HUMAN Isoform 2 of Vigilin OS=Homo sapiens GN=HDLBP;>tr|H0Y394|H0Y394_HUMAN Vigilin (Fragment) OS=Homo sapiens GN=HDLBP PE=4 SV=1 0.04 0.02 -0.07 -0.06 0.41 0.21 0.11 -0.07 0.7406975 -0.180648672 alcohol metabolic process;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;cholesterol metabolic process;cytokinesis;cytoskeleton organization;establishment of localization;lipid metabolic process;lipid transport;metabolic process;microtubule cytoskeleton organization;microtubule-based process;organelle organization;organic substance transport;primary metabolic process;small molecule metabolic process;steroid metabolic process;sterol metabolic process;transport binding;lipid binding;nucleic acid binding;RNA binding cell part;cytoplasm;extracellular region part;high-density lipoprotein particle;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;nucleus;organelle;plasma lipoprotein particle;plasma membrane;protein-lipid complex 0 26 68 66 55.4

P53396;P53396-2;B4E3P0;K7ESG8;K7EIE7;REV__J3KRN3;REV__J3KTL5;REV__J3QRY7;REV__J3QQW3;REV__Q12767;REV__C9JL75;REV__Q12767-2 ATP-citrate synthase ACLY >sp|P53396|ACLY_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3;>sp|P53396-2|ACLY_HUMAN Isoform 2 of ATP-citrate synthase OS=Homo sapiens GN=ACLY;>tr|B4E3P0|B4E3P0_HUMAN ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=2 SV=1 0.05 -0.06 0.03 -0.04 -0.34 0.18 0.55 0.11 0.275367014 -0.130121883 acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;ATP catabolic process;ATP metabolic process;biological regulation;biosynthetic process;carbohydrate metabolic process;carboxylic acid metabolic process;catabolic process;cellular biosynthetic process;cellular carbohydrate metabolic process;cellular catabolic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular nitrogen compound catabolic process;cellular nitrogen compound metabolic process;cellular process;citrate metabolic process;coenzyme A metabolic process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;generation of precursor metabolites and energy;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;heterocycle catabolic process;heterocycle metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;nitrogen compound metabolic process;nucleobase-containing compound catabolic process;nucleobase-containing compound metabolic process;nucleobase-containing small molecule metabolic process;nucleoside bisphosphate metabolic process;nucleoside metabolic process;nucleoside phosphate metabolic process;nucleoside triphosphate catabolic process;nucleoside triphosphate metabolic process;nucleotide catabolic process;nucleotide metabolic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;primary metabolic process;purine nucleoside metabolic process;purine nucleoside triphosphate catabolic process;purine nucleoside triphosphate metabolic process;purine nucleotide catabolic process;purine nucleotide metabolic process;purine ribonucleoside metabolic process;purine ribonucleoside triphosphate catabolic process;purine ribonucleoside triphosphate metabolic process;purine ribonucleotide catabolic process;purine ribonucleotide metabolic process;purine-containing compound catabolic process;purine-containing compound metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;ribonucleoside metabolic process;ribonucleoside triphosphate catabolic process;ribonucleoside triphosphate metabolic process;ribonucleotide catabolic process;ribonucleotide metabolic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;tricarboxylic acid metabolic process;triglyceride biosynthetic process;triglyceride metabolic process "acid-thiol ligase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATP citrate synthase activity;binding;catalytic activity;cation binding;CoA-ligase activity;cofactor binding;ion binding;ligase activity;ligase activity, forming carbon-sulfur bonds;metal ion binding;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;succinate-CoA ligase (ADP-forming) activity;succinate-CoA ligase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer" cell part;citrate lyase complex;cytoplasm;cytoplasmic part;cytosol;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;mitochondrion;nucleus;organelle;plasma membrane;protein complex Carbon fixation pathways in prokaryotes;Citrate cycle (TCA cycle) 0 12 71 71 62.6

K7EKI8;O60437;K7EQ71 Periplakin PPL >tr|K7EKI8|K7EKI8_HUMAN Periplakin OS=Homo sapiens GN=PPL PE=4 SV=1;>sp|O60437|PEPL_HUMAN Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4;>tr|K7EQ71|K7EQ71_HUMAN Periplakin (Fragment) OS=Homo sapiens GN=PPL PE=4 SV=1 -0.07 0.22 0.85 0.17 0.24 0.42 -0.07 -1.17 0.437373093 0.435127703 developmental process;keratinization structural constituent of cytoskeleton;structural molecule activity anchoring junction;cell junction;cell part;cell-cell junction;cytoplasmic part;cytoskeleton;desmosome;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;membrane;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;nucleus;organelle;plasma membrane 0 3 72 72 46.4

P12111-2;P12111;E7ENL6;E9PCV6;P12111-4;P12111-5;P12111-3;C9JNG9;I3L392 Collagen alpha-3(VI) chain COL6A3 >sp|P12111-2|CO6A3_HUMAN Isoform 2 of Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3;>sp|P12111|CO6A3_HUMAN Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5;>tr|E7ENL6|E7ENL6_HUMAN Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE -0.16 1.07 -0.88 -0.82 2.30 2.44 -0.95 0.47 0.575766895 -1.263145573 anatomical structure development;axon guidance;biological adhesion;cell adhesion;cellular component disassembly;cellular component disassembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;collagen catabolic process;collagen metabolic process;developmental process;extracellular matrix disassembly;extracellular matrix organization;extracellular structure organization;locomotion;macromolecule metabolic process;metabolic process;multicellular organismal catabolic process;multicellular organismal macromolecule metabolic process;multicellular organismal metabolic process;multicellular organismal process;muscle organ development;muscle structure development;organ development;response to chemical stimulus;response to external stimulus;response to stimulus;taxis endopeptidase inhibitor activity;endopeptidase regulator activity;enzyme inhibitor activity;enzyme regulator activity;peptidase inhibitor activity;peptidase regulator activity;serine-type endopeptidase inhibitor activity anchoring collagen;cell part;collagen;collagen type VI;cytoplasmic part;endoplasmic reticulum lumen;endoplasmic reticulum part;extracellular matrix part;extracellular region part;extracellular space;intracellular organelle lumen;intracellular organelle part;intracellular part;membrane;membrane-enclosed lumen;organelle lumen;organelle part;plasma membrane;sarcolemma ECM-receptor interaction;Focal adhesion;Protein digestion and absorption 0 9 77 77 33.1

P42704;B8ZZ38;C9JCA9;H7C3W8;Q9NP80-3;Q9NP80-2;J3KPL1;Q9NP80 "Leucine-rich PPR motif-containing protein, mitochondrial" LRPPRC ">sp|P42704|LPPRC_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3" -0.23 0.25 0.10 0.17 -0.39 -0.26 -1.03 -0.48 1.264221346 0.615167068 "acid secretion;alcohol catabolic process;alcohol metabolic process;amine catabolic process;amine metabolic process;arachidonic acid metabolic process;arachidonic acid secretion;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;carboxylic acid transport;catabolic process;cell death;cellular amine metabolic process;cellular biogenic amine catabolic process;cellular biogenic amine metabolic process;cellular biosynthetic process;cellular catabolic process;cellular component movement;cellular ketone metabolic process;cellular lipid catabolic process;cellular lipid metabolic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cytoskeleton-dependent intracellular transport;death;establishment of localization;establishment of localization in cell;establishment of mitochondrion localization;establishment of mitochondrion localization, microtubule-mediated;establishment of organelle localization;establishment of RNA localization;ethanolamine catabolic process;ethanolamine metabolic process;ethanolamine-containing compound metabolic process;fatty acid biosynthetic process;fatty acid metabolic process;fatty acid transport;glycerolipid biosynthetic process;glycerolipid catabolic process;glycerolipid metabolic process;glycerophospholipid biosynthetic process;glycerophospholipid catabolic process;glycerophospholipid metabolic process;icosanoid biosynthetic process;icosanoid metabolic process;icosanoid secretion;icosanoid transport;intracellular transport;linoleic acid metabolic process;lipid biosynthetic process;lipid catabolic process;lipid metabolic process;lipid transport;long-chain fatty acid metabolic process;long-chain fatty acid transport;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;microtubule-based movement;microtubule-based process;microtubule-based transport;mitochondrion transport along microtubule;monocarboxylic acid metabolic process;monocarboxylic acid transport;mRNA transport;nitrogen compound metabolic process;nucleic acid metabolic process;nucleic acid transport;nucleobase-containing compound metabolic process;nucleobase-containing compound transport;organelle transport along microtubule;organic acid biosynthetic process;organic acid metabolic process;organic acid transport;organic substance transport;organophosphate metabolic process;oxoacid metabolic process;phosphatidylcholine catabolic process;phosphatidylcholine metabolic process;phosphatidylethanolamine catabolic process;phosphatidylethanolamine metabolic process;phospholipid biosynthetic process;phospholipid catabolic process;phospholipid metabolic process;primary metabolic process;prostaglandin biosynthetic process;prostaglandin metabolic process;prostanoid biosynthetic process;prostanoid metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription, DNA-dependent;RNA biosynthetic process;RNA metabolic process;RNA transport;secretion;small molecule biosynthetic process;small molecule catabolic process;small molecule metabolic process;transcription, DNA-dependent;transport;unsaturated fatty acid biosynthetic process;unsaturated fatty acid metabolic process;very long-chain fatty acid metabolic process" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;beta-tubulin binding;binding;calcium-independent phospholipase A2 activity;carboxylic ester hydrolase activity;catalytic activity;cytoskeletal protein binding;DNA binding;hydrolase activity;hydrolase activity, acting on ester bonds;lipase activity;lysophospholipase activity;microtubule binding;nucleic acid binding;nucleotide binding;phospholipase A2 activity;phospholipase activity;protein binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;single-stranded DNA binding;structure-specific DNA binding;tubulin binding" cell part;chromosome;condensed chromosome;condensed nuclear chromosome;cytoplasmic part;cytoskeletal part;endoplasmic reticulum membrane;endoplasmic reticulum part;Golgi apparatus part;Golgi membrane;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;microbody;microbody membrane;microbody part;microtubule;mitochondrial nucleoid;mitochondrial part;mitochondrion;non-membrane-bounded organelle;nuclear chromosome;nuclear inner membrane;nuclear membrane;nuclear outer membrane;nuclear part;nucleoid;nucleoplasm;organelle;organelle inner membrane;organelle membrane;organelle outer membrane;organelle part;outer membrane;perinuclear region of cytoplasm;peroxisomal membrane;peroxisomal part;protein complex 0 8 79 79 56.5

P07814;REV__H0YGN0;REV__F5GWI9;REV__F5GXZ7;REV__F5GZ97;REV__Q9Y3C0 Bifunctional glutamate/proline--tRNA ligase;Glutamate--tRNA ligase;Proline--tRNA ligase EPRS >sp|P07814|SYEP_HUMAN Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 -0.08 -0.08 0.10 0.00 0.08 -0.14 0.21 -0.43 0.138740549 0.056230331 amine metabolic process;amino acid activation;biological regulation;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular component assembly;cellular component organization;cellular component organization or biogenesis;cellular ketone metabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to chemical stimulus;cellular response to cytokine stimulus;cellular response to interferon-gamma;cellular response to organic substance;cellular response to stimulus;glutamyl-tRNA aminoacylation;macromolecular complex assembly;macromolecular complex subunit organization;macromolecule metabolic process;metabolic process;ncRNA metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of cellular protein metabolic process;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of protein metabolic process;negative regulation of translation;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organic acid metabolic process;oxoacid metabolic process;posttranscriptional regulation of gene expression;primary metabolic process;prolyl-tRNA aminoacylation;protein complex assembly;protein complex subunit organization;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation;response to chemical stimulus;response to cytokine stimulus;response to interferon-gamma;response to organic substance;response to stimulus;RNA metabolic process;small molecule metabolic process;tRNA aminoacylation;tRNA aminoacylation for protein translation;tRNA metabolic process "adenyl nucleotide binding;adenyl ribonucleotide binding;aminoacyl-tRNA ligase activity;ATP binding;binding;catalytic activity;glutamate-tRNA ligase activity;ligase activity;ligase activity, forming aminoacyl-tRNA and related compounds;ligase activity, forming carbon-oxygen bonds;nucleic acid binding;nucleotide binding;proline-tRNA ligase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;RNA binding;RNA stem-loop binding" cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;ribonucleoprotein complex Aminoacyl-tRNA biosynthesis;Porphyrin and chlorophyll metabolism 0 6 82 80 53.9

Q92616 Translational activator GCN1 GCN1L1 >sp|Q92616|GCN1L_HUMAN Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 0.31 -0.03 0.00 -0.16 0.12 -0.27 0.33 -0.42 0.16384583 0.089133902 biological regulation;posttranscriptional regulation of gene expression;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of primary metabolic process;regulation of protein metabolic process;regulation of translation "binding;nucleic acid binding;RNA binding;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular part;macromolecular complex;non-membrane-bounded organelle;organelle;ribonucleoprotein complex;ribosome 0 1 81 81 36.2

P13639 Elongation factor 2 EEF2 >sp|P13639|EF2_HUMAN Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 0.16 -0.09 -0.12 -0.02 -0.07 0.00 0.44 -0.07 0.262456695 -0.092923437 biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;macromolecule biosynthetic process;macromolecule metabolic process;metabolic process;translational elongation "binding;catalytic activity;GTP binding;GTPase activity;guanyl nucleotide binding;guanyl ribonucleotide binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;nucleic acid binding;nucleoside-triphosphatase activity;nucleotide binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding;RNA binding;translation elongation factor activity;translation factor activity, nucleic acid binding" cell part;cytoplasmic part;cytosol;intracellular part;macromolecular complex;polysome;ribonucleoprotein complex 0 1 82 81 79.3

Q14152;F5H335 Eukaryotic translation initiation factor 3 subunit A EIF3A >sp|Q14152|EIF3A_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1;>tr|F5H335|F5H335_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=2 SV=1 0.20 -0.02 0.16 -0.04 -0.04 -0.20 0.13 -0.49 0.668069638 0.228188979 cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular process;formation of translation initiation complex;macromolecular complex assembly;macromolecular complex subunit organization;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization "binding;nucleic acid binding;RNA binding;structural molecule activity;translation factor activity, nucleic acid binding;translation initiation factor activity" cell part;cytoplasm;cytoplasmic part;cytosol;eukaryotic translation initiation factor 3 complex;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;non-membrane-bounded organelle;nuclear part;nucleolus;organelle;organelle part;protein complex RNA transport 0 2 82 82 56.5

P14625;Q58FF3;H0YIV0;F8W026;F8VPC7;REV__Q8TCB0 Endoplasmin HSP90B1 >sp|P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 0.04 0.05 -0.45 -0.28 0.21 -0.21 0.18 -0.01 0.54398586 -0.202525356 actin cytoskeleton organization;actin filament organization;actin filament-based process;actin rod assembly;activation of immune response;activation of innate immune response;activation of signaling protein activity involved in unfolded protein response;biological regulation;catabolic process;cellular catabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecule catabolic process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cellular response to ATP;cellular response to chemical stimulus;cellular response to organic substance;cellular response to stimulus;cytoskeleton organization;defense response;ER-associated protein catabolic process;establishment of localization;establishment of protein localization;immune response;immune response-activating signal transduction;immune response-regulating signaling pathway;immune system process;innate immune response;innate immune response-activating signal transduction;macromolecule catabolic process;macromolecule metabolic process;maintenance of location;metabolic process;modification-dependent macromolecule catabolic process;modification-dependent protein catabolic process;negative regulation of apoptosis;negative regulation of biological process;negative regulation of cell death;negative regulation of cellular process;negative regulation of programmed cell death;organelle organization;pattern recognition receptor signaling pathway;positive regulation of biological process;positive regulation of catalytic activity;positive regulation of defense response;positive regulation of hydrolase activity;positive regulation of immune response;positive regulation of immune system process;positive regulation of innate immune response;positive regulation of kinase activity;positive regulation of molecular function;positive regulation of nuclease activity;positive regulation of protein kinase activity;positive regulation of response to stimulus;positive regulation of transferase activity;primary metabolic process;proteasomal protein catabolic process;proteasomal ubiquitin-dependent protein catabolic process;protein folding;protein metabolic process;protein transport;proteolysis;proteolysis involved in cellular protein catabolic process;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of catalytic activity;regulation of cell death;regulation of cellular metabolic process;regulation of cellular process;regulation of cellular protein metabolic process;regulation of defense response;regulation of dephosphorylation;regulation of hydrolase activity;regulation of immune response;regulation of immune system process;regulation of innate immune response;regulation of kinase activity;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nuclease activity;regulation of phosphatase activity;regulation of phosphate metabolic process;regulation of phosphoprotein phosphatase activity;regulation of phosphorus metabolic process;regulation of phosphorylation;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein kinase activity;regulation of protein metabolic process;regulation of protein modification process;regulation of protein phosphorylation;regulation of response to stimulus;regulation of response to stress;regulation of transferase activity;response to ATP;response to chemical stimulus;response to hypoxia;response to organic substance;response to oxygen levels;response to stimulus;response to stress;sequestering of calcium ion;sequestering of metal ion;signal transduction;toll-like receptor signaling pathway;transport;ubiquitin-dependent protein catabolic process adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;calcium ion binding;cation binding;enzyme binding;ion binding;lipoprotein particle receptor binding;low-density lipoprotein particle receptor binding;metal ion binding;nucleic acid binding;nucleotide binding;phosphatase binding;protein binding;protein phosphatase binding;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;receptor binding;ribonucleotide binding;RNA binding;virion binding cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;endoplasmic reticulum;endoplasmic reticulum lumen;endoplasmic reticulum membrane;endoplasmic reticulum part;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle lumen;intracellular organelle part;intracellular part;melanosome;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;membrane-enclosed lumen;midbody;organelle;organelle lumen;organelle membrane;organelle part;perinuclear region of cytoplasm;pigment granule;plasma membrane part;vesicle NOD-like receptor signaling pathway;Pathways in cancer;Plant-pathogen interaction;Prostate cancer;Protein processing in endoplasmic reticulum 0 6 84 82 75.2

P78527;E7EUY0;P78527-2;F5GX40;H0YG84;Q9UI33-2;Q9UI33-3;Q9UI33 DNA-dependent protein kinase catalytic subunit PRKDC >sp|P78527|PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3;>tr|E7EUY0|E7EUY0_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=2 SV=1;>sp|P78527-2|PRKDC_HUMAN Isoform 2 of DNAdep 0.27 -0.05 -0.02 -0.08 0.22 -0.54 -0.30 -0.69 0.705751477 0.356738653 "anatomical structure development;anatomical structure formation involved in morphogenesis;anatomical structure homeostasis;anterior/posterior pattern specification;apoptosis;B cell lineage commitment;biological regulation;brain development;cell activation;cell death;cell differentiation;cell fate commitment;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular process involved in reproduction;cellular protein metabolic process;cellular response to chemical stimulus;cellular response to endogenous stimulus;cellular response to hormone stimulus;cellular response to insulin stimulus;cellular response to organic substance;cellular response to peptide hormone stimulus;cellular response to stimulus;cellular response to stress;chromosome organization;death;developmental process;developmental process involved in reproduction;developmental programmed cell death;DNA metabolic process;DNA recombination;DNA repair;double-strand break repair;double-strand break repair via nonhomologous end joining;germ cell programmed cell death;heart development;hemopoietic progenitor cell differentiation;homeostatic process;immune system process;immunoglobulin V(D)J recombination;leukocyte activation;leukocyte differentiation;lymphocyte activation;lymphocyte differentiation;lymphoid progenitor cell differentiation;macromolecule metabolic process;macromolecule modification;metabolic process;nitrogen compound metabolic process;non-recombinational repair;nucleic acid metabolic process;nucleobase-containing compound metabolic process;organ development;organelle organization;pattern specification process;peptidyl-amino acid modification;peptidyl-serine modification;peptidyl-serine phosphorylation;phosphate-containing compound metabolic process;phosphorus metabolic process;phosphorylation;positive regulation of apoptosis;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cell death;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of programmed cell death;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;posttranscriptional regulation of gene expression;primary metabolic process;pro-B cell differentiation;programmed cell death;protein destabilization;protein metabolic process;protein modification process;protein phosphorylation;regionalization;regulation of apoptosis;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cell death;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of programmed cell death;regulation of protein stability;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;reproductive process;response to abiotic stimulus;response to chemical stimulus;response to DNA damage stimulus;response to drug;response to endogenous stimulus;response to gamma radiation;response to hormone stimulus;response to insulin stimulus;response to ionizing radiation;response to organic substance;response to peptide hormone stimulus;response to radiation;response to stimulus;response to stress;segmentation;somatic cell DNA recombination;somatic diversification of immune receptors;somatic diversification of immune receptors via germline recombination within a single locus;somatic diversification of immunoglobulins;somatic diversification of T cell receptor genes;somatic recombination of immunoglobulin gene segments;somatic recombination of T cell receptor gene segments;somitogenesis;T cell activation;T cell differentiation;T cell differentiation in thymus;T cell lineage commitment;T cell receptor V(D)J recombination;telomere maintenance;telomere organization;V(D)J recombination" "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;binding;catalytic activity;cation channel activity;cation transmembrane transporter activity;channel activity;DNA binding;DNA-dependent protein kinase activity;gated channel activity;ion channel activity;ion transmembrane transporter activity;kinase activity;nucleic acid binding;nucleotide binding;passive transmembrane transporter activity;phosphotransferase activity, alcohol group as acceptor;protein kinase activity;protein serine/threonine kinase activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;ribonucleotide binding;sodium channel activity;substrate-specific channel activity;substrate-specific transmembrane transporter activity;substrate-specific transporter activity;transferase activity;transferase activity, transferring phosphorus-containing groups;transmembrane transporter activity;transporter activity;voltage-gated cation channel activity;voltage-gated channel activity;voltage-gated ion channel activity;voltage-gated sodium channel activity" axon;cation channel complex;cell part;cell projection;C-fiber;DNA-dependent protein kinase-DNA ligase 4 complex;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;ion channel complex;macromolecular complex;membrane part;membrane-bounded organelle;neuron projection;nonhomologous end joining complex;non-membrane-bounded organelle;nuclear part;nucleolus;nucleoplasm part;nucleus;organelle;organelle part;plasma membrane part;protein complex;sodium channel complex;transcription factor complex;voltage-gated sodium channel complex Cell cycle;Non-homologous end-joining 0 8 116 115 32.1

Q13813;Q13813-2;A6NG51;Q13813-3 "Spectrin alpha chain, non-erythrocytic 1" SPTAN1 ">sp|Q13813|SPTN1_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3;>sp|Q13813-2|SPTN1_HUMAN Isoform 2 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1;>tr|A6NG51|A6NG51_HUMAN Spectrin alpha chain, non-e" -0.09 -0.04 0.19 -0.03 0.12 0.02 0.03 -0.33 0.153415858 0.049581614 actin filament capping;axon guidance;biological regulation;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular process;chemotaxis;locomotion;negative regulation of actin filament depolymerization;negative regulation of actin filament polymerization;negative regulation of biological process;negative regulation of cellular component organization;negative regulation of cellular process;negative regulation of cytoskeleton organization;negative regulation of organelle organization;negative regulation of protein complex assembly;negative regulation of protein complex disassembly;negative regulation of protein polymerization;regulation of actin cytoskeleton organization;regulation of actin filament depolymerization;regulation of actin filament length;regulation of actin filament polymerization;regulation of actin filament-based process;regulation of actin polymerization or depolymerization;regulation of anatomical structure size;regulation of biological process;regulation of biological quality;regulation of cellular component biogenesis;regulation of cellular component organization;regulation of cellular component size;regulation of cellular process;regulation of cytoskeleton organization;regulation of organelle organization;regulation of protein complex assembly;regulation of protein complex disassembly;regulation of protein polymerization;response to chemical stimulus;response to external stimulus;response to stimulus;taxis actin binding;binding;calcium ion binding;cation binding;cytoskeletal protein binding;ion binding;metal ion binding;protein binding;structural constituent of cytoskeleton;structural molecule activity adherens junction;anchoring junction;cell cortex part;cell junction;cell part;cell-cell adherens junction;cell-cell junction;contractile fiber part;cuticular plate;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;fascia adherens;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;lateral plasma membrane;membrane;membrane part;membrane-bounded organelle;microtubule cytoskeleton;non-membrane-bounded organelle;organelle;organelle part;plasma membrane part;spectrin;Z disc 0 4 133 133 58.1

P49327;J3KTF0;J3QL89 Fatty acid synthase;[Acyl-carrier-protein] S-acetyltransferase;[Acyl-carrier-protein] S-malonyltransferase;3-oxoacyl-[acyl-carrier-protein] synthase;3-oxoacyl-[acyl-carrier-protein] reductase;3-hydroxyacyl-[acyl-carrier-protein] dehydratase;Enoyl-[acyl-carrier-protein] reductase;Oleoyl-[acyl-carrier-protein] hydrolase FASN >sp|P49327|FAS_HUMAN Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3 0.11 -0.11 0.05 0.01 -0.91 -0.97 0.12 -0.73 1.051649747 0.637269291 acetyl-CoA metabolic process;acyl-CoA biosynthetic process;acyl-CoA metabolic process;acylglycerol biosynthetic process;acylglycerol metabolic process;amine metabolic process;biological regulation;biosynthetic process;carboxylic acid biosynthetic process;carboxylic acid metabolic process;cellular amine metabolic process;cellular amino acid metabolic process;cellular biosynthetic process;cellular ketone metabolic process;cellular lipid metabolic process;cellular metabolic process;cellular modified amino acid metabolic process;cellular nitrogen compound metabolic process;cellular process;coenzyme biosynthetic process;coenzyme metabolic process;cofactor biosynthetic process;cofactor metabolic process;energy derivation by oxidation of organic compounds;energy reserve metabolic process;fatty acid biosynthetic process;fatty acid metabolic process;fatty-acyl-CoA biosynthetic process;fatty-acyl-CoA metabolic process;generation of precursor metabolites and energy;glycerol ether biosynthetic process;glycerol ether metabolic process;glycerolipid biosynthetic process;glycerolipid metabolic process;lipid biosynthetic process;lipid metabolic process;long-chain fatty-acyl-CoA biosynthetic process;long-chain fatty-acyl-CoA metabolic process;metabolic process;monocarboxylic acid metabolic process;neutral lipid biosynthetic process;neutral lipid metabolic process;nitrogen compound metabolic process;organic acid biosynthetic process;organic acid metabolic process;organic ether metabolic process;oxidation-reduction process;oxoacid metabolic process;pantothenate metabolic process;positive regulation of biological process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of metabolic process;primary metabolic process;regulation of biological process;regulation of cellular metabolic process;regulation of cellular process;regulation of metabolic process;small molecule biosynthetic process;small molecule metabolic process;thioester biosynthetic process;thioester metabolic process;triglyceride biosynthetic process;triglyceride metabolic process;vitamin metabolic process;water-soluble vitamin metabolic process "[acyl-carrier-protein] S-acetyltransferase activity;[acyl-carrier-protein] S-malonyltransferase activity;3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity;3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase activity;3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity;3-oxoacyl-[acyl-carrier-protein] reductase (NADPH) activity;3-oxoacyl-[acyl-carrier-protein] synthase activity;acetyltransferase activity;acyl-[acyl-carrier-protein] hydrolase activity;binding;carbon-oxygen lyase activity;catalytic activity;cation binding;coenzyme binding;cofactor binding;drug binding;enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity;fatty acid synthase activity;hydrolase activity;hydrolase activity, acting on ester bonds;hydro-lyase activity;ion binding;lyase activity;malonyltransferase activity;metal ion binding;myristoyl-[acyl-carrier-protein] hydrolase activity;NADP binding;NADPH binding;nucleotide binding;oleoyl-[acyl-carrier-protein] hydrolase activity;oxidoreductase activity;oxidoreductase activity, acting on CH-OH group of donors;oxidoreductase activity, acting on the CH-CH group of donors;oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor;oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor;palmitoyl-[acyl-carrier-protein] hydrolase activity;S-acetyltransferase activity;S-acyltransferase activity;S-malonyltransferase activity;thiolester hydrolase activity;transferase activity;transferase activity, transferring acyl groups;transferase activity, transferring acyl groups other than amino-acyl groups;transition metal ion binding;zinc ion binding" cell part;cytoplasmic membrane-bounded vesicle;cytoplasmic part;cytoplasmic vesicle;cytosol;glycogen granule;Golgi apparatus;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;melanosome;membrane;membrane-bounded organelle;membrane-bounded vesicle;mitochondrion;organelle;pigment granule;plasma membrane;vesicle Fatty acid biosynthesis;Insulin signaling pathway 0 3 149 147 64.1

P21333-2;P21333;Q5HY54;E9PHF0;F8WE98;H0Y5C6;H0Y5F3;H7C2E7 Filamin-A FLNA >sp|P21333-2|FLNA_HUMAN Isoform 2 of Filamin-A OS=Homo sapiens GN=FLNA;>sp|P21333|FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4;>tr|Q5HY54|Q5HY54_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=2 SV=1 -0.06 -0.15 -0.13 -0.02 -0.06 -0.35 0.21 -0.36 0.131299166 0.051155195 "actin crosslink formation;actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament organization;actin filament-based process;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;biological regulation;cAMP-mediated signaling;cell activation;cell cycle process;cell junction assembly;cell junction organization;cell morphogenesis;cell morphogenesis involved in differentiation;cell projection assembly;cell projection organization;cell surface receptor linked signaling pathway;cellular component assembly;cellular component assembly at cellular level;cellular component assembly involved in morphogenesis;cellular component morphogenesis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular localization;cellular macromolecule localization;cellular membrane organization;cellular process;cellular protein localization;cellular response to stimulus;cilium assembly;cyclic-nucleotide-mediated signaling;cytoplasmic sequestering of protein;cytoskeleton organization;developmental process;dopamine receptor signaling pathway;early endosome to late endosome transport;endosome transport;epithelial to mesenchymal transition;establishment of localization;establishment of localization in cell;establishment of protein localization;exocytosis;G-protein coupled receptor protein signaling pathway;G-protein signaling, coupled to cAMP nucleotide second messenger;G-protein signaling, coupled to cyclic nucleotide second messenger;inhibition of adenylate cyclase activity by dopamine receptor signaling pathway;inhibition of adenylate cyclase activity by G-protein signaling pathway;intracellular signal transduction;intracellular transport;localization;macromolecule localization;maintenance of location;maintenance of location in cell;maintenance of protein location;maintenance of protein location in cell;membrane organization;microtubule cytoskeleton organization;microtubule-based process;mitotic spindle organization;negative regulation of adenylate cyclase activity;negative regulation of biological process;negative regulation of catabolic process;negative regulation of catalytic activity;negative regulation of cyclase activity;negative regulation of lyase activity;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of molecular function;negative regulation of protein catabolic process;negative regulation of protein metabolic process;negative regulation of protein transport;negative regulation of sequence-specific DNA binding transcription factor activity;negative regulation of transport;organelle assembly;organelle organization;platelet activation;platelet degranulation;positive regulation of biological process;positive regulation of cell communication;positive regulation of cellular process;positive regulation of I-kappaB kinase/NF-kappaB cascade;positive regulation of intracellular protein kinase cascade;positive regulation of intracellular protein transport;positive regulation of intracellular transport;positive regulation of nucleocytoplasmic transport;positive regulation of protein import into nucleus;positive regulation of protein transport;positive regulation of response to stimulus;positive regulation of signal transduction;positive regulation of signaling;positive regulation of transcription factor import into nucleus;positive regulation of transmembrane transport;positive regulation of transport;posttranscriptional regulation of gene expression;protein localization;protein localization at cell surface;protein localization in membrane;protein stabilization;receptor clustering;regulation of adenylate cyclase activity;regulation of biological process;regulation of biological quality;regulation of biosynthetic process;regulation of cAMP biosynthetic process;regulation of cAMP metabolic process;regulation of catabolic process;regulation of catalytic activity;regulation of cell communication;regulation of cellular biosynthetic process;regulation of cellular localization;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of cyclase activity;regulation of cyclic nucleotide biosynthetic process;regulation of cyclic nucleotide metabolic process;regulation of establishment of protein localization;regulation of gene expression;regulation of I-kappaB kinase/NF-kappaB cascade;regulation of intracellular protein kinase cascade;regulation of intracellular protein transport;regulation of intracellular transport;regulation of localization;regulation of lyase activity;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of molecular function;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of nucleocytoplasmic transport;regulation of nucleotide biosynthetic process;regulation of nucleotide metabolic process;regulation of primary metabolic process;regulation of protein catabolic process;regulation of protein import into nucleus;regulation of protein localization;regulation of protein metabolic process;regulation of protein stability;regulation of protein transport;regulation of response to stimulus;regulation of RNA metabolic process;regulation of sequence-specific DNA binding transcription factor activity;regulation of signal transduction;regulation of signaling;regulation of transcription factor import into nucleus;regulation of transcription, DNA-dependent;regulation of transmembrane transport;regulation of transport;response to stimulus;second-messenger-mediated signaling;secretion;secretion by cell;signal transduction;spindle assembly;spindle assembly involved in mitosis;spindle organization;transport;vesicle-mediated transport" actin binding;actin filament binding;binding;cytoskeletal protein binding;enzyme binding;Fc-gamma receptor I complex binding;glycoprotein binding;GTPase binding;identical protein binding;immunoglobulin receptor binding;molecular transducer activity;protein binding;protein dimerization activity;protein homodimerization activity;Rac GTPase binding;Ral GTPase binding;Ras GTPase binding;receptor binding;Rho GTPase binding;signal transducer activity;small GTPase binding actin cytoskeleton;cell cortex;cell part;chromosomal part;cytoplasm;cytoplasmic part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus part;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane-bounded organelle;membrane-bounded vesicle;Myb complex;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;protein complex;trans-Golgi network;vesicle Focal adhesion;MAPK signaling pathway 0 8 181 164 74.1

Q8IVF2-3;Q8IVF2;Q8IVF2-2 Protein AHNAK2 AHNAK2 >sp|Q8IVF2-3|AHNK2_HUMAN Isoform 3 of Protein AHNAK2 OS=Homo sapiens GN=AHNAK2;>sp|Q8IVF2|AHNK2_HUMAN Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2 -0.32 0.08 -0.06 0.06 -0.68 -0.28 0.24 0.16 0.121050934 0.078645786 cell part;intracellular membrane-bounded organelle;intracellular organelle;intracellular part;membrane-bounded organelle;nucleus;organelle 0 3 174 174 60.8

P35579;P35579-2;Q5BKV1;B1AH99;REV__Q08AF3;REV__E7EQT4;REV__Q9UKV3-5;REV__Q9UKV3 Myosin-9 MYH9 >sp|P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4;>sp|P35579-2|MYH9_HUMAN Isoform 2 of Myosin-9 OS=Homo sapiens GN=MYH9 -0.13 0.62 -0.06 0.58 -0.03 0.43 -0.14 0.52 0.078506714 0.059087804 actin cytoskeleton organization;actin cytoskeleton reorganization;actin filament-based movement;actin filament-based process;anatomical structure formation involved in morphogenesis;anatomical structure morphogenesis;angiogenesis;axon guidance;biological adhesion;biological regulation;blood vessel endothelial cell migration;cell adhesion;cell cycle phase;cell cycle process;cell differentiation;cell migration;cell morphogenesis;cell morphogenesis involved in differentiation;cell motility;cell projection organization;cell surface receptor linked signaling pathway;cell-cell adhesion;cellular component morphogenesis;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular process;cellular response to stimulus;chemotaxis;chordate embryonic development;cytokinesis;cytoskeleton organization;developmental process;embryo development;embryo development ending in birth or egg hatching;endothelial cell migration;establishment of cell polarity;establishment of localization;establishment of localization in cell;establishment of lymphocyte polarity;establishment of meiotic spindle localization;establishment of organelle localization;establishment of protein localization;establishment of spindle localization;establishment of T cell polarity;establishment or maintenance of cell polarity;immune system process;in utero embryonic development;integrin-mediated signaling pathway;leukocyte differentiation;leukocyte migration;locomotion;macromolecule metabolic process;meiotic metaphase I;meiotic spindle organization;membrane protein ectodomain proteolysis;membrane protein proteolysis;metabolic process;metaphase;microtubule cytoskeleton organization;microtubule-based process;monocyte differentiation;myeloid cell differentiation;myeloid leukocyte differentiation;myoblast fusion;negative regulation of biological process;negative regulation of cell communication;negative regulation of cellular process;negative regulation of G-protein coupled receptor protein signaling pathway;negative regulation of response to stimulus;negative regulation of signal transduction;negative regulation of signaling;organelle organization;platelet formation;primary metabolic process;protein metabolic process;protein transport;proteolysis;regulation of anatomical structure morphogenesis;regulation of biological process;regulation of biological quality;regulation of cell communication;regulation of cell morphogenesis;regulation of cell shape;regulation of cellular component organization;regulation of cellular process;regulation of developmental process;regulation of G-protein coupled receptor protein signaling pathway;regulation of response to stimulus;regulation of signal transduction;regulation of signaling;response to chemical stimulus;response to external stimulus;response to stimulus;signal transduction;spindle organization;syncytium formation;syncytium formation by plasma membrane fusion;taxis;termination of G-protein coupled receptor signaling pathway;termination of signal transduction;transport;uropod organization "actin binding;actin filament binding;actin-dependent ATPase activity;adenyl nucleotide binding;adenyl ribonucleotide binding;ADP binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;catalytic activity;cytoskeletal protein binding;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;identical protein binding;microfilament motor activity;motor activity;nucleoside-triphosphatase activity;nucleotide binding;protein anchor;protein binding;protein dimerization activity;protein homodimerization activity;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;ribonucleotide binding" actin filament bundle;actomyosin;actomyosin contractile ring;adherens junction;anchoring junction;cell cortex part;cell division site part;cell junction;cell part;cell projection;cell-cell adherens junction;cell-cell junction;cleavage furrow;contractile ring;cortical cytoskeleton;cytoplasmic part;cytoskeletal part;cytoskeleton;cytosol;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;immunological synapse;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;myosin complex;myosin II complex;neuromuscular junction;non-membrane-bounded organelle;nucleus;organelle;organelle part;plasma membrane;plasma membrane part;protein complex;ruffle;spindle;stress fiber;synapse;uropod;vesicle Tight junction;Viral myocarditis 0 8 244 207 78.7

Q14204;H0YJ21;B4DLR6;B4DQ29;P32247;REV__Q8IYI6;D6RIG4;Q9HCL0-2;Q9HCL0 Cytoplasmic dynein 1 heavy chain 1 DYNC1H1 >sp|Q14204|DYHC1_HUMAN Cytoplasmic dynein 1 heavy chain 1

OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 0.17 -0.04 -0.11 -0.15 0.32 0.00 0.36 -0.13 0.502259916 -0.170212832 adult behavior;adult feeding behavior;alcohol metabolic process;anatomical structure development;antigen processing and presentation;antigen processing and presentation of exogenous antigen;antigen processing and presentation of exogenous peptide antigen;antigen processing and presentation of exogenous peptide antigen via MHC class II;antigen processing and presentation of peptide antigen;antigen processing and presentation of peptide antigen via MHC class II;antigen processing and presentation of peptide or polysaccharide antigen via MHC class II;behavior;biological adhesion;biological regulation;brain development;carbohydrate metabolic process;cell adhesion;cell cycle process;cell death;cell-cell adhesion;cellular carbohydrate metabolic process;cellular component assembly;cellular component assembly at cellular level;cellular component movement;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular macromolecular complex assembly;cellular macromolecular complex subunit organization;cellular metabolic process;cellular process;cytoplasmic mRNA processing body assembly;cytoskeleton organization;death;developmental process;establishment of localization;feeding behavior;G2/M transition of mitotic cell cycle;glucose metabolic process;hexose metabolic process;homophilic cell adhesion;immune system process;macromolecular complex assembly;macromolecular complex subunit organization;metabolic process;microtubule cytoskeleton organization;microtubule-based movement;microtubule-based process;mitotic spindle organization;monosaccharide metabolic process;multicellular organismal process;organ development;organelle organization;primary metabolic process;regulation of biological quality;regulation of blood pressure;response to stimulus;ribonucleoprotein complex assembly;ribonucleoprotein complex subunit organization;small molecule metabolic process;spindle organization;stress granule assembly;transport "adenyl nucleotide binding;adenyl ribonucleotide binding;ATP binding;ATPase activity;ATPase activity, coupled;binding;bombesin receptor activity;calcium ion binding;catalytic activity;cation binding;G-protein coupled receptor activity;hydrolase activity;hydrolase activity, acting on acid anhydrides;hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides;ion binding;metal ion binding;microtubule motor activity;molecular transducer activity;motor activity;neuropeptide binding;neuropeptide receptor activity;neurotransmitter binding;neurotransmitter receptor activity;nucleoside-triphosphatase activity;nucleotide binding;peptide binding;peptide receptor activity;peptide receptor activity, G-protein coupled;purine nucleotide binding;purine ribonucleoside triphosphate binding;purine ribonucleotide binding;pyrophosphatase activity;receptor activity;ribonucleotide binding;signal transducer activity;signaling receptor activity;transmembrane signaling receptor activity" cell body;cell part;cell projection;centrosome;cytoplasmic dynein complex;cytoplasmic part;cytoskeletal part;cytosol;dynein complex;extracellular membrane-bounded organelle;extracellular organelle;extracellular region part;extracellular vesicular exosome;Golgi apparatus;integral to membrane;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;intrinsic to membrane;macromolecular complex;membrane;membrane part;membrane-bounded organelle;membrane-bounded vesicle;microtubule;microtubule associated complex;microtubule organizing center;neuron projection;neuronal cell body;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;protein complex;vesicle Neuroactive ligand-receptor interaction;Phagosome;Vasopressin-regulated water reabsorption 0 9 215 215 48.7

P15924;P15924-2;J3QLM5;REV__C0H5Y3;REV__P49279 Desmoplakin DSP >sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3;>sp|P15924-2|DESP_HUMAN Isoform DPII of Desmoplakin OS=Homo sapiens GN=DSP -0.22 -0.06 0.47 0.12 -0.70 -0.34 0.22 -0.84 0.756950965 0.493702362 adherens junction organization;anatomical structure development;anatomical structure morphogenesis;biological adhesion;cardiac muscle tissue morphogenesis;cell adhesion;cell differentiation;cell junction organization;cell-cell adhesion;cell-cell junction organization;cellular component disassembly;cellular component disassembly at cellular level;cellular component disassembly involved in apoptosis;cellular component organization;cellular component organization at cellular level;cellular component organization or biogenesis;cellular component organization or biogenesis at cellular level;cellular developmental process;cellular macromolecule metabolic process;cellular metabolic process;cellular process;cellular protein metabolic process;cytoskeleton organization;developmental process;epidermal cell differentiation;epidermis development;epithelial cell differentiation;intermediate filament cytoskeleton organization;intermediate filament organization;intermediate filament-based process;keratinocyte differentiation;localization;macromolecule localization;macromolecule metabolic process;macromolecule modification;metabolic process;muscle tissue morphogenesis;organelle organization;peptide cross-linking;primary metabolic process;protein localization;protein localization to adherens junction;protein metabolic process;protein modification process;skin development;tissue development;tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis;ventricular compact myocardium morphogenesis "binding;binding, bridging;protein binding;protein binding, bridging;structural constituent of cytoskeleton;structural molecule activity" anchoring junction;basolateral plasma membrane;cell junction;cell part;cell-cell contact zone;cell-cell junction;cornified envelope;cytoplasmic part;cytoskeletal part;cytoskeleton;desmosome;intercalated disc;intermediate filament;intracellular membrane-bounded organelle;intracellular non-membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane;membrane part;membrane-bounded organelle;mitochondrion;non-membrane-bounded organelle;organelle;organelle part;plasma membrane;plasma membrane part;protein complex Arrhythmogenic right ventricular cardiomyopathy (ARVC) 0 5 262 260 73.2

Q09666;E9PKR9;E9PLK4;E9PJZ0;E9PJC6;Q09666-2;E9PQE3;P48552 Neuroblast differentiation-associated protein AHNAK AHNAK >sp|Q09666|AHNK_HUMAN Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 -0.07 -0.02 0.03 -0.03 0.10 -0.10 0.05 -0.17 0.051224118 0.010021349 "anatomical structure development;androgen receptor signaling pathway;biological regulation;biosynthetic process;cellular biosynthetic process;cellular macromolecule biosynthetic process;cellular macromolecule metabolic process;cellular metabolic process;cellular nitrogen compound metabolic process;cellular process;cellular response to stimulus;developmental process;intracellular receptor mediated signaling pathway;lipid localization;lipid storage;localization;macromolecule biosynthetic process;macromolecule localization;macromolecule metabolic process;metabolic process;negative regulation of biological process;negative regulation of biosynthetic process;negative regulation of cellular biosynthetic process;negative regulation of cellular macromolecule biosynthetic process;negative regulation of cellular metabolic process;negative regulation of cellular process;negative regulation of gene expression;negative regulation of macromolecule biosynthetic process;negative regulation of macromolecule metabolic process;negative regulation of metabolic process;negative regulation of nitrogen compound metabolic process;negative regulation of nucleobase-containing compound metabolic process;negative regulation of RNA metabolic process;negative regulation of transcription from RNA polymerase II promoter;negative regulation of transcription, DNA-dependent;nervous system development;nitrogen compound metabolic process;nucleic acid metabolic process;nucleobase-containing compound metabolic process;ovarian follicle rupture;ovulation cycle process;positive regulation of biological process;positive regulation of biosynthetic process;positive regulation of cellular biosynthetic process;positive regulation of cellular metabolic process;positive regulation of cellular process;positive regulation of gene expression;positive regulation of macromolecule biosynthetic process;positive regulation of macromolecule metabolic process;positive regulation of metabolic process;positive regulation of nitrogen compound metabolic process;positive regulation of nucleobase-containing compound metabolic process;positive regulation of RNA metabolic process;positive regulation of transcription from RNA polymerase II promoter;positive regulation of transcription, DNA-dependent;primary metabolic process;regulation of biological process;regulation of biosynthetic process;regulation of cellular biosynthetic process;regulation of cellular macromolecule biosynthetic process;regulation of cellular metabolic process;regulation of cellular process;regulation of gene expression;regulation of macromolecule biosynthetic process;regulation of macromolecule metabolic process;regulation of metabolic process;regulation of nitrogen compound metabolic process;regulation of nucleobase-containing compound metabolic process;regulation of primary metabolic process;regulation of RNA metabolic process;regulation of transcription from RNA polymerase II promoter;regulation of transcription, DNA-dependent;response to stimulus;rhythmic process;RNA biosynthetic process;RNA metabolic process;signal transduction;steroid hormone receptor signaling pathway;system development;transcription, DNA-dependent" androgen receptor binding;binding;hormone receptor binding;nuclear hormone receptor binding;protein binding;protein binding transcription factor activity;receptor binding;steroid hormone receptor binding;transcription coactivator activity;transcription cofactor activity;transcription corepressor activity;transcription factor binding transcription factor activity cell part;chromatin remodeling complex;histone deacetylase complex;intracellular membrane-bounded organelle;intracellular organelle;intracellular organelle part;intracellular part;macromolecular complex;membrane-bounded organelle;nuclear part;nucleoplasm part;nucleus;organelle;organelle part;protein complex 0 8 420 420 86.9